

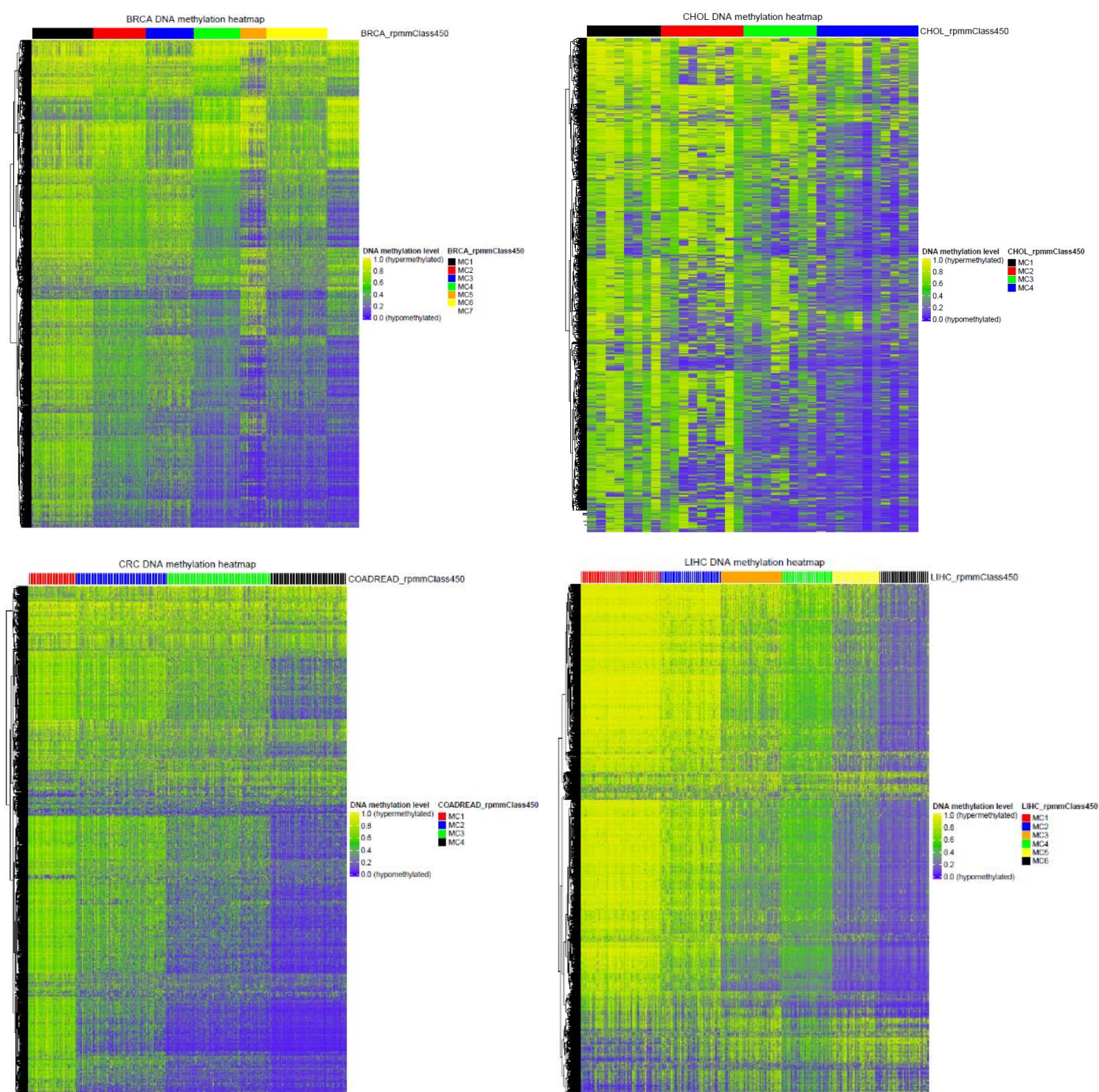
Discovery of Novel DNA Methylation Biomarker Panels for the Diagnosis and Differentiation between Common Adenocarcinomas and Their Liver Metastases

Tina Draškovič, Nina Hauptman

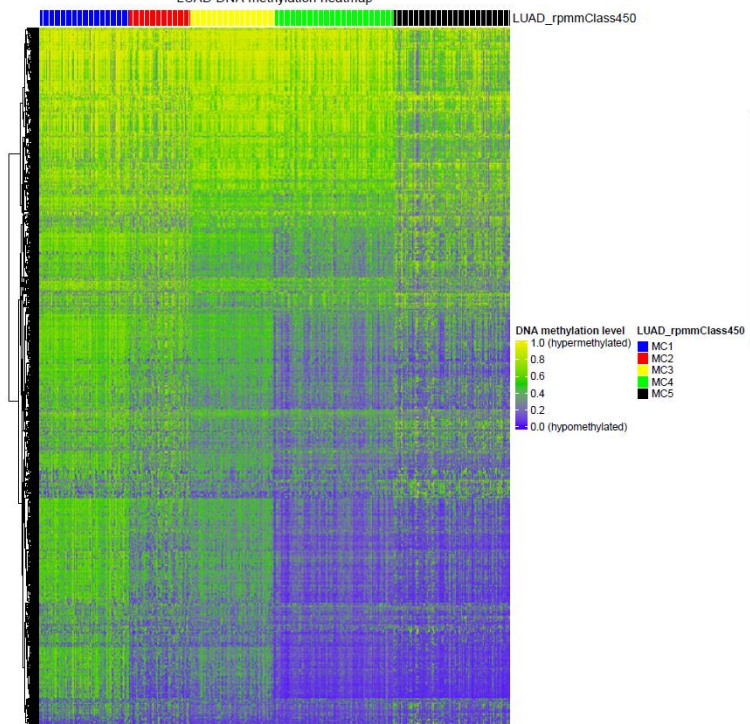
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Supplementary Figures

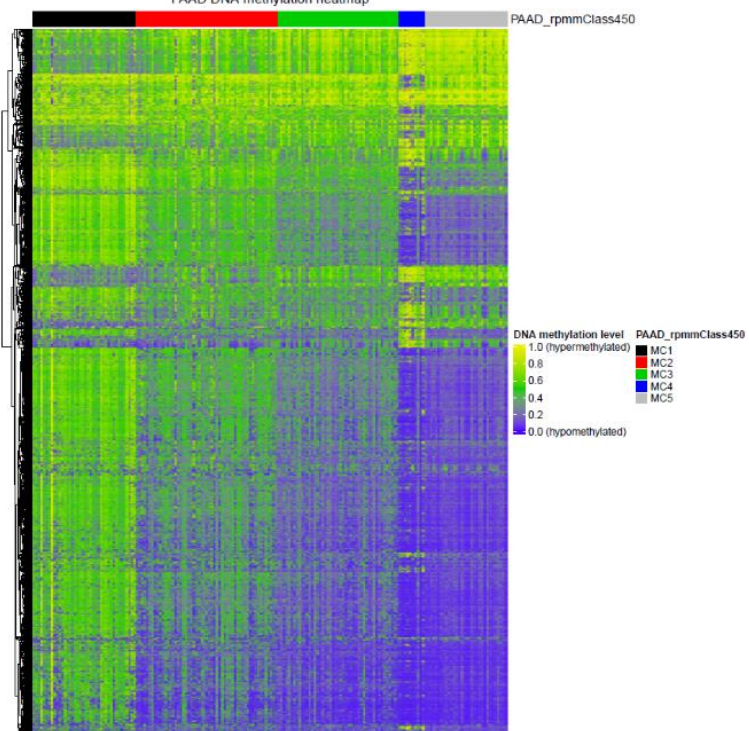
Fig. S1: DNA methylation heatmaps showing HM450 DNA methylation levels and RPMM-based classification of included adenocarcinomas.



LUAD DNA methylation heatmap



PAAD DNA methylation heatmap



STAD DNA methylation heatmap

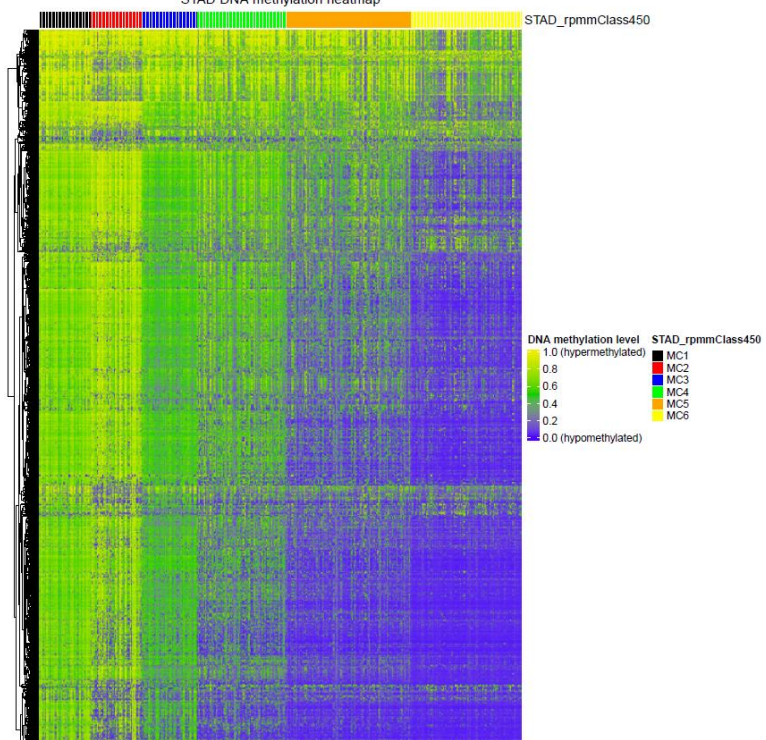
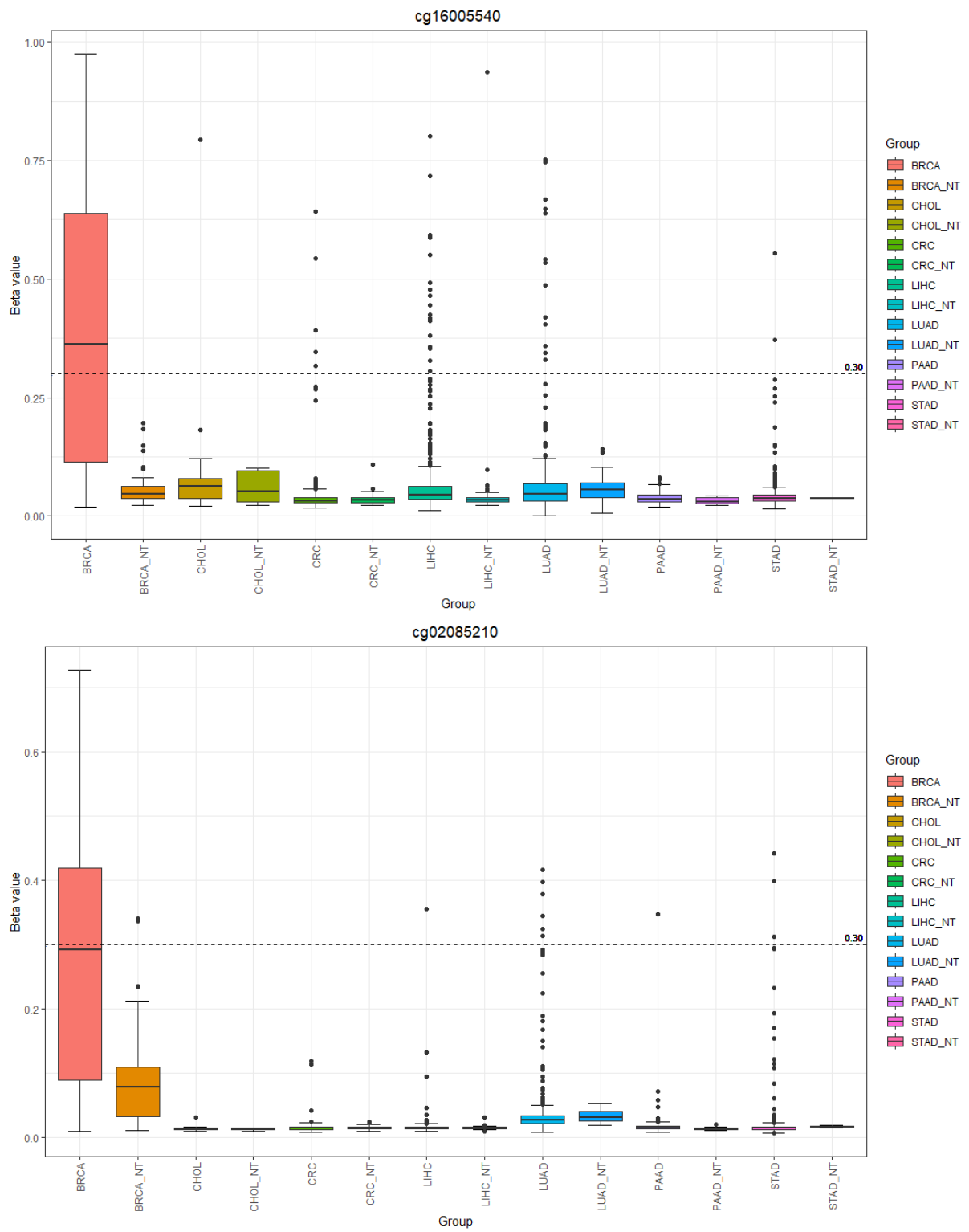
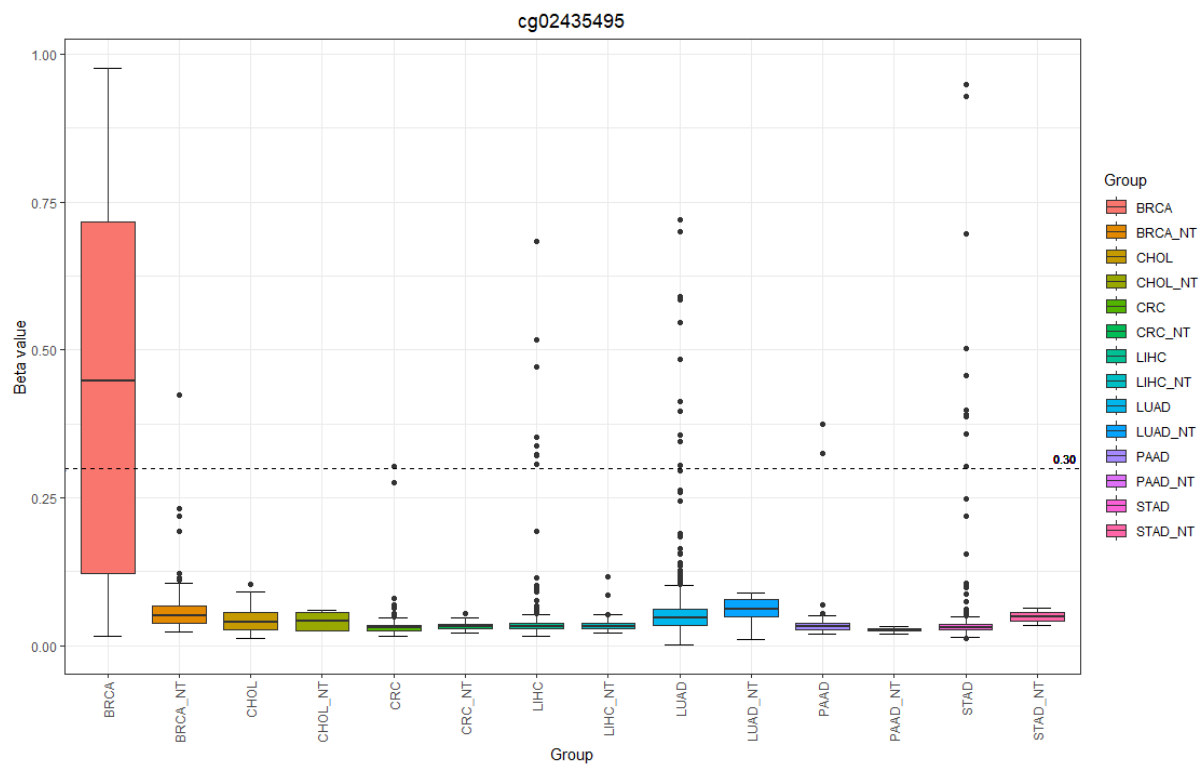
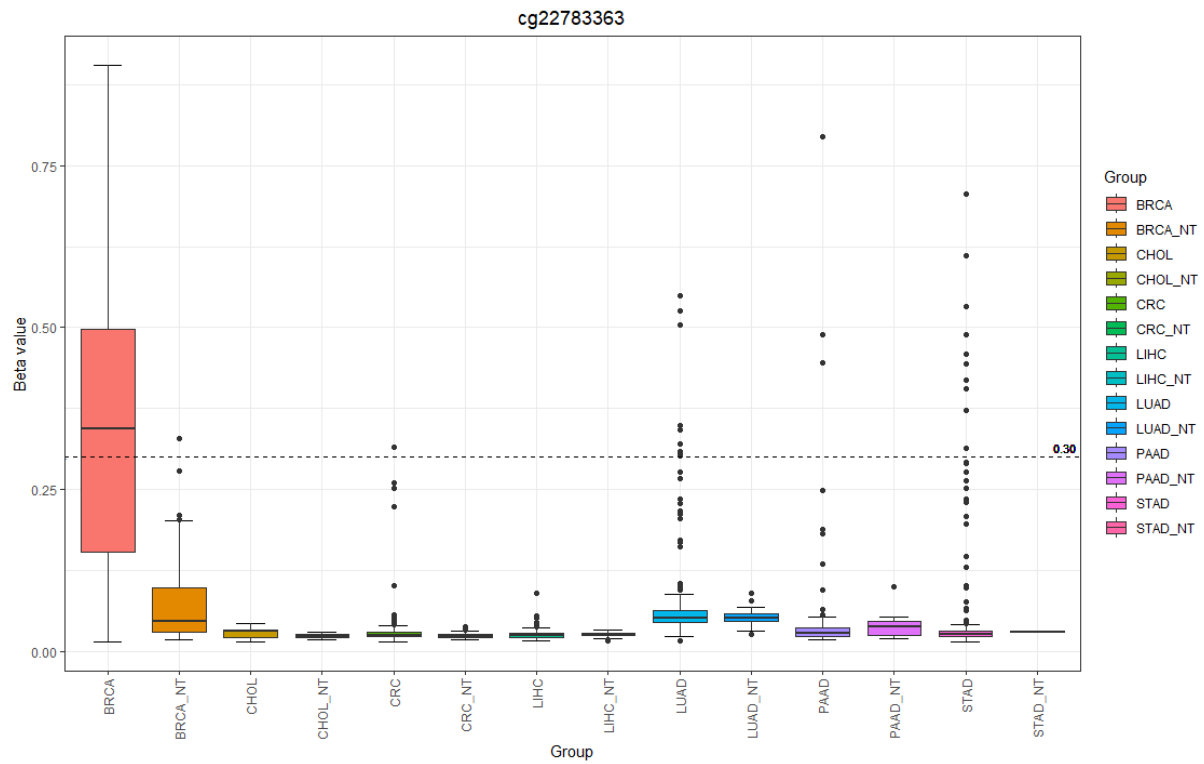
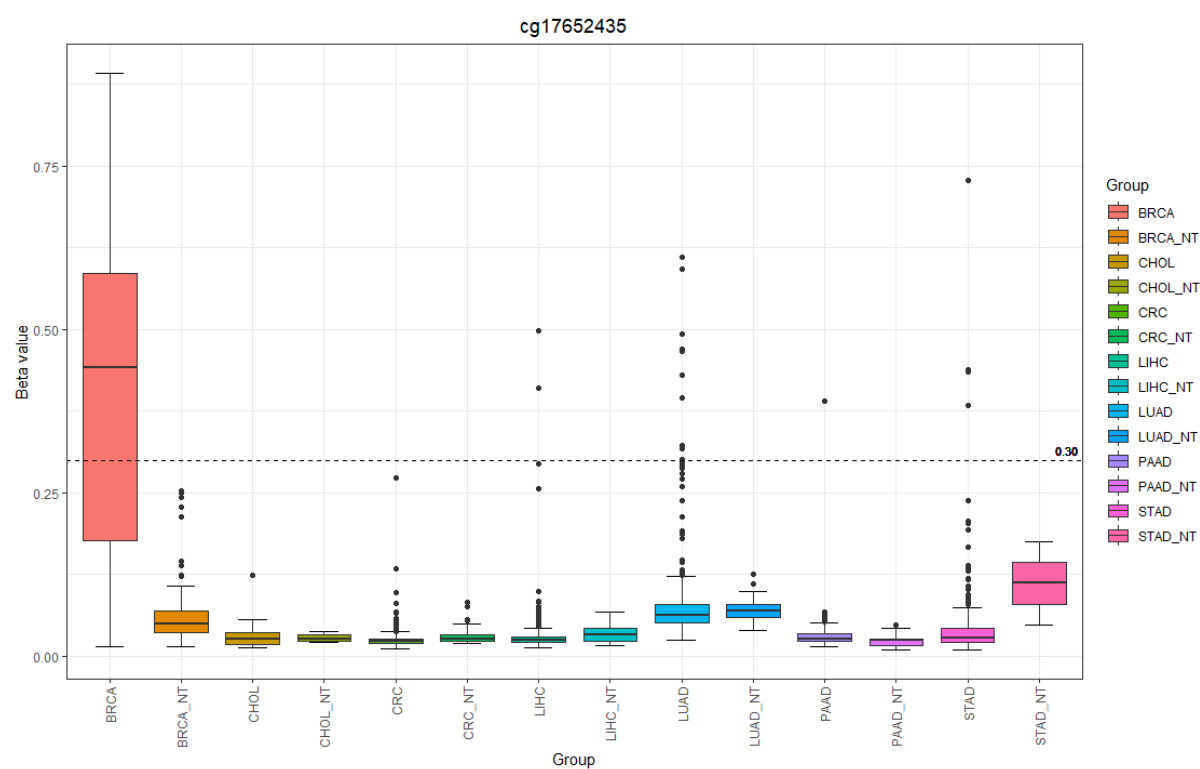
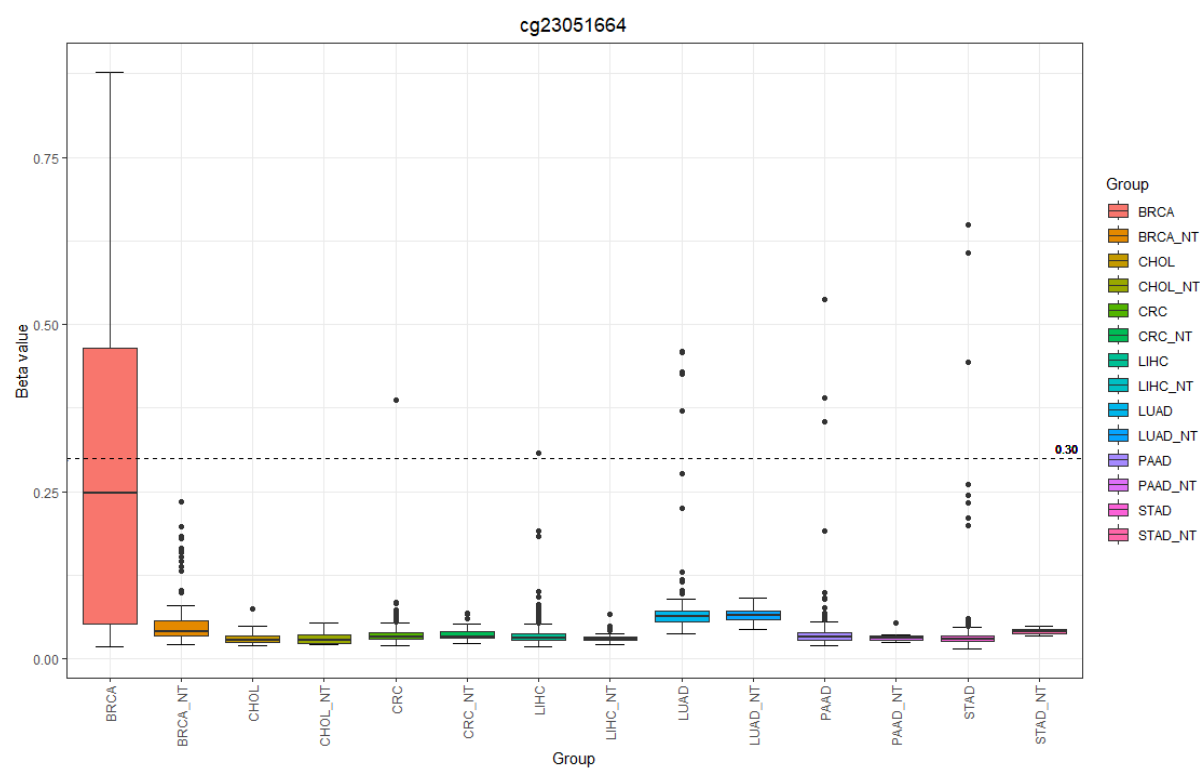
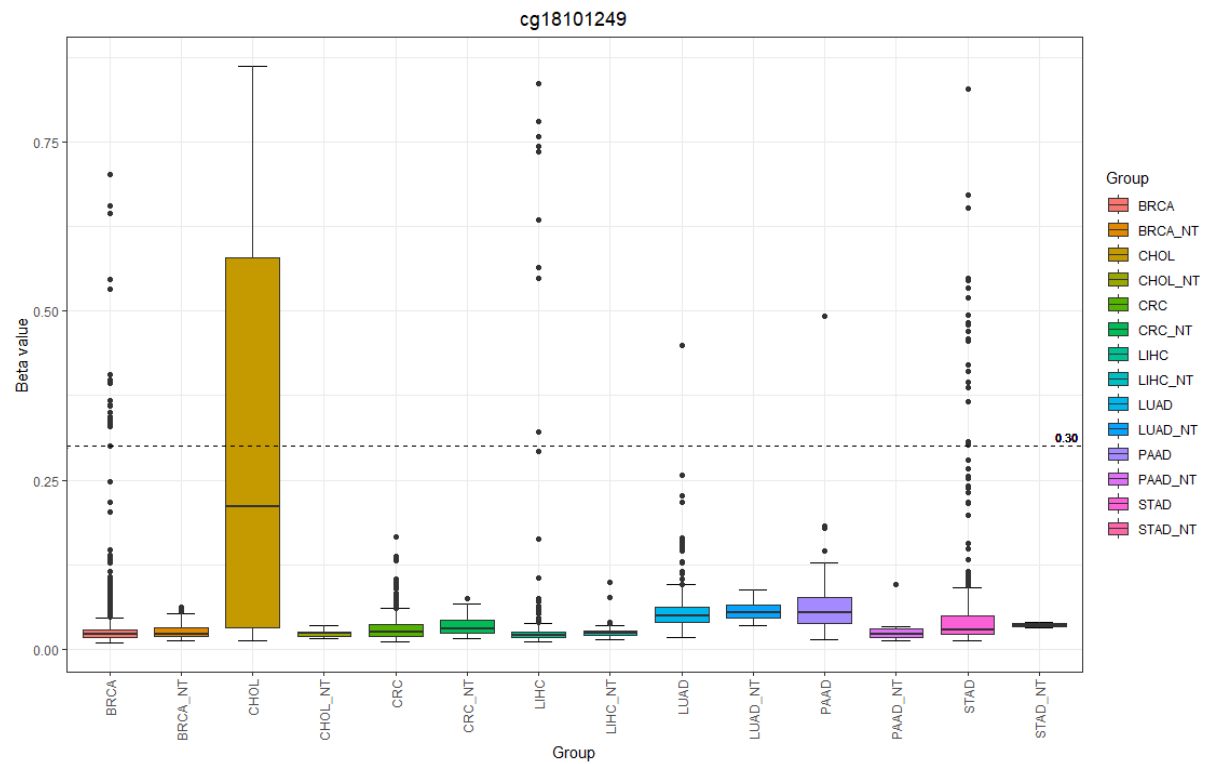
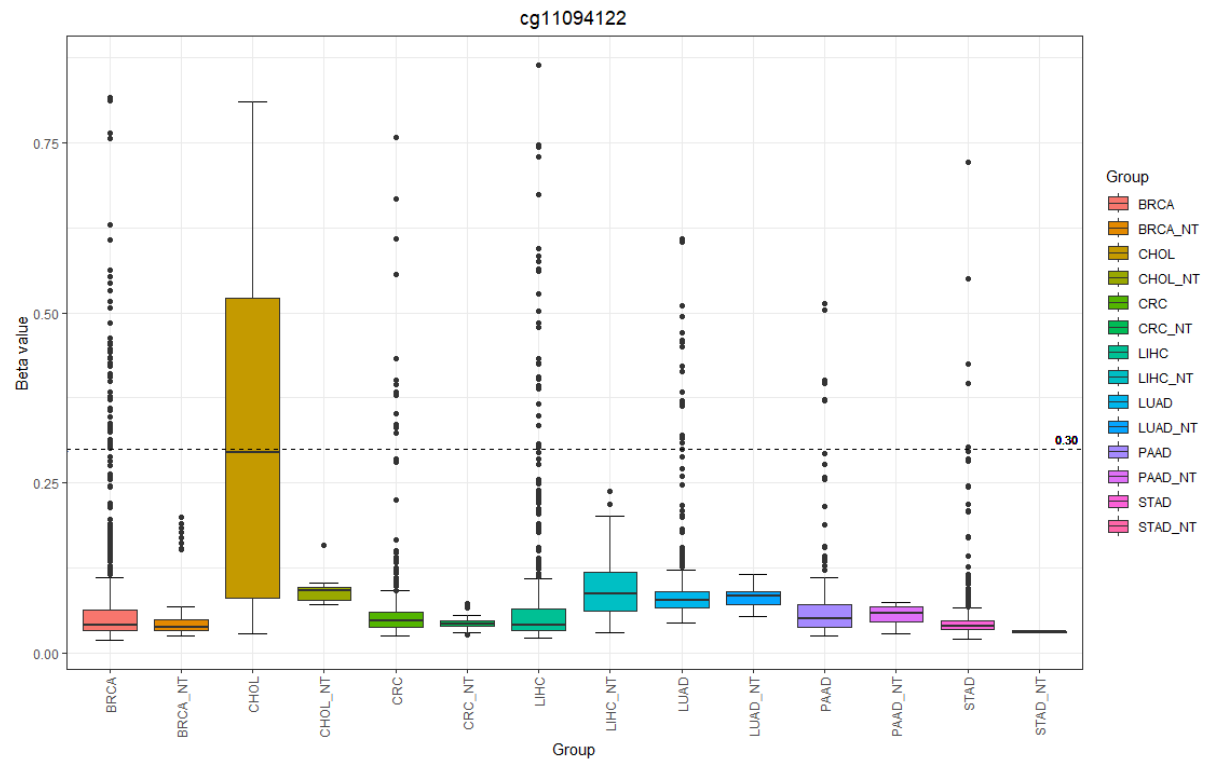


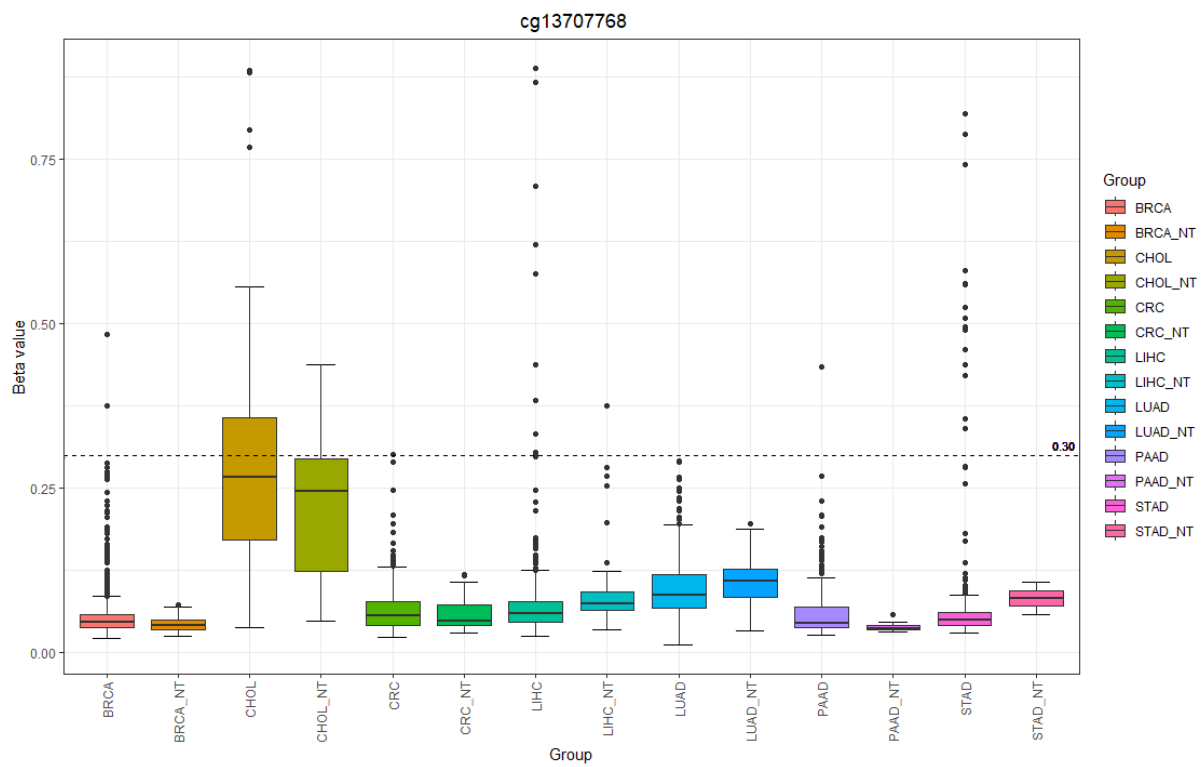
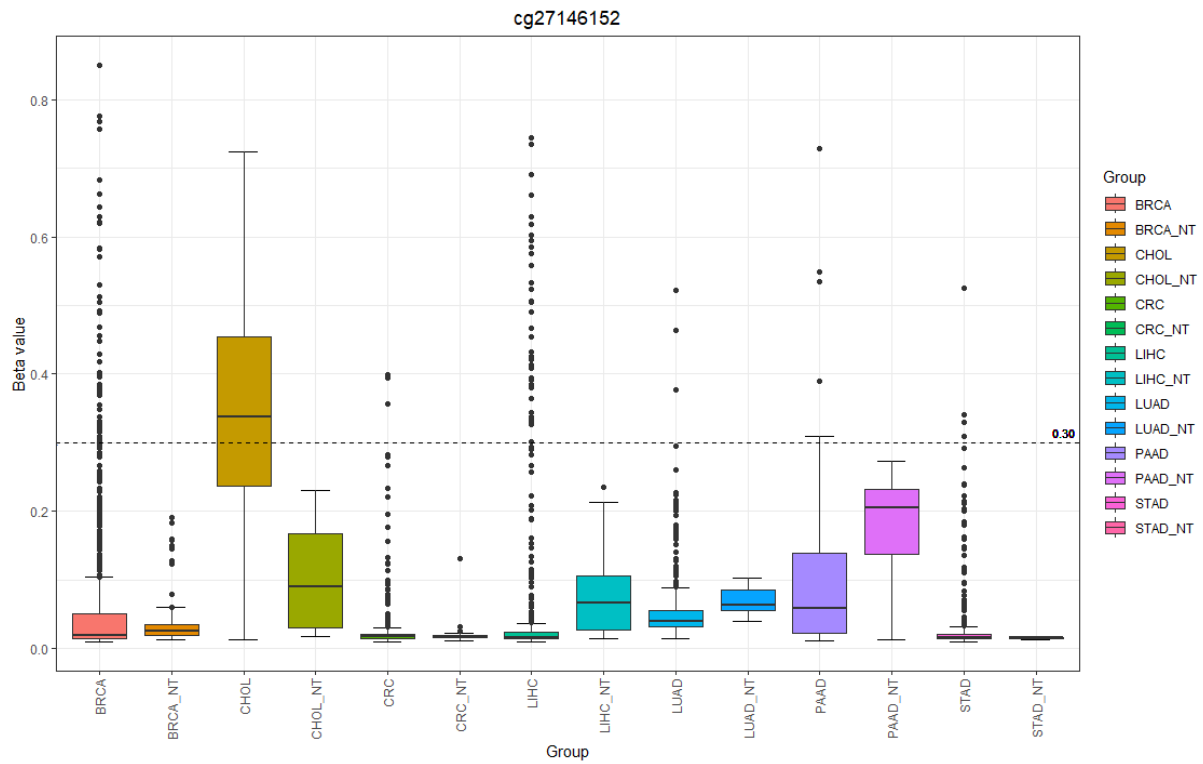
Fig. S2: Boxplots showing the distribution of beta values of selected probes from the non-clustered approach across the included tumor samples and the normal tissue samples.

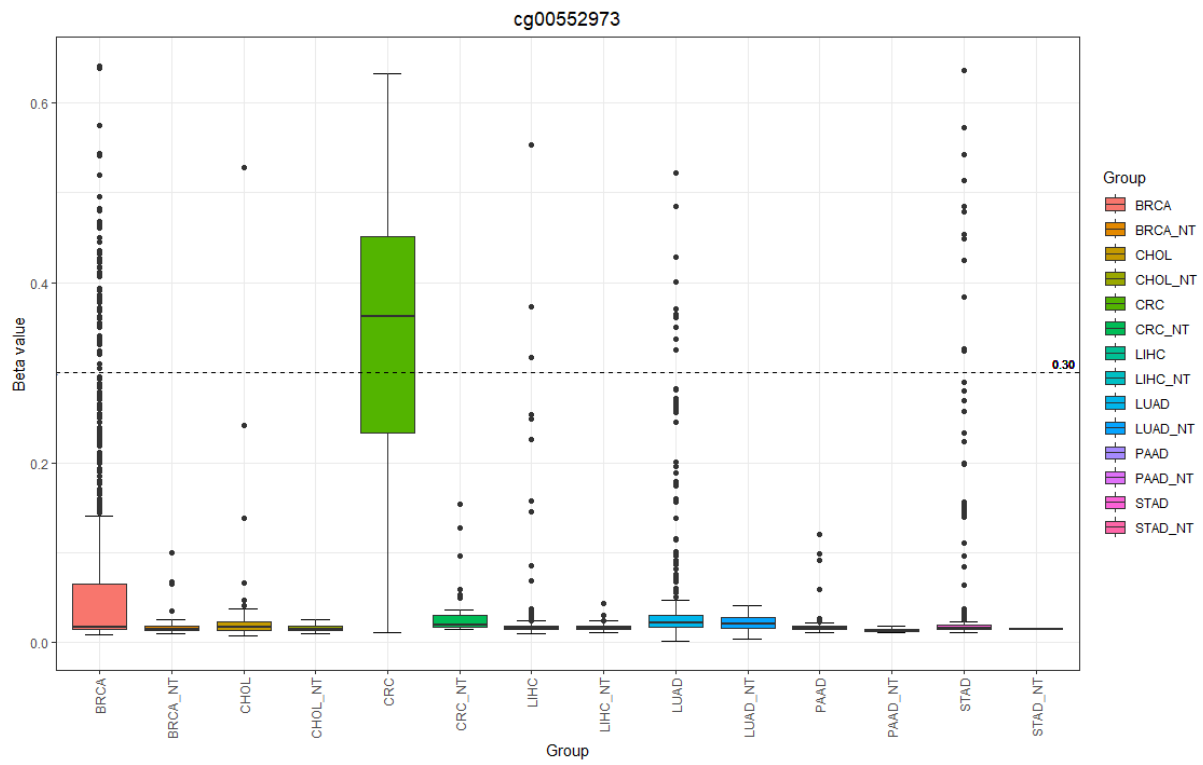
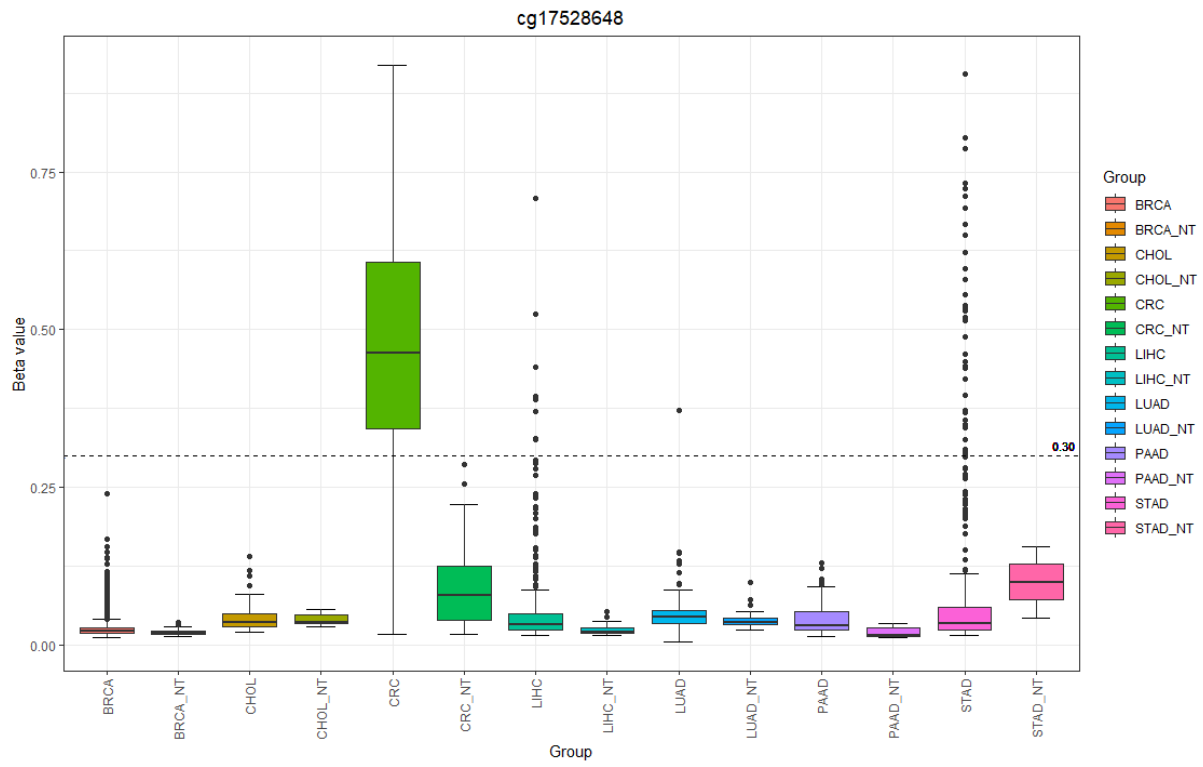


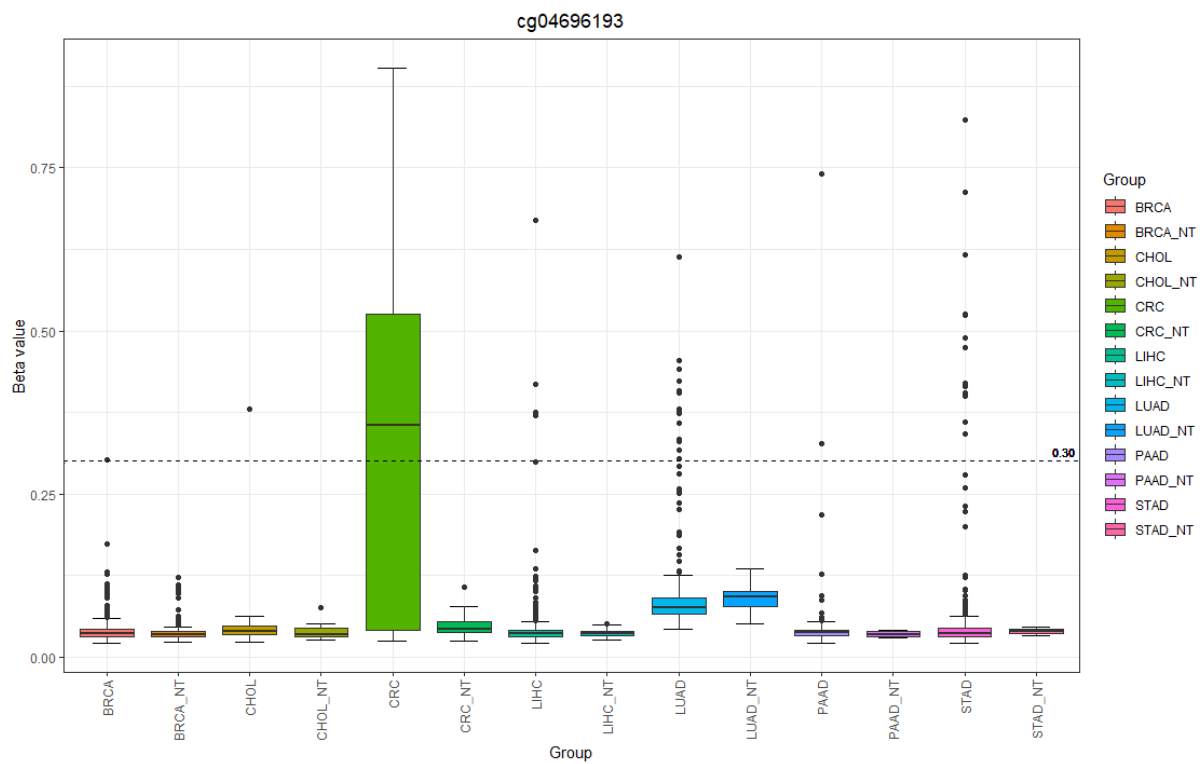
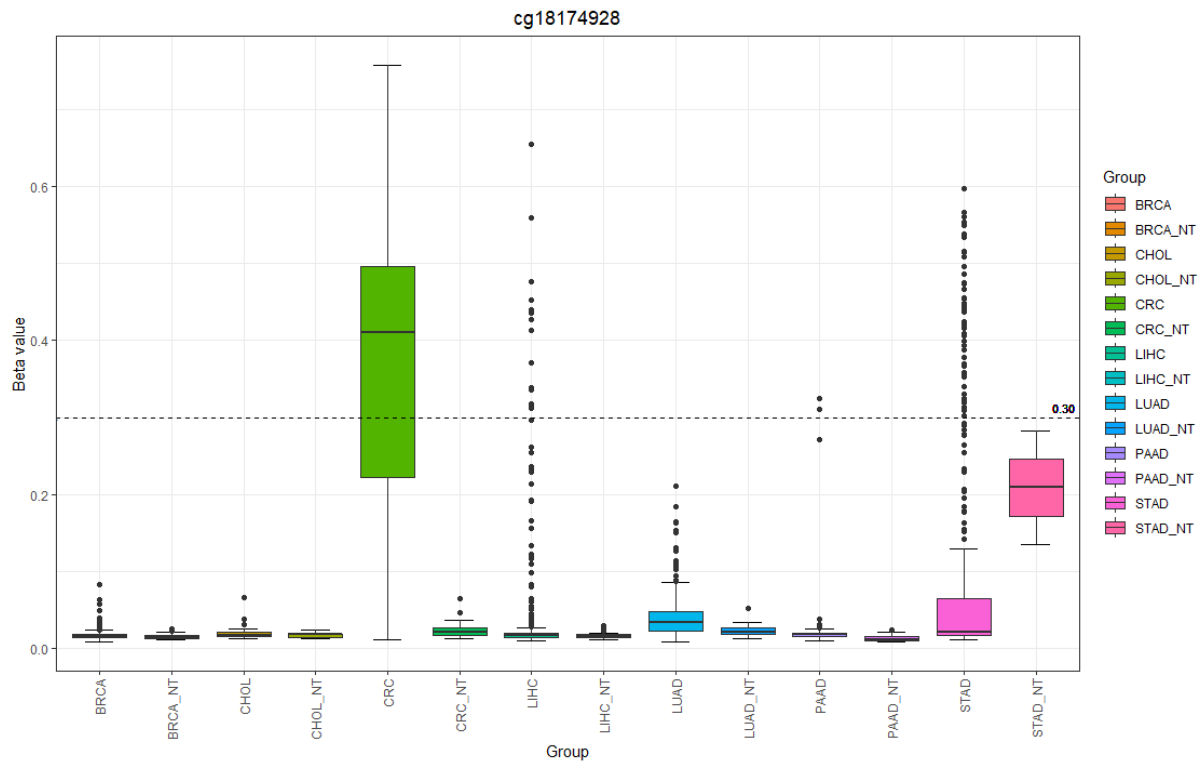


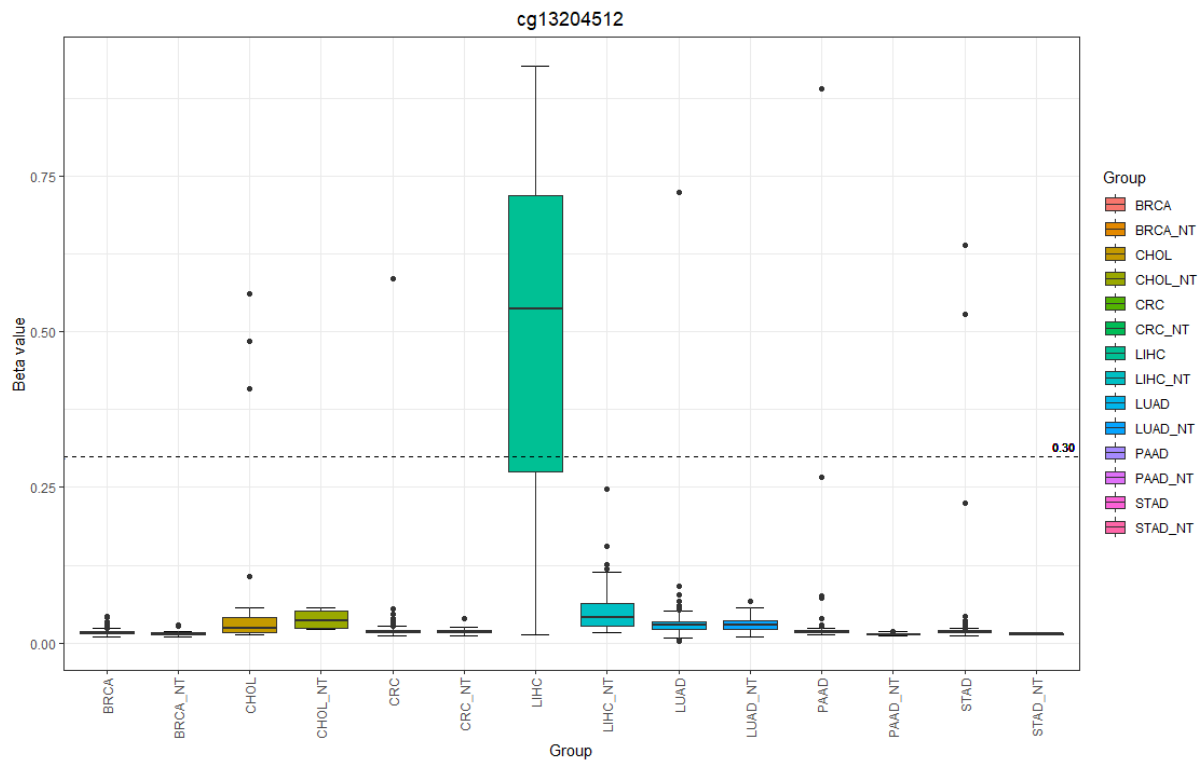
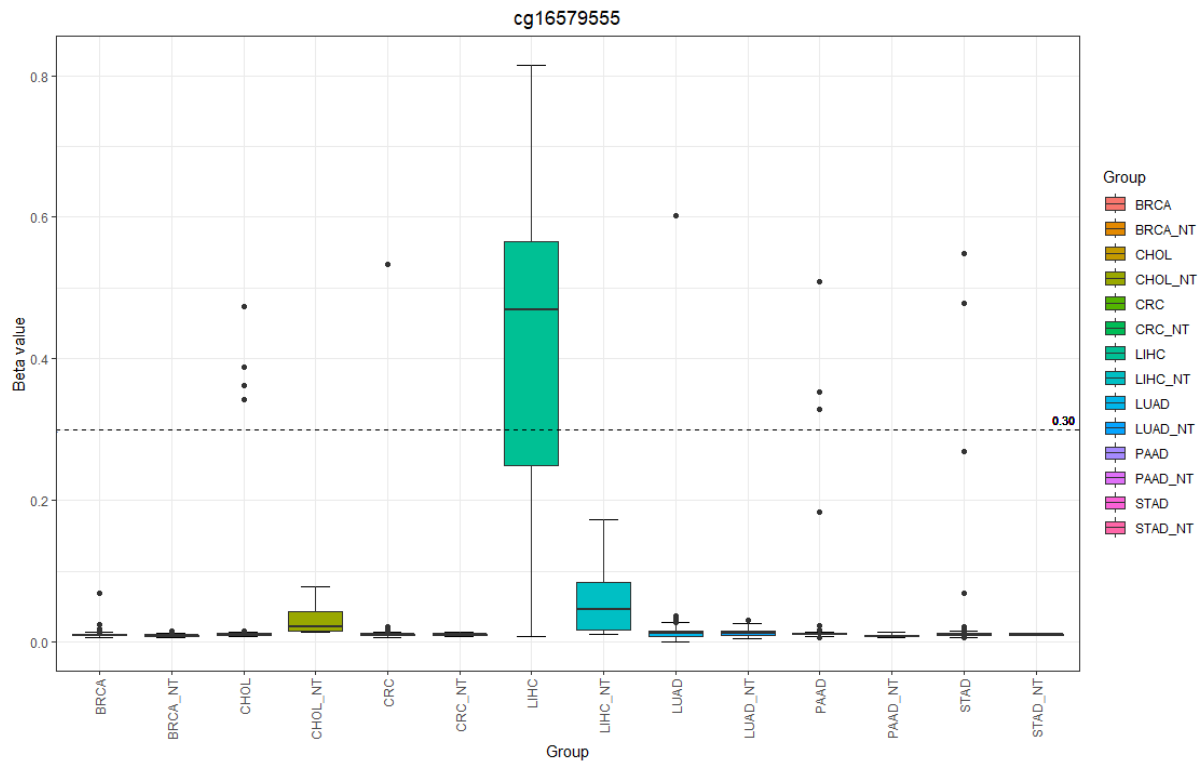


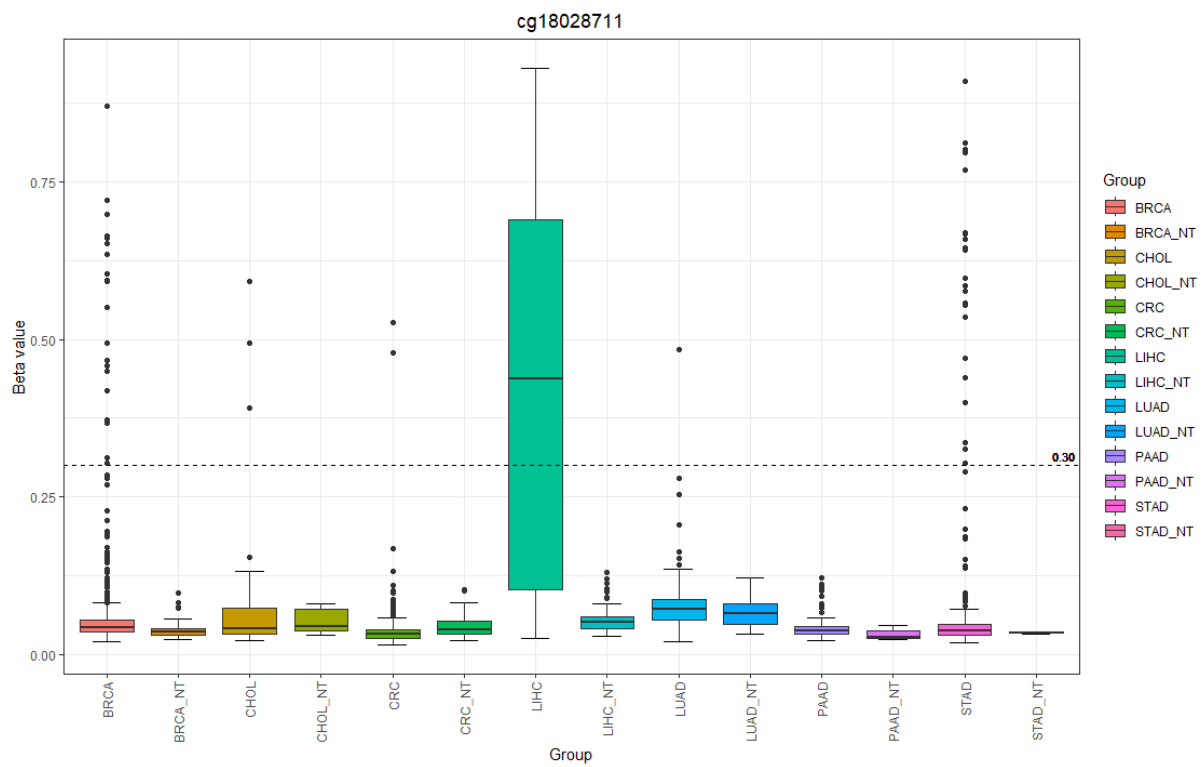
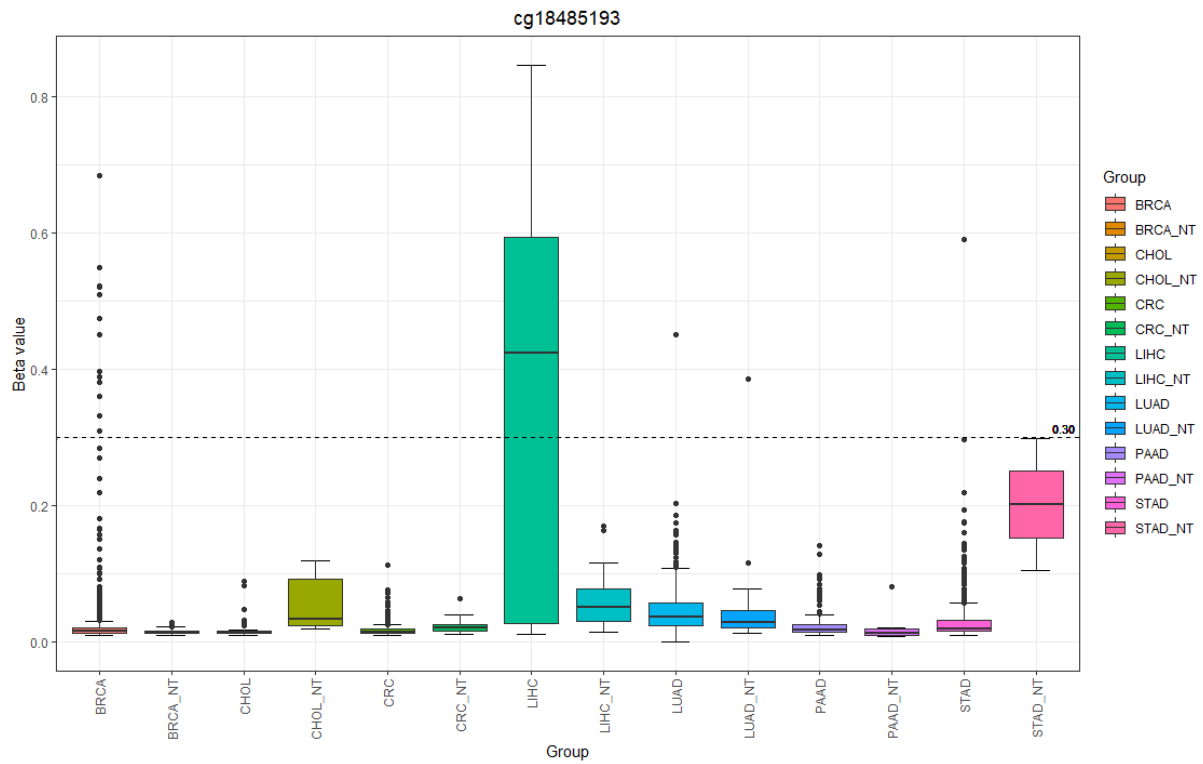


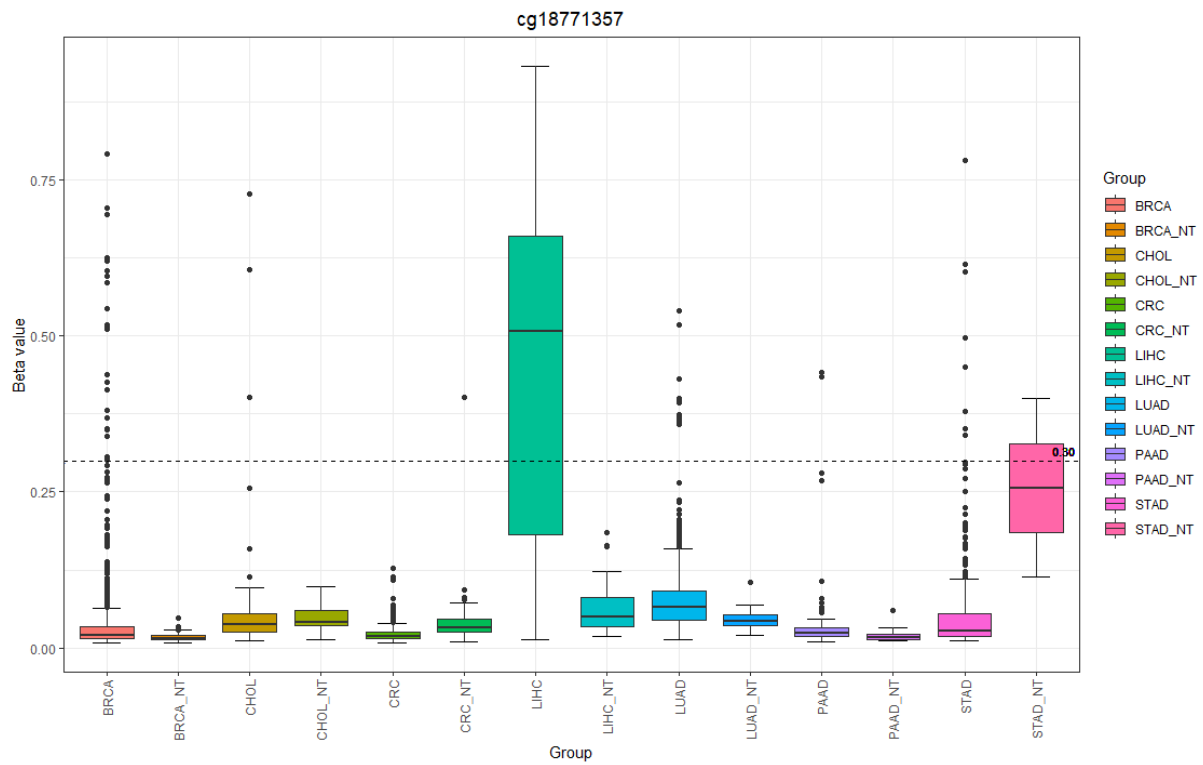
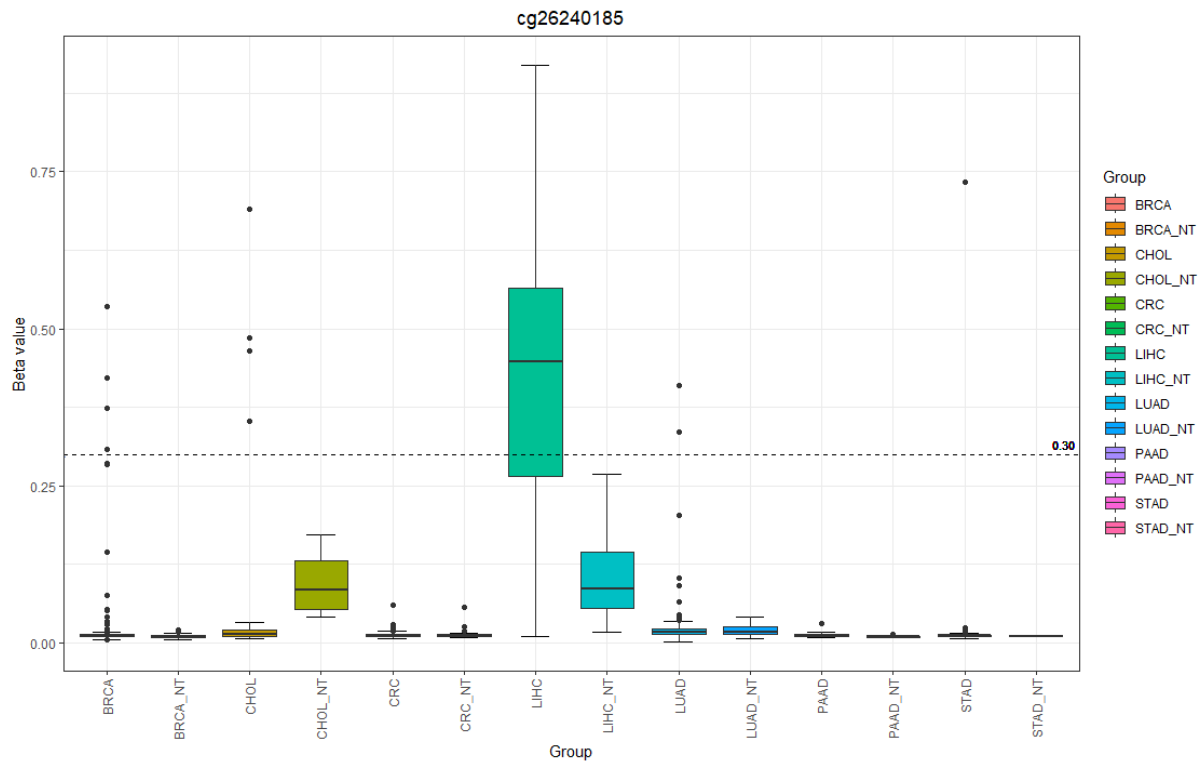


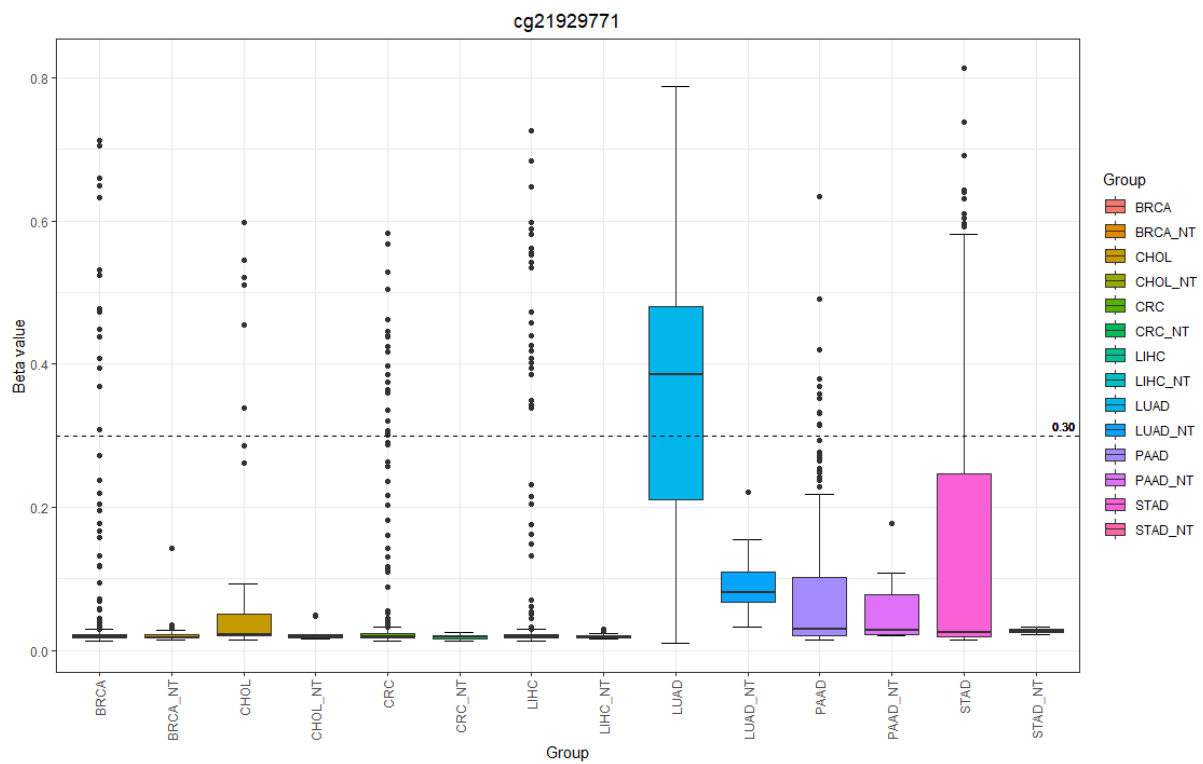
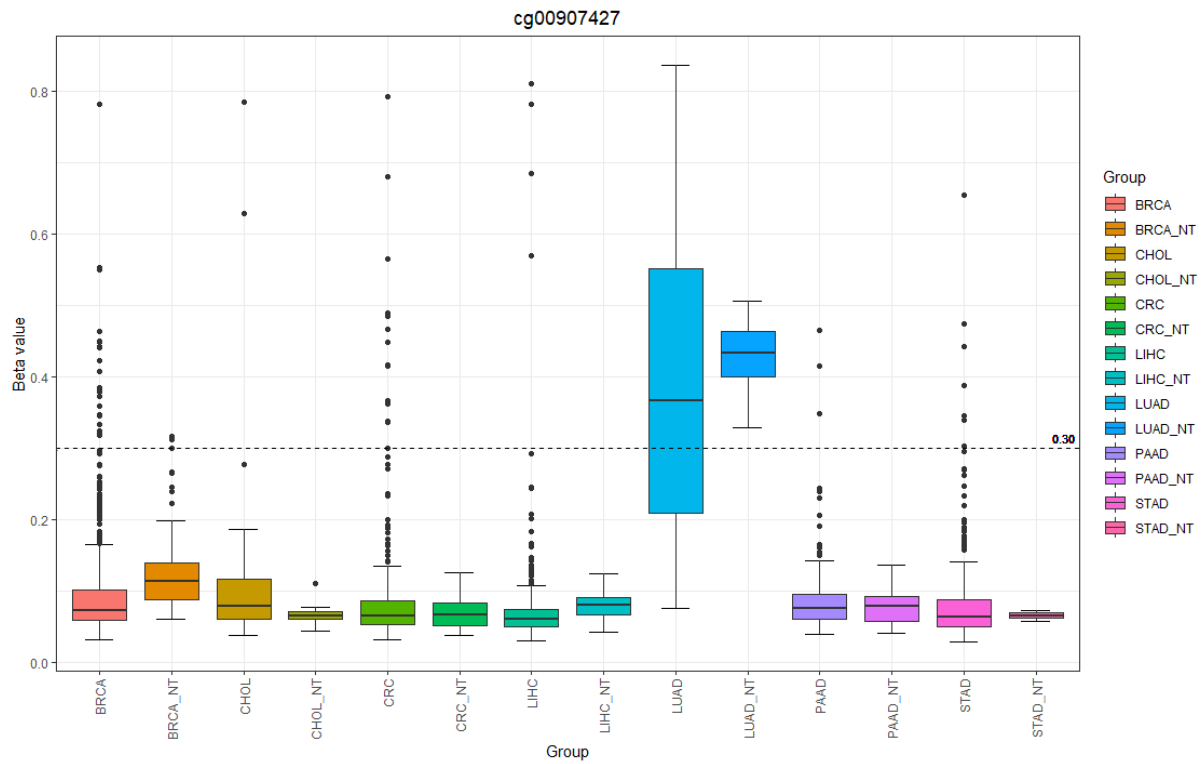


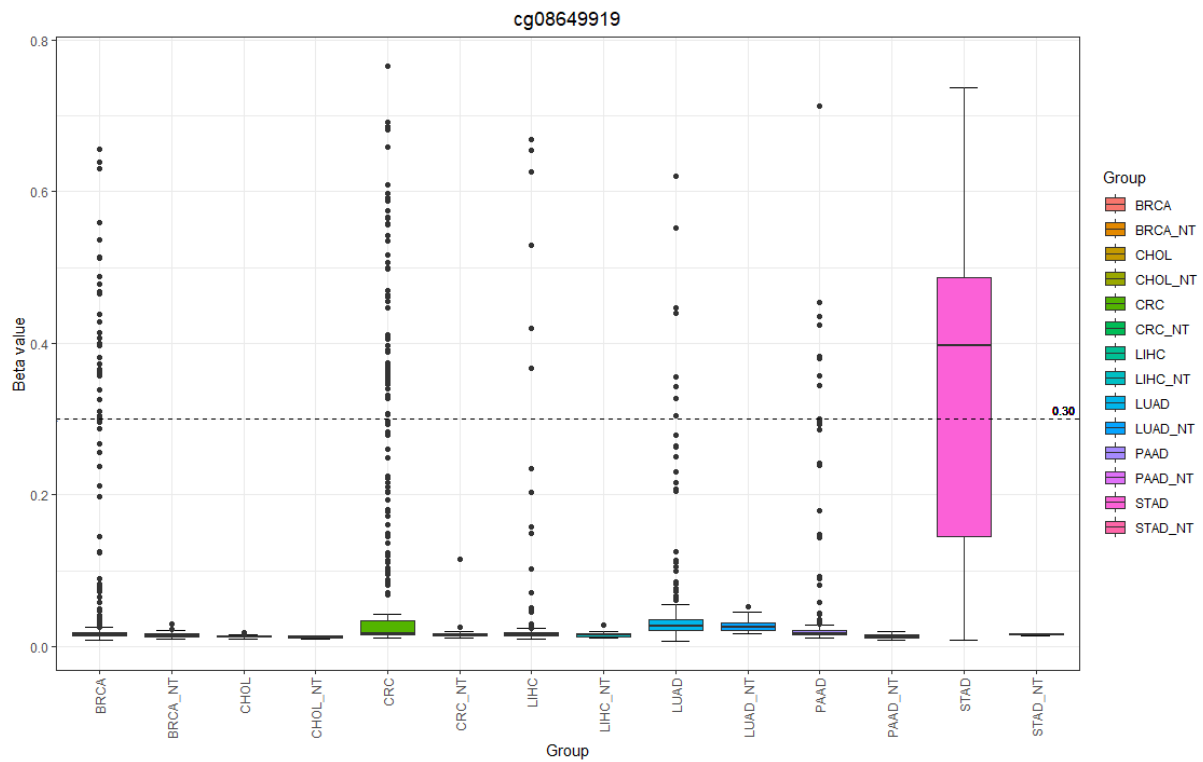
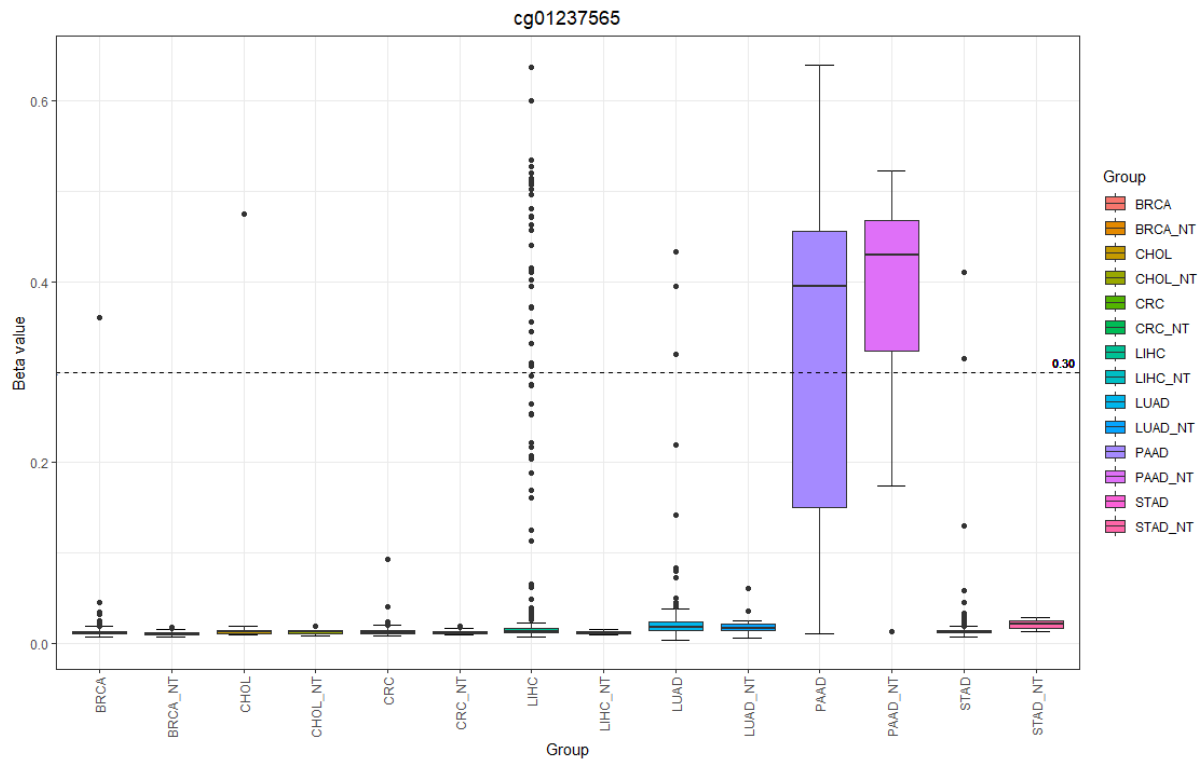


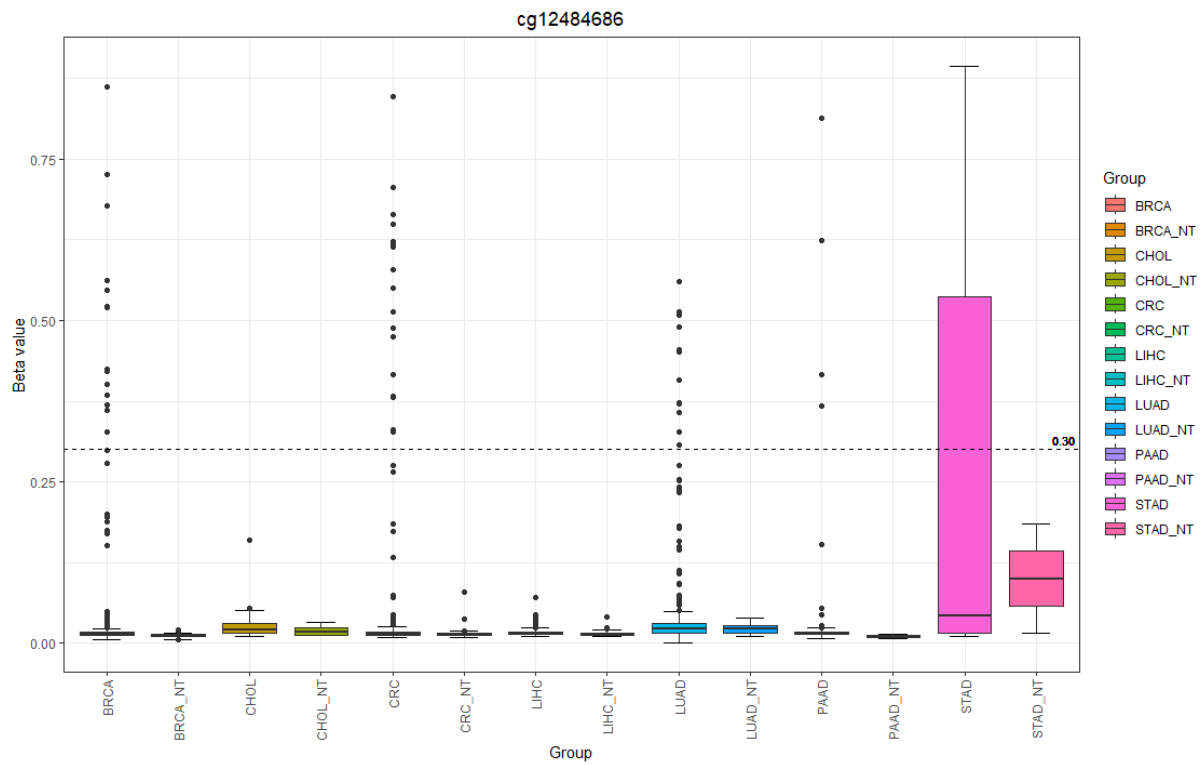
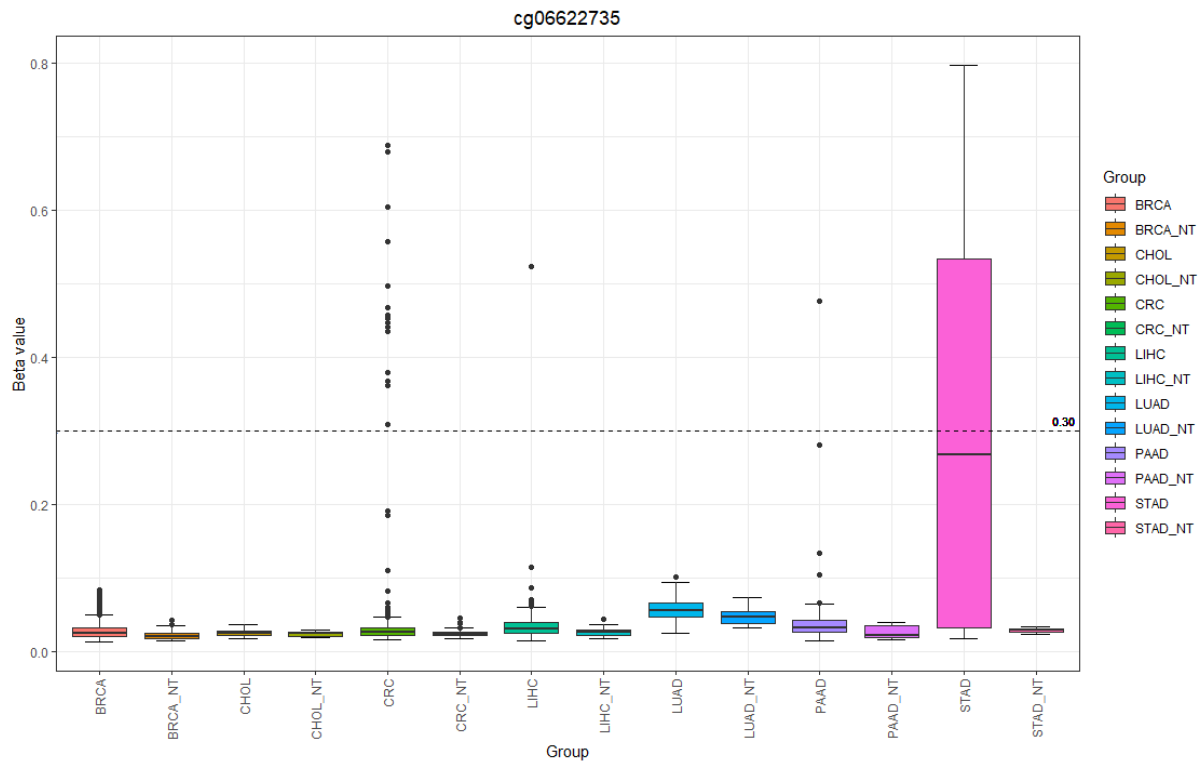












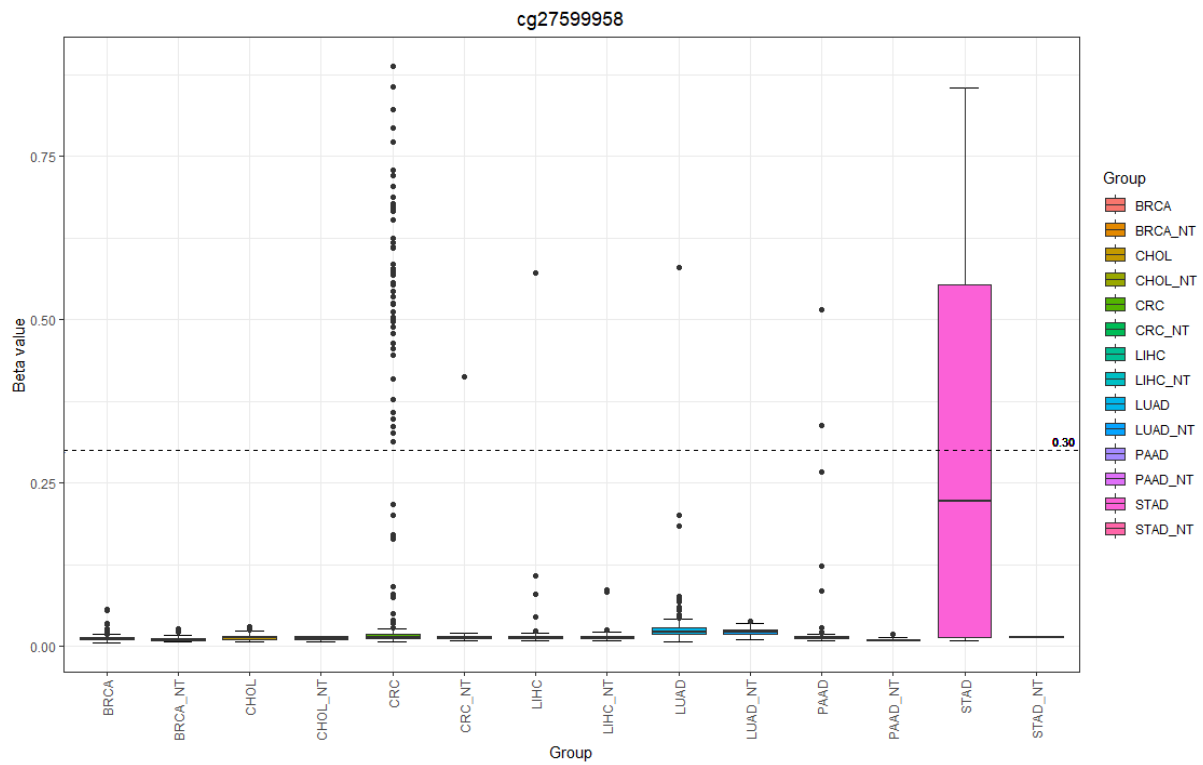
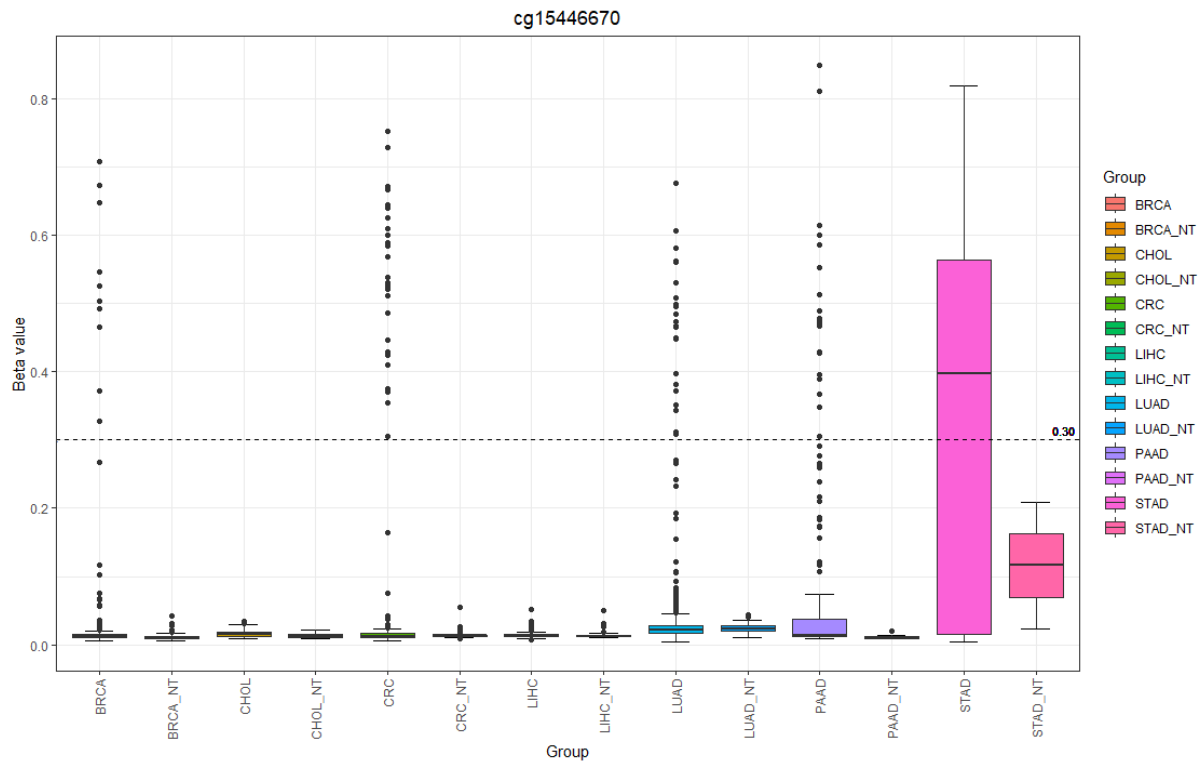
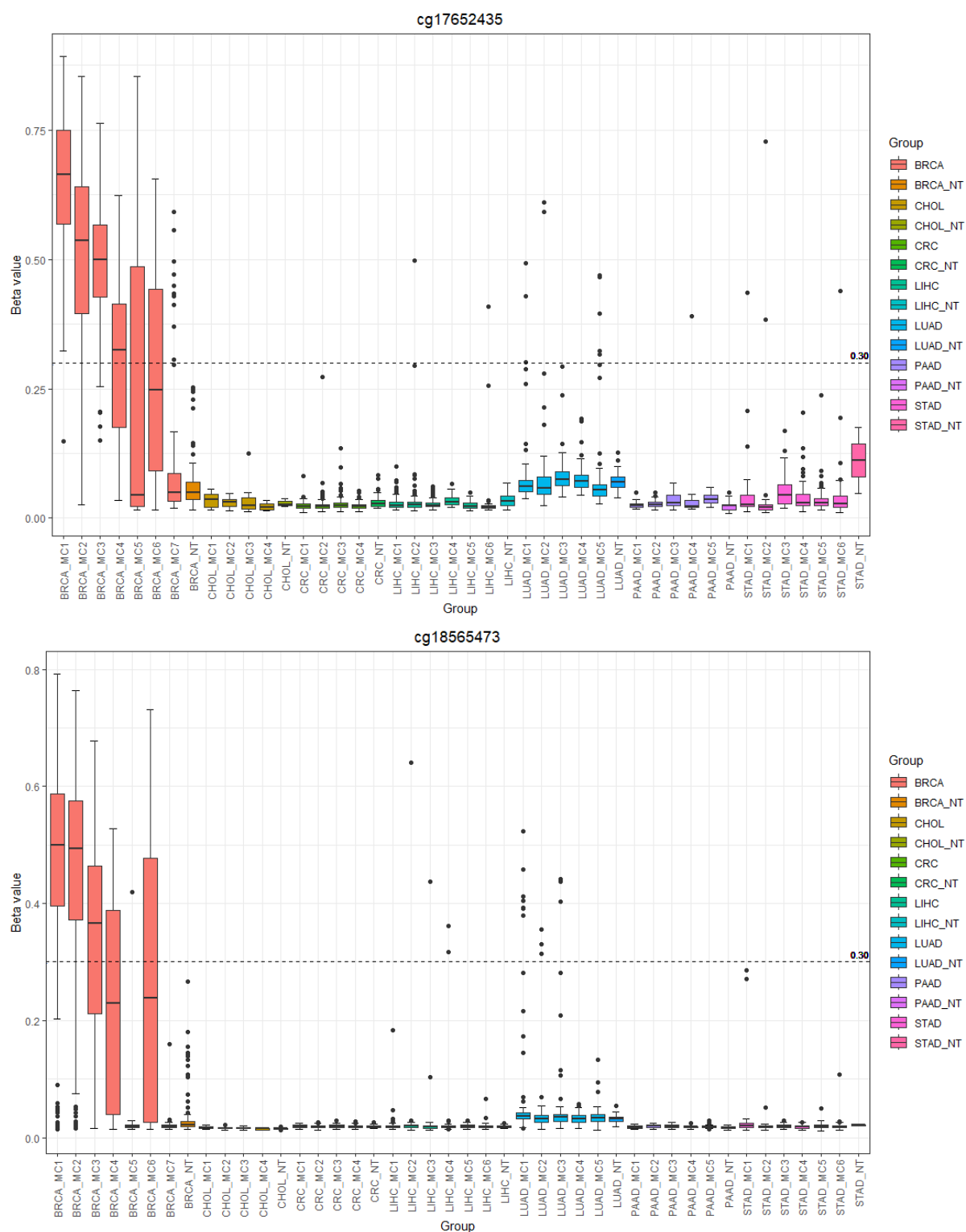
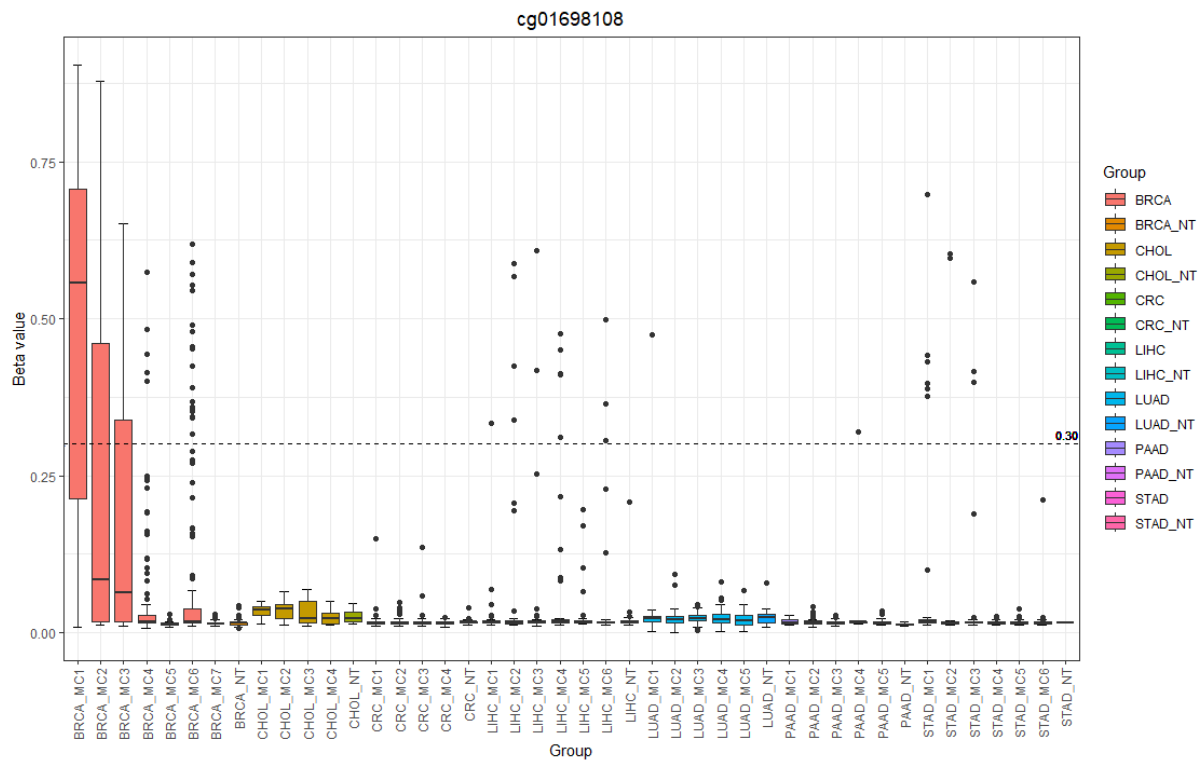
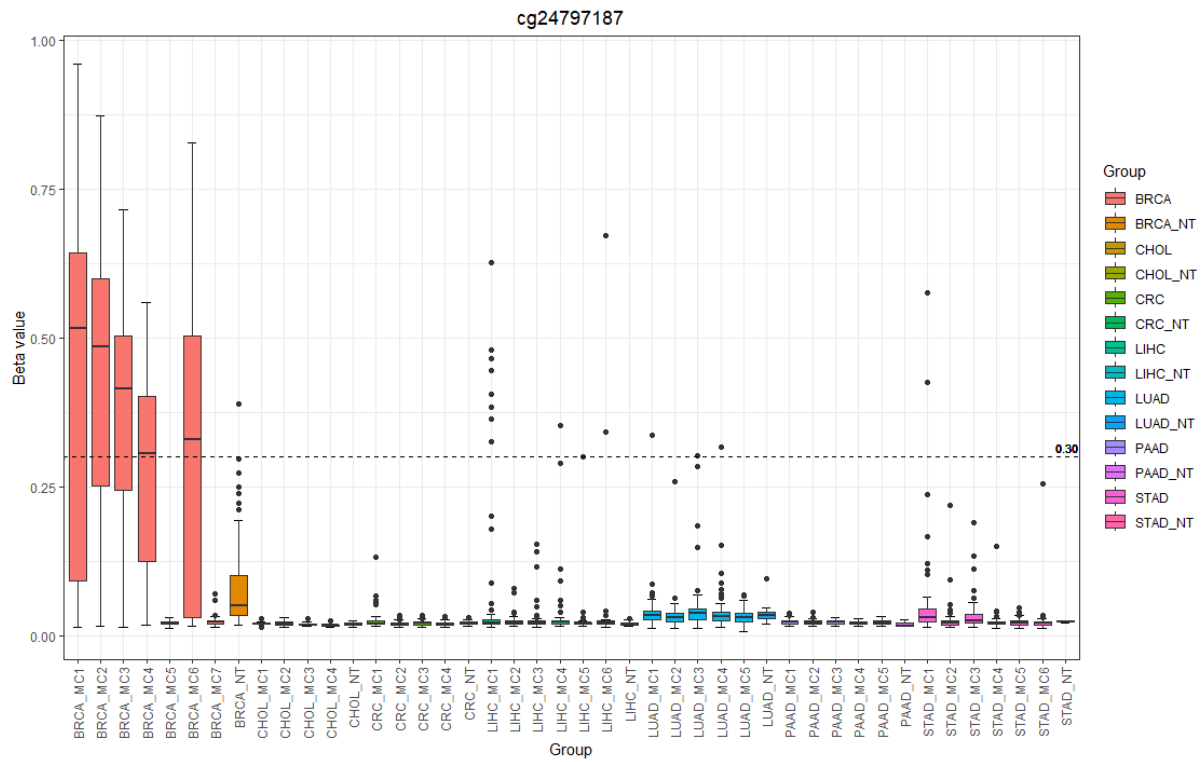
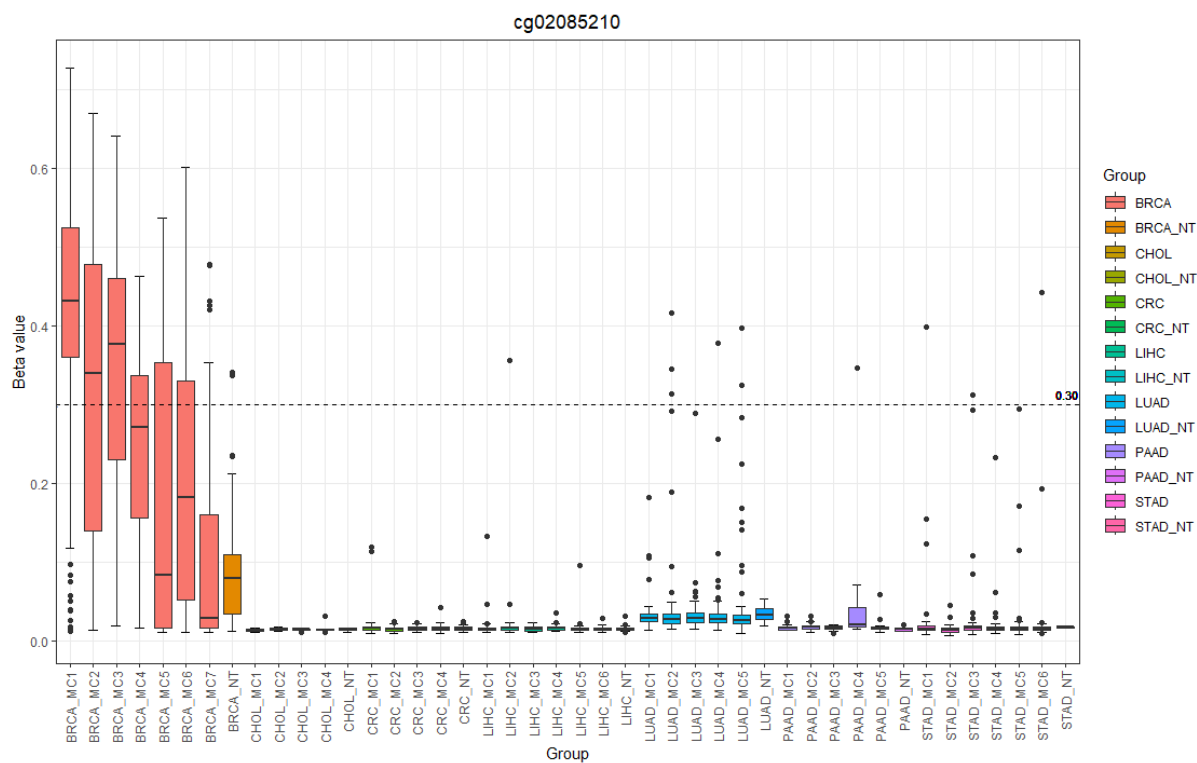
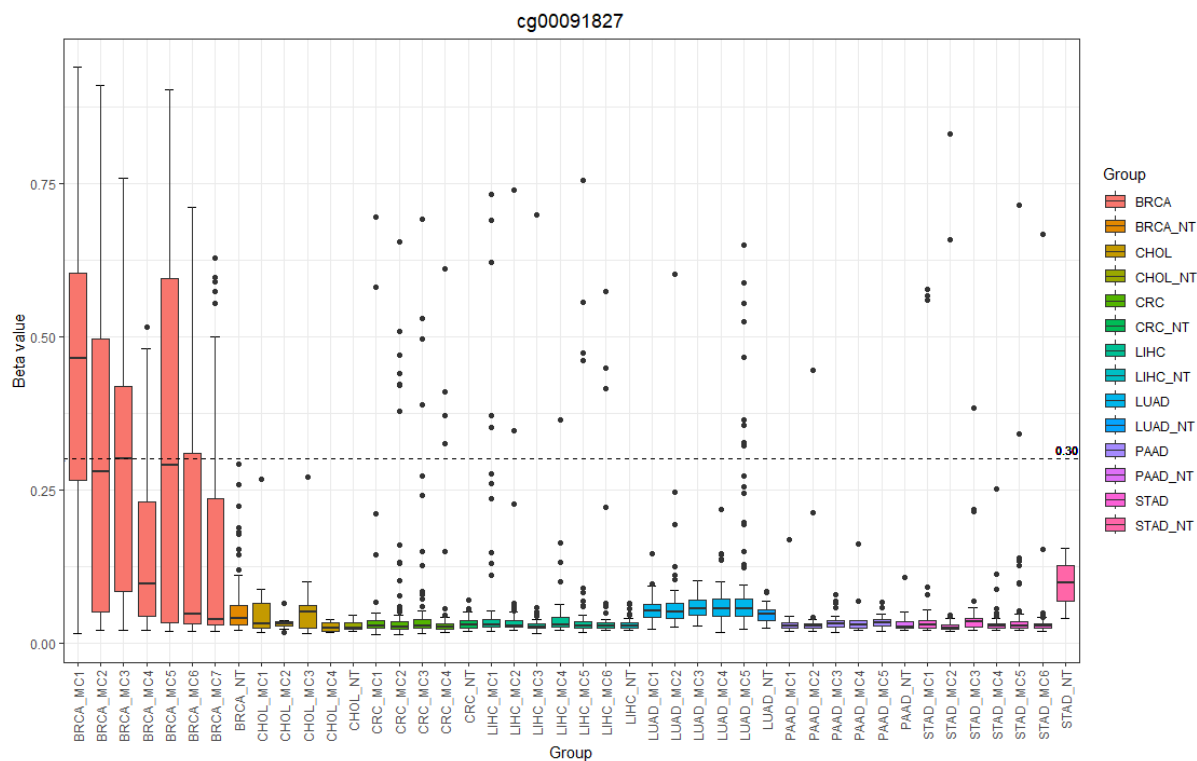


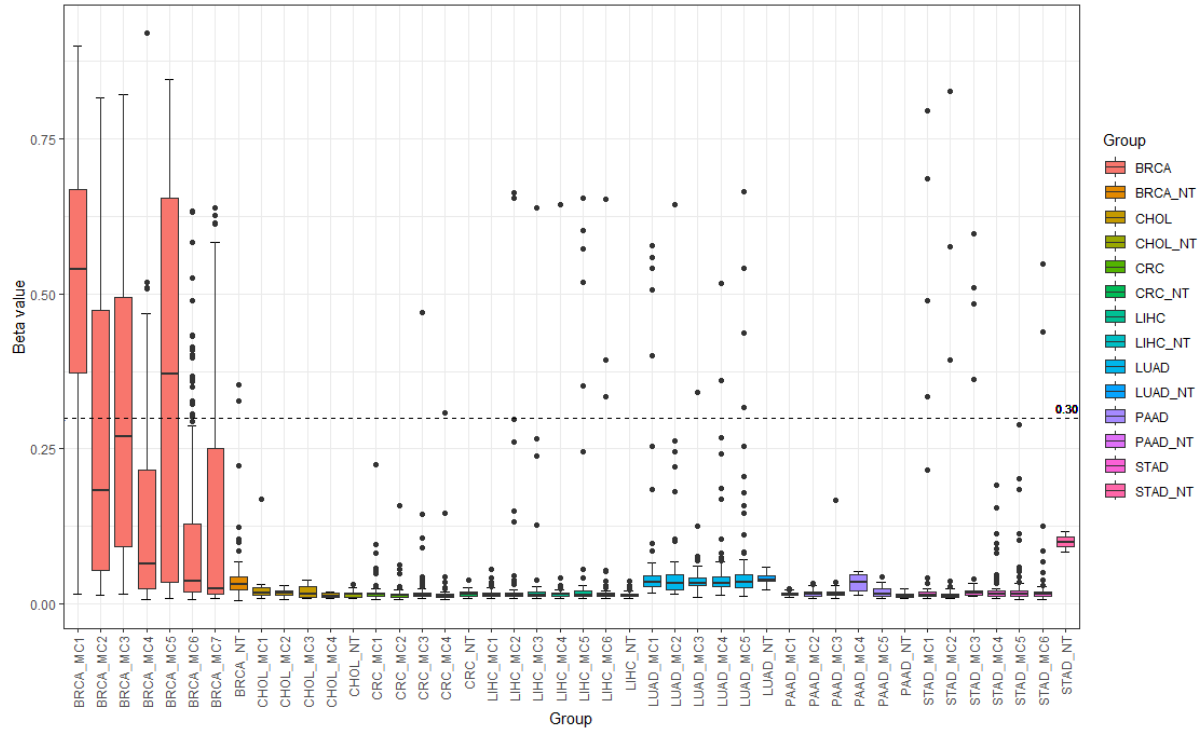
Fig. S3: Boxplots showing the distribution of beta values of selected probes from the clustered approach across the included tumor samples and the normal tissue samples.



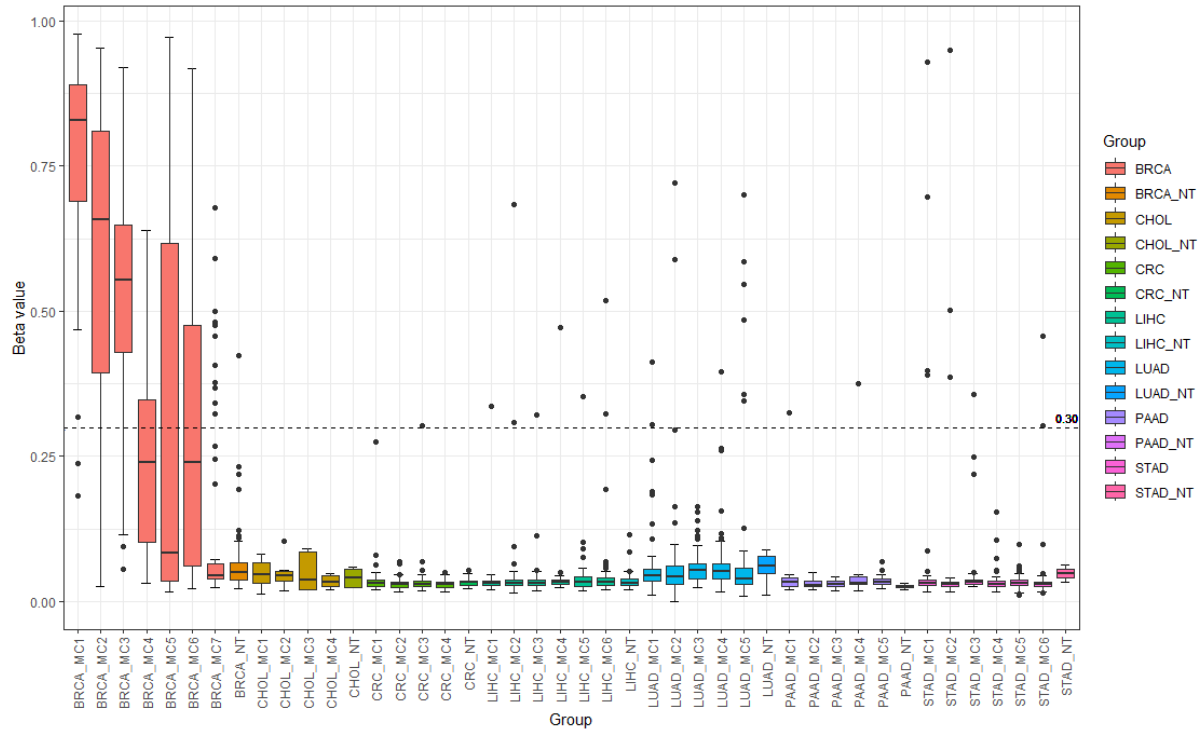


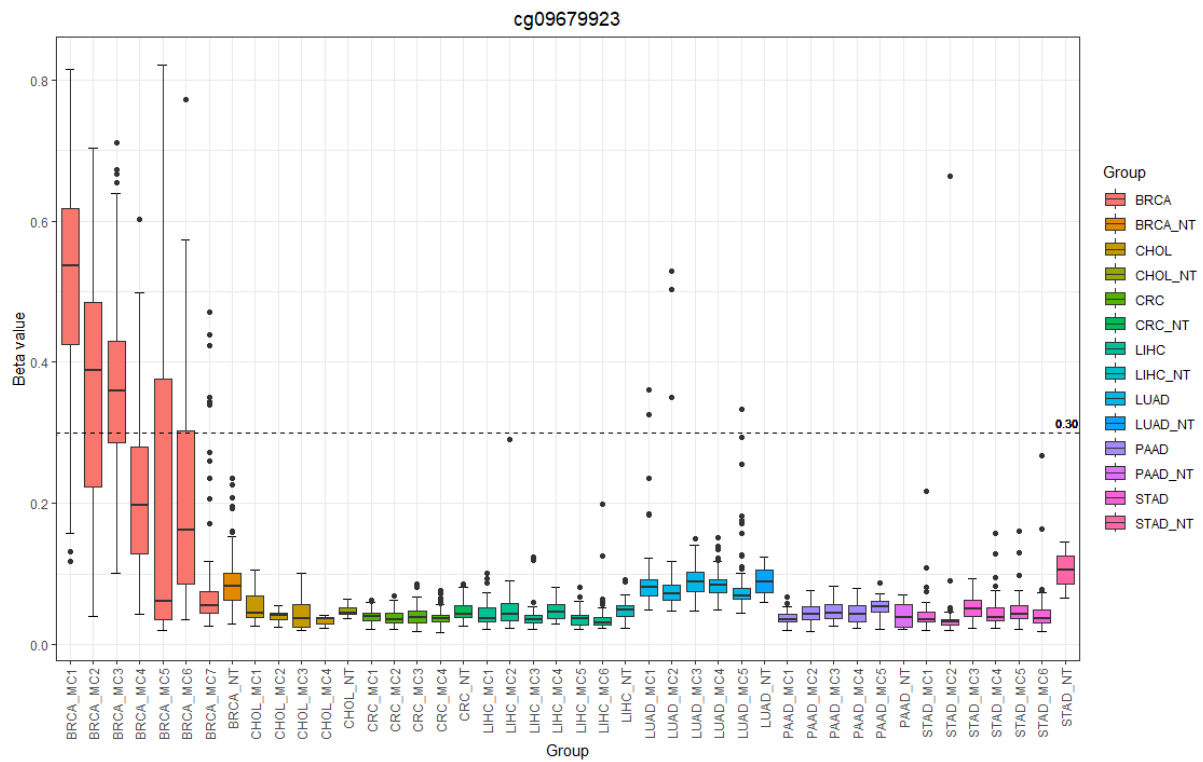
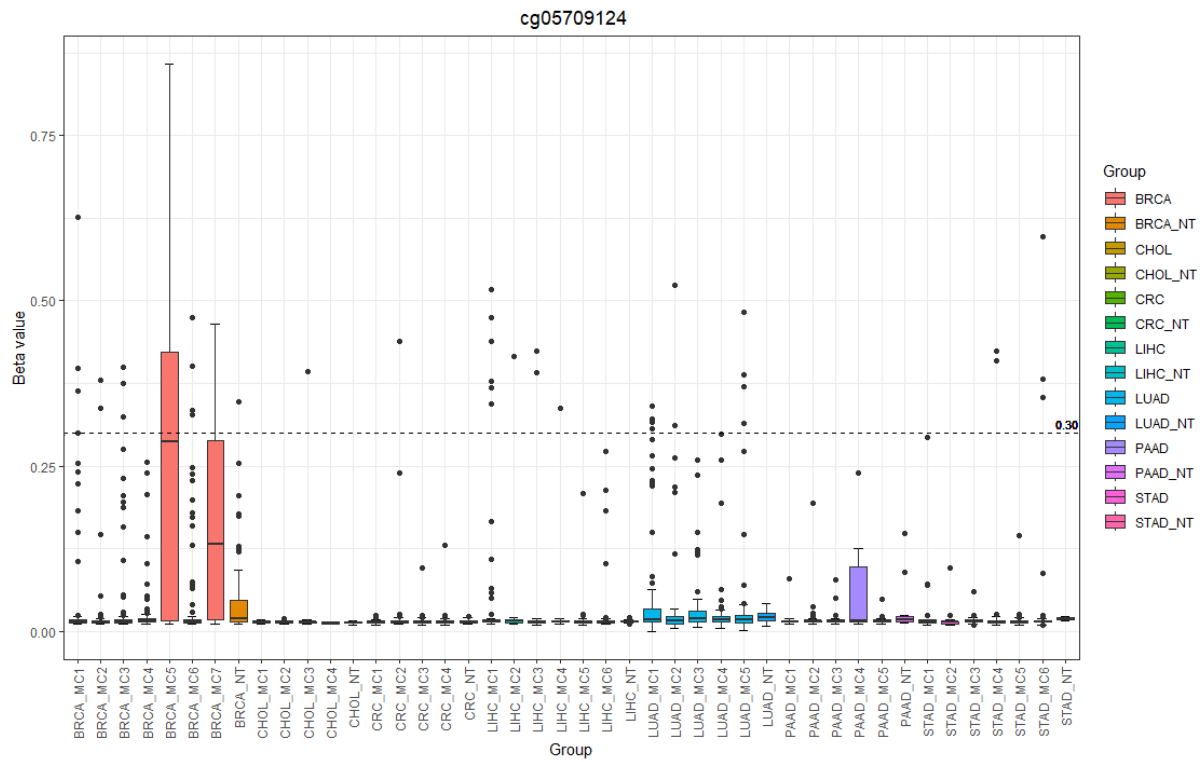


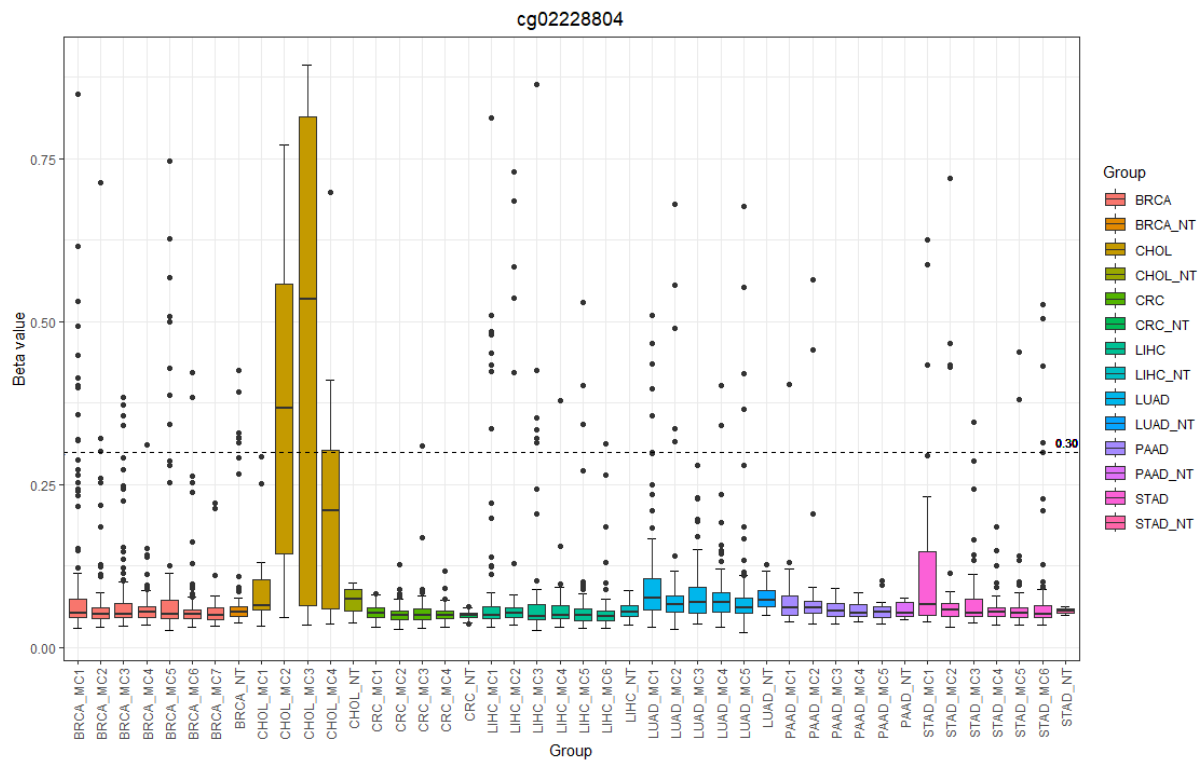
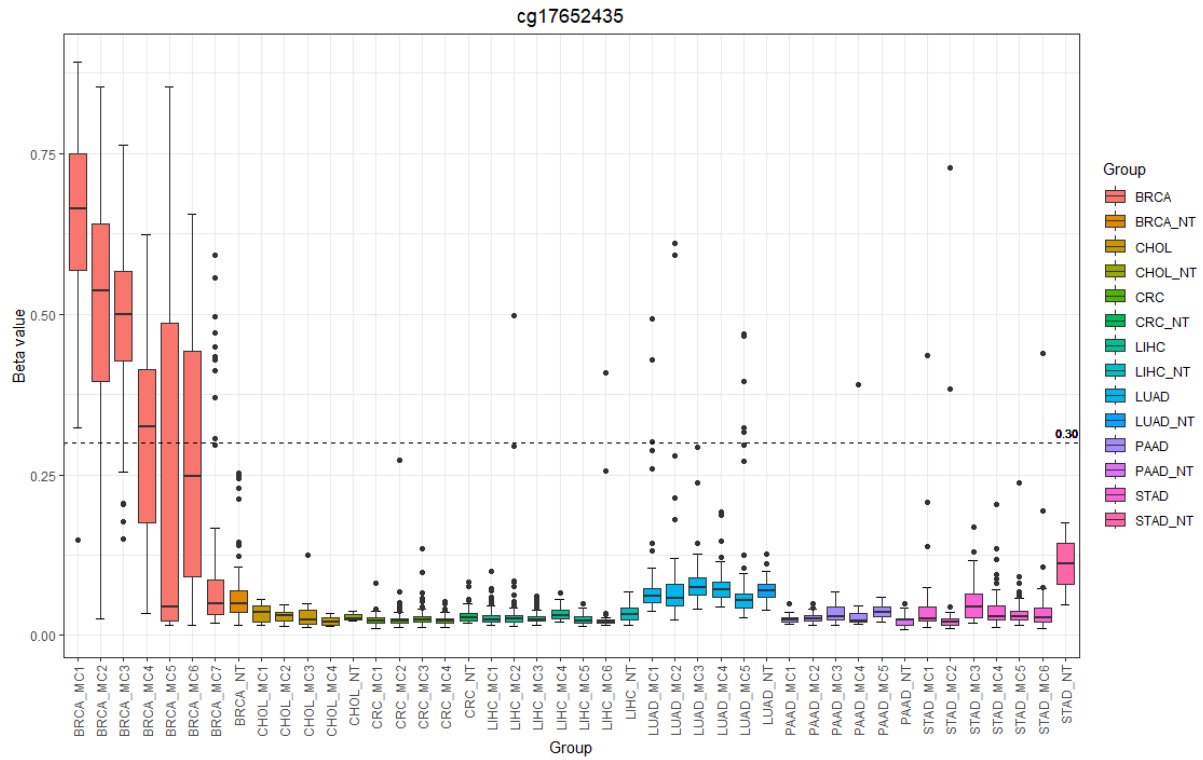
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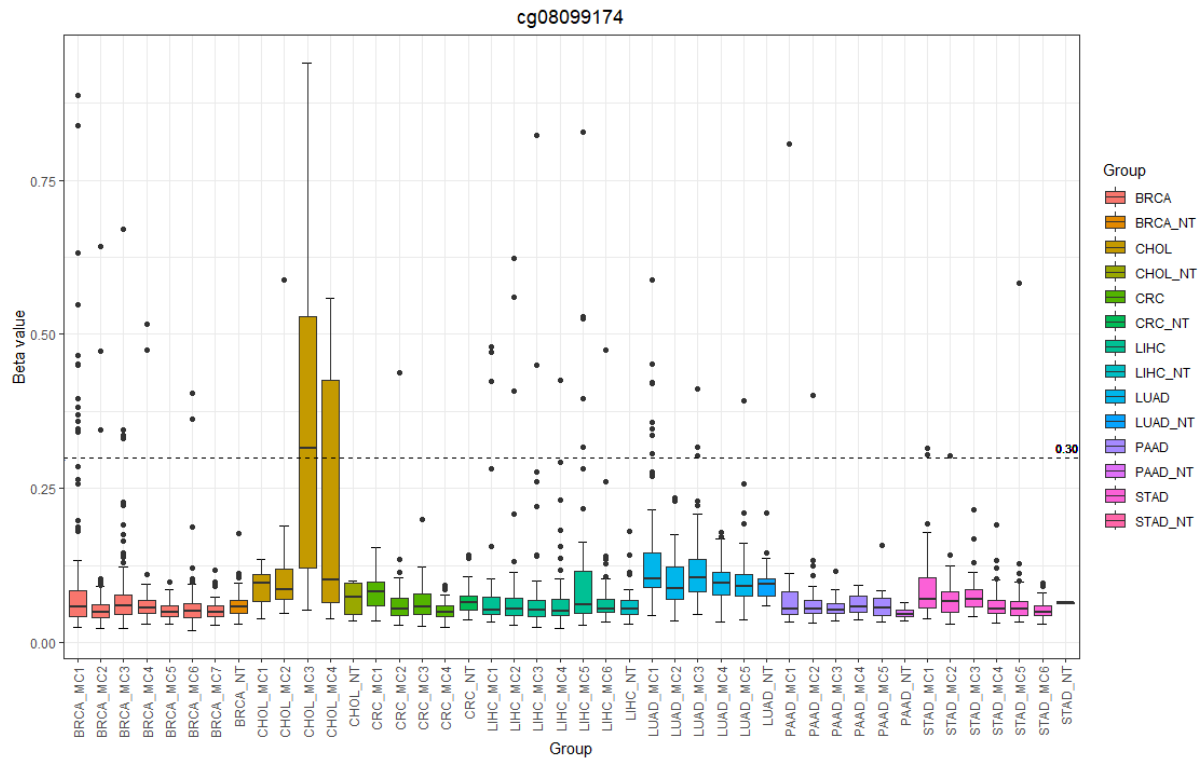
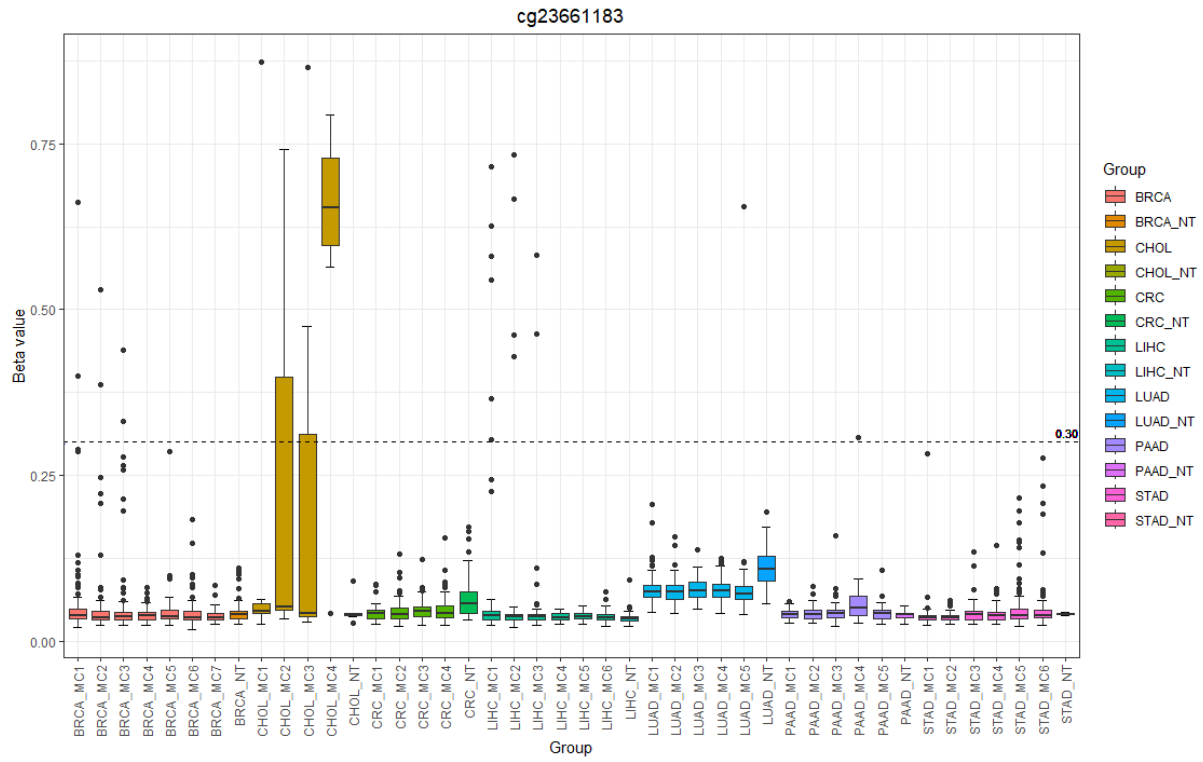


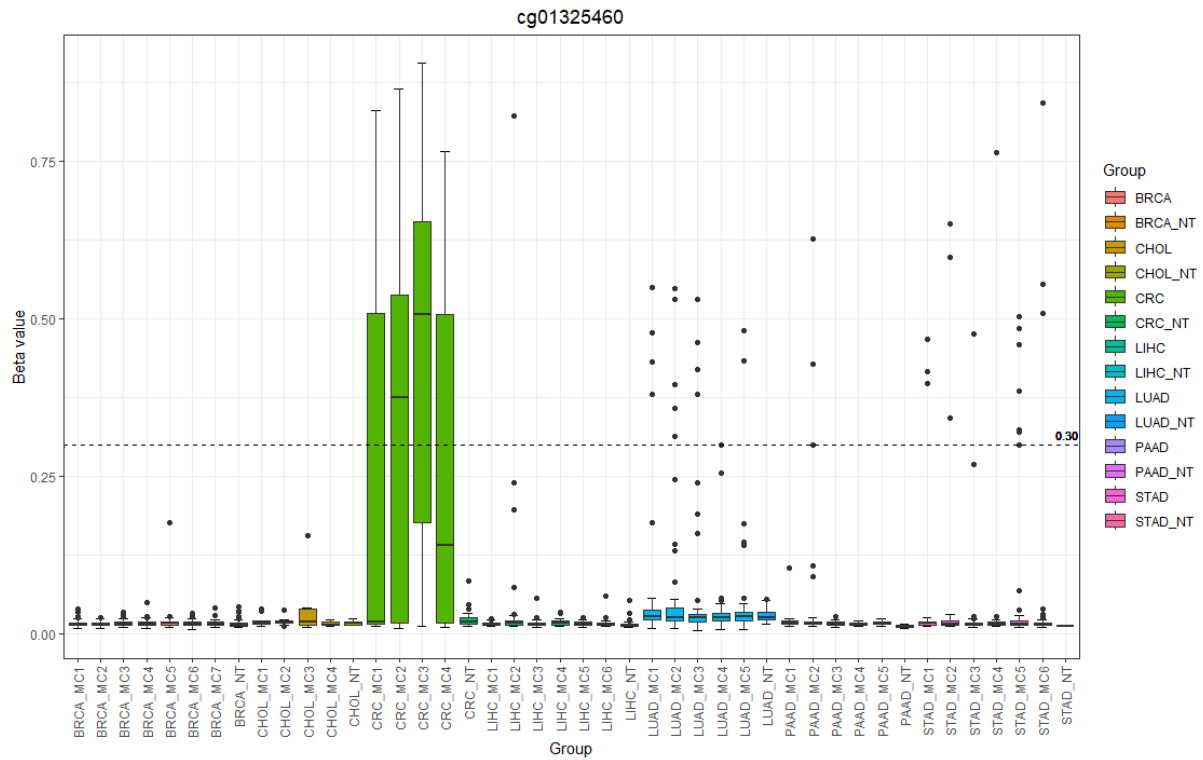
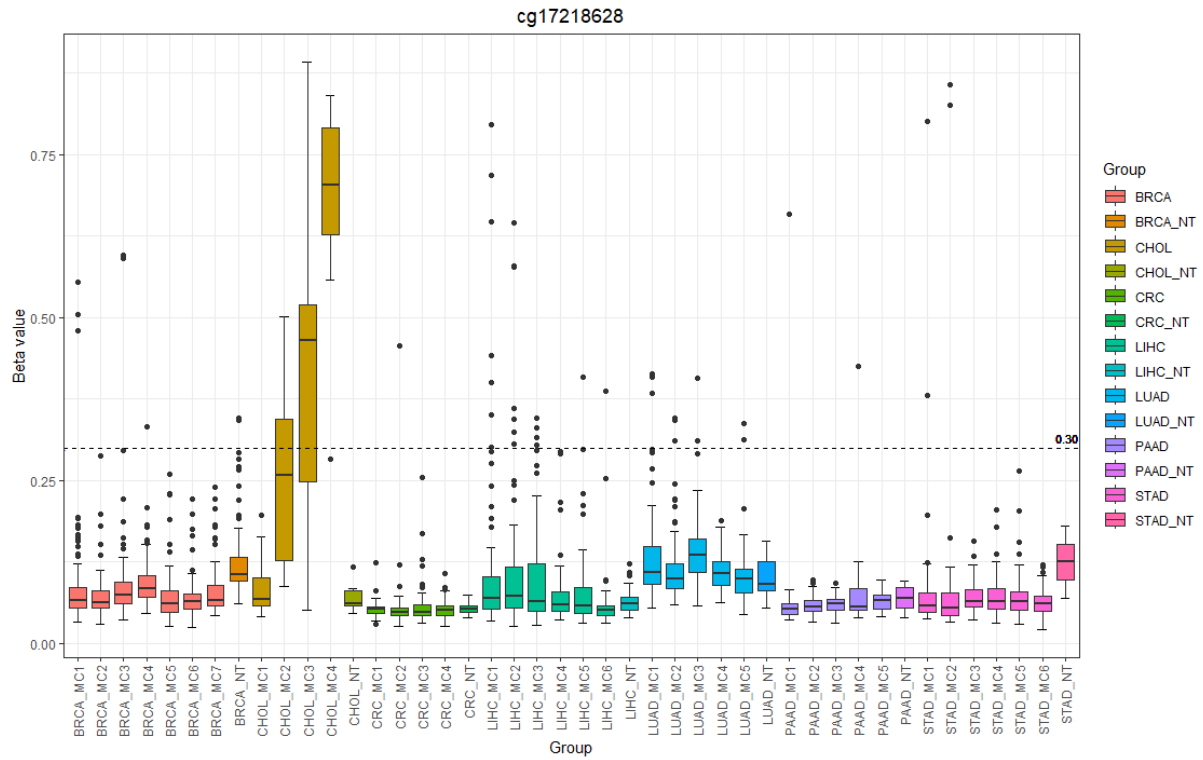
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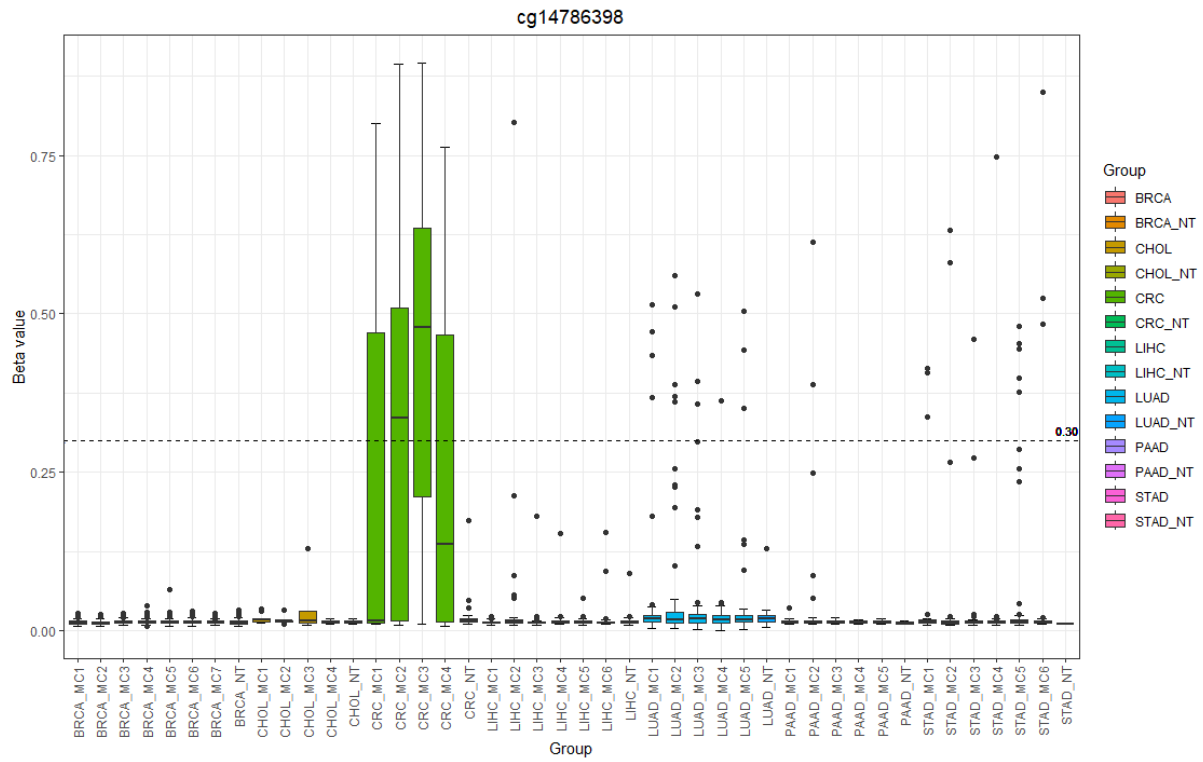
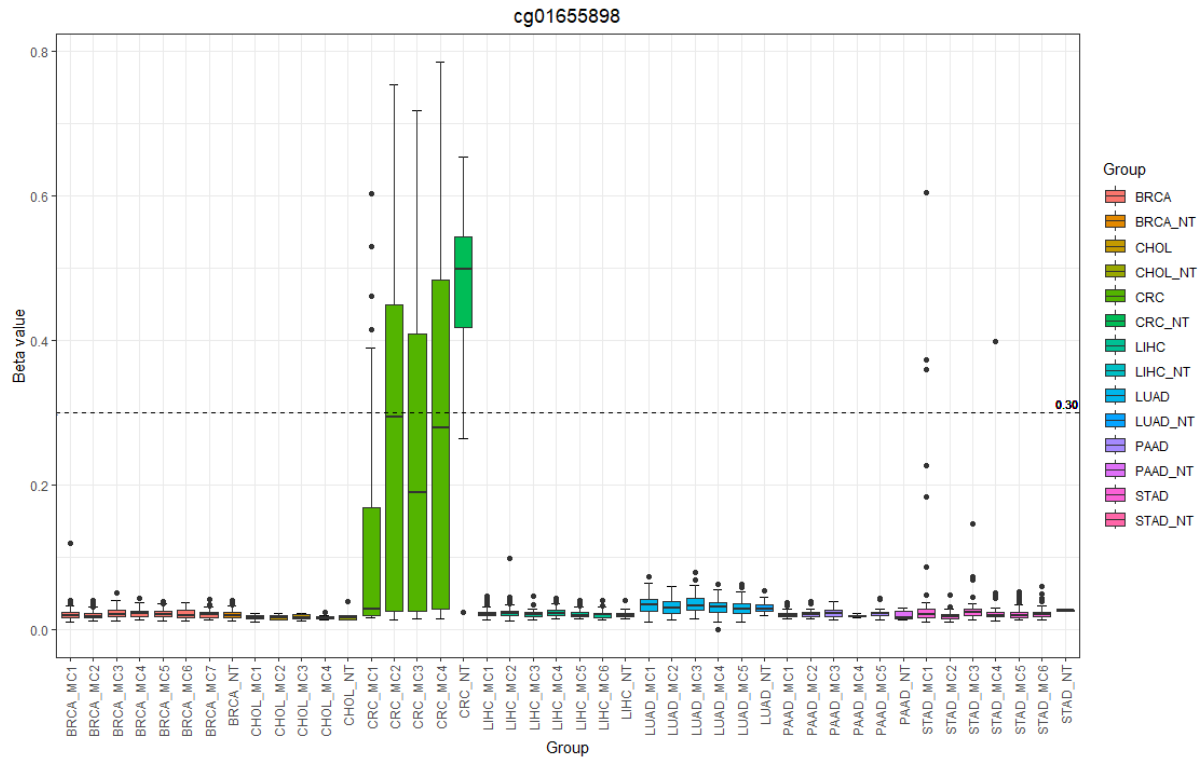


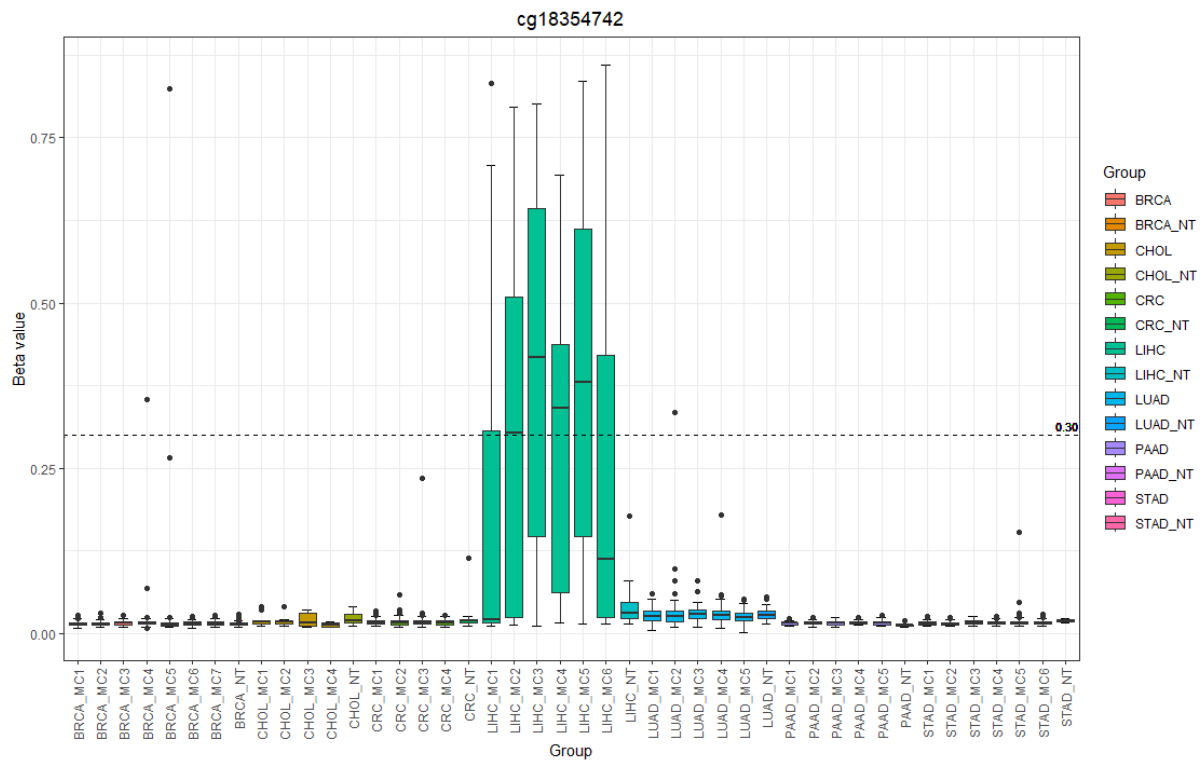
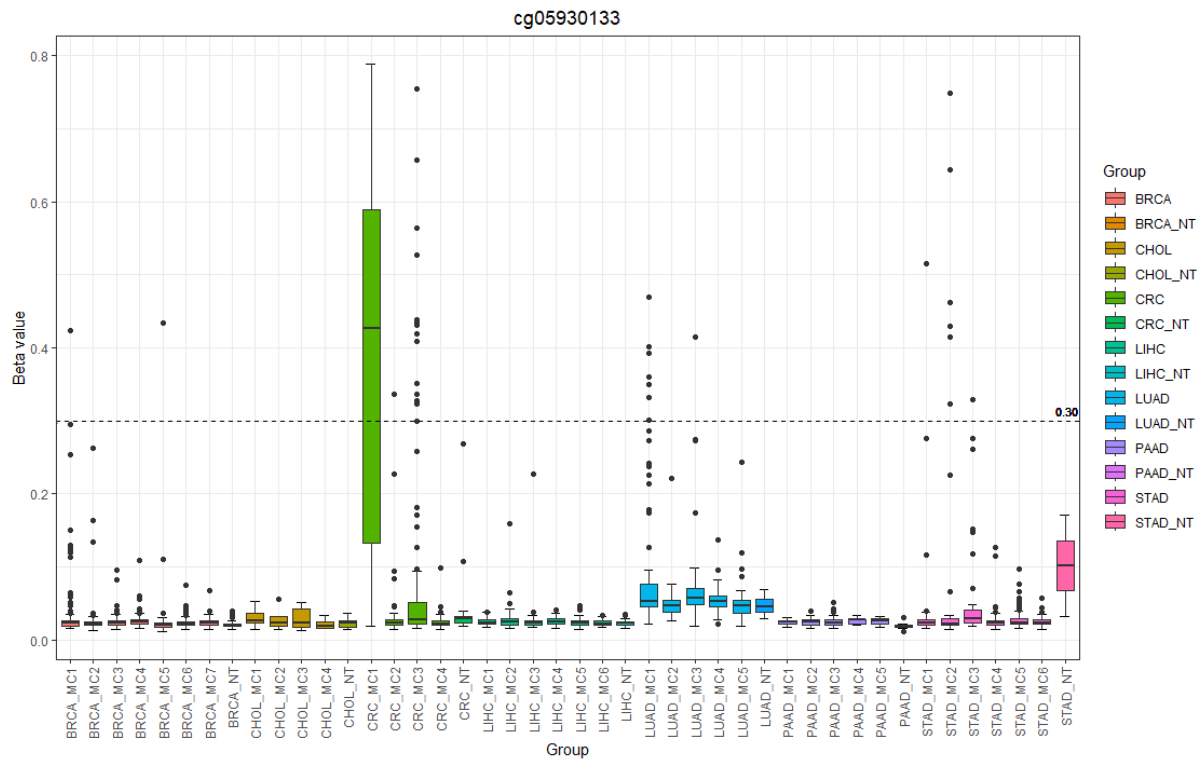


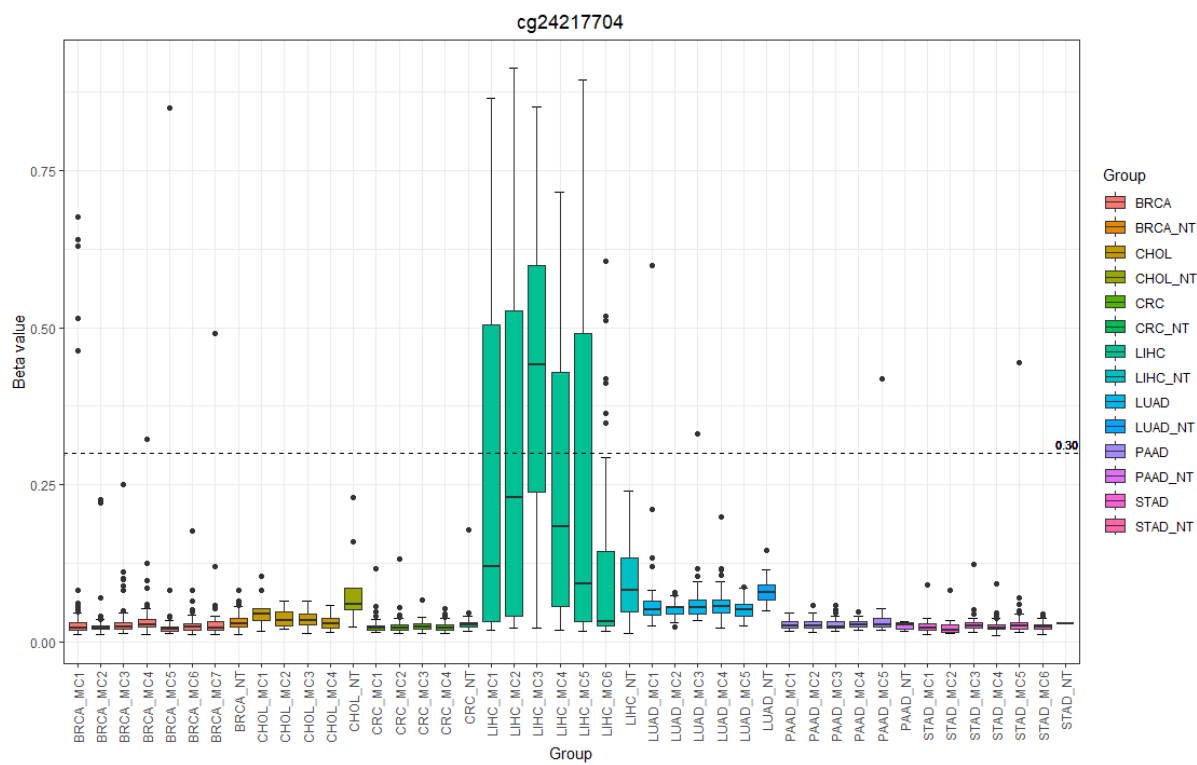
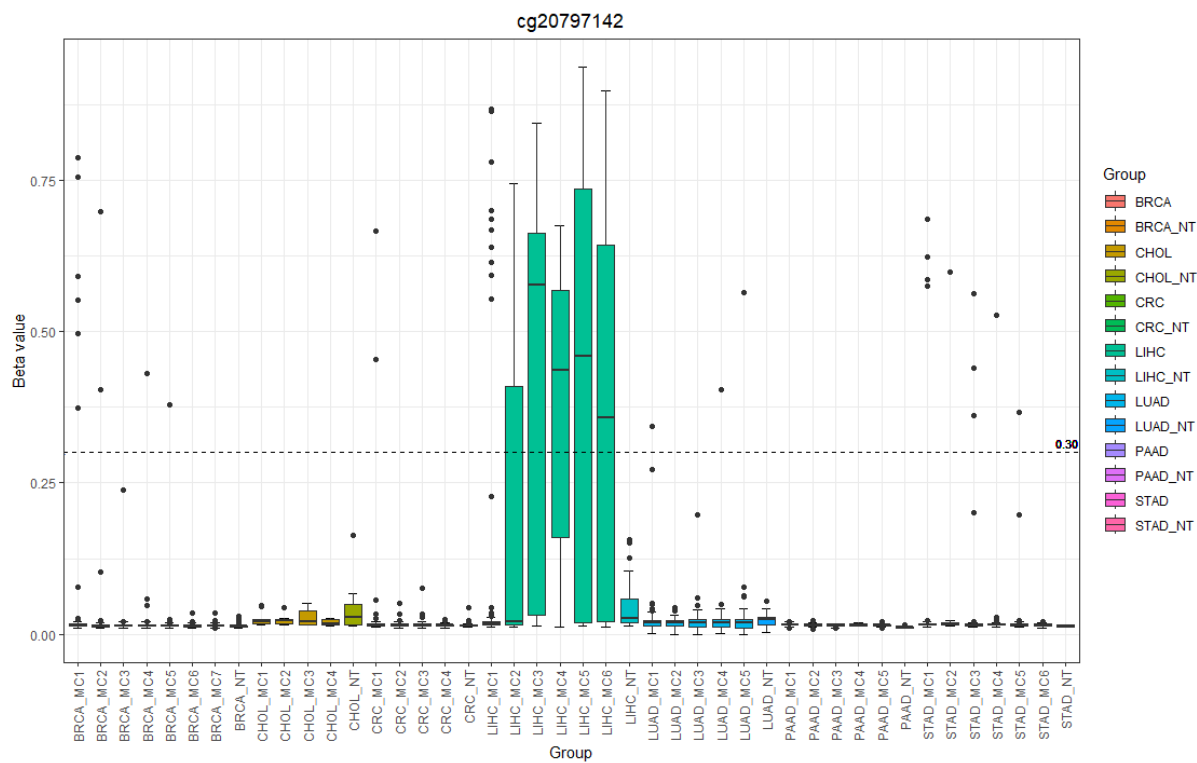


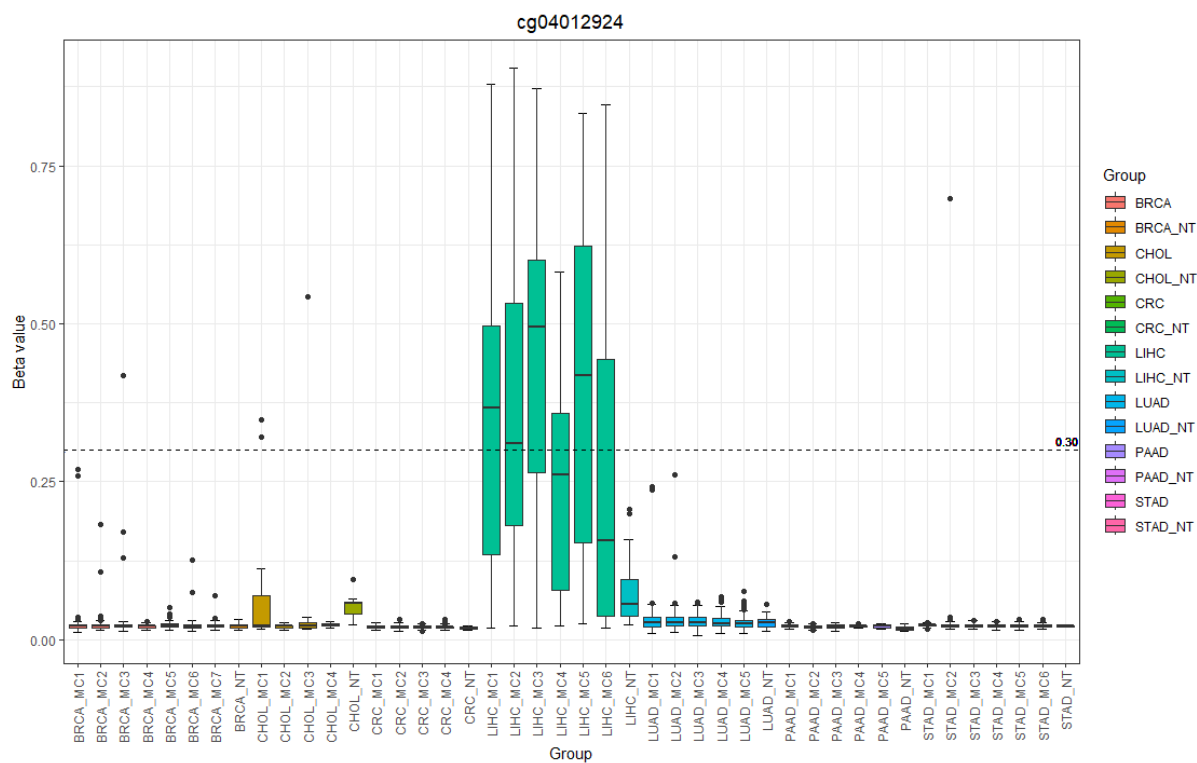
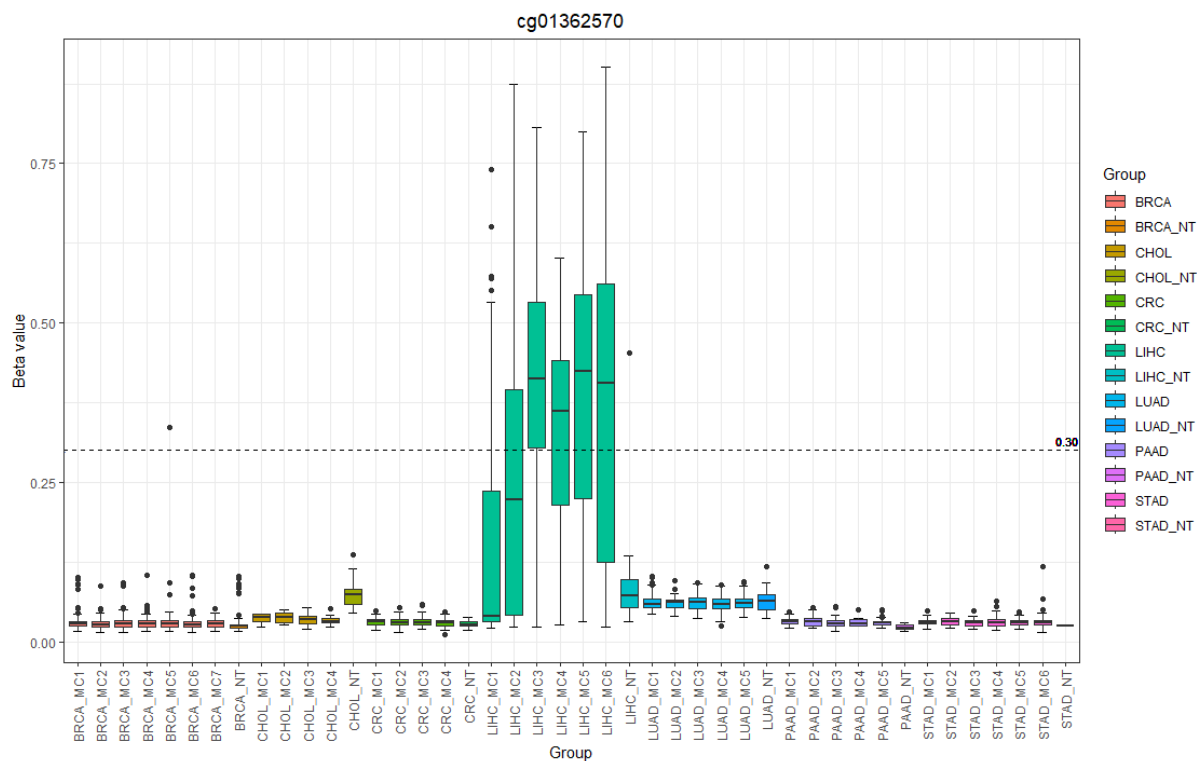


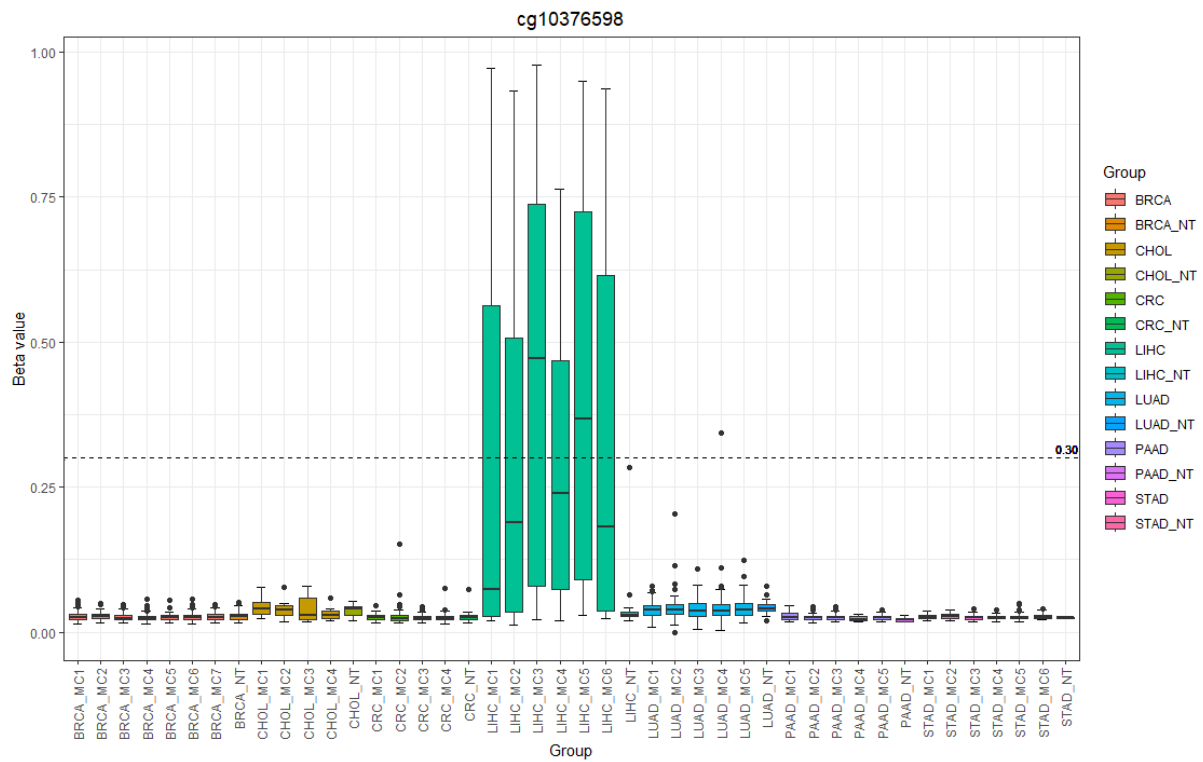
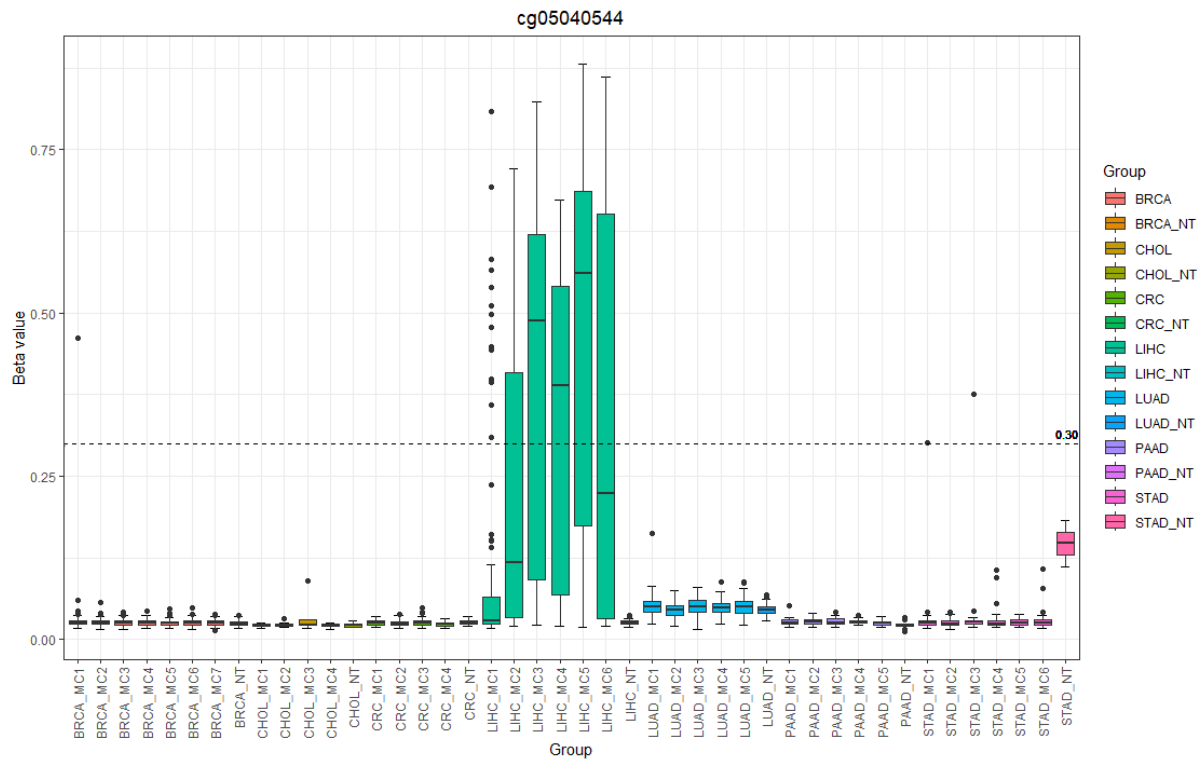


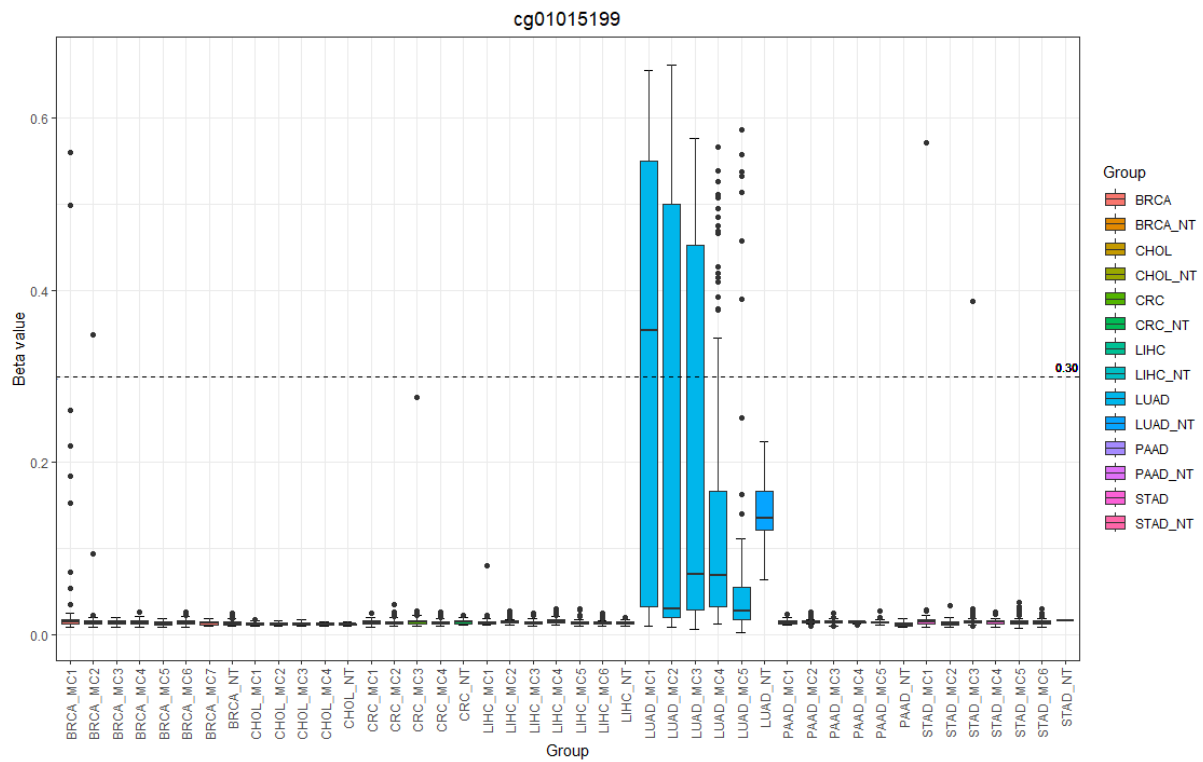
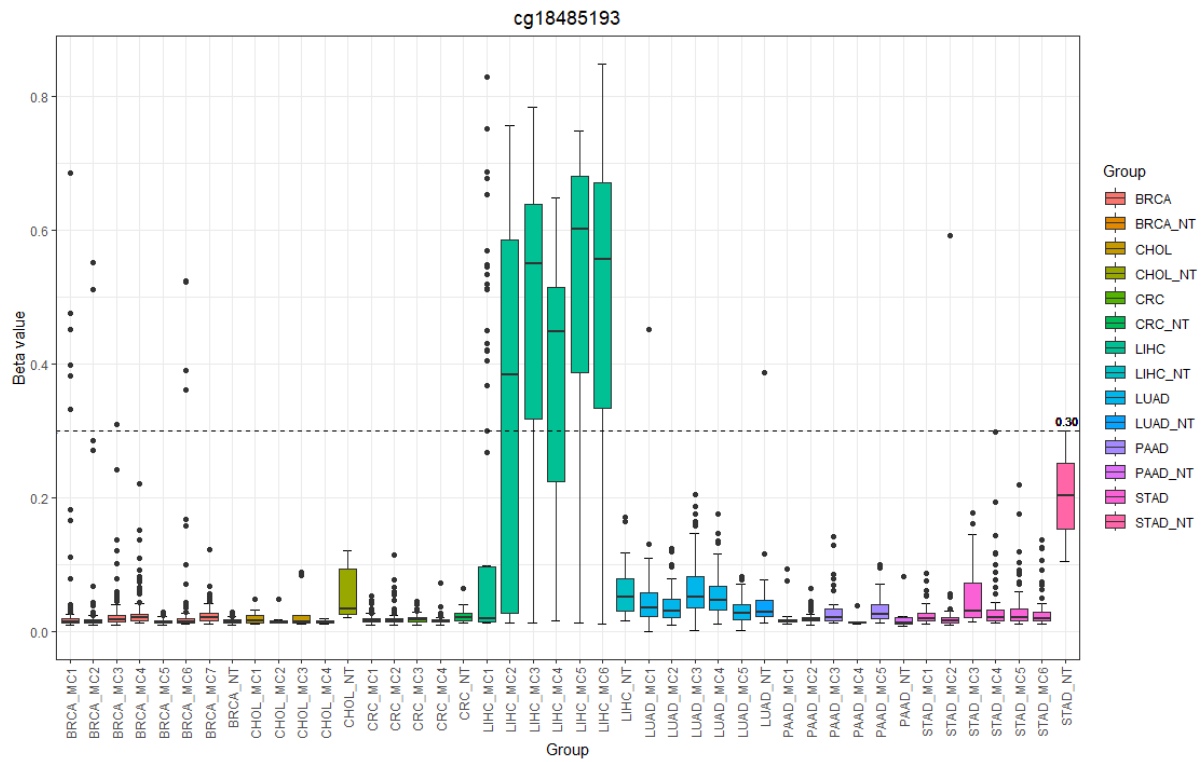


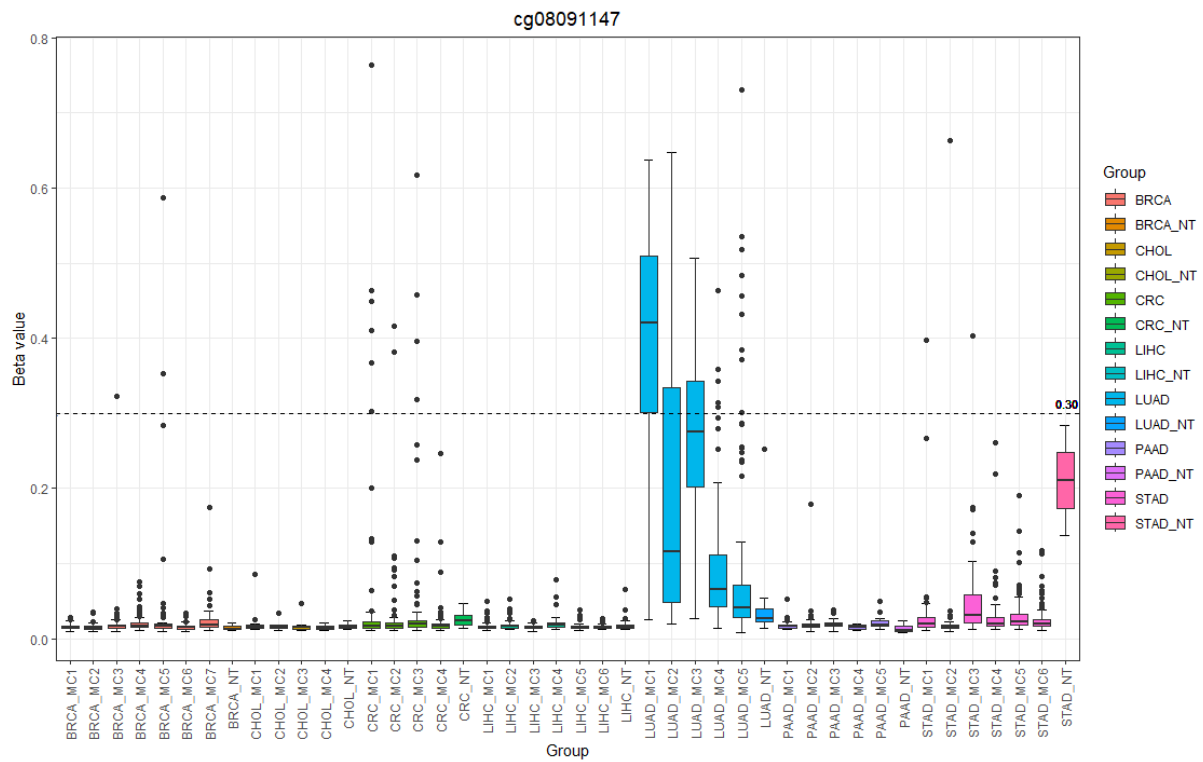
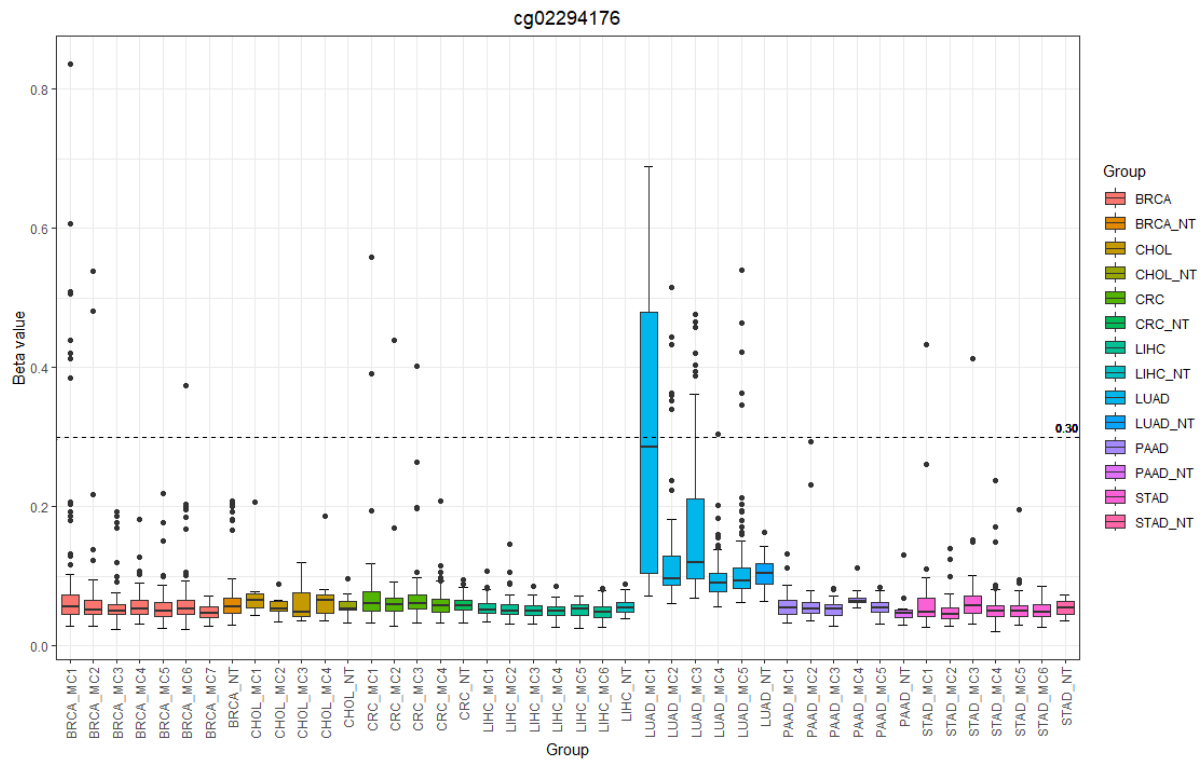


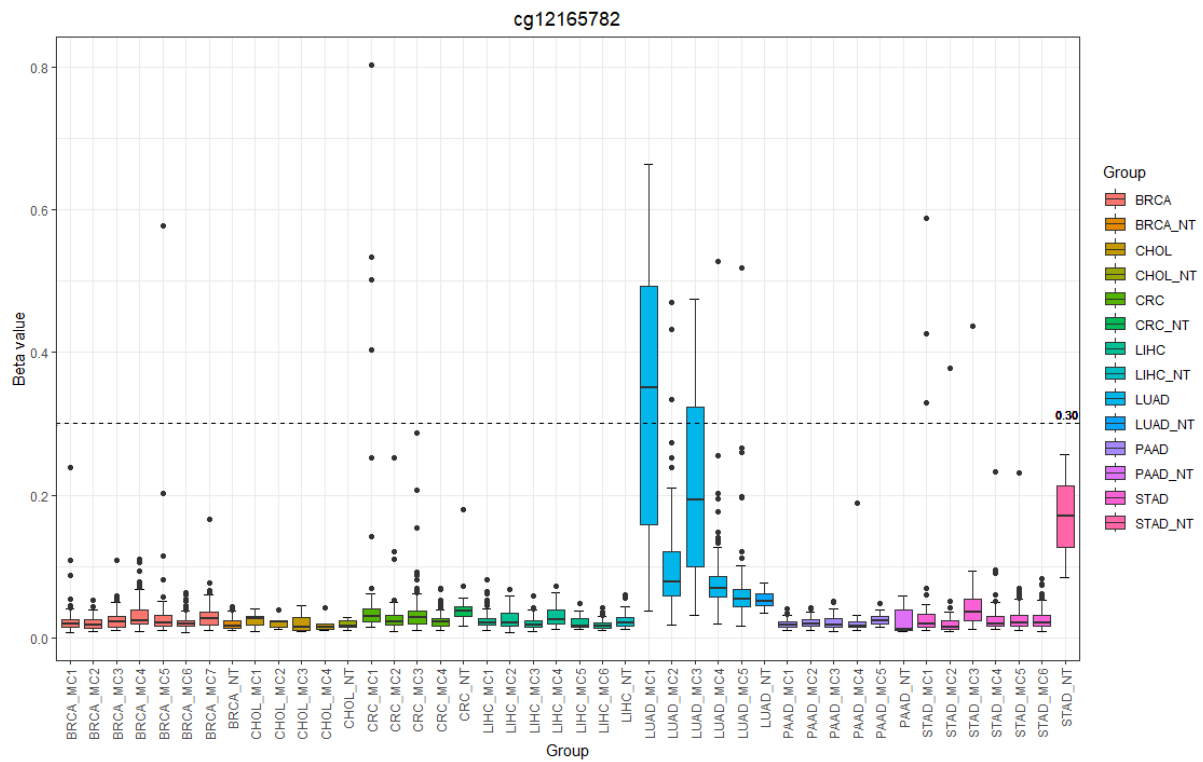
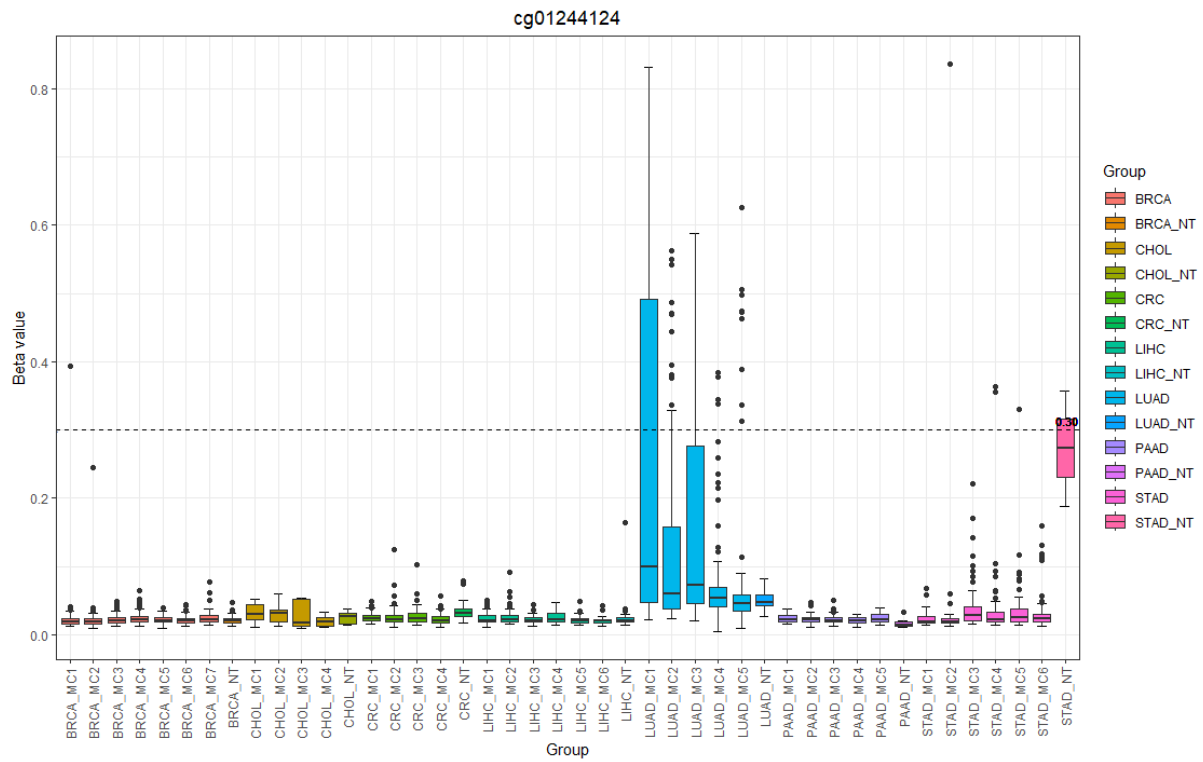


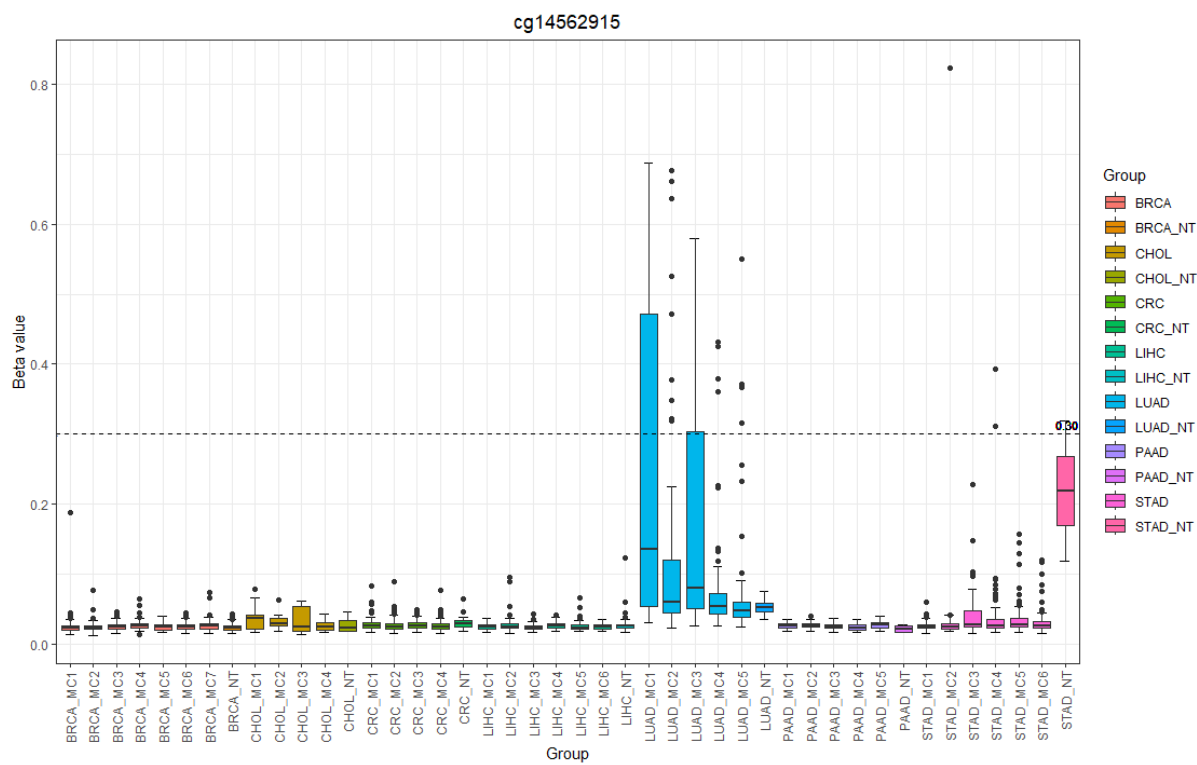
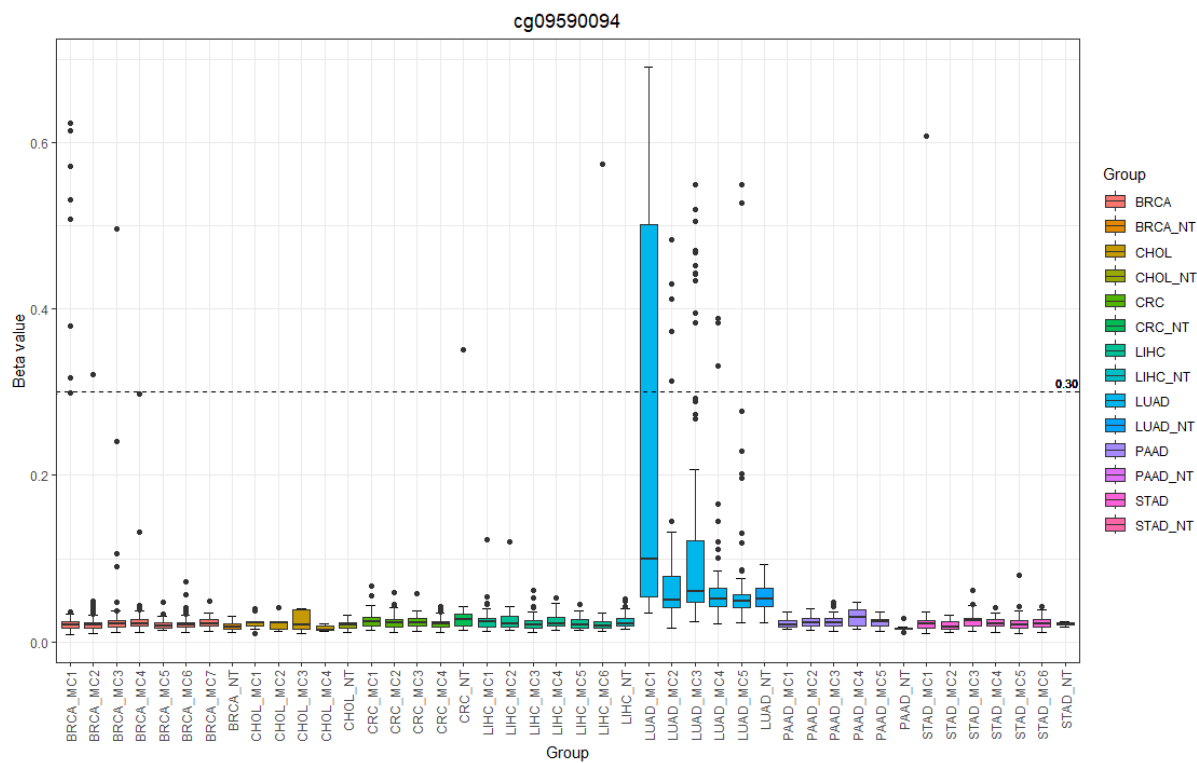


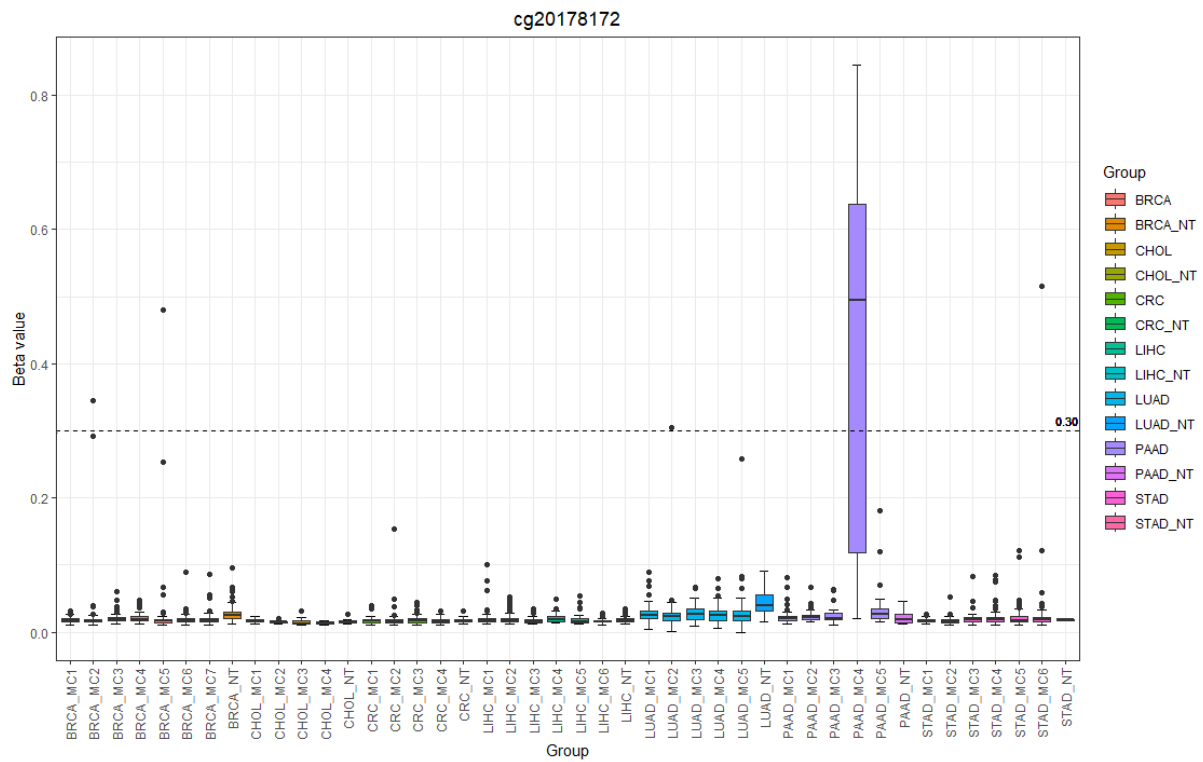
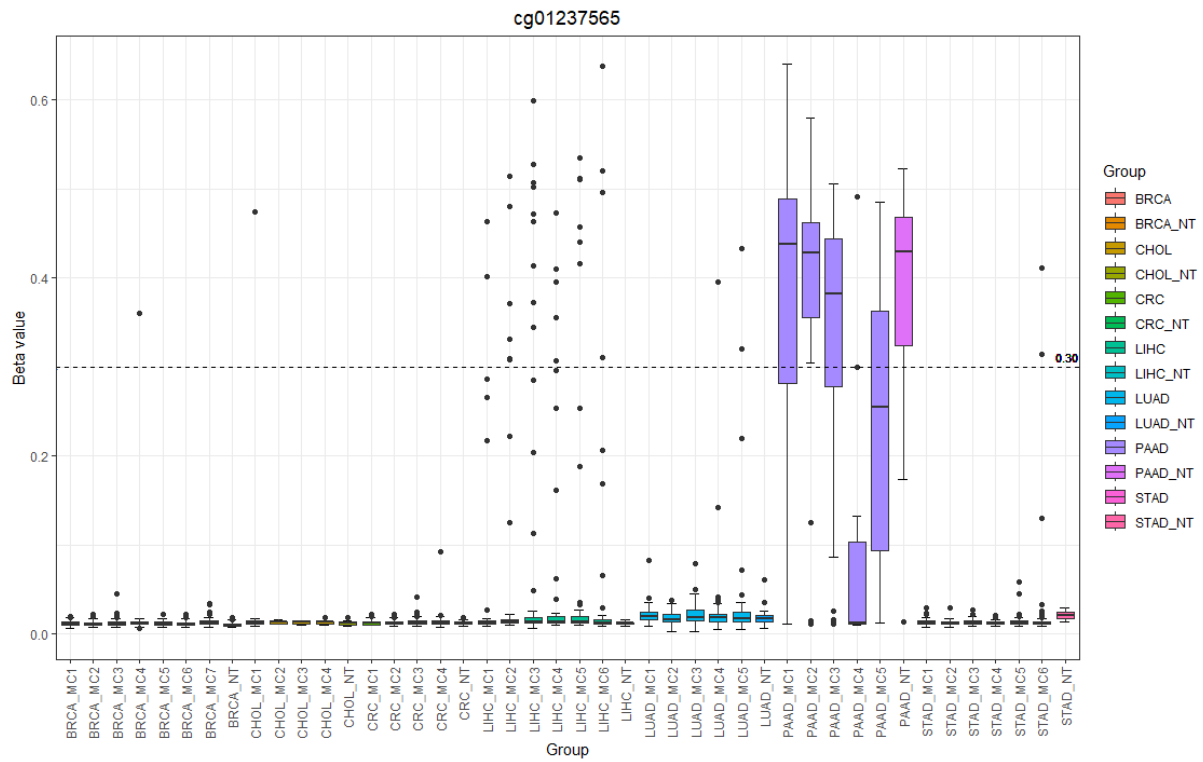


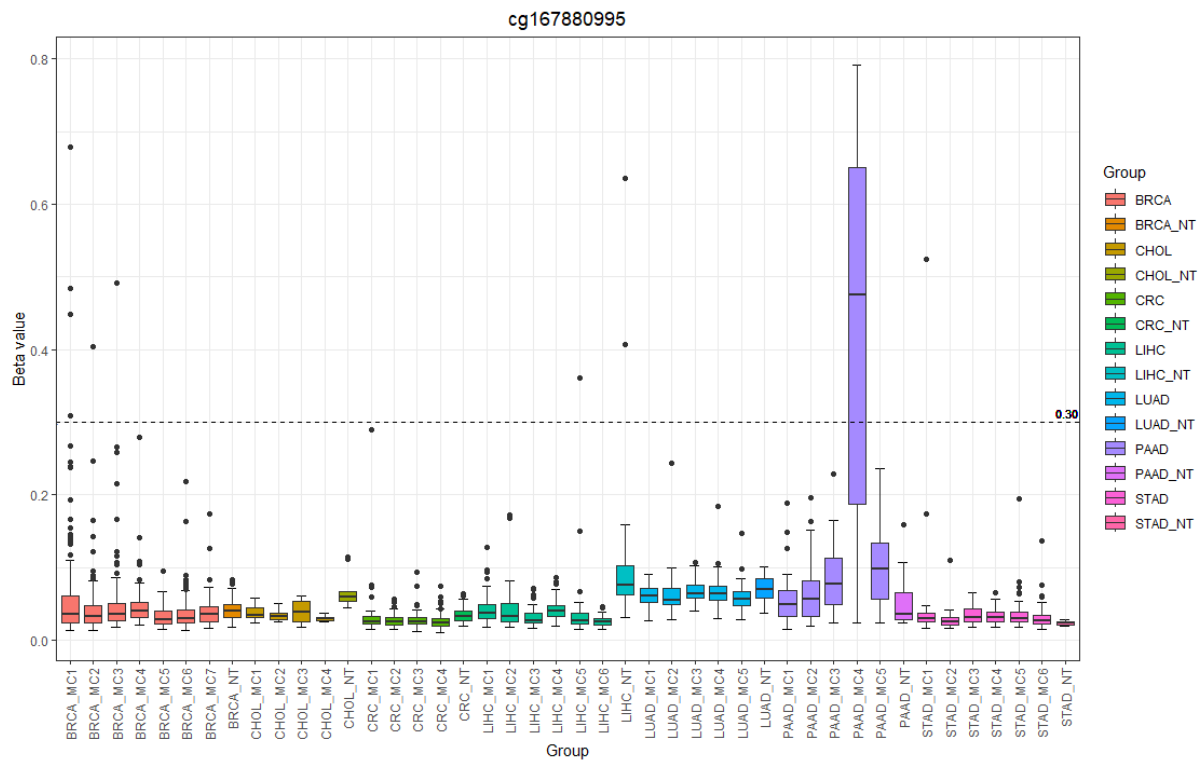
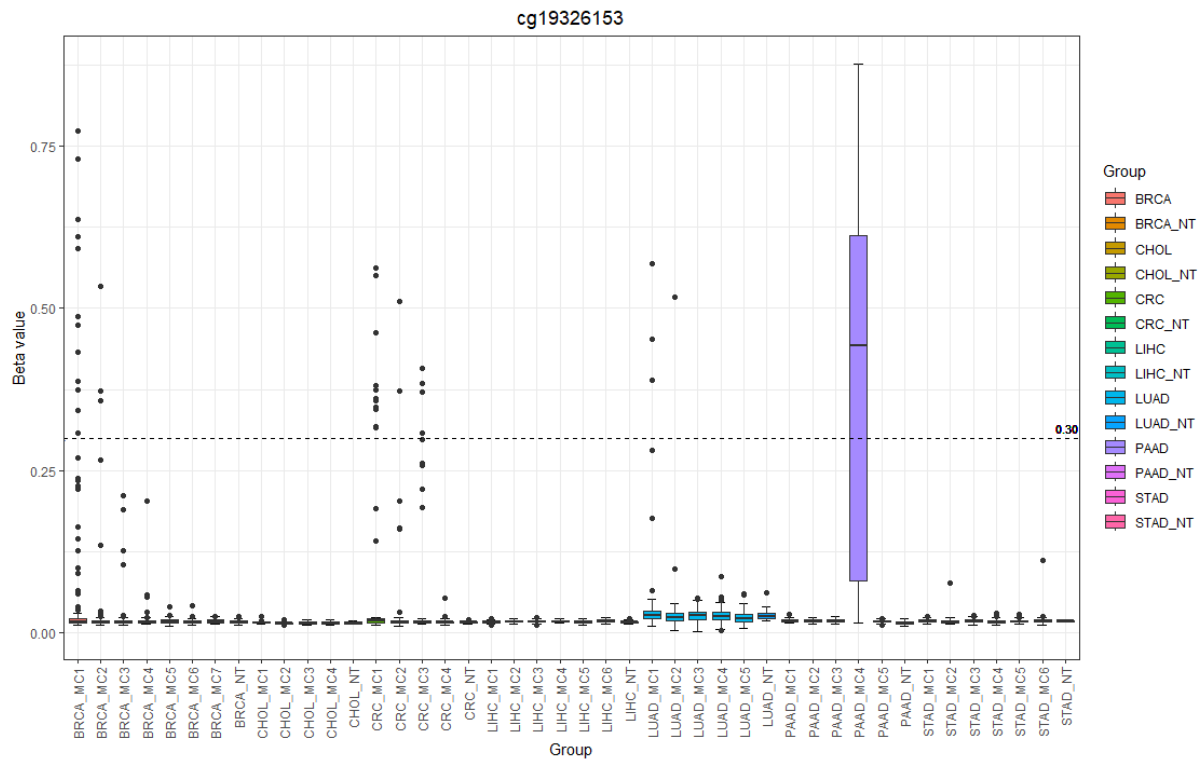


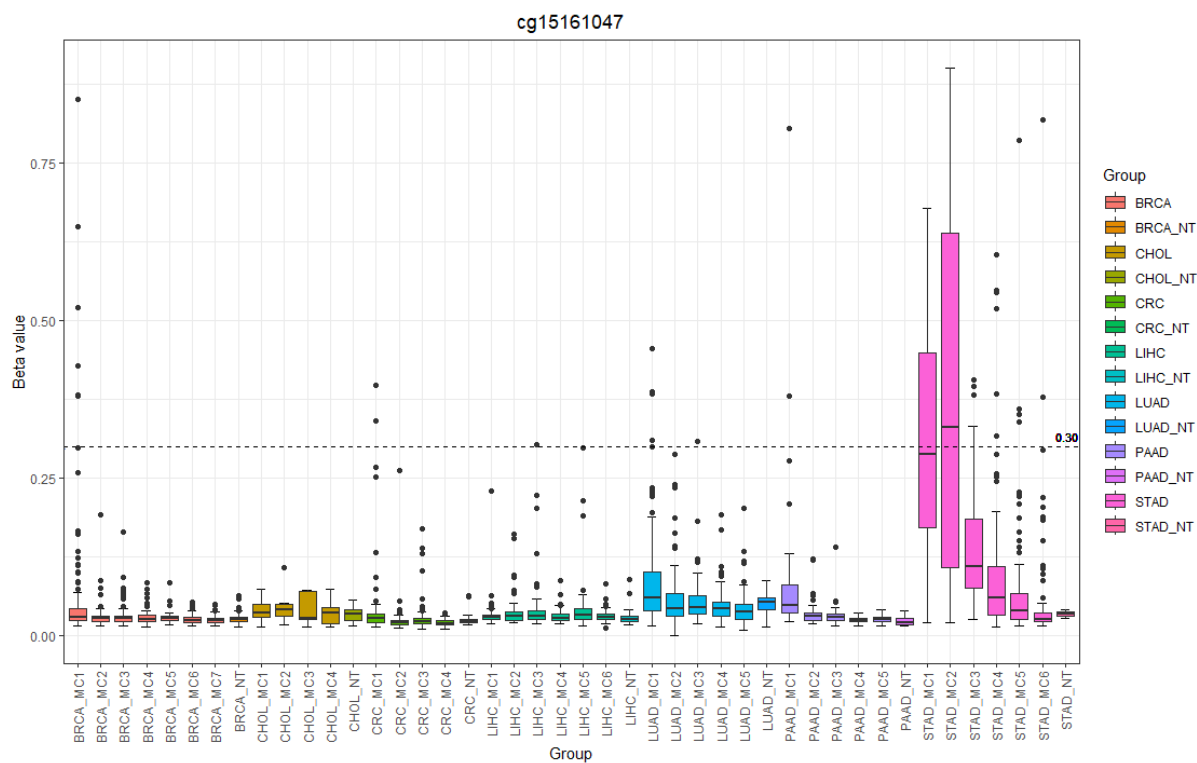
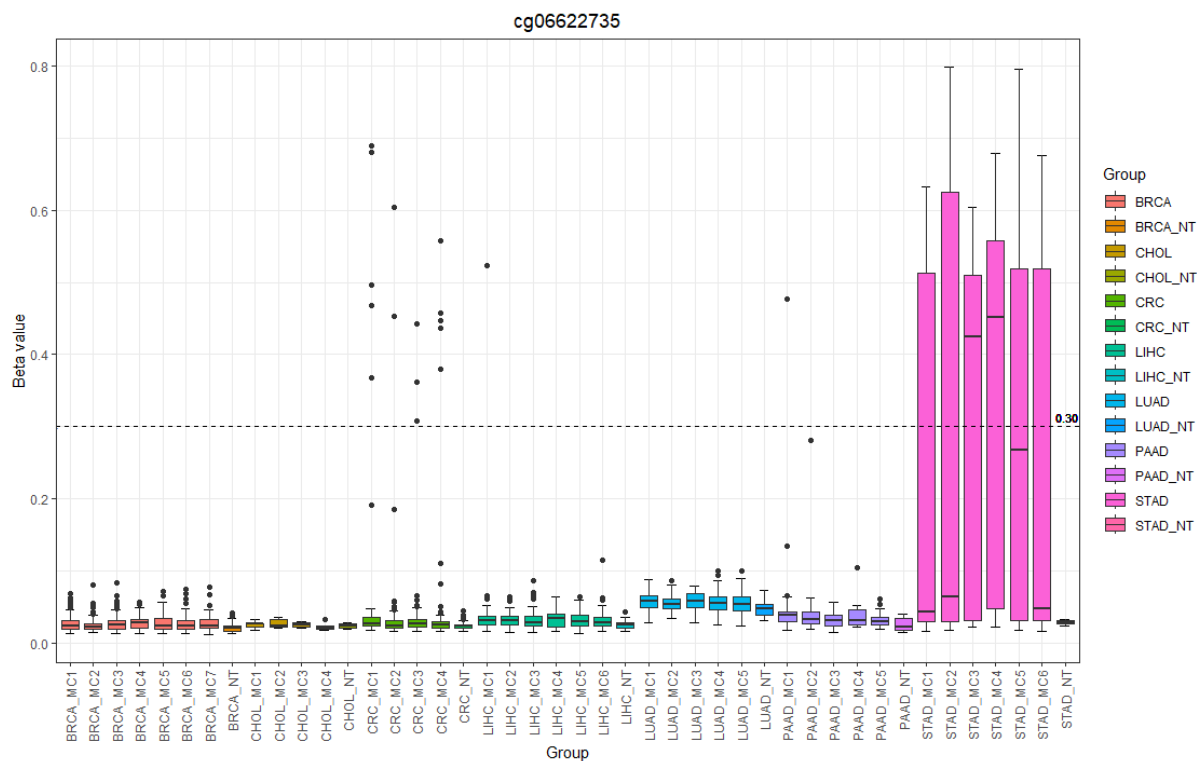


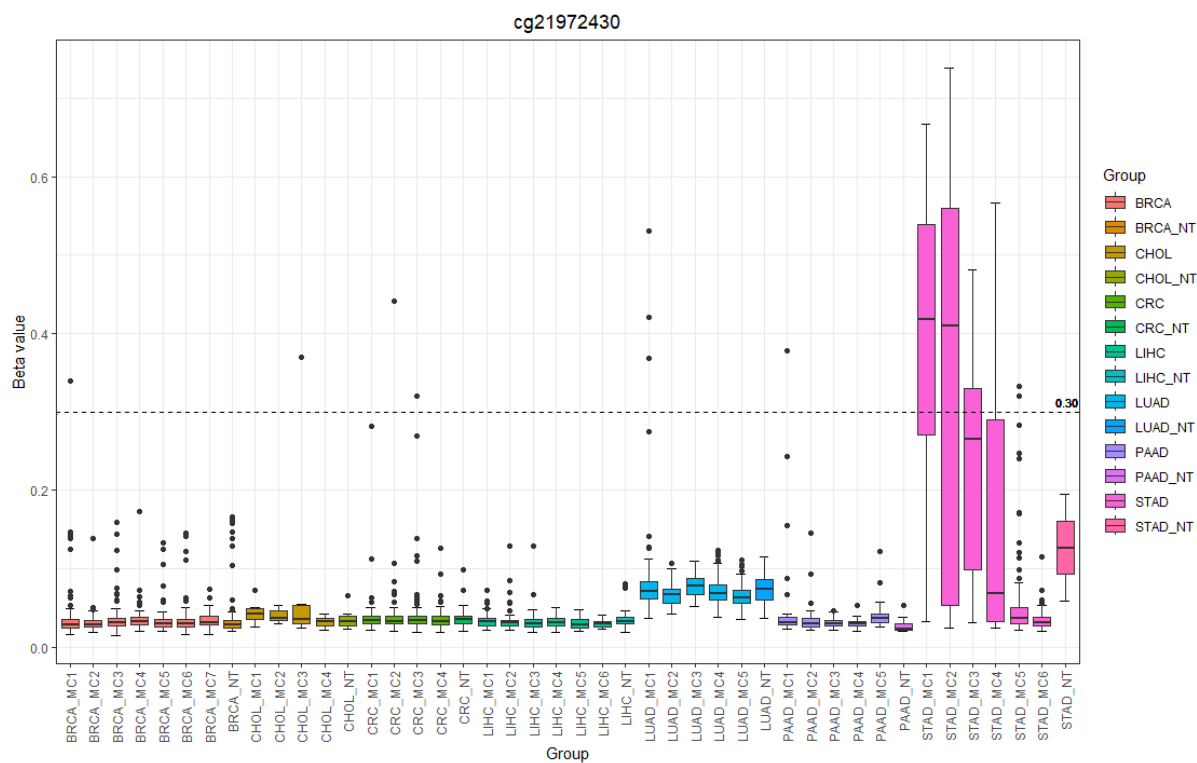
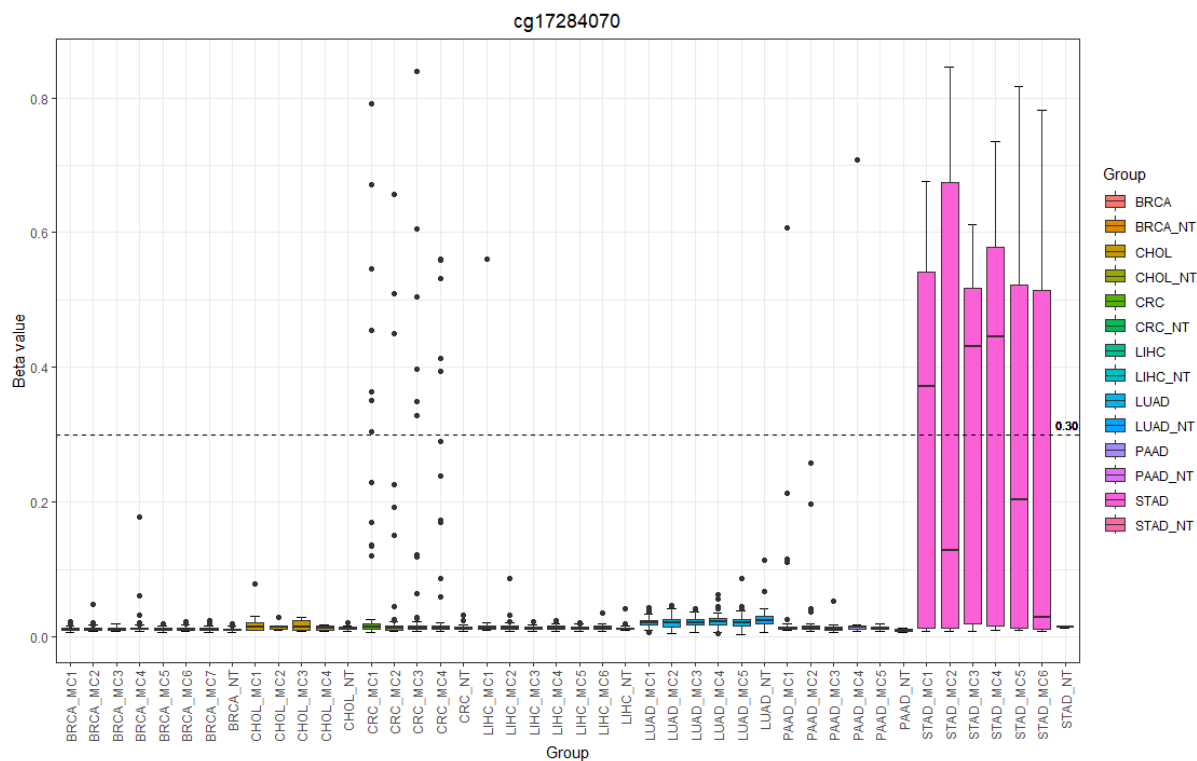


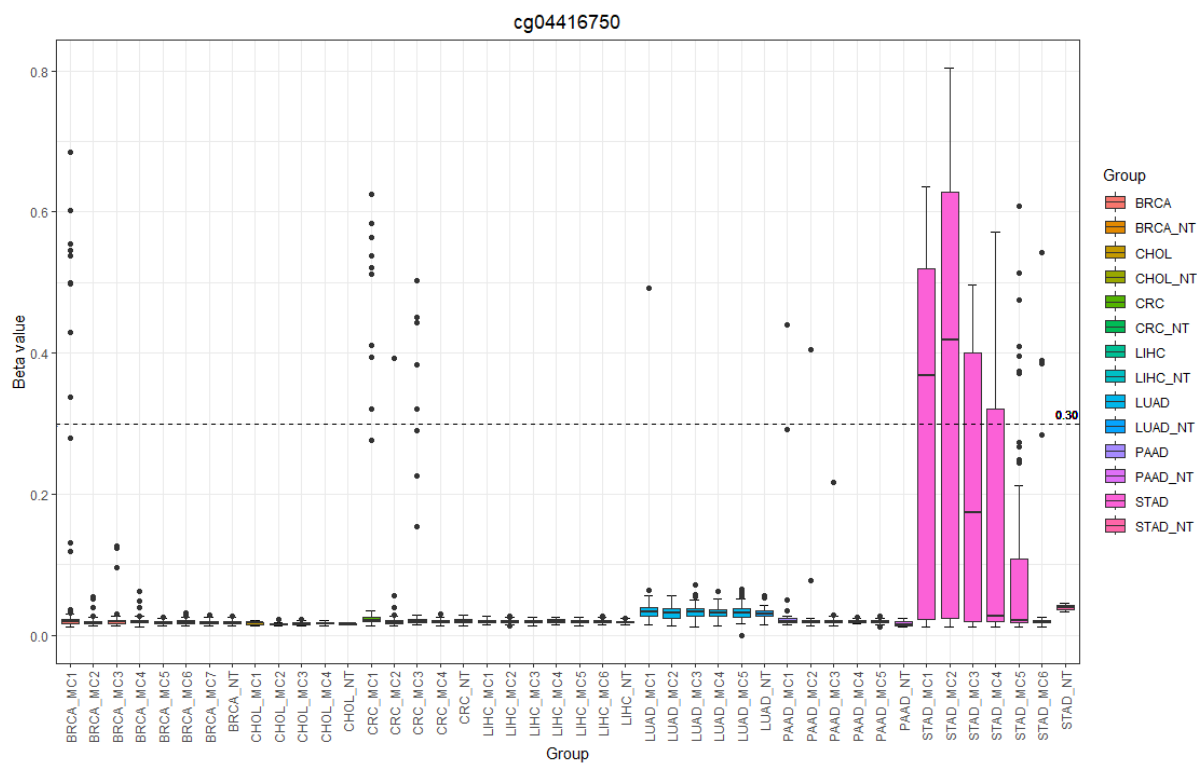
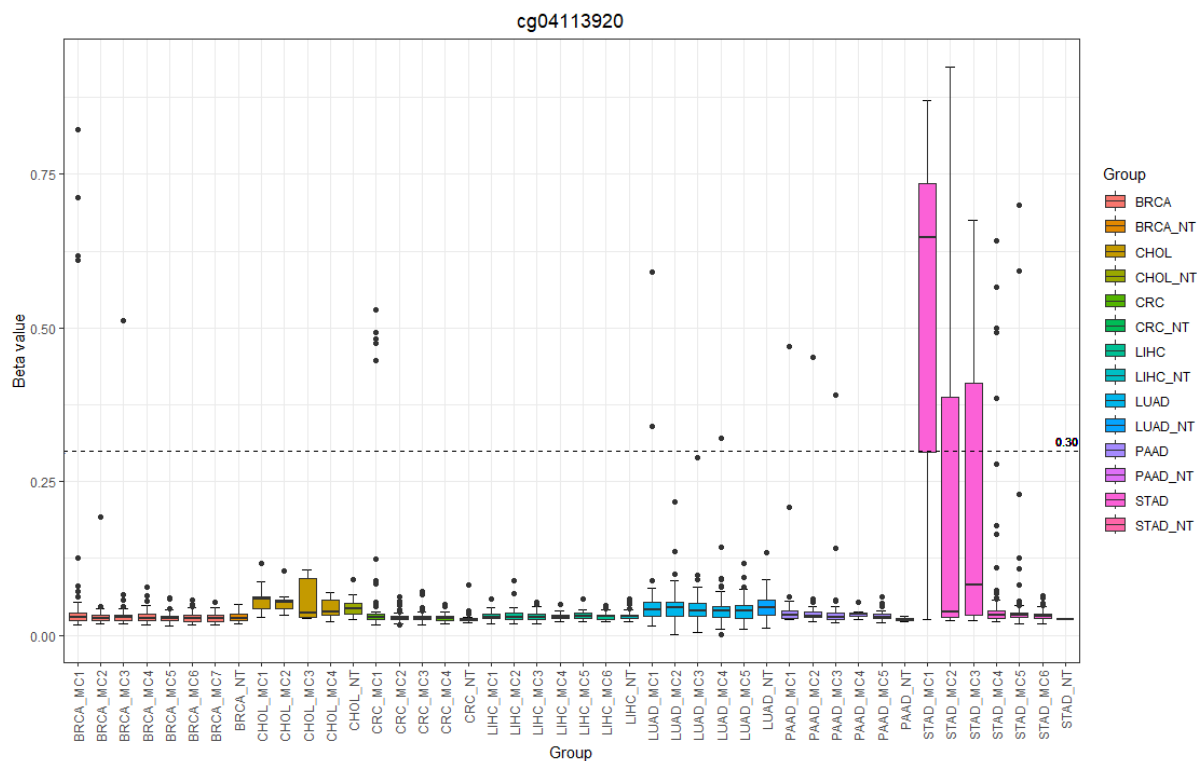


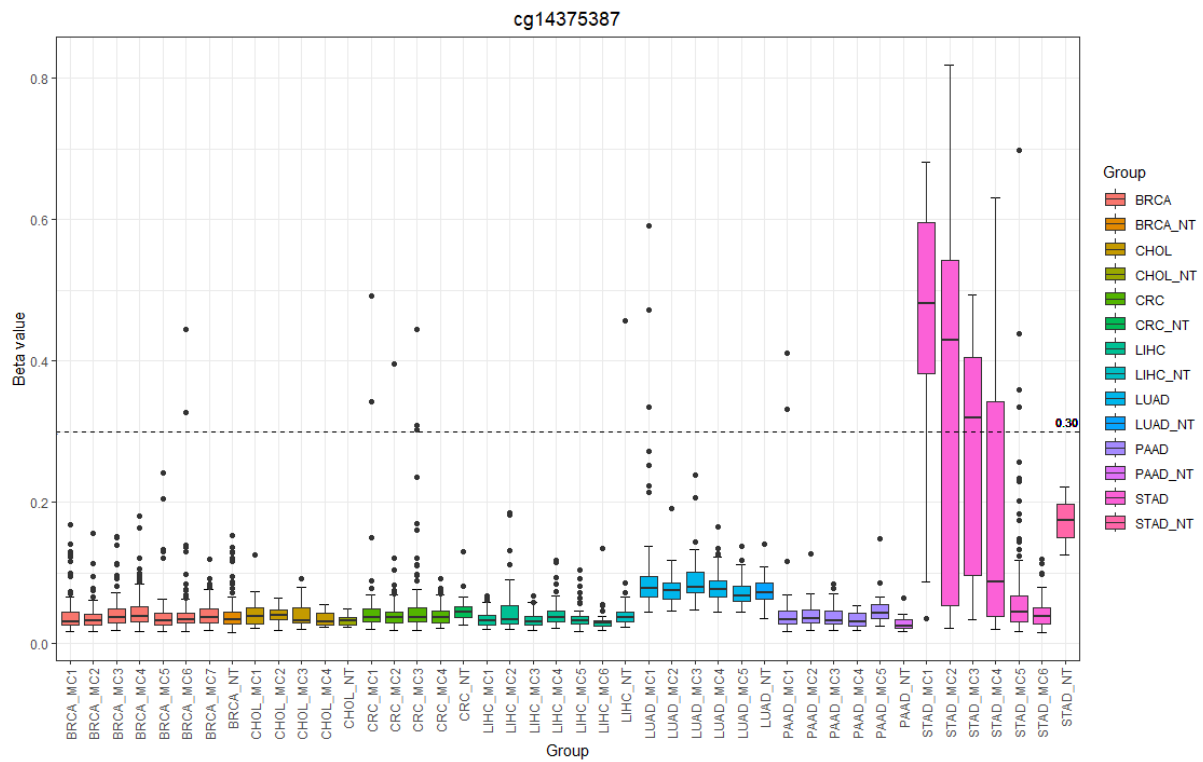
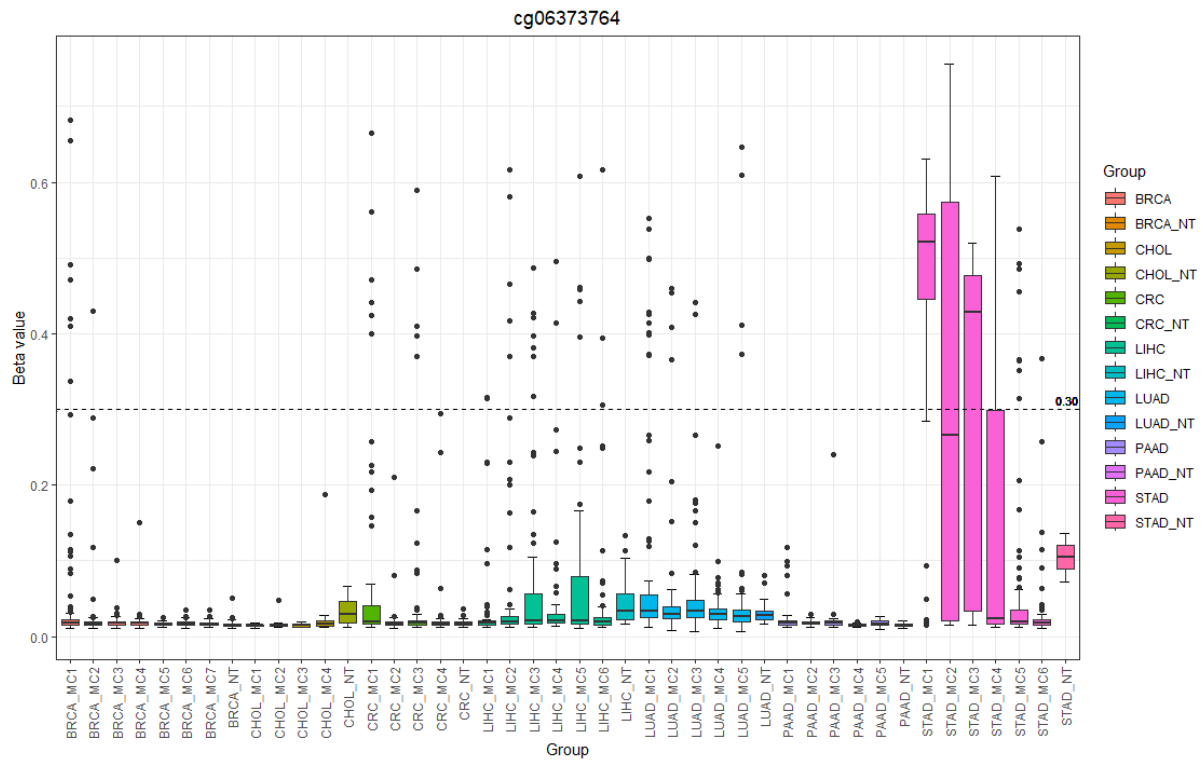












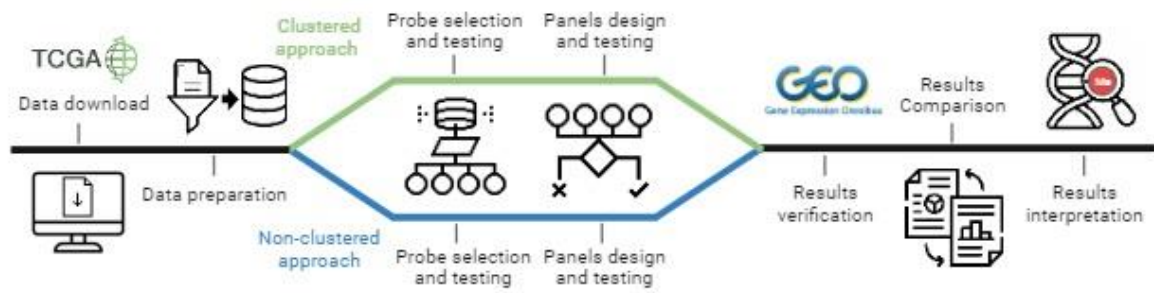


Fig. S4: Simple study workflow. After downloading and preparation, the TCGA dataset were analyzed using two different approaches: a non-clustered approach (no clustering was performed) and a clustered approach (unsupervised clustering was performed within each project). Separate results were obtained for each of these approaches (probe candidates were selected and tested, followed by a panel design and testing for each cancer type). The results were verified by an independent GEO dataset. At the end, results from both approaches were compared and interpreted.

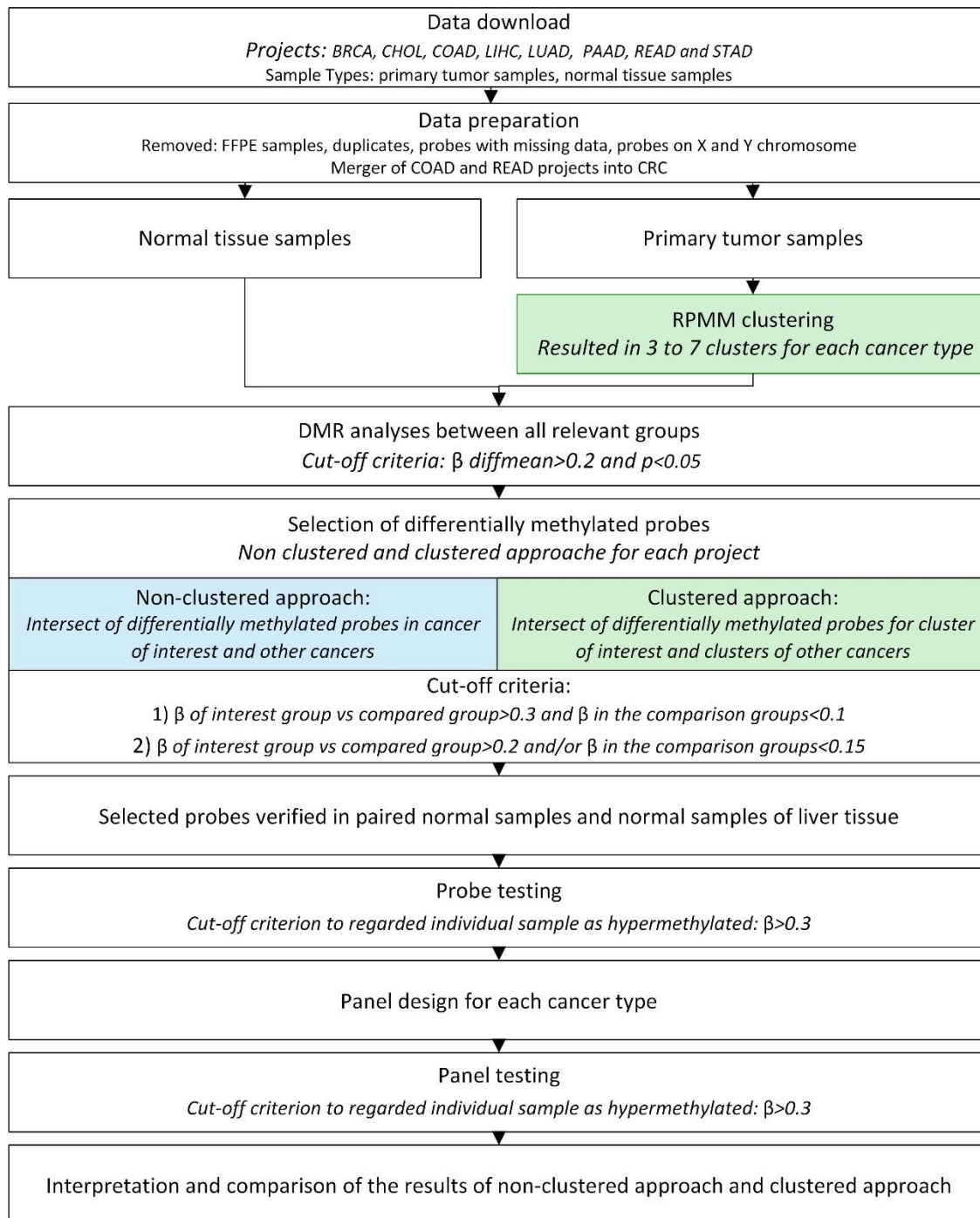


Fig. S5: Detailed workflow showing the probe selection and panel design steps for the non-clustered and clustered approaches. After data download, data preparation and clustering of primary tumor samples in a clustered approach, differentially methylated regions (DMR) analyses were performed. Candidate probes that were differentially methylated in different cancer types were selected and tested in normal tissue samples. After testing the candidate probes, panels were designed and tested for each cancer type. The blue colored steps were used only for the non-clustered approach and the green colored steps were used only for the clustered approach. The white colored steps were used in both approaches.