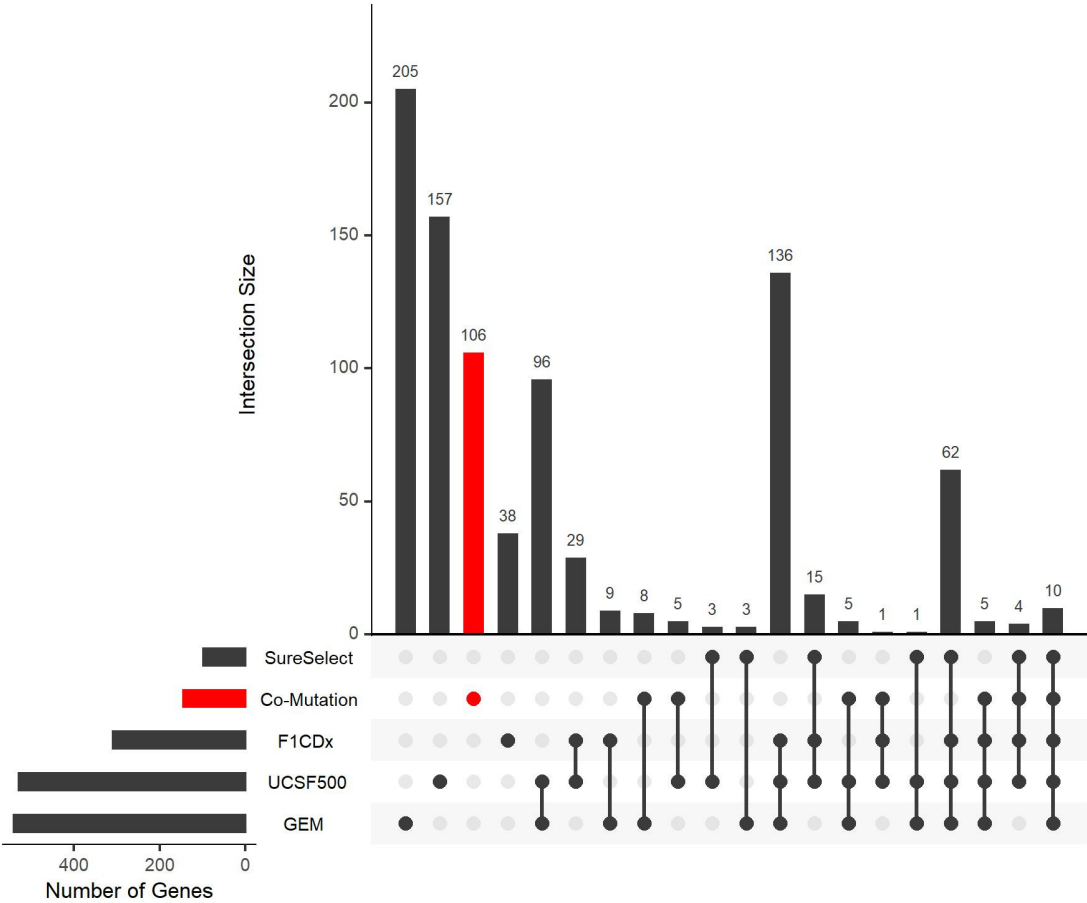


Supplementary Figure S1. The twenty most frequently mutated genes in the three cancer data consortiums separately. A. The Cancer Genome Atlas (TCGA). B. International Cancer Genome Consortium (ICGC). C. Cancer Dependency Map (DepMap). Each row of the heatmap represents a gene, and each column represents a subject showing mutation in at least one gene. Gene names in black denote protein-coding genes, and gene names in pink denote non-coding genes. Two barplots are attached at the left side of the heatmap to annotate two distinct features of the mutated genes. One barplot denotes the mutation frequency of each gene across all cohorts of one same consortium; the other barplot visualizes the gene length with the corresponding rank specified. Available phenotypic variables of subjects were indicated with color bars on the top of the heatmap. Subjects bearing mutations in all 20 genes are identified below the heatmap.



Supplementary Figure S2. Intersection analysis plot among five different cancer-related gene sets. The five gene sets included our identified co-mutation genes (red) and four clinical cancer gene panels (black), whose identification and gene number are depicted as horizontal barplot on the bottom left panel. The unitary, binary, tertiary, quaternary, and quinary intersection relations were illustrated with line segments on the bottom panel. The actual size of each intersection set formed by one, two, three, four, or five sets out of the total five was depicted in the vertical barplot on the top main panel. For example, the first verticle bar (205), represents the unique genes in GEM cancer gene panel and these 205 genes are not included in the other four gene sets. The last column

(10) represents the overall intersection of the five gene sets. The fourth to the last column (62), represents the intersection of the four cancer panels minus co-mutation gene sets. Thus, the four cancer gene panels share $62 + 10 = 72$ genes. SureSelect, Agilent SureSelect. F1CDx, FoundationOne CDx. UCSF500, University of California San Francisco UCSF500. GEM, Ashion Genomic Enabled Medicine.