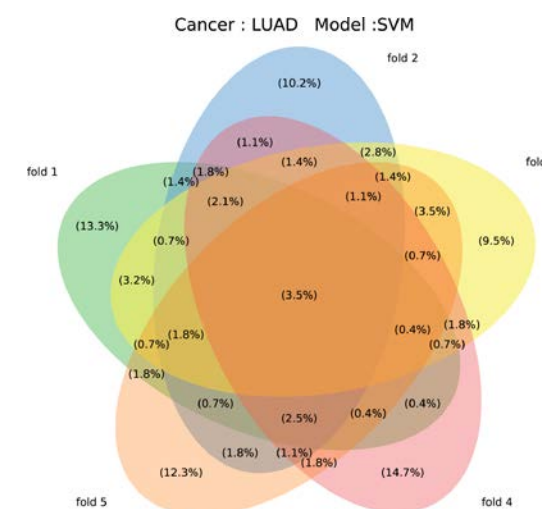
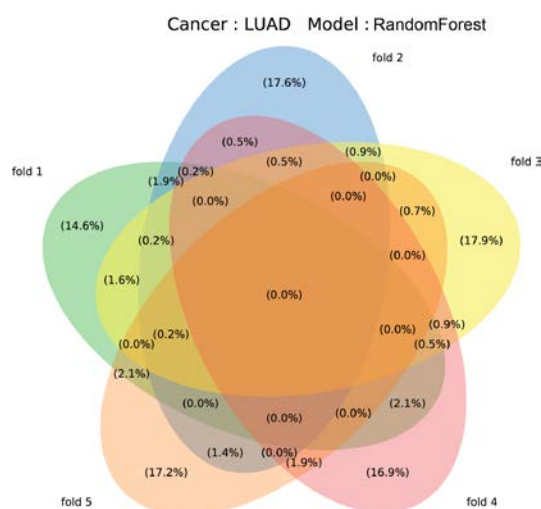
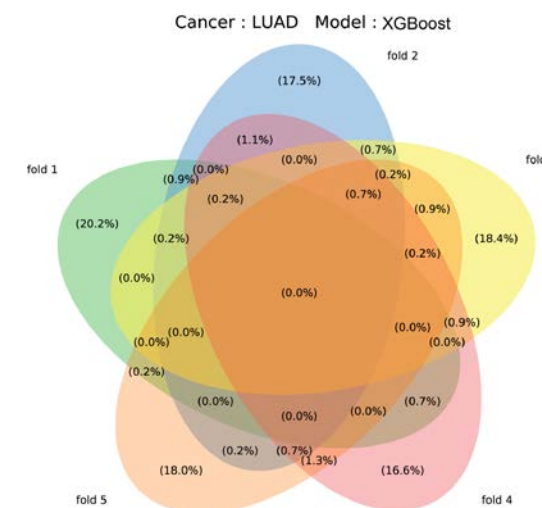
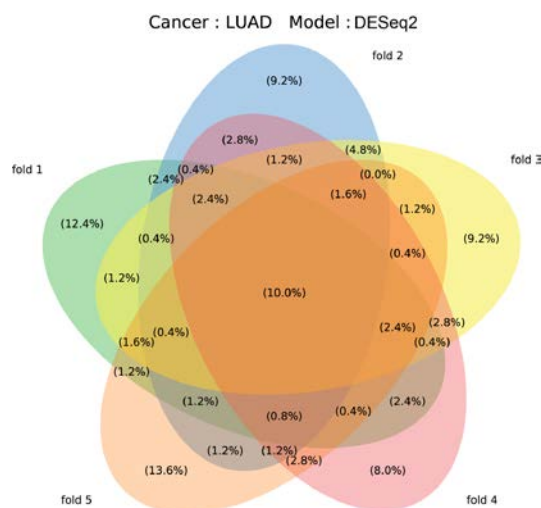
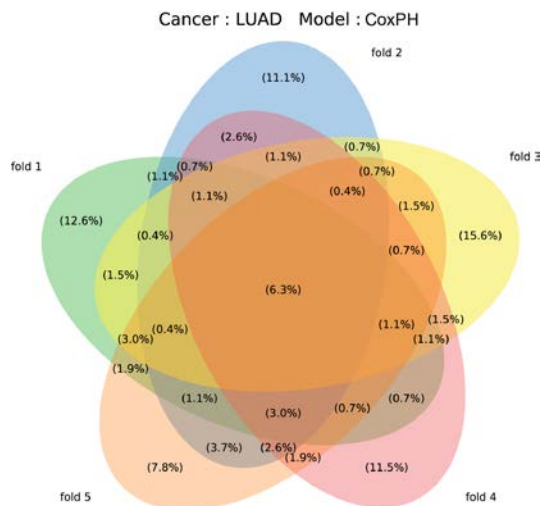
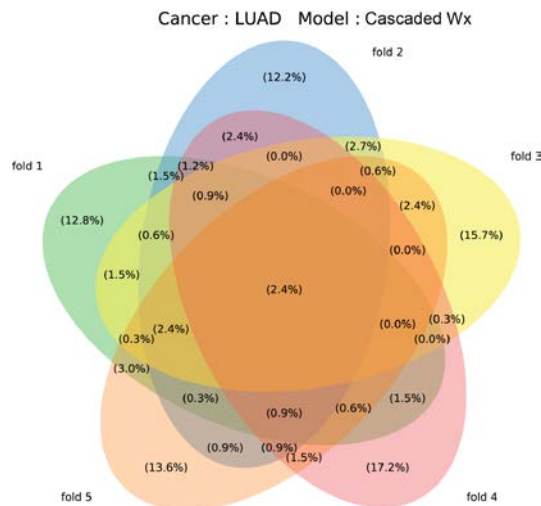
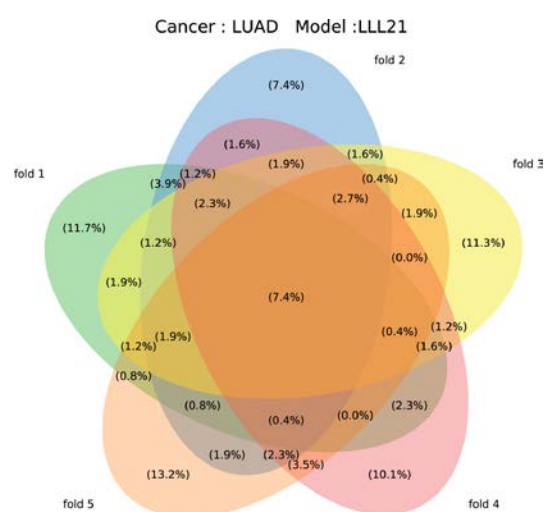
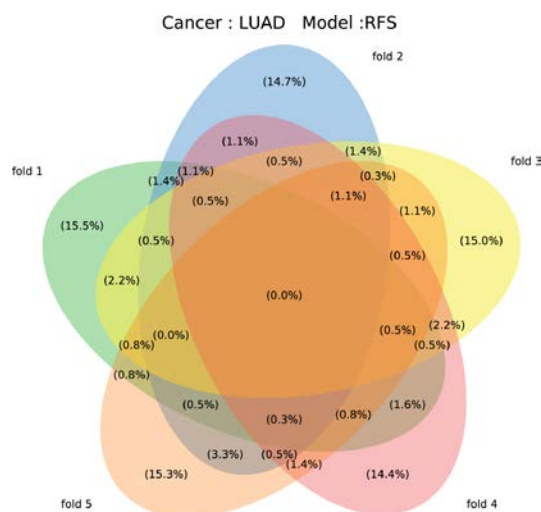
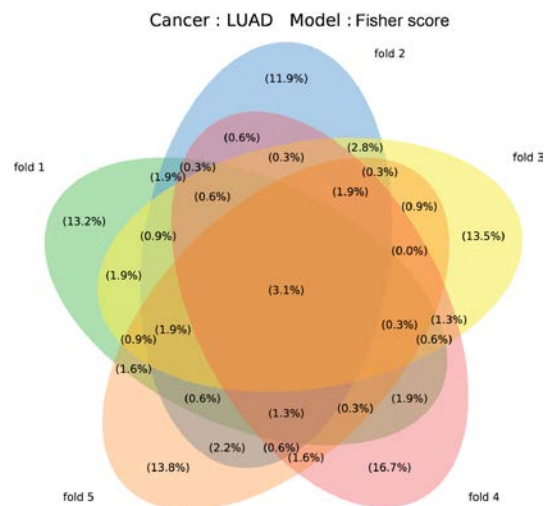
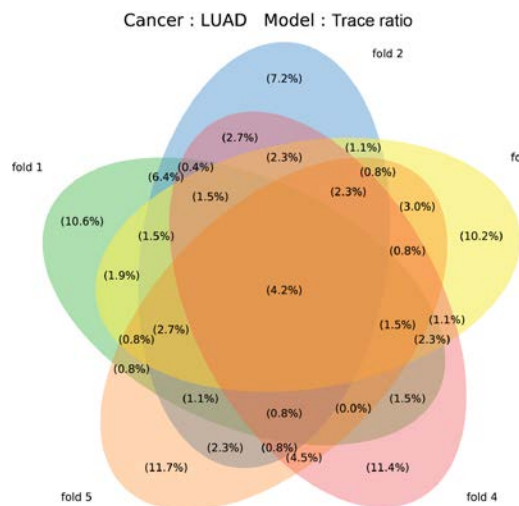
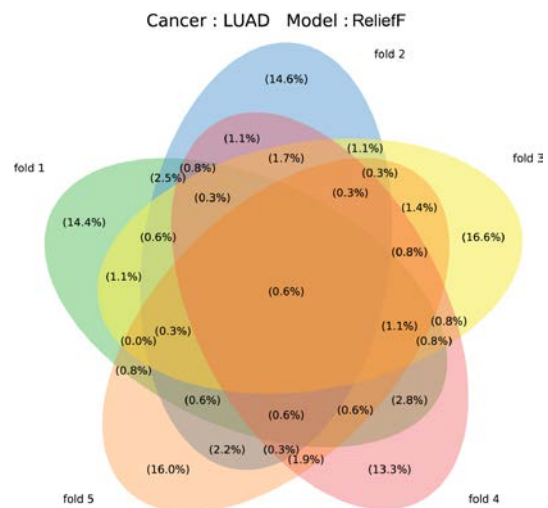
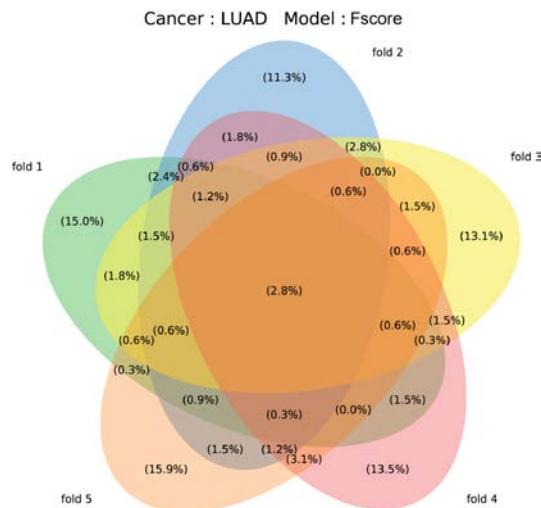
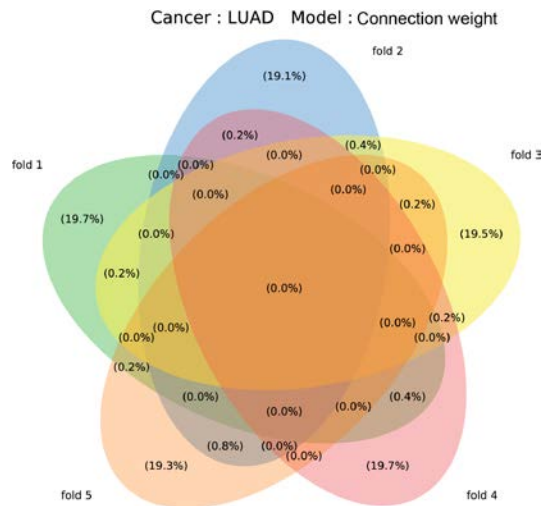


**Figure S1. Comparison of feature selection algorithms with cumulative top-k genes**

Violin plot shows  $c$ -indexes of the top genes (cumulative from 1 to 100,  $n = 100$ ) identified by each algorithm (left panel). White circles indicate the medians; box limits inside the polygons indicate the 25th and 75th percentiles as determined by R software; whiskers extend 1.5 times the interquartile range from the 25th and 75th percentiles; polygons represent density estimates of data and extend to extreme values. Asterisks (\* $P < 0.05$ ; \*\*\* $P < 0.001$ ; n.s., not significant) indicate results of one-way ANOVA ( $P$  value  $< 0.0001$ ) with post hoc test (pairwise t-test with Bonferroni-Holm correction). The x-axis and y-axis indicate the number of cumulative top genes and  $c$ -index, respectively (right panel).







**Figure S2. Intersection of genes between five folds (groups).** Venn diagrams show the intersection of selected genes in the 5-fold cross-validation using feature-selection algorithms.