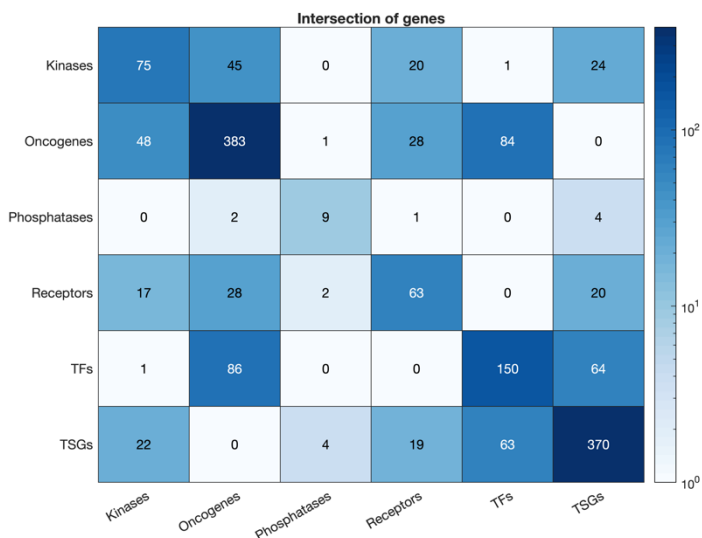
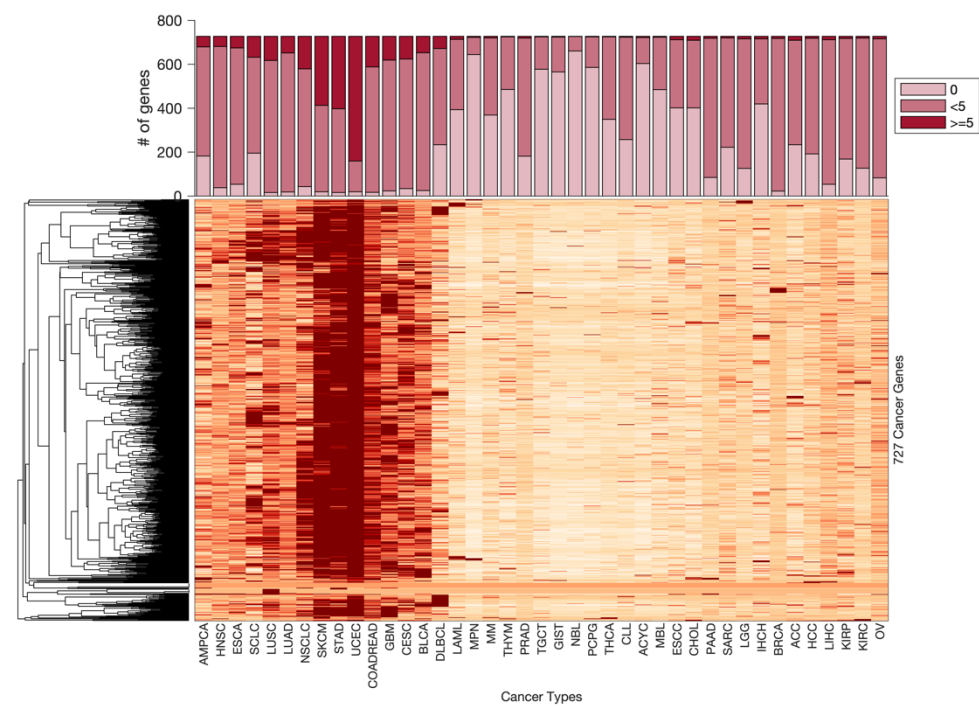


Mutational Landscape of Cancer-Driver Genes Across Human Cancers

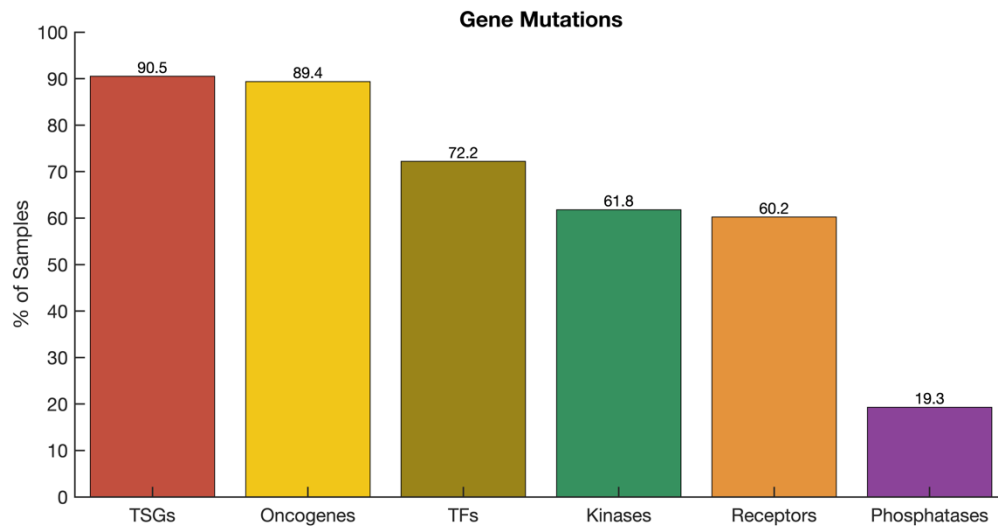
Supplemental Information



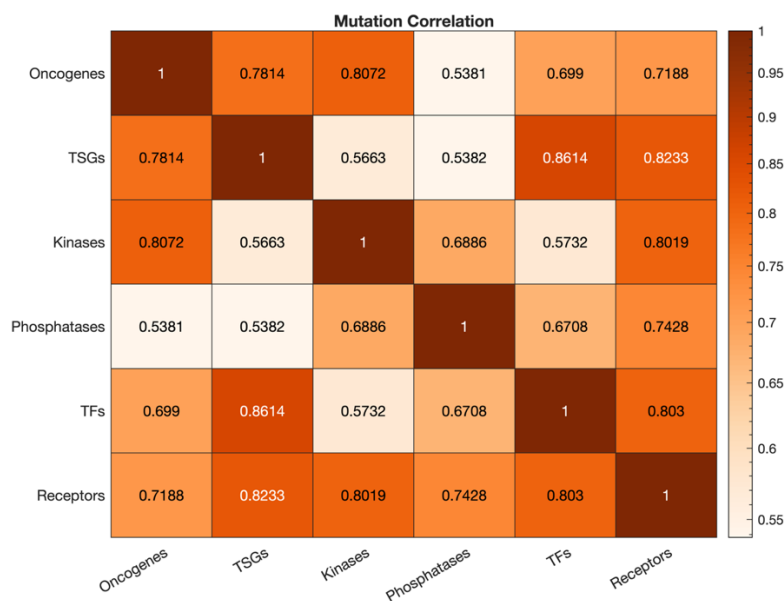
Supplementary Figure 1: Categories of known cancer genes with the main diagonal of the heatmap indicating the total gene count in each category. Off-diagonal numbers show the number of shared genes between the categories indicated by the rows and columns.



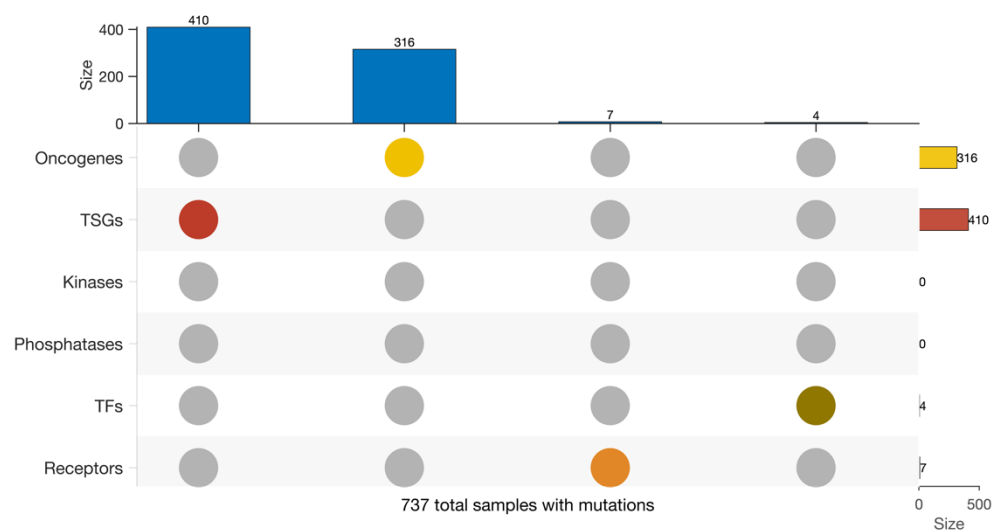
Supplementary Figure 2: Unsupervised hierarchical clustering of tumours based on mutation frequency of driver genes, with a grouped bar graph at the top indicating the number of driver genes mutated in $\geq 5\%$ (dark), $< 5\%$ (intermediate), or 0% (light) of the samples.



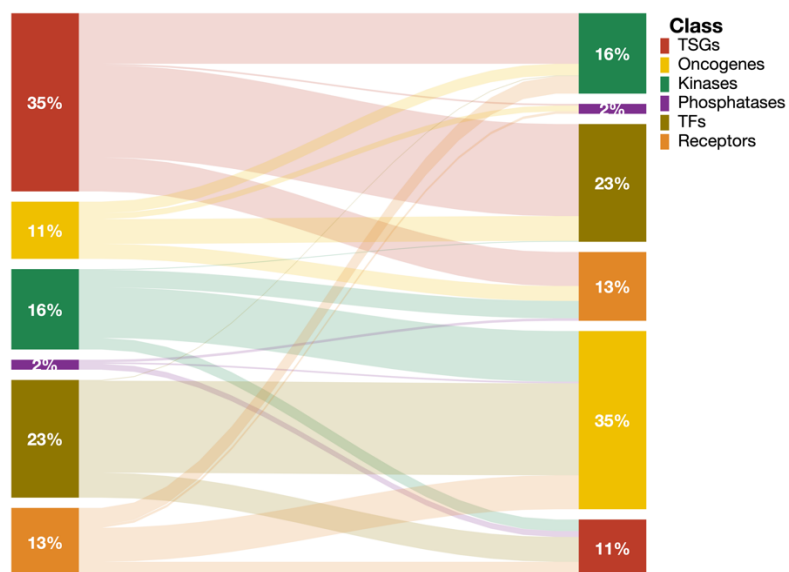
Supplementary Figure 3: *Frequency of driver genes from various classes across all tumour samples.*



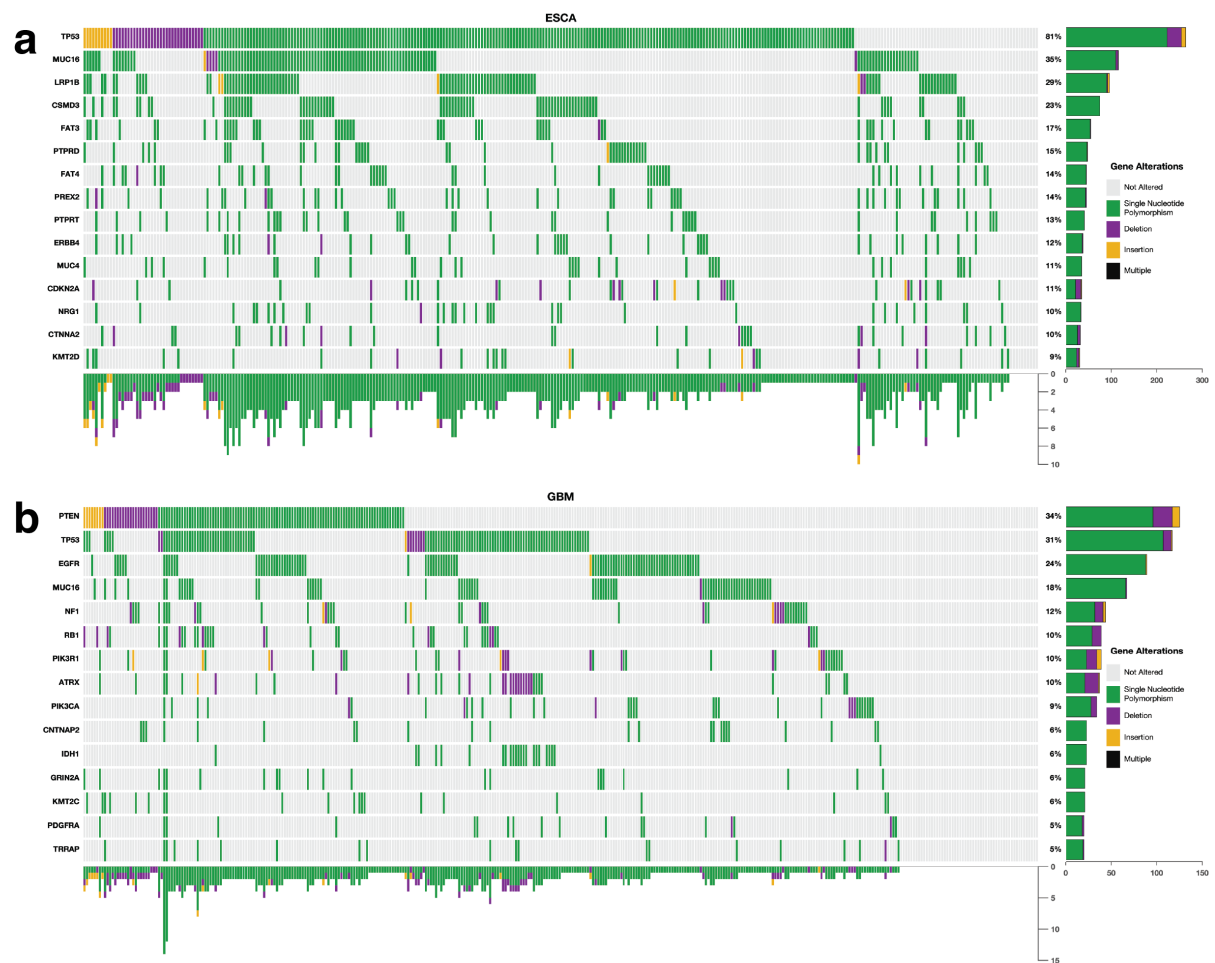
Supplementary Figure 4: *Correlation of mutation signature of cancer gene categories across 41 cancers. Heatmap numbers indicate Pearson's correlation scores, with increasing color intensity showing higher correlation.*



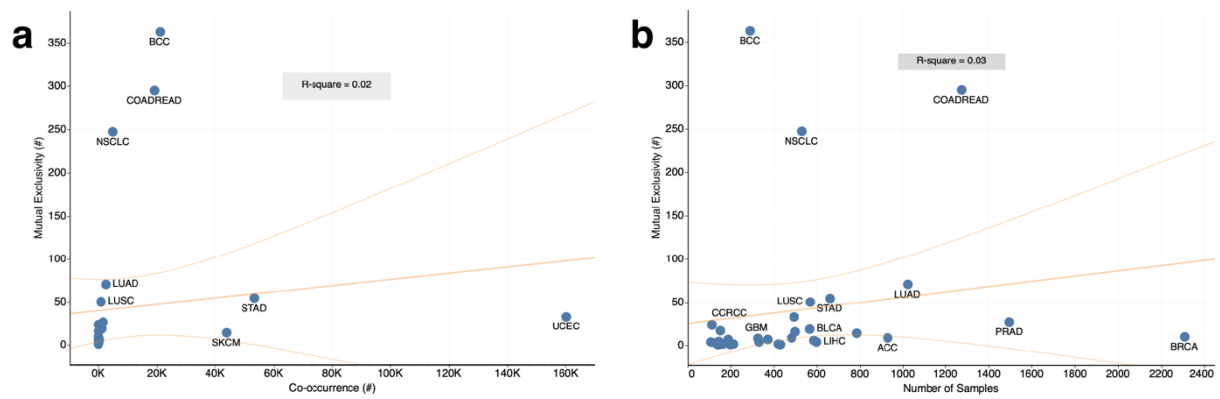
Supplementary Figure 5: Upset plot of the count of mutually exclusive mutated driver genes in all tumour samples.



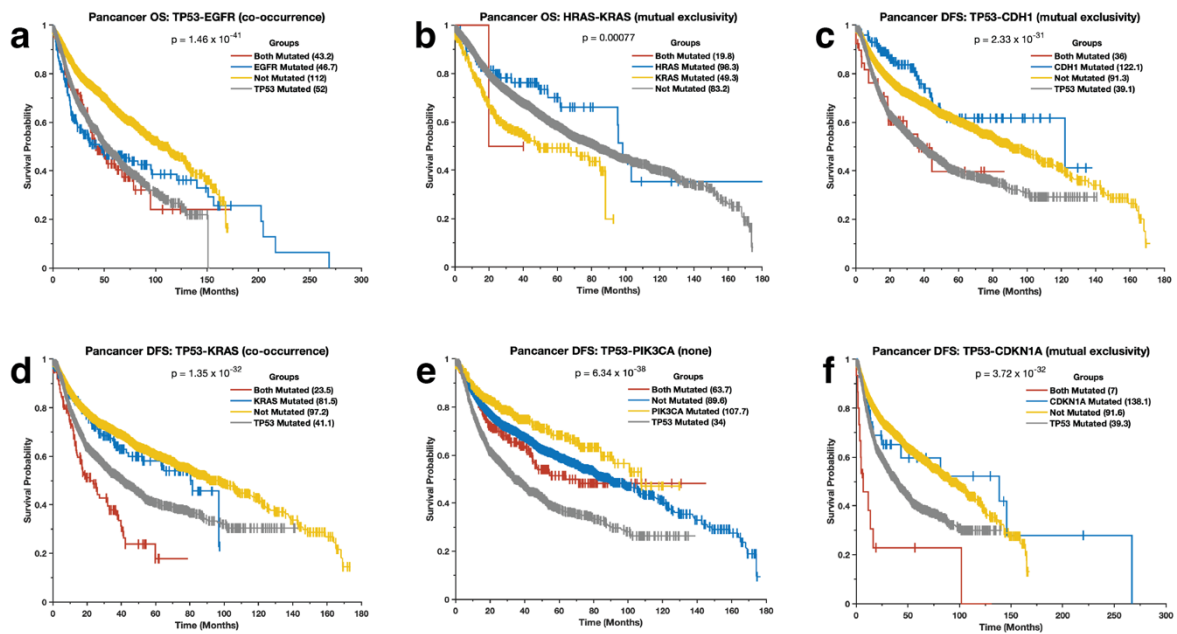
Supplementary Figure 6: Percentage of mutated cancer genes belonging to multiple categories. Note, the plotted data includes on the genes that have multiple cancer gene categories.



Supplementary Figure 7: Example of mutation signature plot with co-occurrence and exclusivity of mutations in oesophageal (a) and kidney (b) cancer, displaying only the 15 most mutated genes.



Supplementary Figure 8: Correlation between the number of co-occurring (a) and exclusive (b) mutations in gene pairs vs the number of profiled samples in each cancer type.



Supplementary Figure 9: Kaplan-Meier curve showing disease-free and overall survival of patients with tumours that have two mutated driver gene pairs, one mutated gene, or no mutated genes in the pair.

