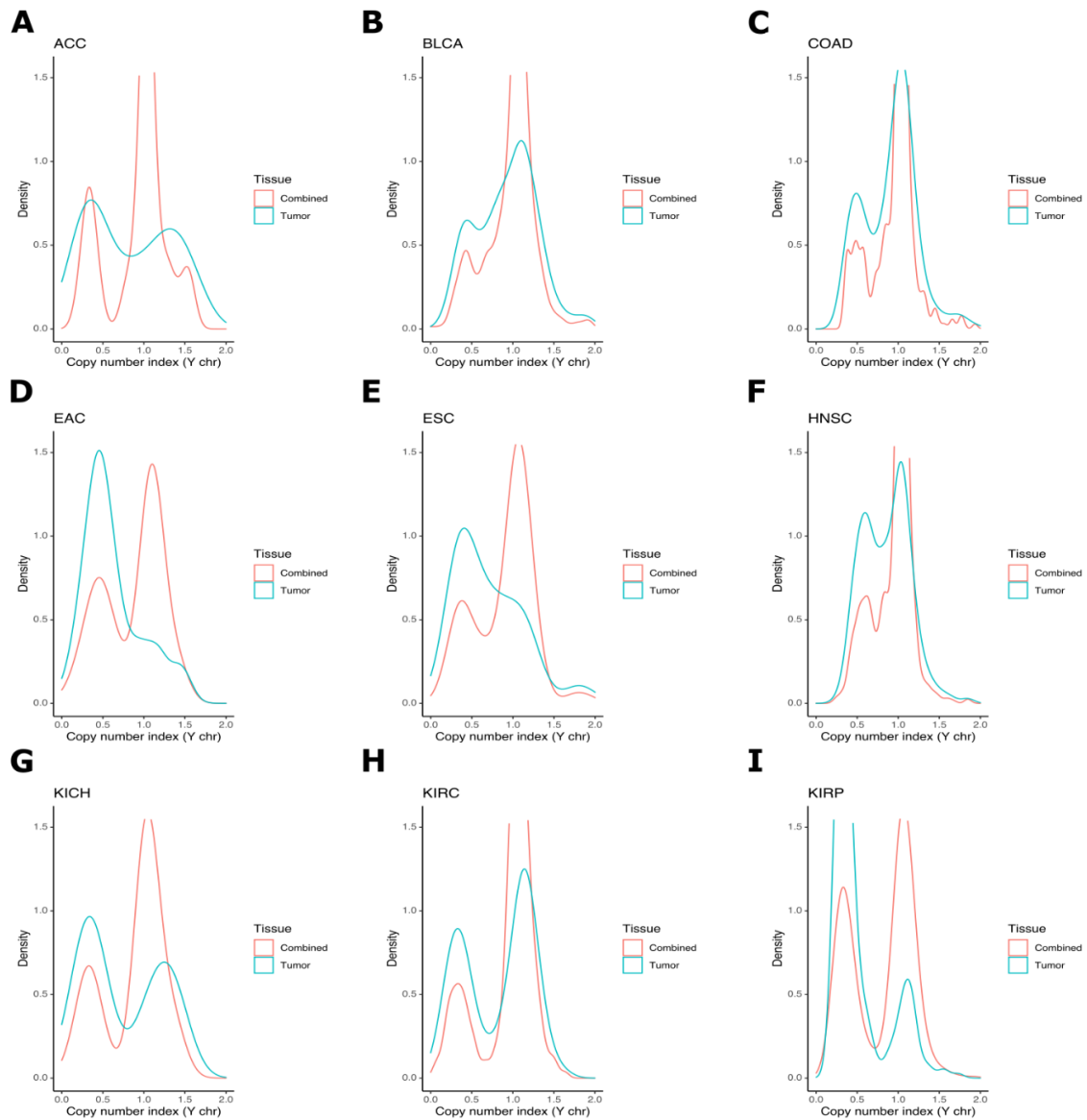
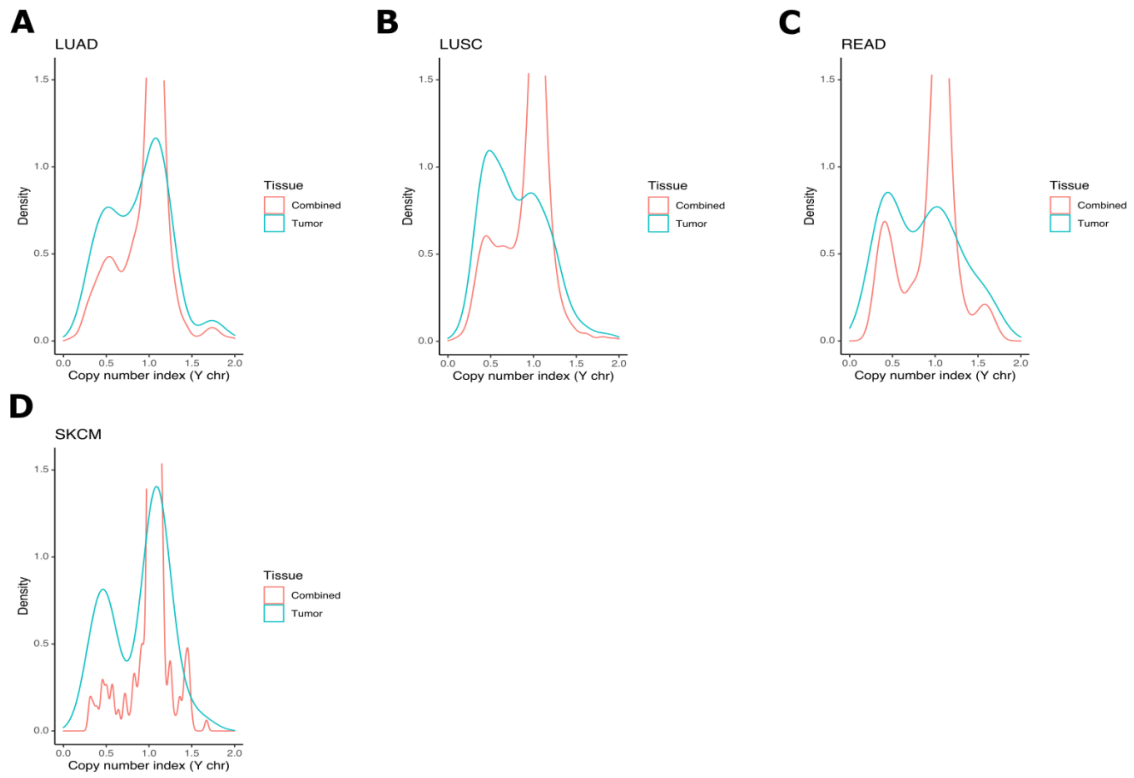


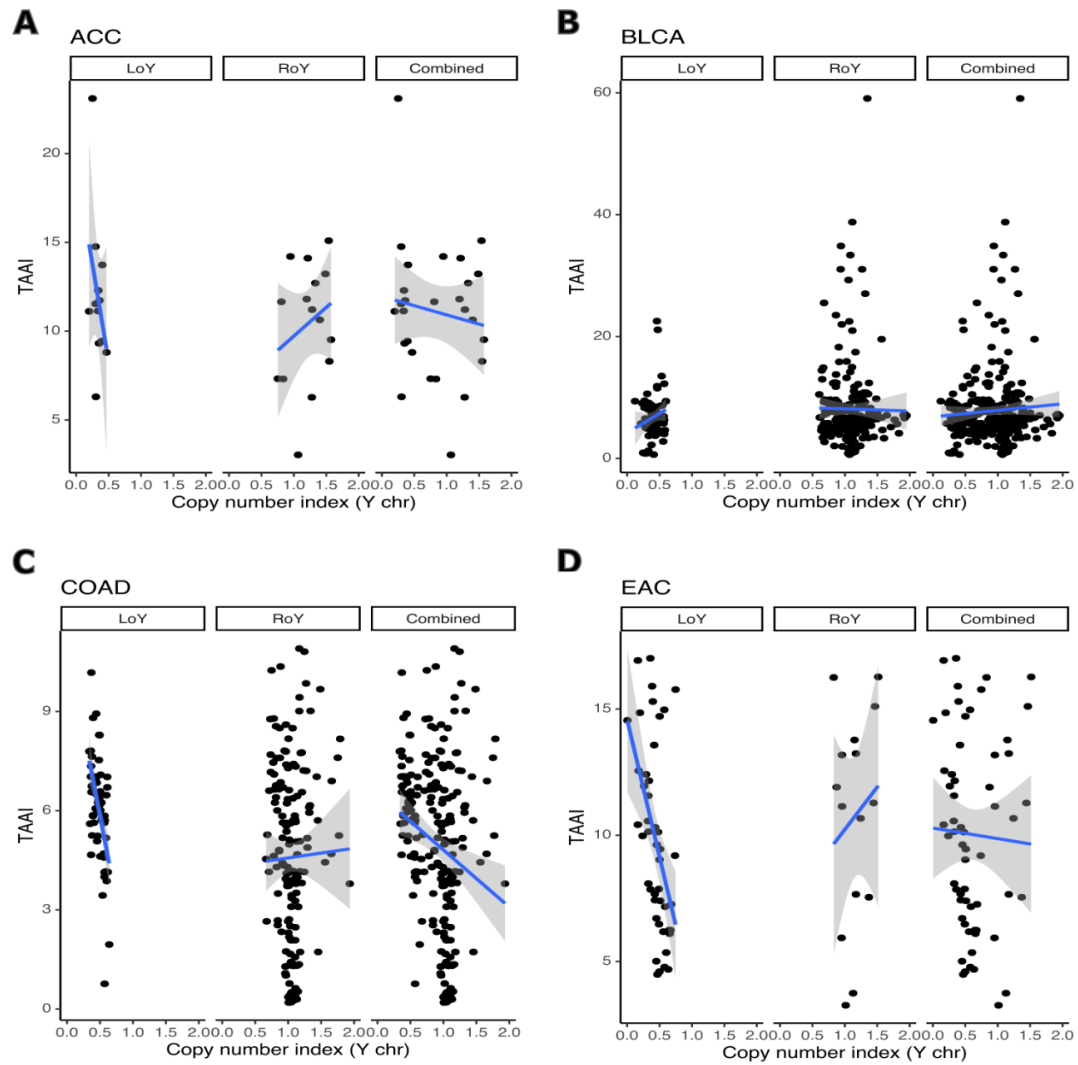
Supplement

Supplementary Figures

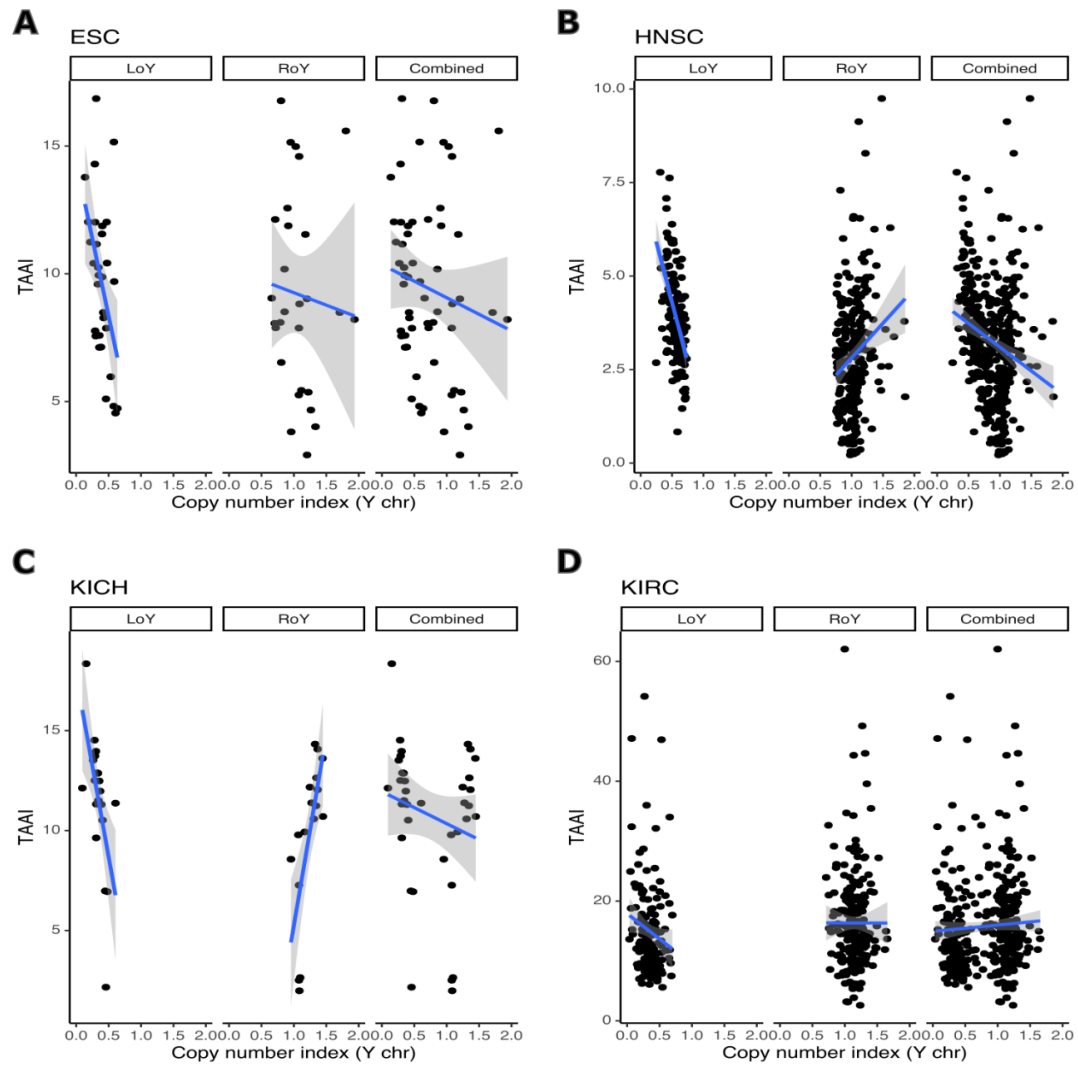




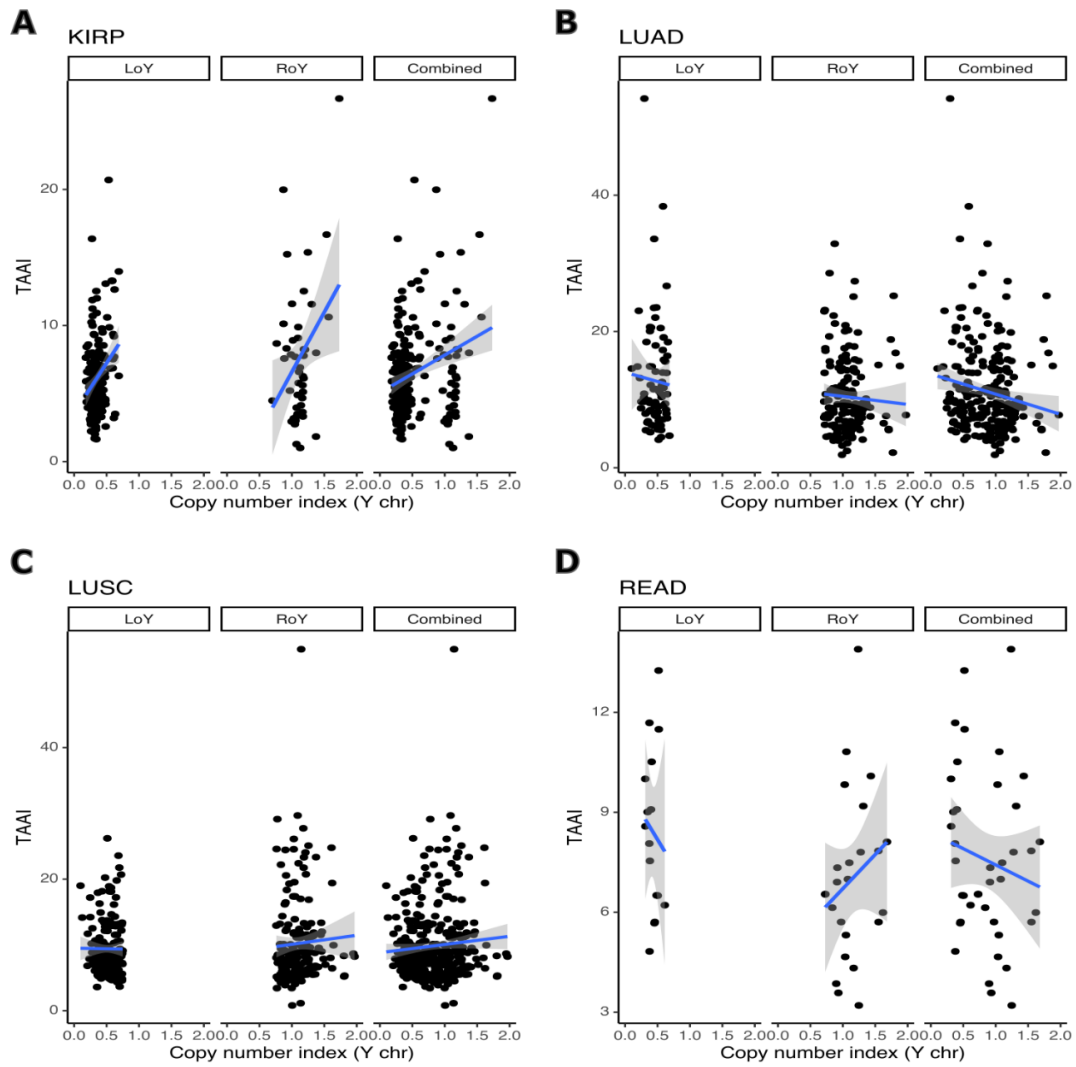
Supp. Fig. 2. Density plot of Y copy number index. Density curves are colored by tissue: tumor (blue) and tumor-normal combined (red). The plots show data of the cancer types: (A) LUAD, (B) LUSC, (C) READ, (D) SKCM.



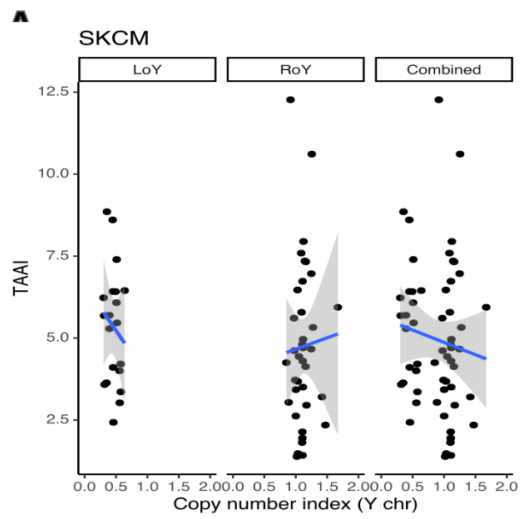
Supp. Fig. 3. Comparison of the Y copy number index and the autosomal aneuploidy index. Each of the depicted cancer types shows three correlation plots for the subsets of LoY, RoY and a mixed/combined one. The four plots show data of the cancer types: (A) ACC, (B) BLCA, (C) COAD, (D) EAC.



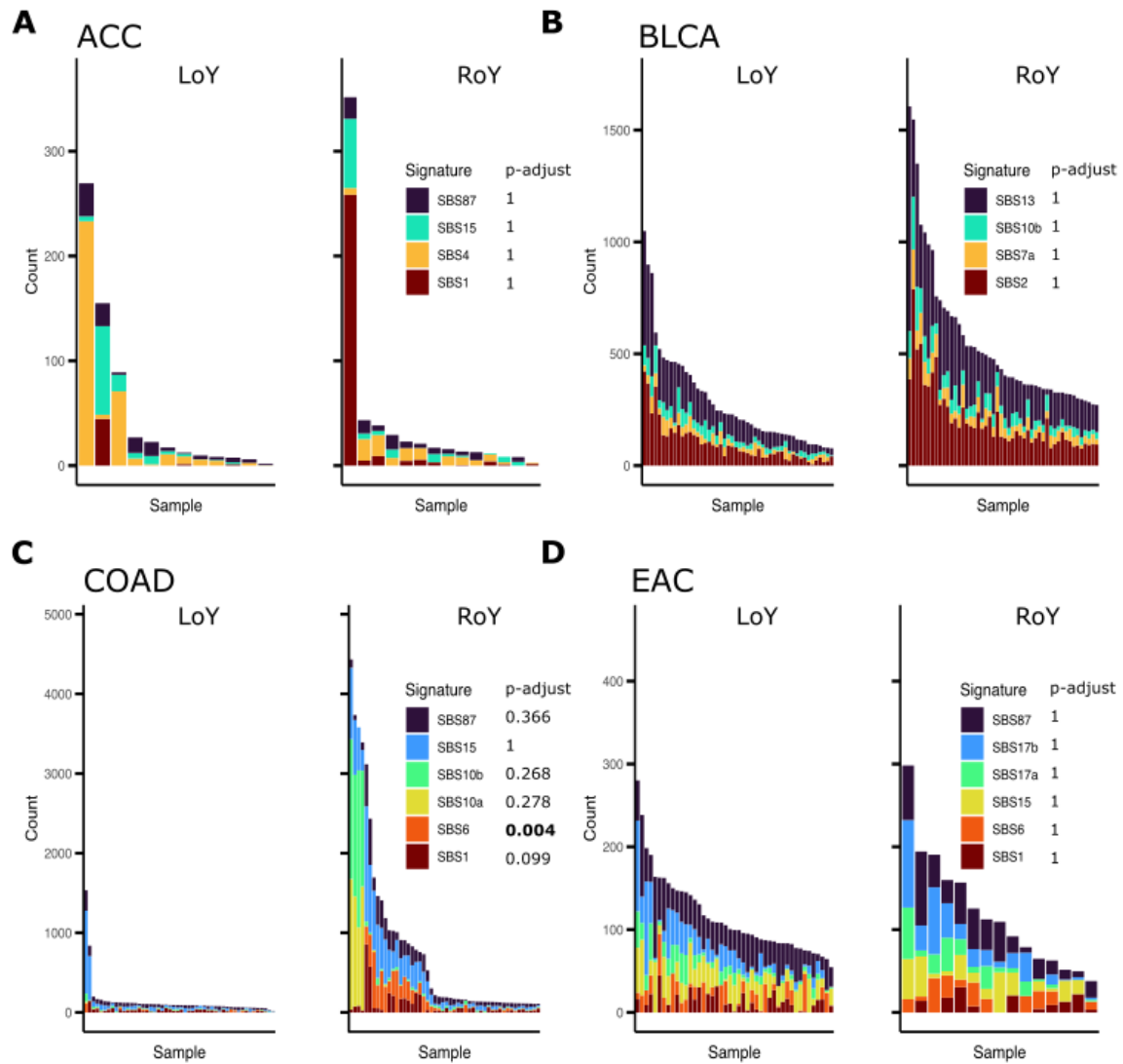
Supp. Fig. 4. Comparison of the Y copy number index and the autosomal aneuploidy index. Each of the depicted cancer types shows three correlation plots for the subsets of LoY, RoY and a mixed/combined one. The plots show data of the cancer types: (A) ESC, (B) HNSC, (C) KICH, (D) KIRC.



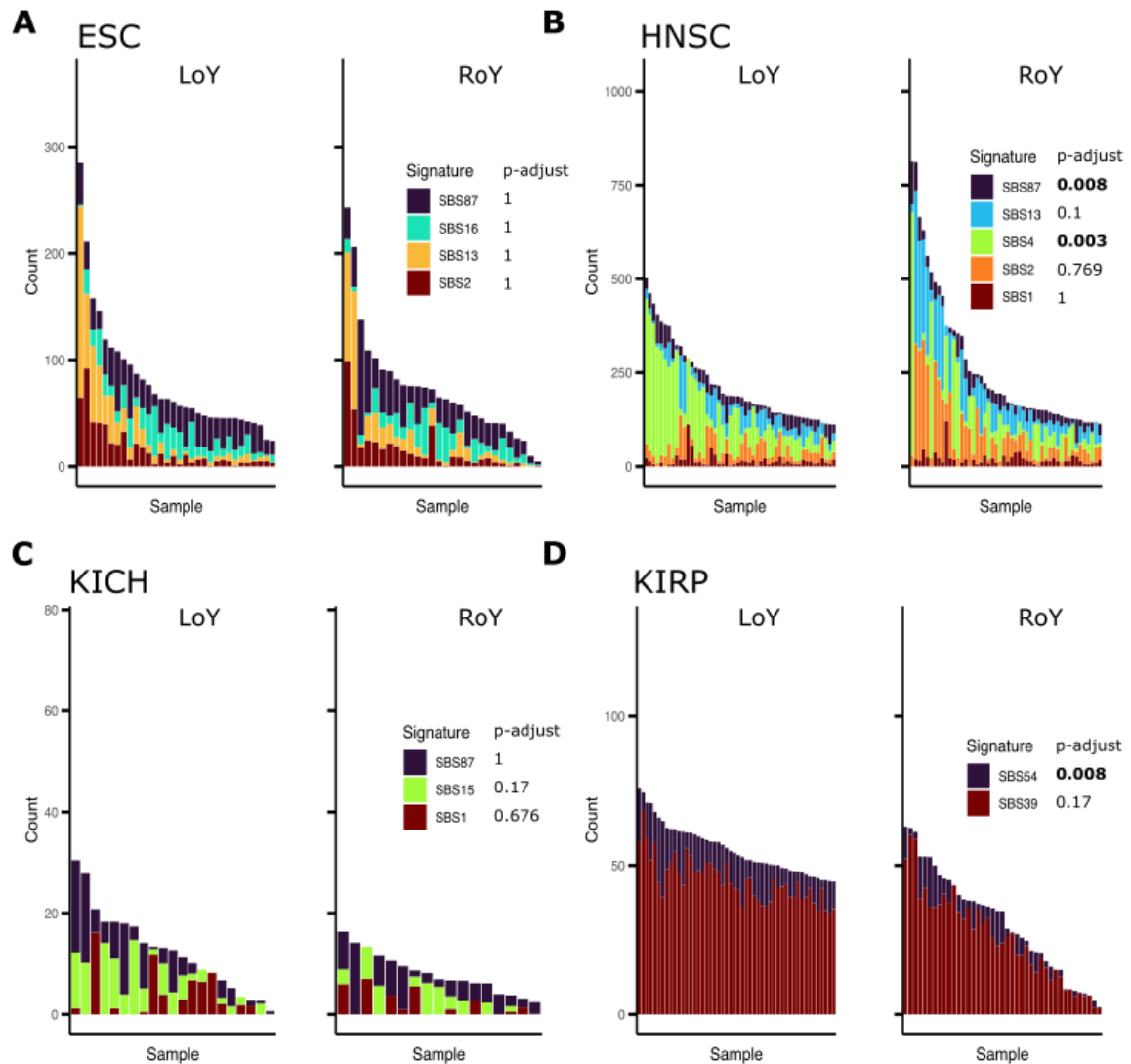
Supp. Fig. 5. Comparison of the Y copy number index and the autosomal aneuploidy index. Each of the depicted cancer types shows three correlation plots for the subsets of LoY, RoY and a mixed/combined one. The plots show data of the cancer types: (A) KIRP, (B) LUAD, (C) LUSC, (D) READ.



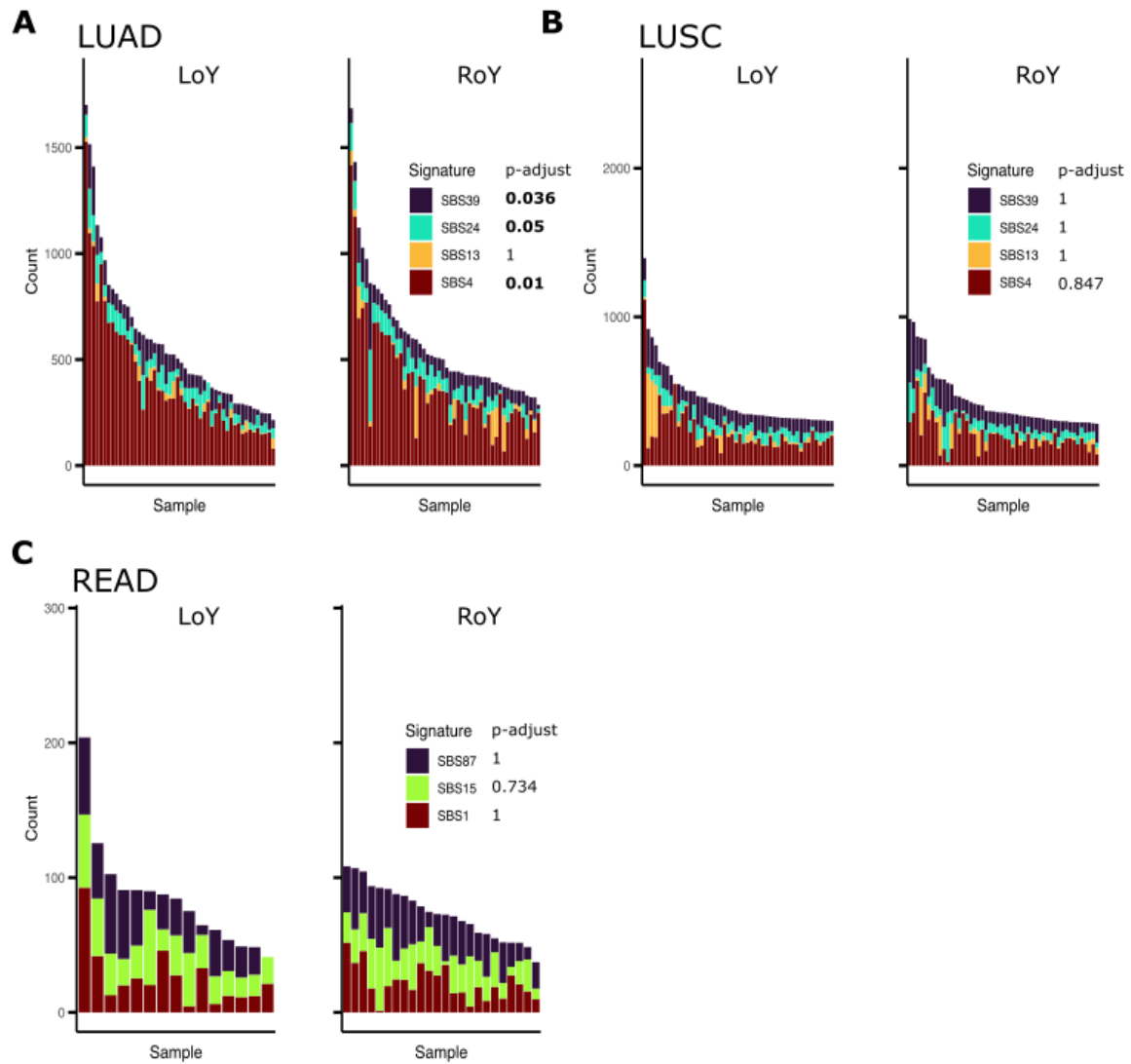
Supp. Fig. 6. Comparison of the Y copy number index and the autosomal aneuploidy index. For SKCM, three correlation plots for the subsets of LoY, RoY and a mixed/combined one are shown.



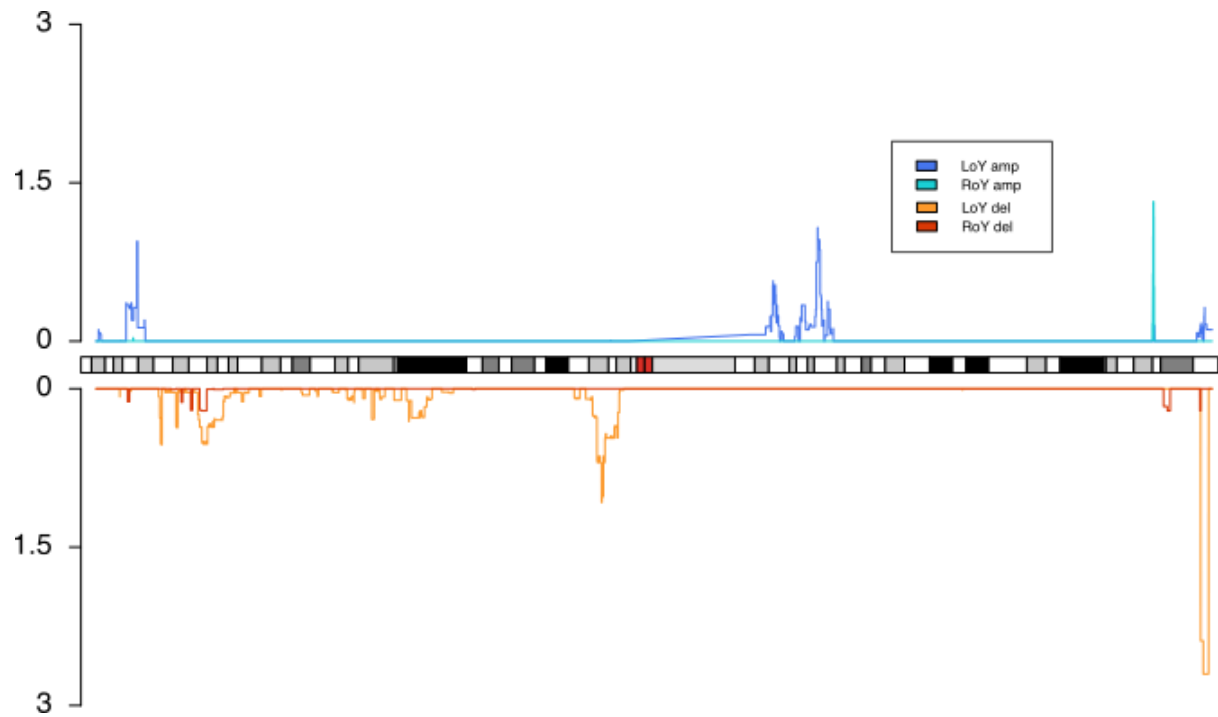
Supp. Fig. 7. Comparison of mutation signatures. Each cancer type contains two bar plots for the Loss and Retain subset. Patients are ordered in a descending fashion based on their mutational burden. The colors represent the fraction of mutations being assigned to the respective COSMIC single based substitution signature as shown in the legend. An additional p-value of the t-test is shown indicating the likelihood of the distributions of the respective signature being significantly different between LoY and RoY. The four plots show data of the cancer types: ACC, BLCA, COAD, and EAC.



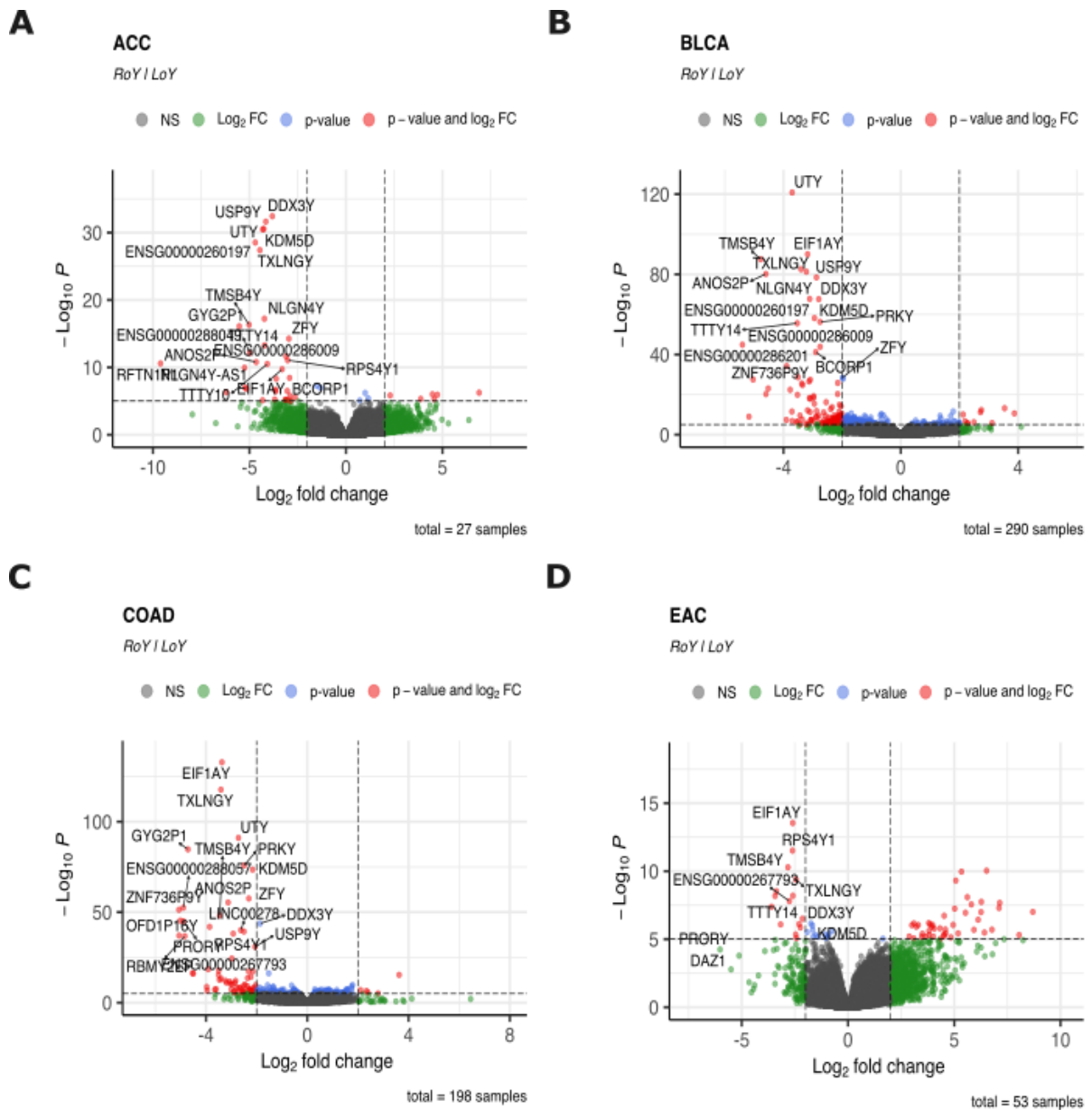
Supp. Fig. 8. Comparison of mutation signatures. Each cancer type contains two bar plots for the Loss and Retain subset. Patients are ordered in a descending fashion based on their mutational burden. The colors represent the fraction of mutations being assigned to the respective COSMIC single based substitution signature as shown in the legend. An additional p-value of the t-test is shown indicating the likelihood of the distributions of the respective signature being significantly different between LoY and RoY. The four plots show data of the cancer types: ESC, HNSC, KICH, and KIRP.



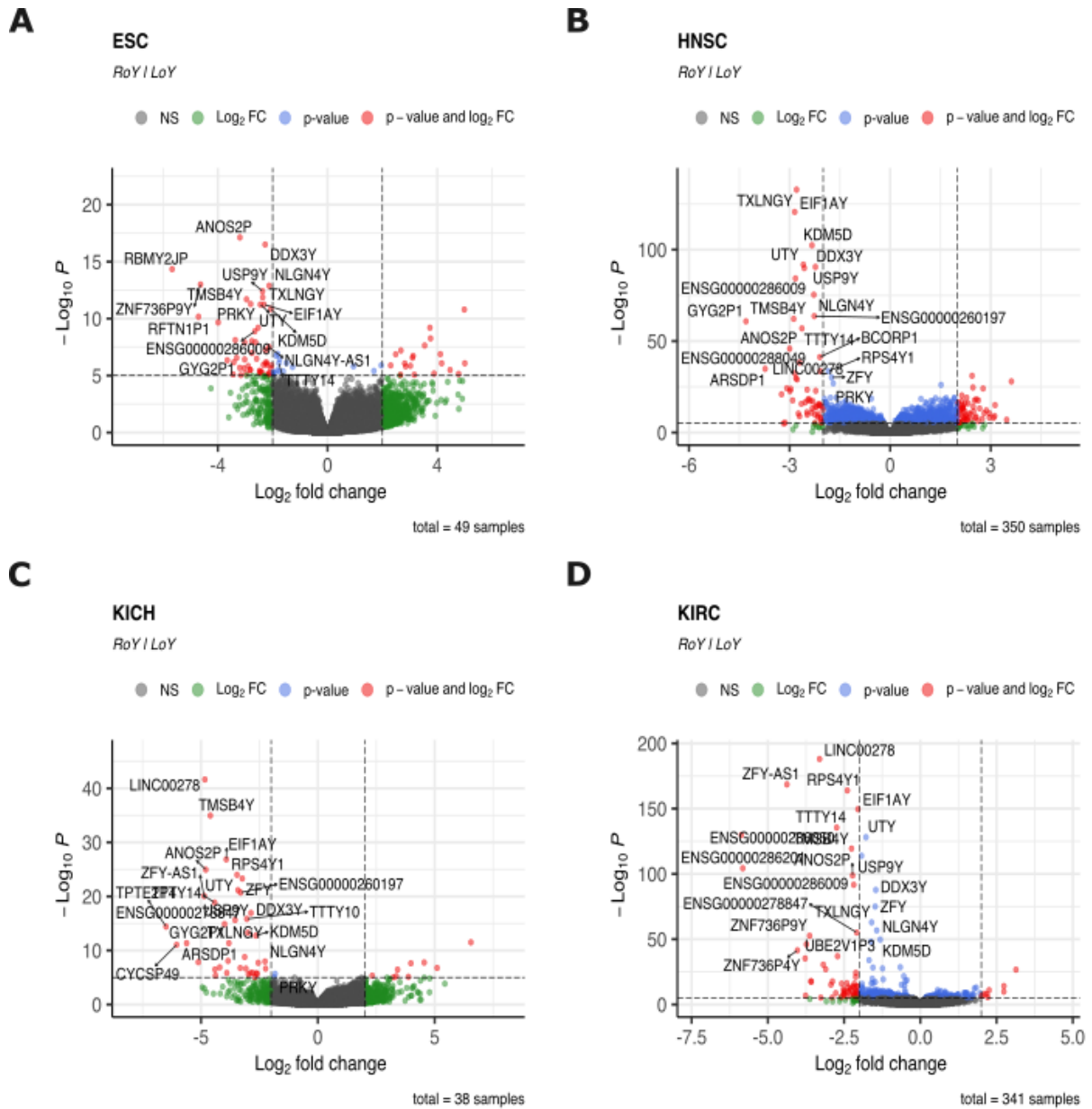
Supp. Fig. 9. Comparison of mutation signatures. Each cancer type contains two bar plots for the Loss and Retain subset. Patients are ordered in a descending fashion based on their mutational burden. The colors represent the fraction of mutations being assigned to the respective COSMIC single based substitution signature as shown in the legend. An additional p-value of the t-test is shown indicating the likelihood of the distributions of the respective signature being significantly different between LoY and RoY. The three plots show data of the cancer types: LUAD, LUSC, and READ.



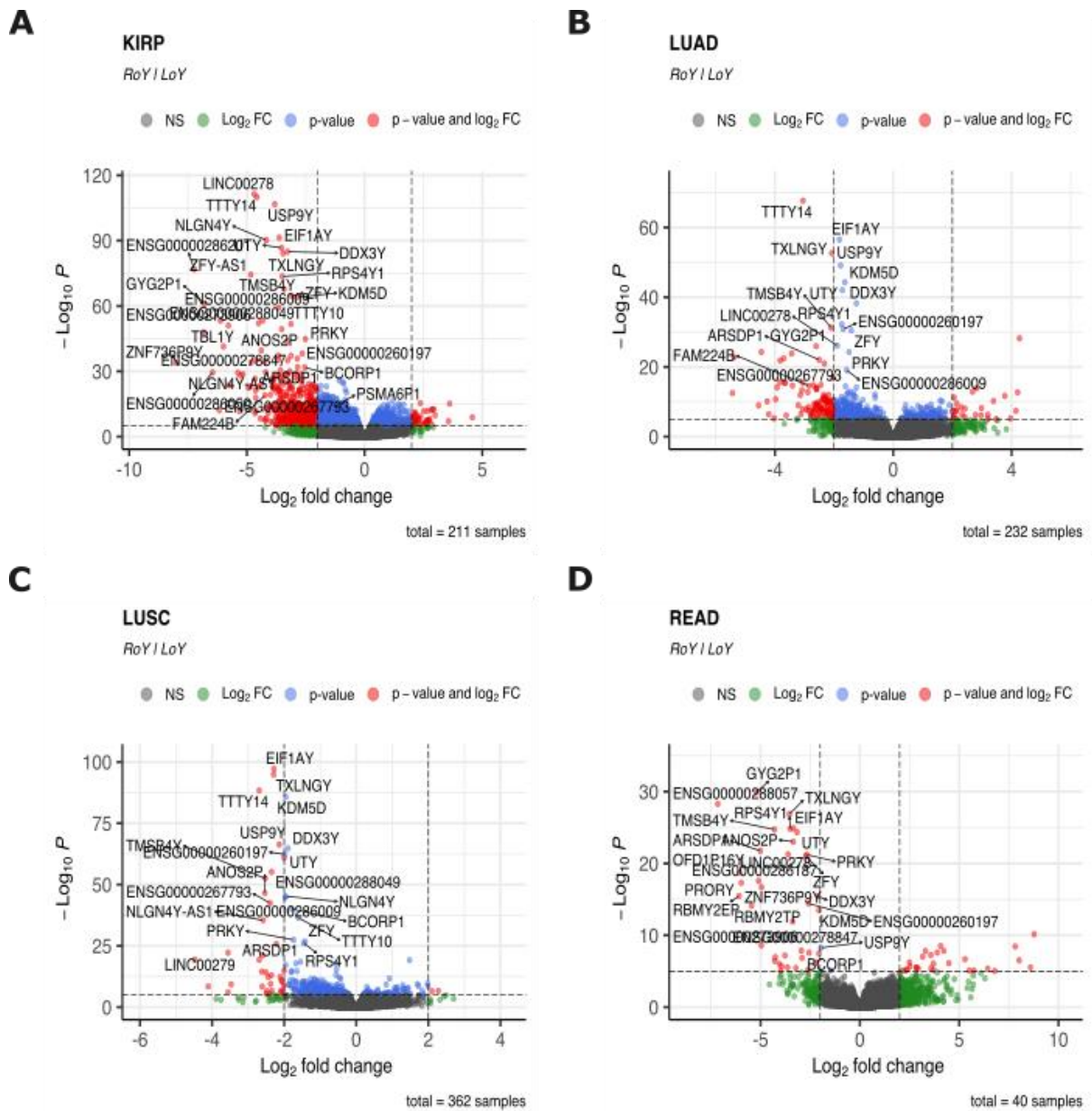
Supp. Fig. 10. GISTIC2.0 output for chromosome 1 of the esophageal adenocarcinoma. G-scores of the GISTIC2.0 analysis for chromosome 1 are shown. Amplified regions are highlighted in blue (LoY) and light blue (RoY). Deleted regions are colored in orange (LoY) and red (RoY).



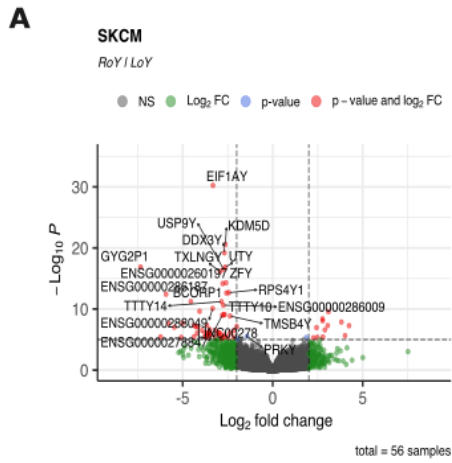
Supp. Fig. 11. Differentially expressed genes. Each of the four depicted volcano plots shows the differentially expressed genes for the respective cancer type with regards to the LoY status. Red dots represent genes that show both a p-value smaller than 0.05 and an absolute log₂ fold change of over 2. The four plots show data of the cancer types: ACC, BLCA, COAD, and EAC.



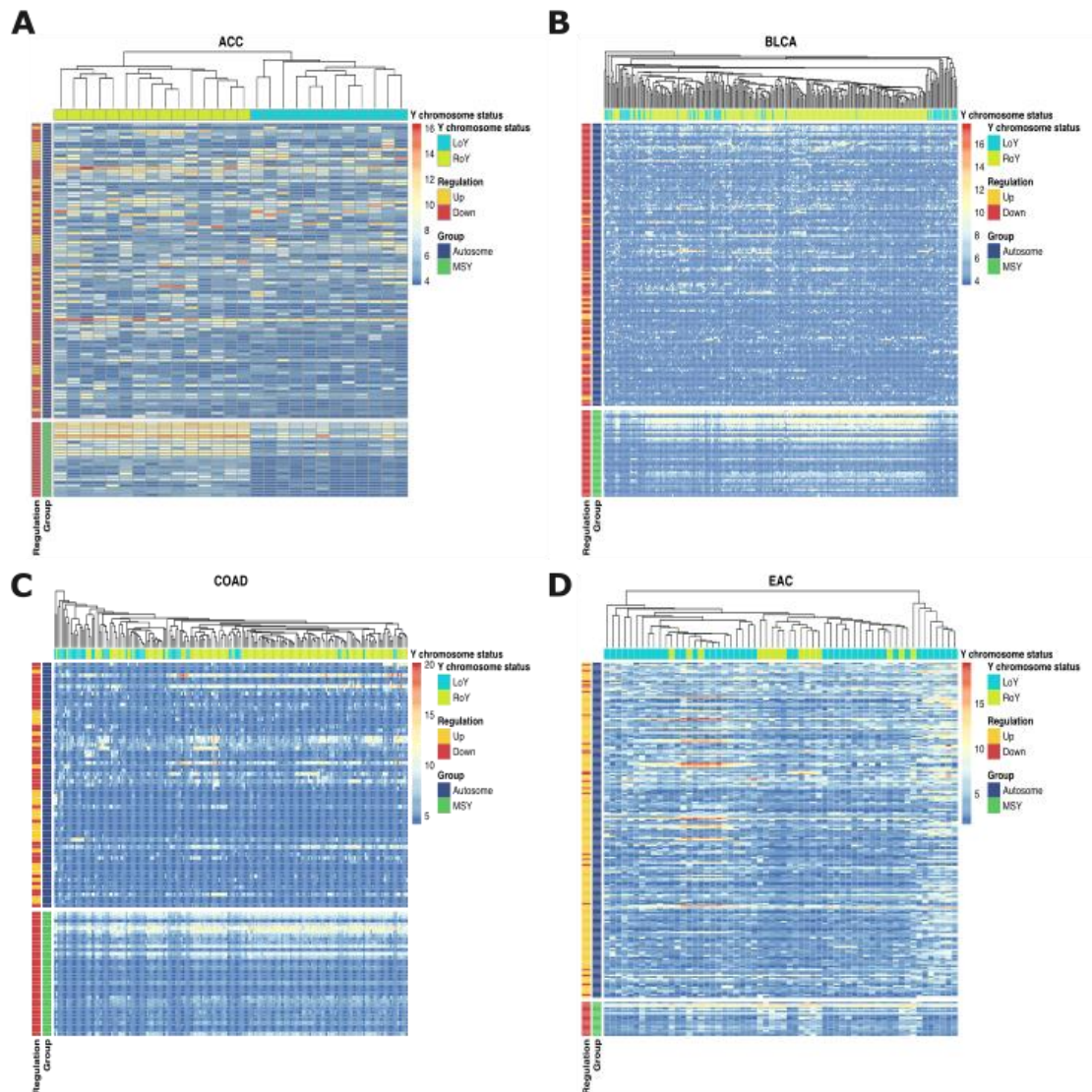
Supp. Fig. 12. Differentially expressed genes. Each of the four depicted volcano plots shows the differentially expressed genes for the respective cancer type with regards to the LoY status. Red dots represent genes that show both a p-value smaller than 0.05 and an absolute log₂ fold change of over 2. The four plots show data of the cancer types: ESC, HNSC, KICH, and KIRC.



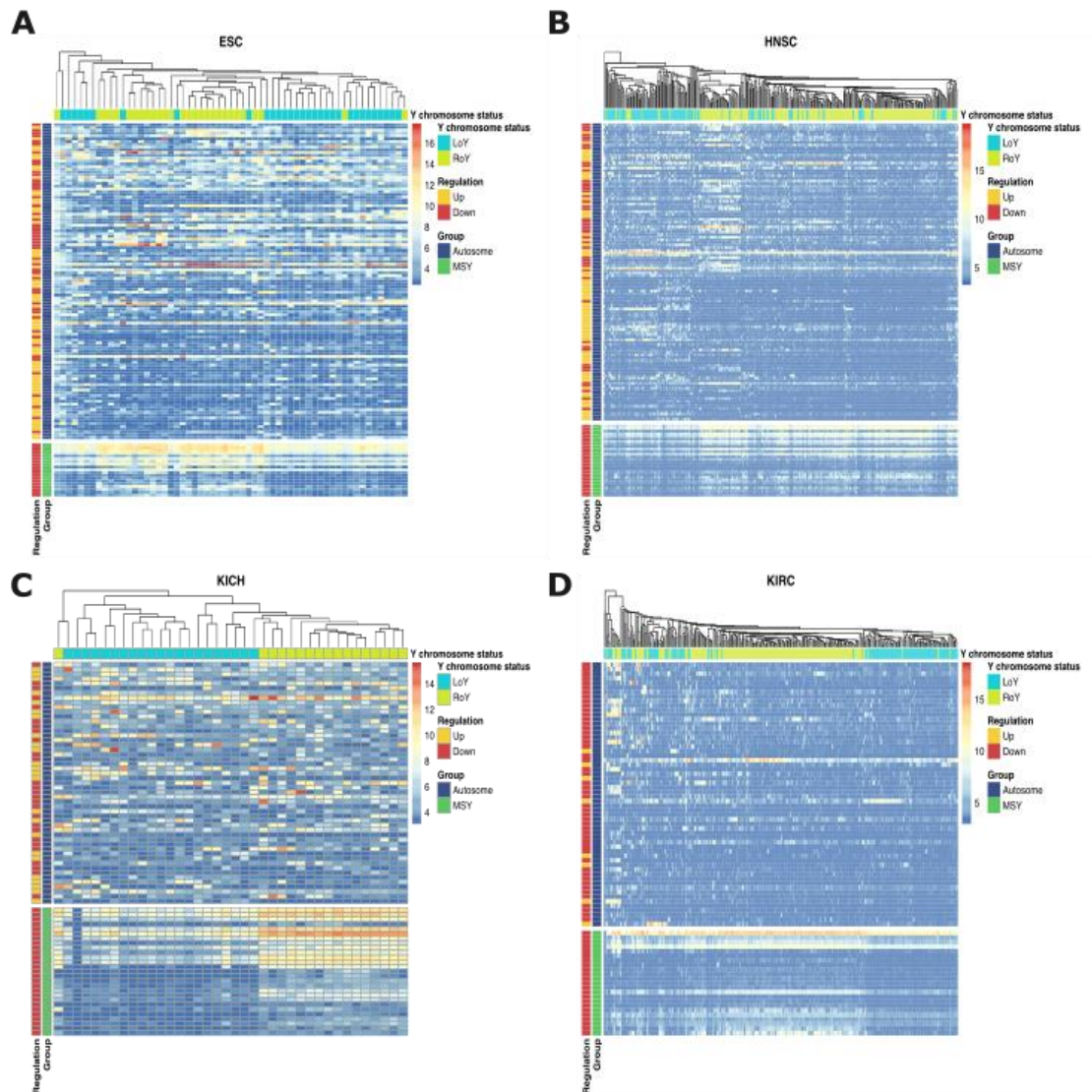
Supp. Fig. 13. Differentially expressed genes. Each of the four depicted volcano plots shows the differentially expressed genes for the respective cancer type with regards to the LoY status. Red dots represent genes that show both a p-value smaller than 0.05 and an absolute log₂ fold change of over 2. The four plots show data of the cancer types: KIRP, LUAD, LUSC, and READ.



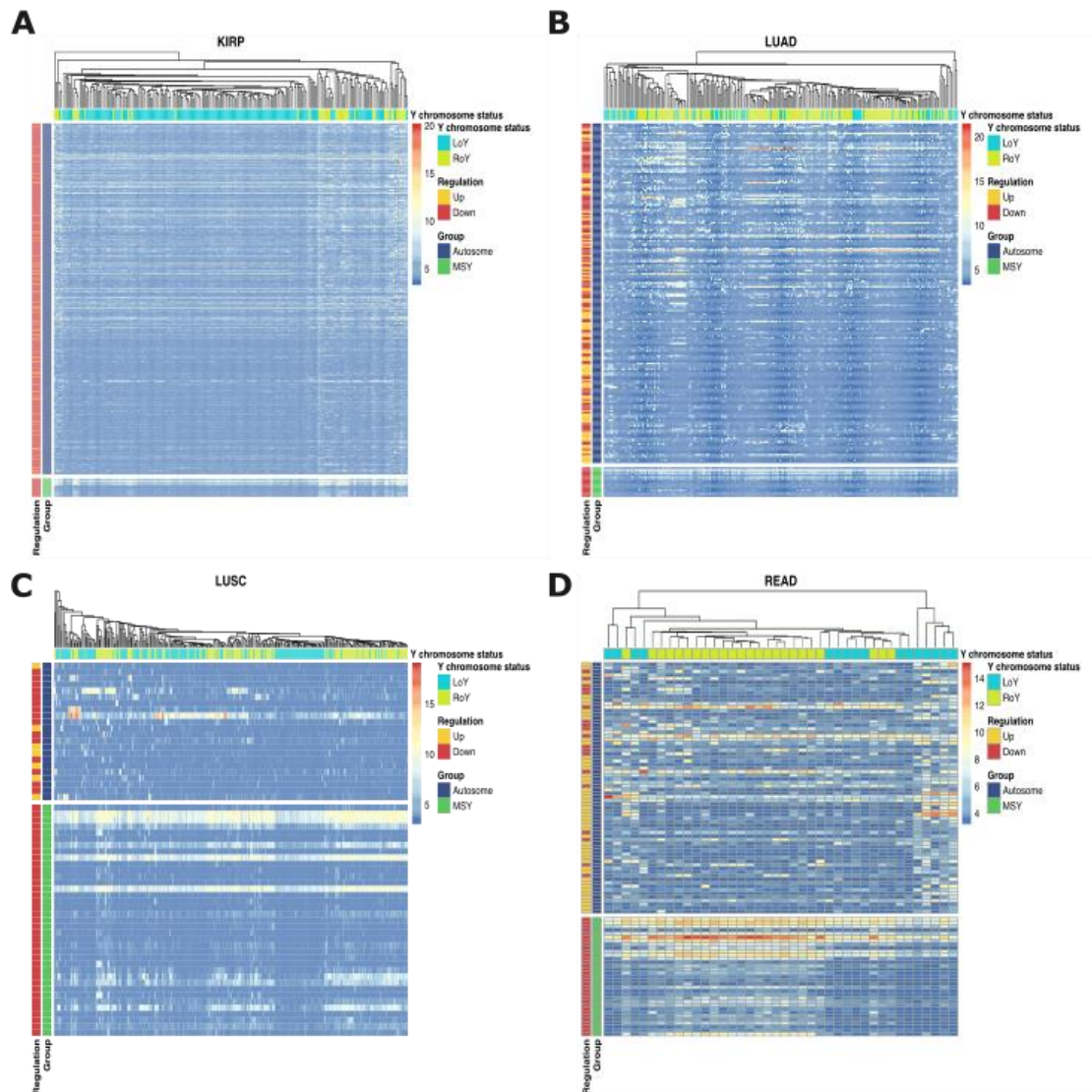
Supp. Fig. 14. Differentially expressed genes. The volcano plots shows the differentially expressed genes for SKCM with regards to the LoY status. Red dots represent genes that show both a p-value smaller than 0.05 and an absolute log₂ fold change of over 2.



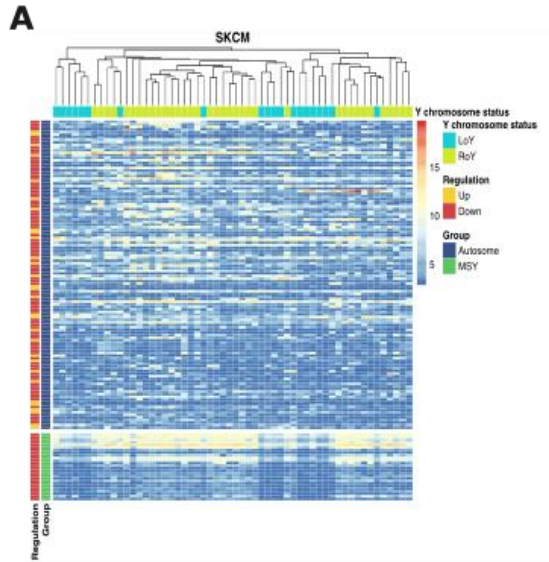
Supp. Fig. 15. Heat map comparison of up- and downregulated genes. The figure shows the heat maps for the cancer types ACC, BLCA, COAD, and EAC. The heat maps show genes (horizontal rows) that are either significantly up- (marked in orange on the left) or down-regulated (marked in red on the left) in LoY patients (vertical columns). On top is an unsupervised clustering dendrogram shown with colored classification of patient's LoY status, loss (turquoise) and retain (light green). Chromosomal origin for each gene is indicated on the left. MSY region (green), autosome (blue).



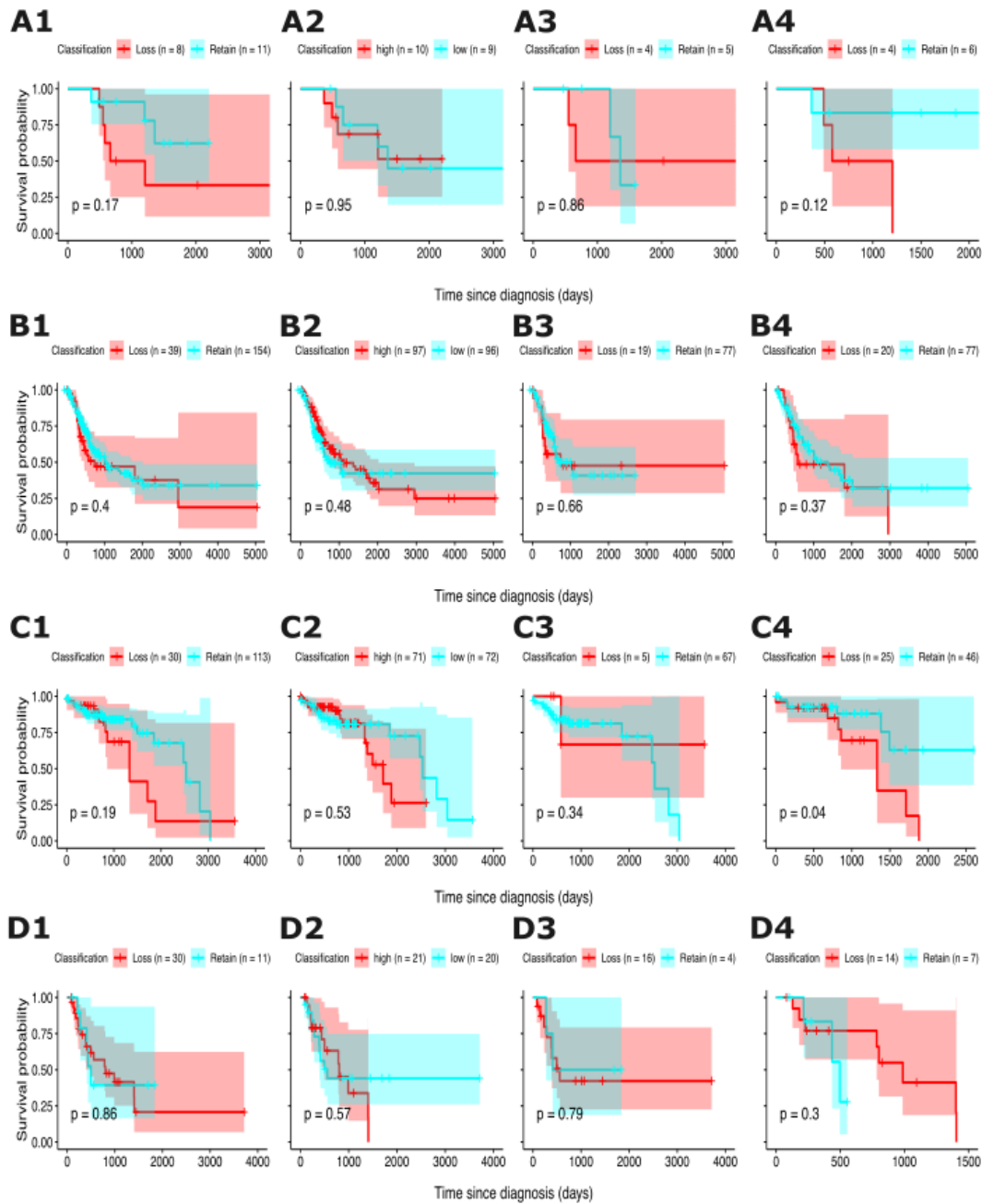
Supp. Fig. 16. Heatmap comparison of up- and downregulated genes. The figure shows the heat maps for the cancer types ESC, HNSC, KICH, and KIRC. The heat maps show genes (horizontal rows) that are either significantly up- (marked in orange on the left) or downregulated (marked in red on the left) in LoY patients (vertical columns). On top is an unsupervised clustering dendrogram shown with colored classification of patient's LoY status, loss (turquoise) and retain (light green). Chromosomal origin for each gene is indicated on the left. MSY region (green), autosome (blue).



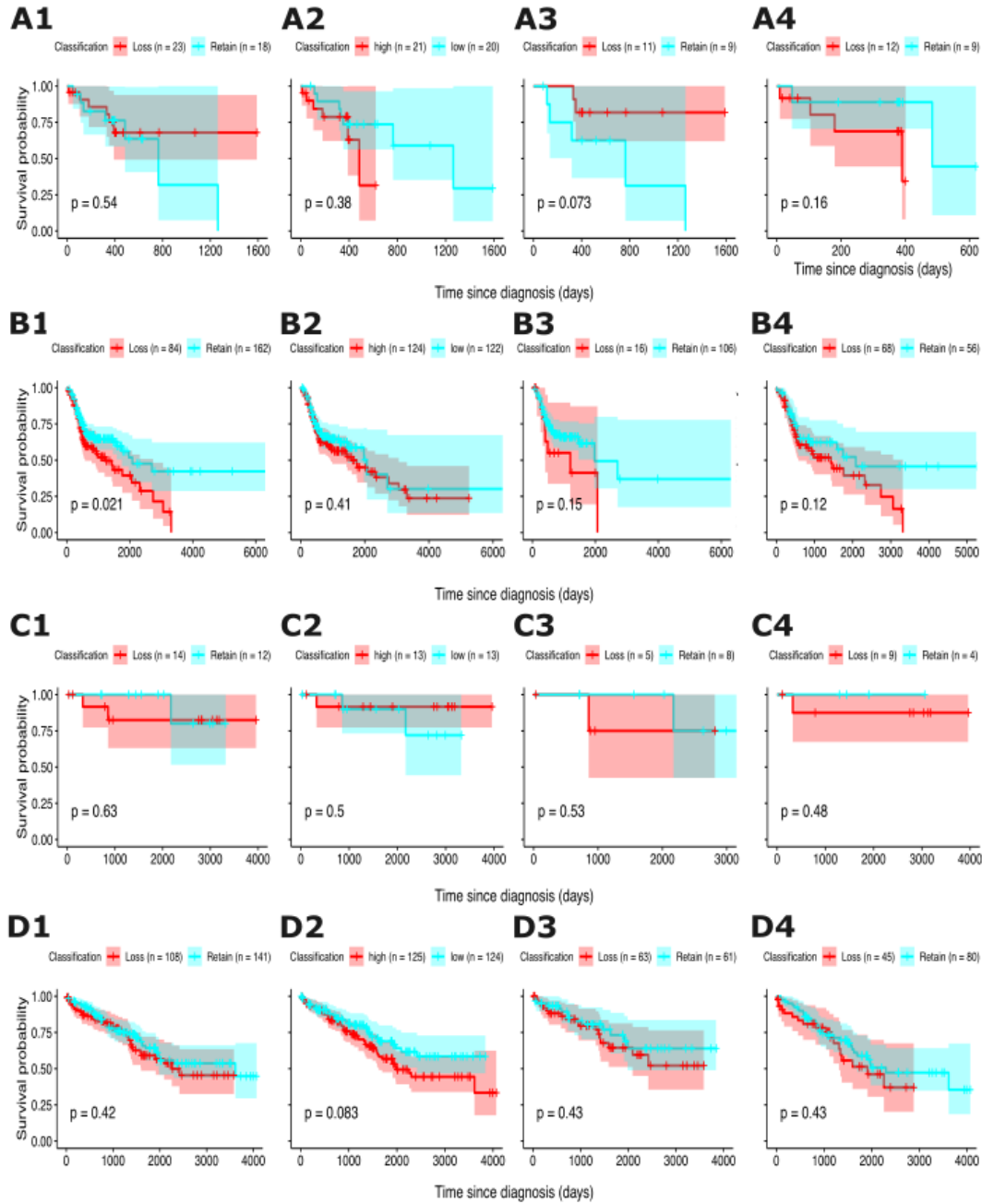
Supp. Fig. 17. Heatmap comparison of up- and downregulated genes. The figure shows the heat maps for the cancer types KIRP, LUAD, LUSC, and READ. The heat maps show genes (horizontal rows) that are either significantly up- (marked in orange on the left) or downregulated (marked in red on the left) in LoY patients (vertical columns). On top is an unsupervised clustering dendrogram shown with colored classification of patient's LoY status, loss (turquoise) and retain (light green). Chromosomal origin for each gene is indicated on the left. MSY region (green), autosome (blue).



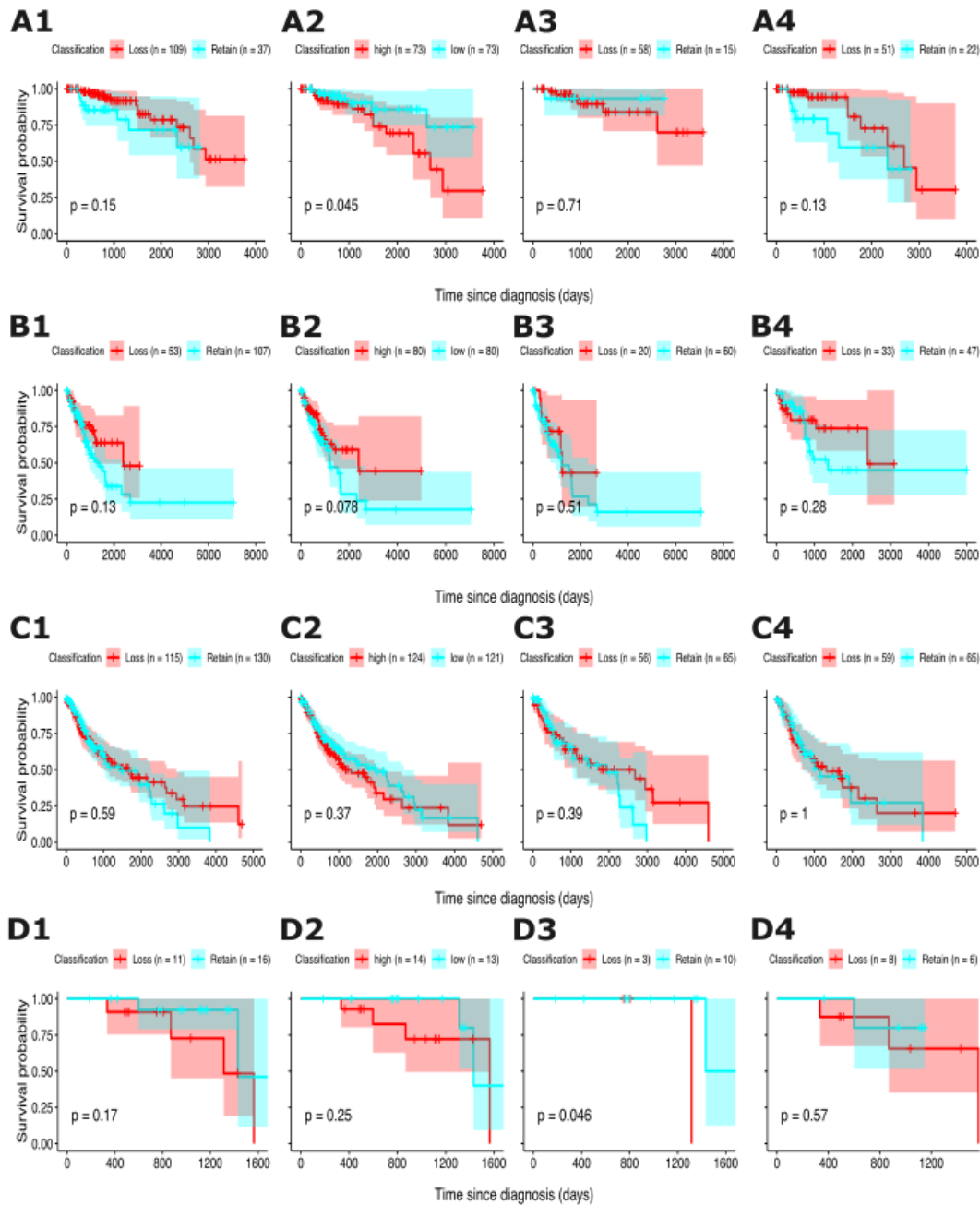
Supp. Fig. 18. Heatmap comparison of up- and downregulated genes of SKCM. The heat maps show genes (horizontal rows) that are either significantly up- (marked in orange on the left) or down-regulated (marked in red on the left) in LoY patients (vertical columns). On top is an unsupervised clustering dendrogram shown with colored classification of patient's LoY status, loss (turquoise) and retain (light green). Chromosomal origin for each gene is indicated on the left. Y chromosome (green), autosome (blue).



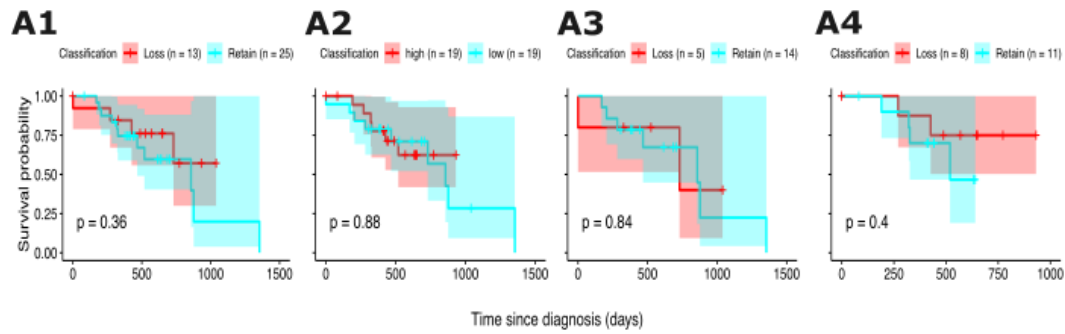
Supp. Fig. 19. Survival analysis for LoY compared with RoY. The figure comprises four separate survival curves for the cancer types (A) ACC, (B) BLCA, (C) COAD, and (D) EAC. (1) Comparison between LoY (red) and RoY (turquoise). (2) Comparison between a high total autosomal aneuploidy index (TAAI, red) and low TAAI (turquoise). (3) Comparison between LoY (red) and RoY (turquoise) for tumors that show a low TAAI. (4) Comparison between LoY (red) and RoY (turquoise) for tumors that show a high TAAI.



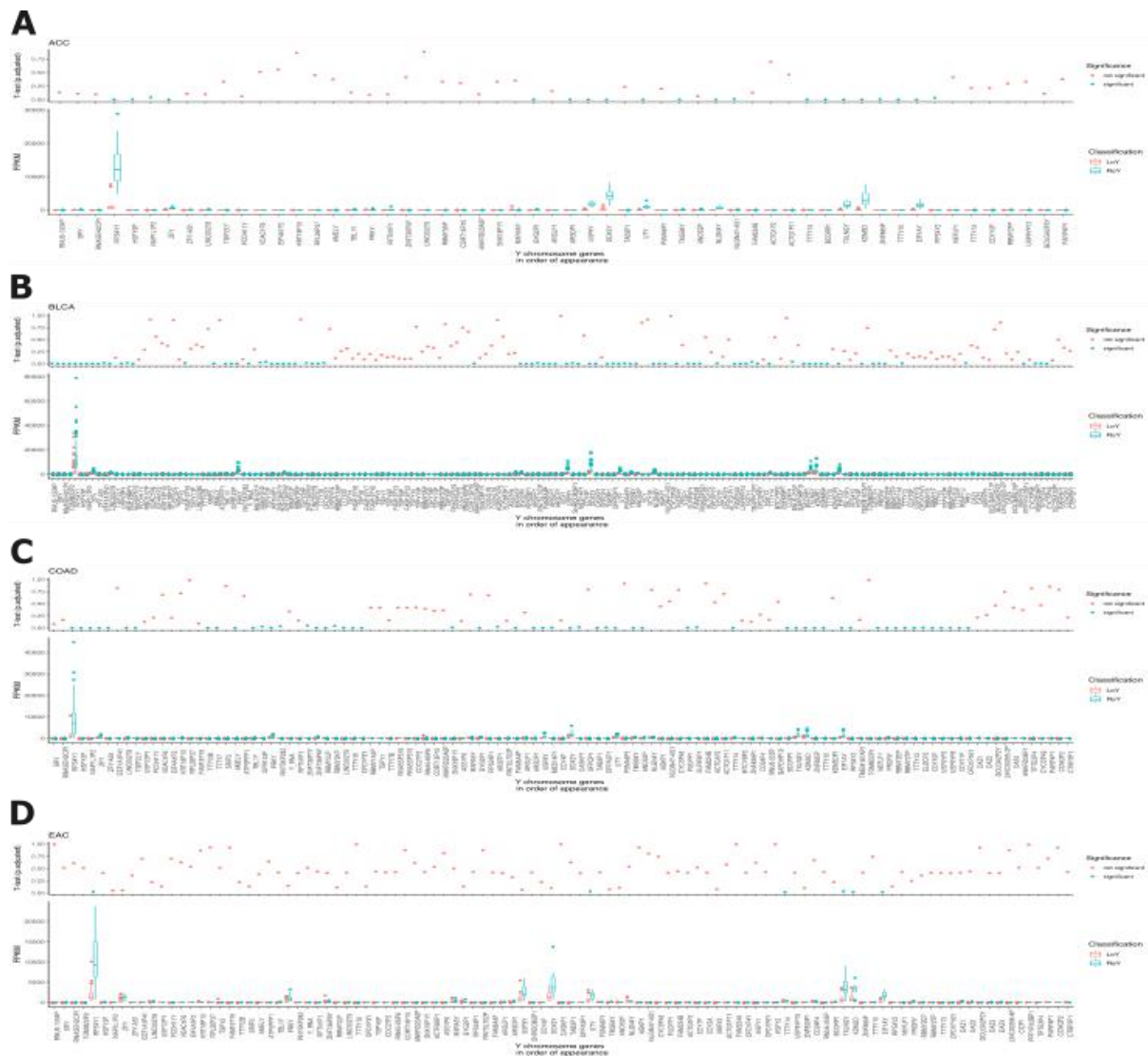
Supp. Fig. 20. Survival analysis for LoY compared with RoY. The figure comprises of four separate survival curves for the cancer types (A) ESC, (B) HNSC, (C) KICH, and (D) KIRC. (1) Comparison between LoY (red) and RoY (turquoise). (2) Comparison between a high TAAI (red) and low TAAI (turquoise). (3) Comparison between LoY (red) and RoY (turquoise) for tumors that show a low TAAI. (4) Comparison between LoY (red) and RoY (turquoise) for tumors that show a high TAAI.



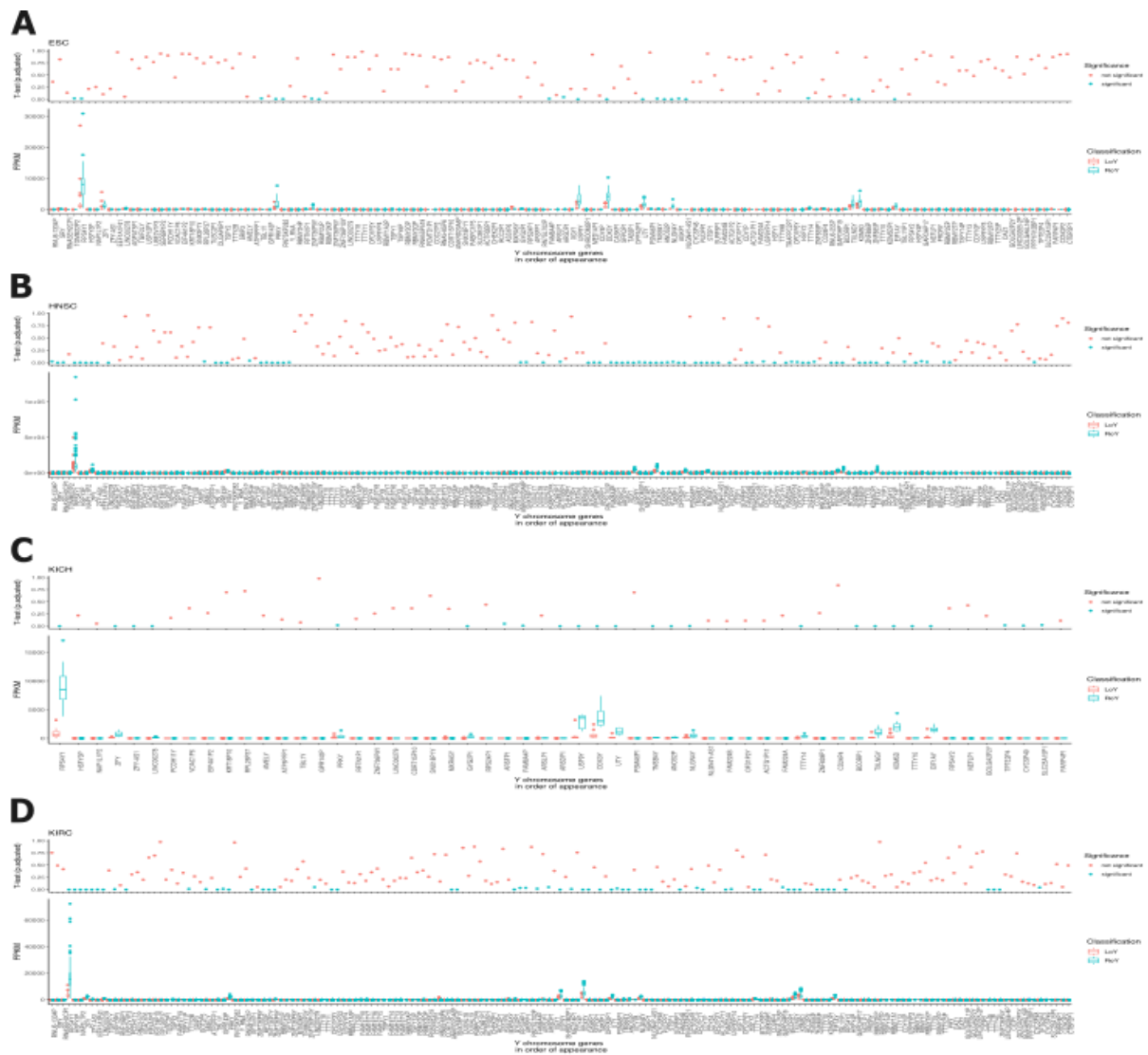
Supp. Fig. 21. Survival analysis for LoY compared with RoY. The figure comprises of four separate survival curves for the cancer types (A) KIRP, (B) LUAD, (C) LUSC, and (D) READ. (1) Comparison between LoY (red) and RoY (turquoise). (2) Comparison between a high TAAI (red) and low TAAI (turquoise). (3) Comparison between LoY (red) and RoY (turquoise) for tumors that show a low TAAI. (4) Comparison between LoY (red) and RoY (turquoise) for tumors that show a high TAAI.



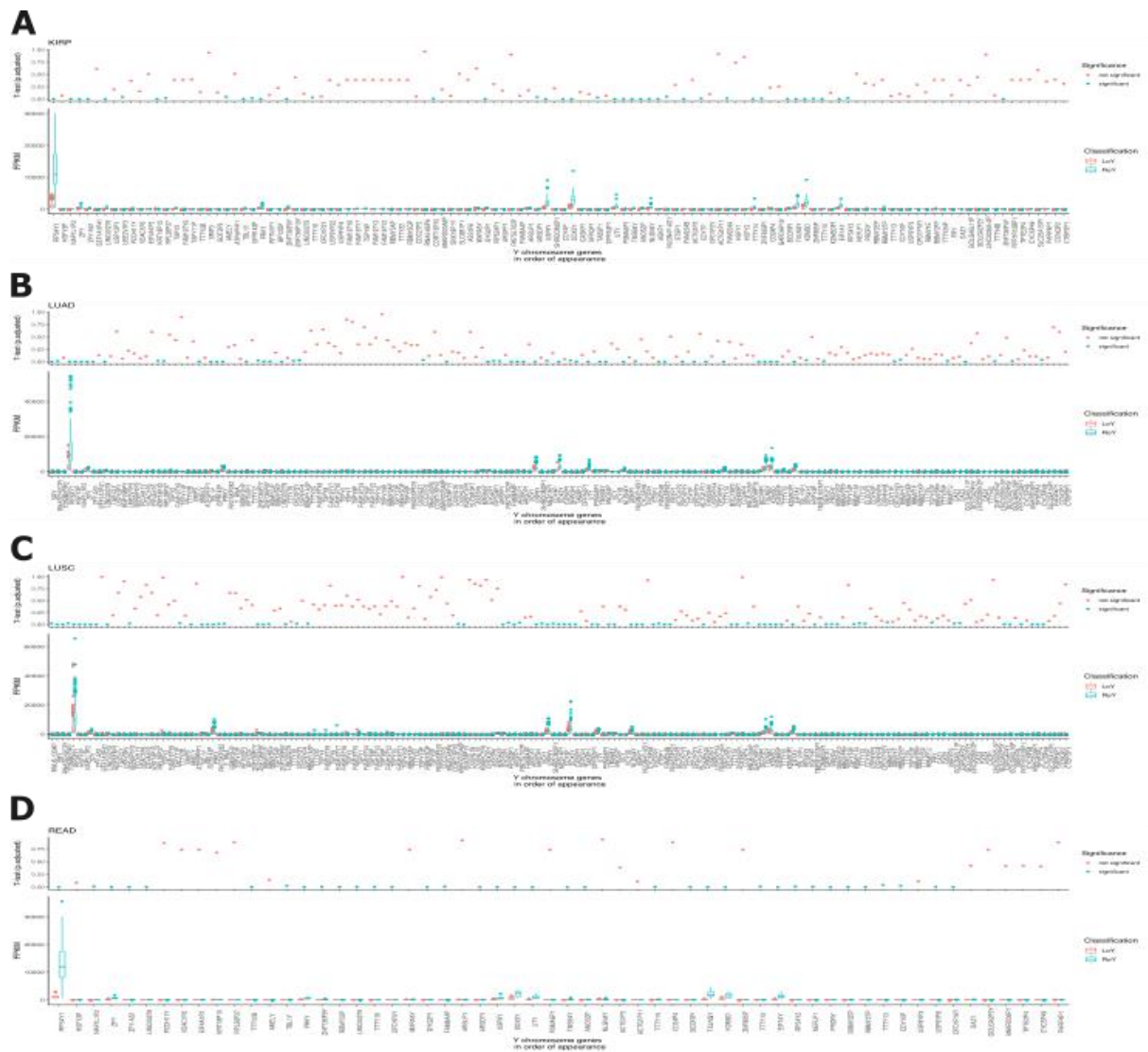
Supp. Fig. 22. Survival analysis for LoY compared with RoY. The figure comprises of four separate survival curves for SKCM. (A1) Comparison between LoY (red) and RoY (turquoise). (A2) Comparison between a high TAAI (red) and low TAAI (turquoise). (3) Comparison between LoY (red) and RoY (turquoise) for tumors that show a low TAAI. (4) Comparison between LoY (red) and RoY (turquoise) for tumors that show a high TAAI.



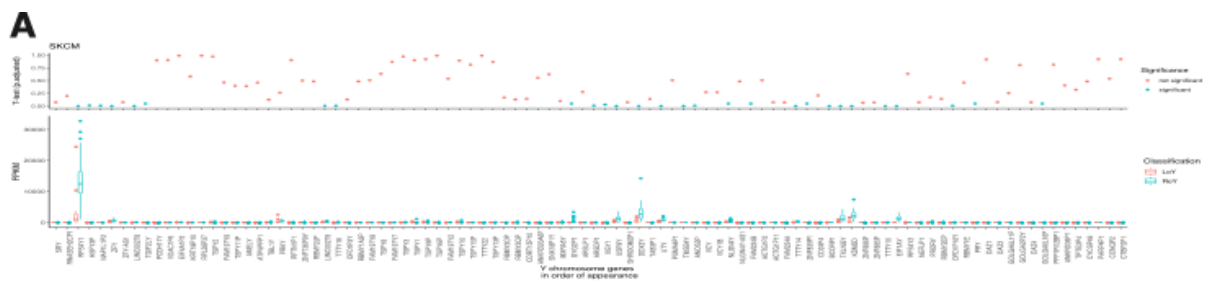
Supp. Fig. 23. Comparison of Y-linked RNA expression levels. Each panel comprises of two subpanels for the cancer types (A) ACC, (B) BLCA, (C) COAD, and (D) EAC. (bottom) FPKM values of genes located on the Y chromosome in order of appearance and colored by Y chromosome status. Loss (red), Retain (turquoise). (top) Respective p-values from a paired t-test. Significant values are marked in red, non-significant values in turquoise.



Supp. Fig. 24. Comparison of Y-linked RNA expression levels. Each panel comprises of two subpanels for the cancer types (A) ESC, (B) HNSC, (C) KICH, and (D) KIRC. (bottom) FPKM values of genes located on the Y chromosome in order of appearance and colored by LoY status. Loss (red), Retain (turquoise). (top) Respective p-values from a paired t-test. Significant values are marked in red, non-significant values in turquoise.



Supp. Fig. 25. Comparison of Y-linked RNA expression levels. Each panel comprises two subpanels for the cancer types (A) KIRP, (B) LUAD, (C) LUSC, and (D) READ. (bottom) FPKM values of genes located on the Y chromosome in order of appearance and colored by LoY status. Loss (red), Retain (turquoise). (top) Respective p-values from a paired t-test. Significant values are marked in red, non-significant values in turquoise.



Supp. Fig. 26. Comparison of Y-linked RNA expression levels. The figure comprises of two subpanels for SKCM. (bottom) FPKM values of genes located on the Y chromosome in order of appearance and colored by LoY status. Loss (red), Retain (turquoise). (top) Respective p-values from a paired t-test. Significant values are marked in red, non-significant values in turquoise.