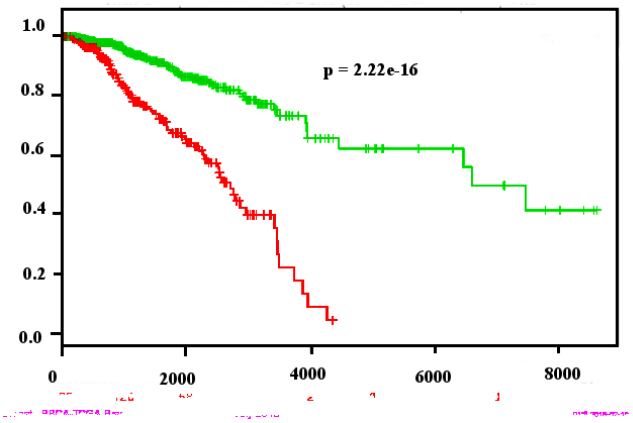

Figure ia: BRCA Top Gain

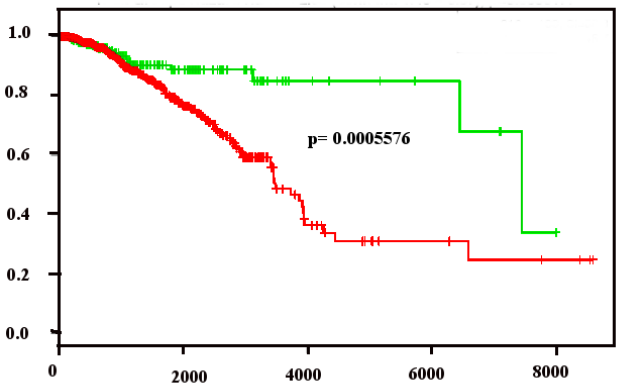

Figure ib: BRCA Specific Top Gain

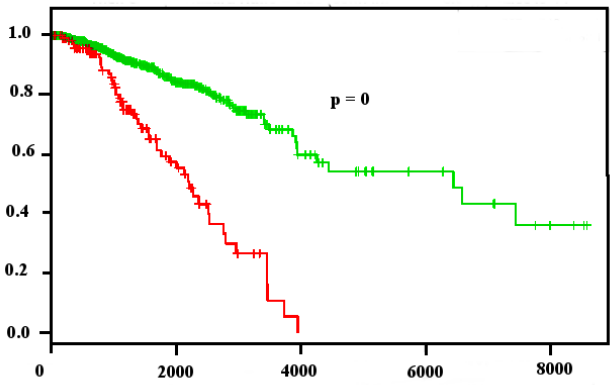

Figure ic: BRCA Top Lost

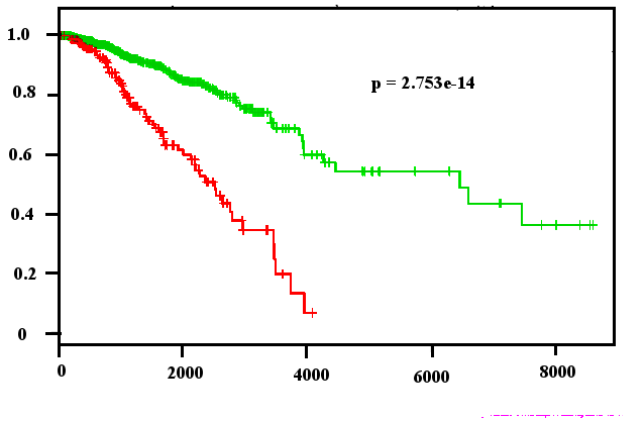

Figure id: BRCA Specific Top Lost

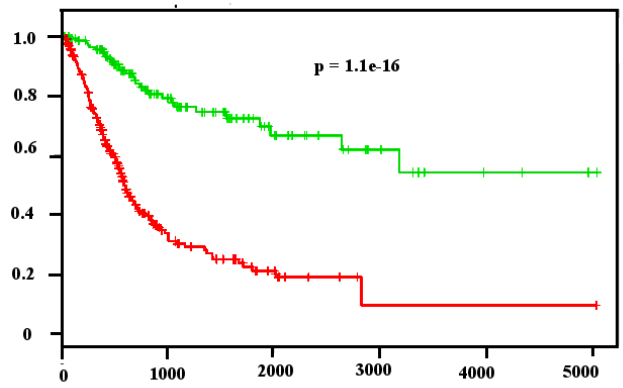

Figure iia: BLCA Top Gain

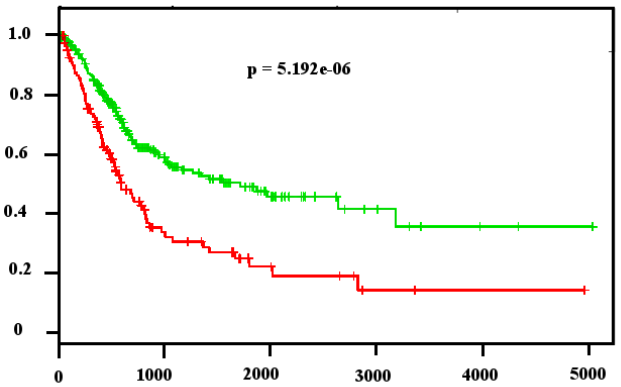

Figure iib: BLCA Specific Top Gain

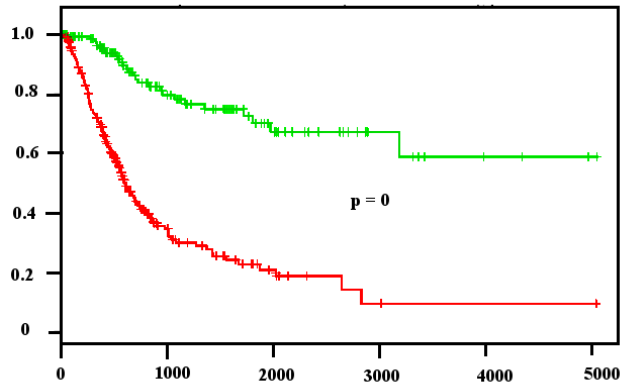

Figure iic: BLCA Top Lost

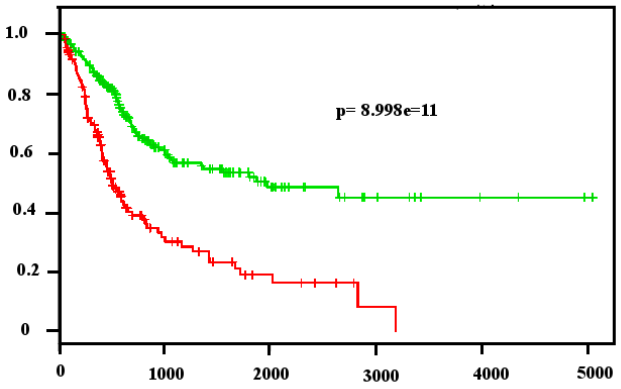

Figure iid: BLCA Specific Top Lost

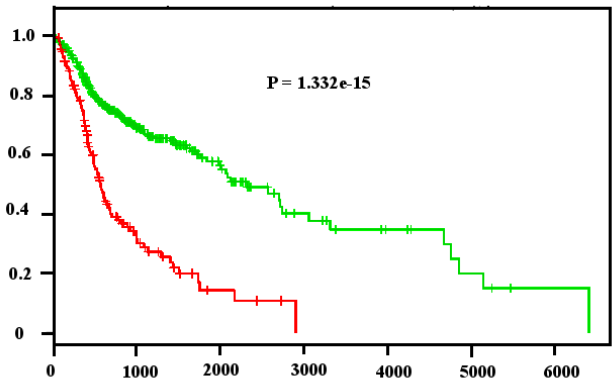

Figure iiia: HNSC Top Gain

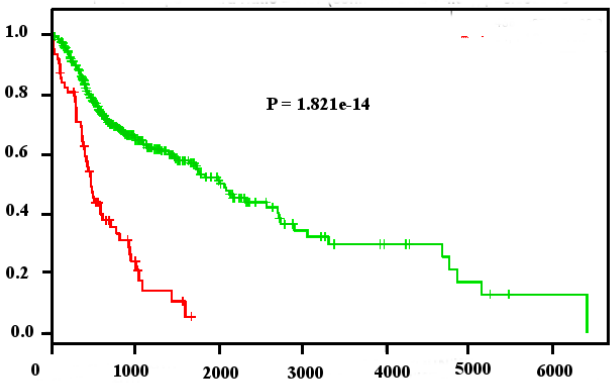

Figure iiib: HNSC Specific Top Gain

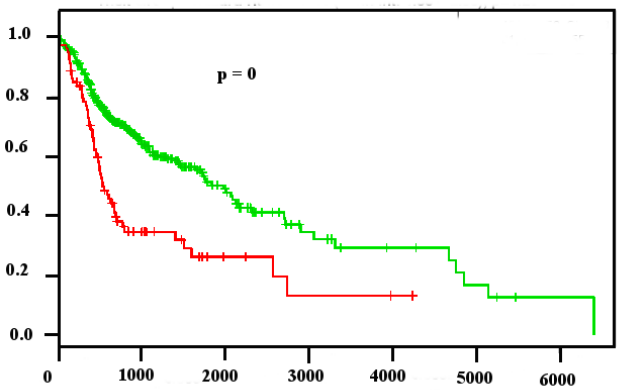

Figure iiic: HNSC Top Lost

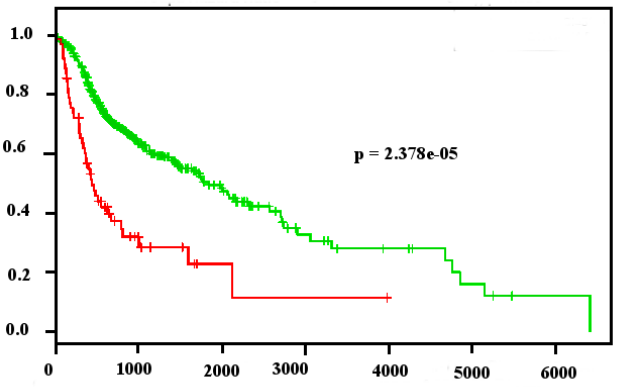

Figure iiid: HNSC Specific Top Lost

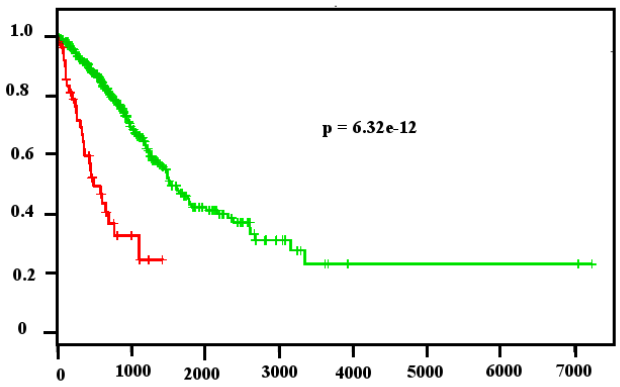

Figure iva: LUAD Top Gain

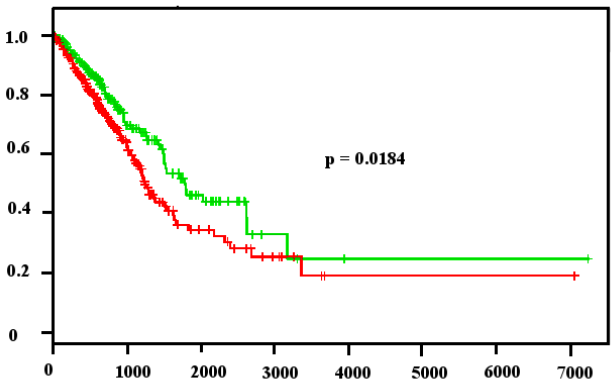

Figure ivb: LUAD Specific Top Gain

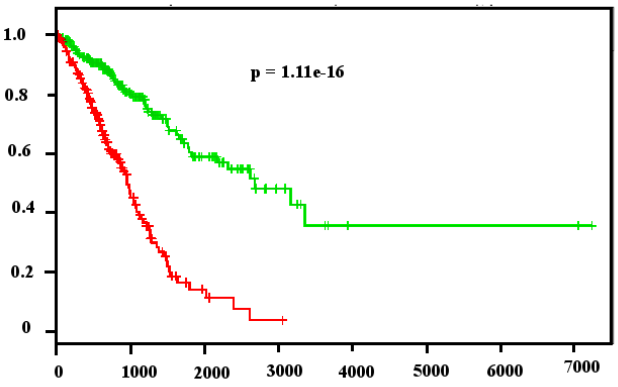

Figure ivc: LUAD Top Lost

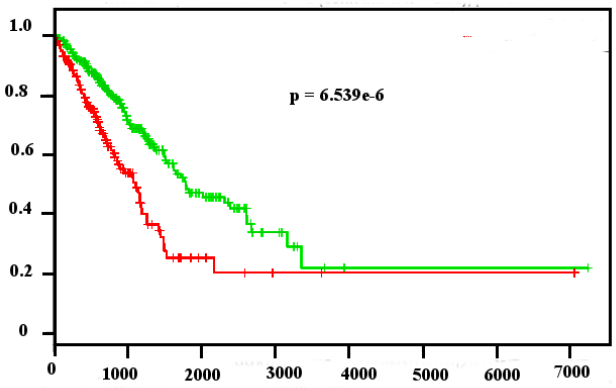

Figure ivd: LUAD Specific Top Lost

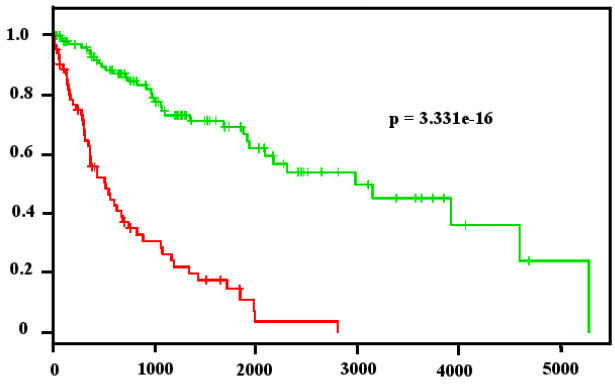

Figure va: LUSC Top Gain

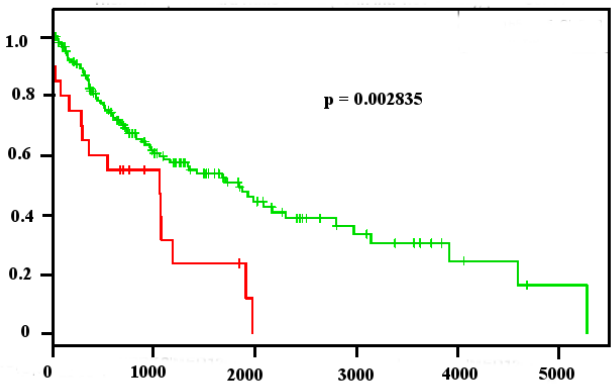

Figure vb: LUSC Specific Top Gain

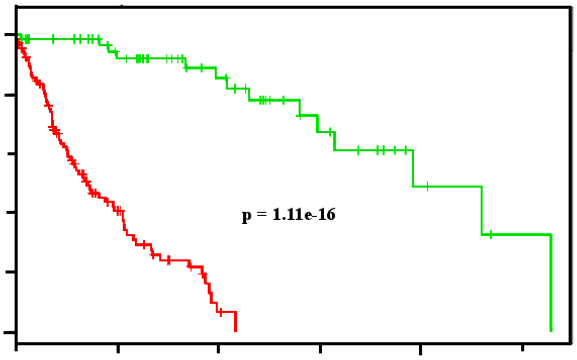

Figure vc: LUSC Top Lost

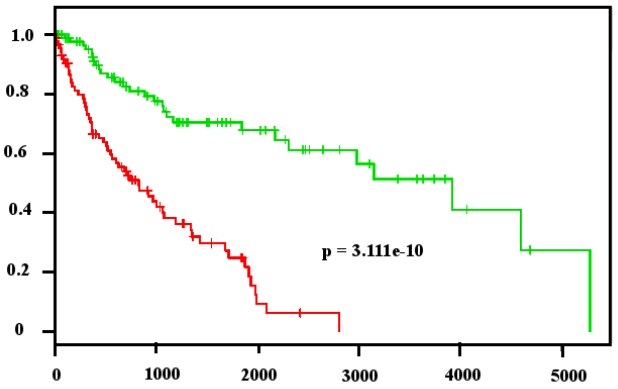

Figure vd: LUSC Specific Top Lost

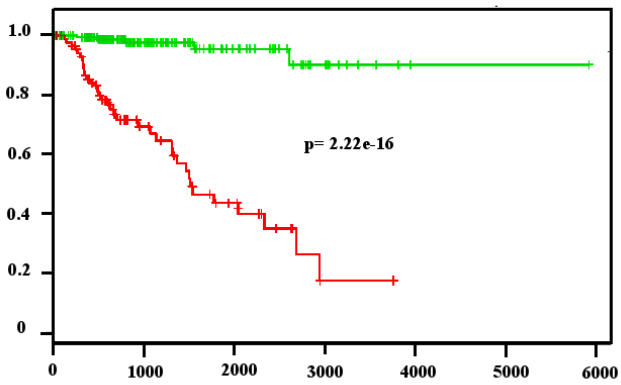

Figure via: KIRP Top Gain

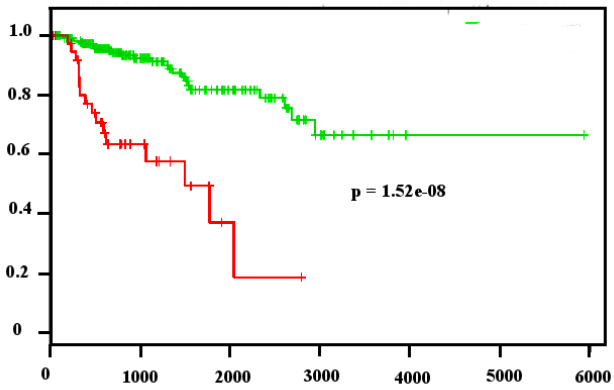

Figure vib: KIRP Specific Top Gain

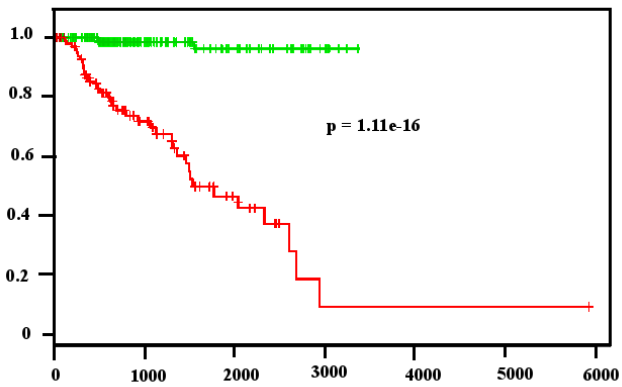

Figure vic: KIRP Top Lost

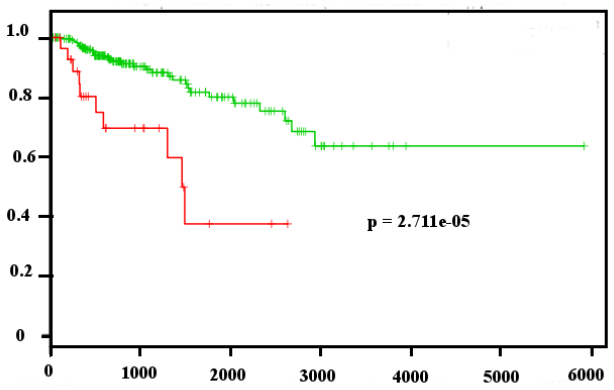

Figure vid: KIRP Specific Top Lost

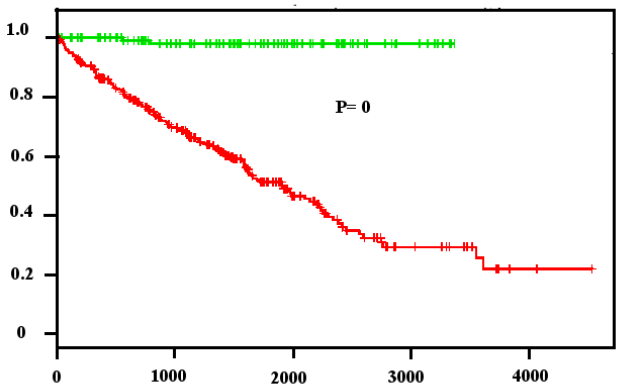

Figure viia: KIRC Top Gain

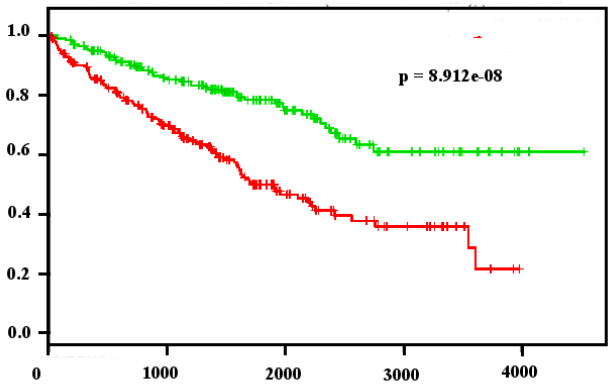

Figure viib: KIRC Specific Top Gain

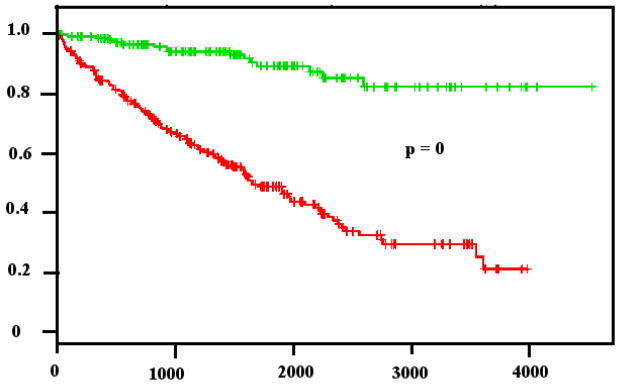

Figure viic: KIRC Top Lost

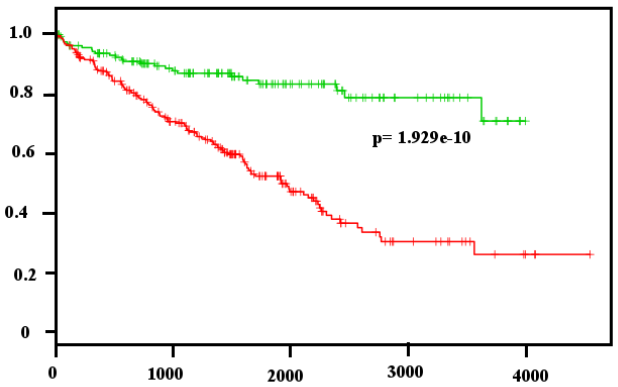

Figure viid: KIRC Specific Top Lost

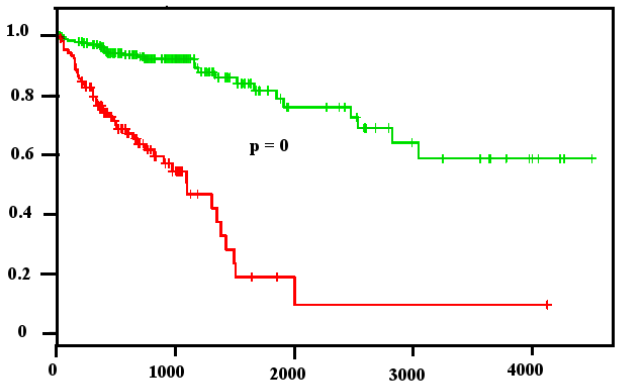

Figure viiia: COAD Top Gain

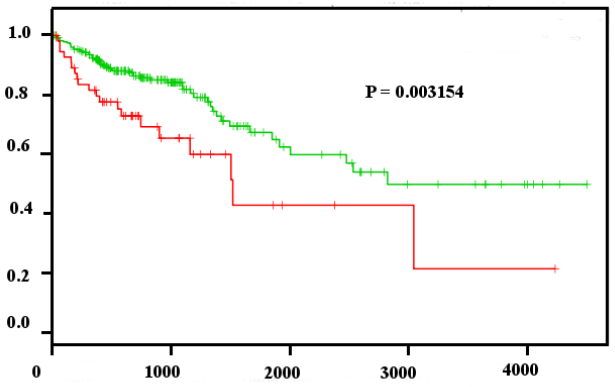

Figure viiib: COAD Specific Top Gain

1

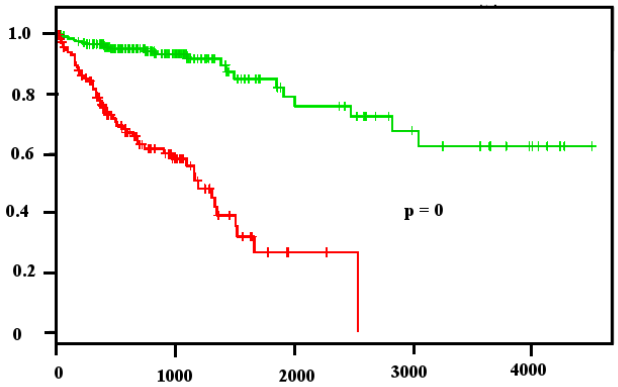

Figure viiic: COAD Top Lost

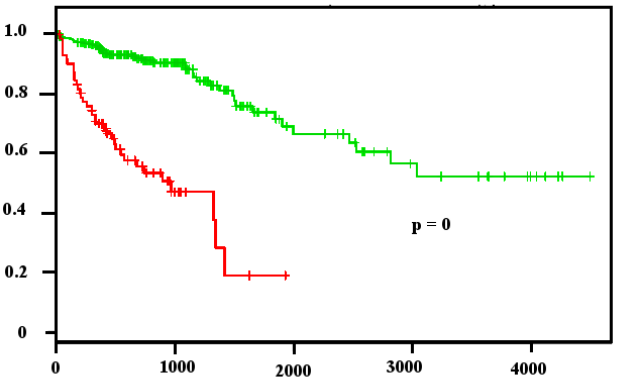

Figure viiid: COAD Specific Top Lost

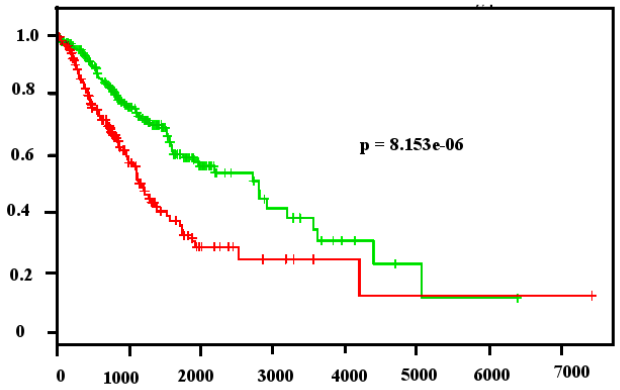

Figure ixa: STES Top Gain

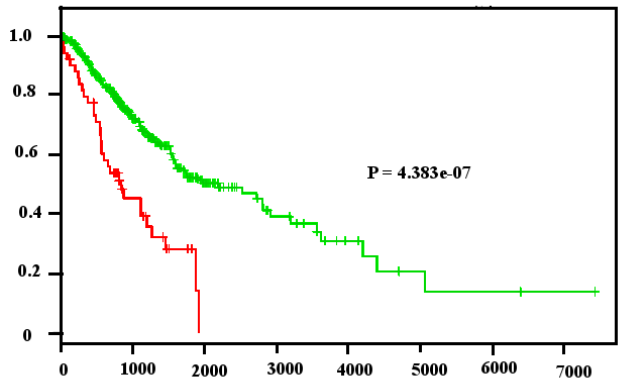

Figure ixb: STES Specific Top Gain

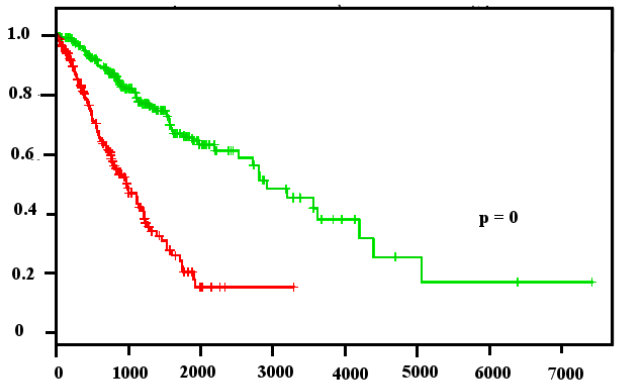

Figure ixc: STES Top Lost

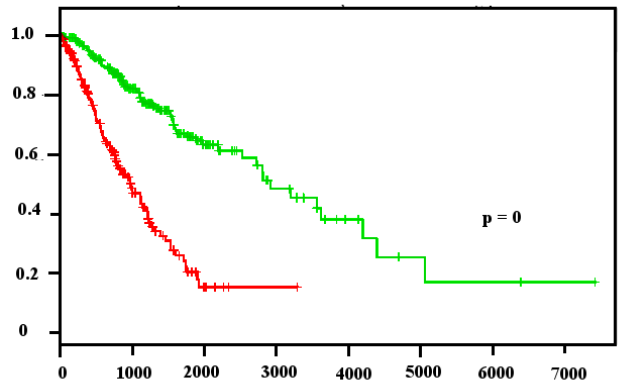

Figure ixd: STES Specific Top Lost

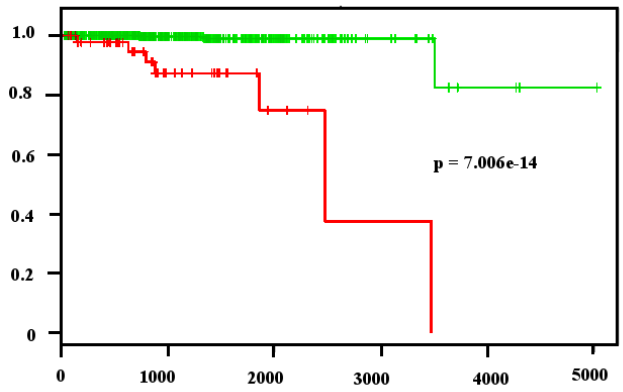

Figure xa: PRAD Top Gain

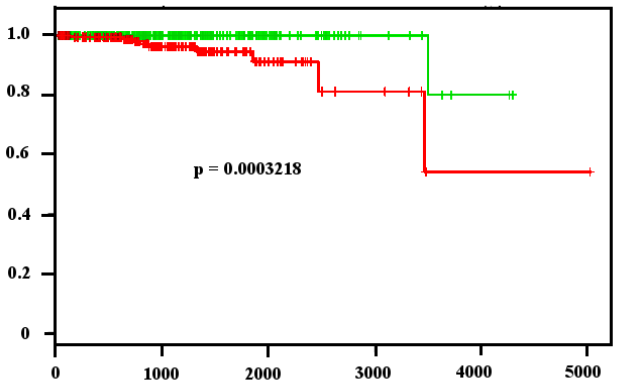

Figure xb: PRAD Specific Top Gain

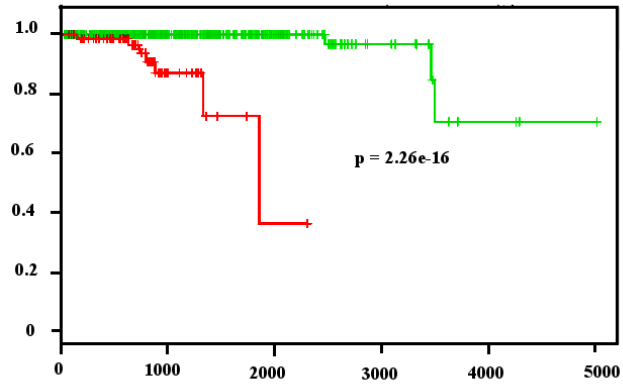

Figure xc: PRAD Top Lost

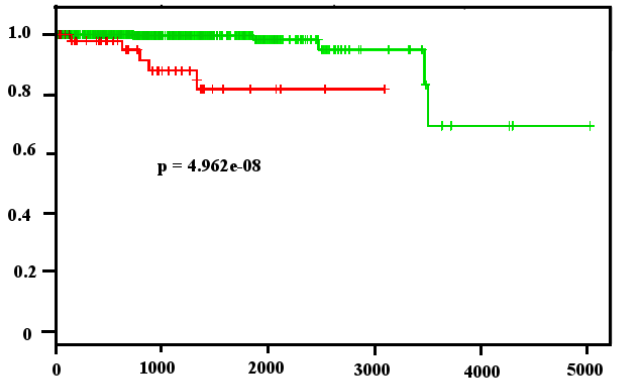

Figure xd: PRAD Specific Top Lost

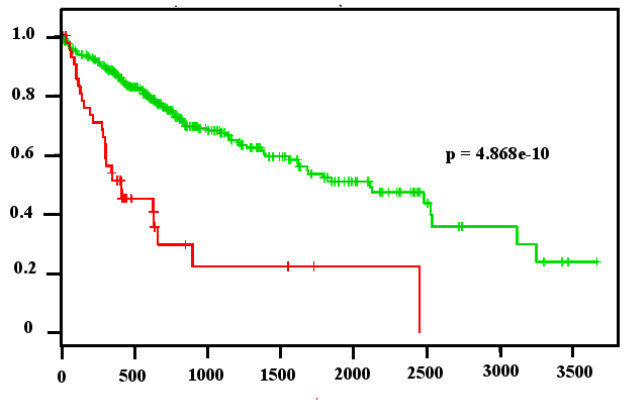

Figure xiia: LIHC Specific Top Gain

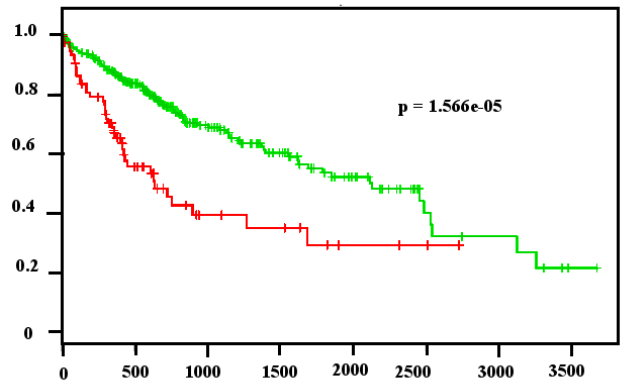

Figure xiib: LIHC Top Lost

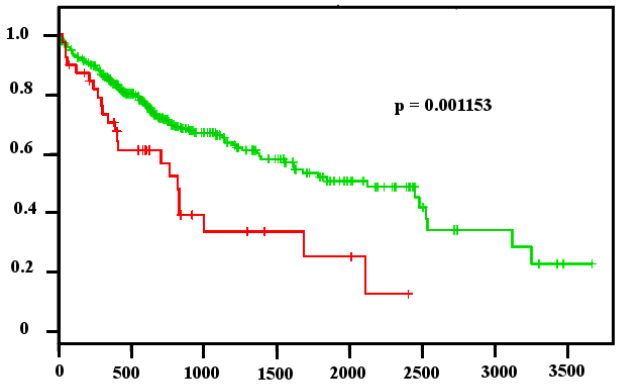

Figure xiic: LIHC Specific Top Lost

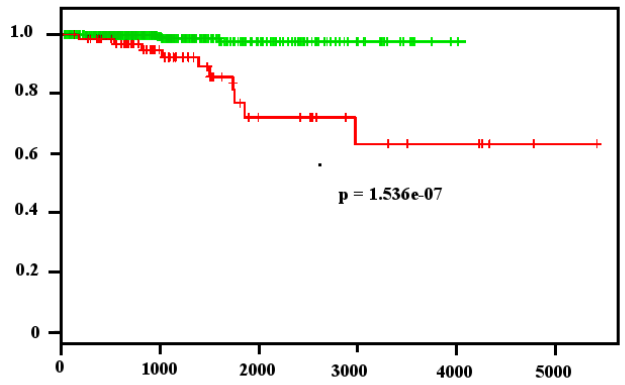

Figure xiiia: THCA Top Gain

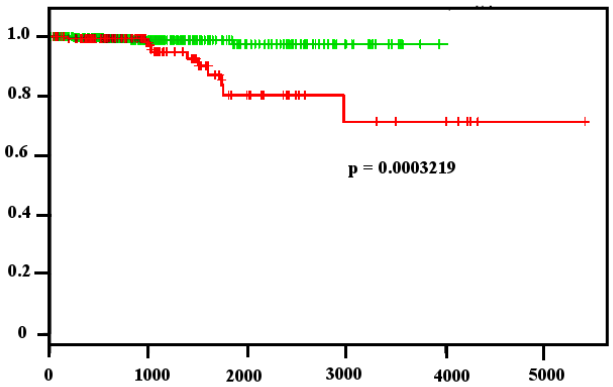

Figure xiiib: THCA Specific Top Gain

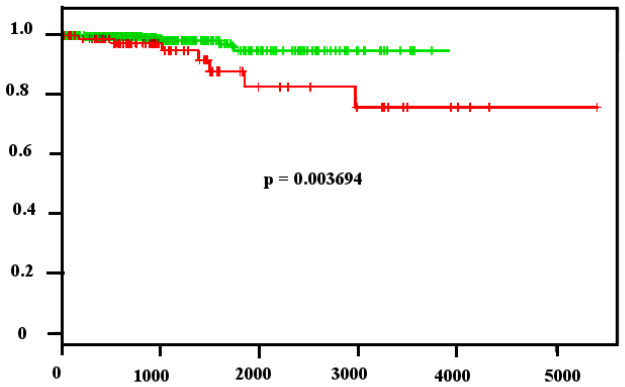

Figure xiiic: THCA Top Lost

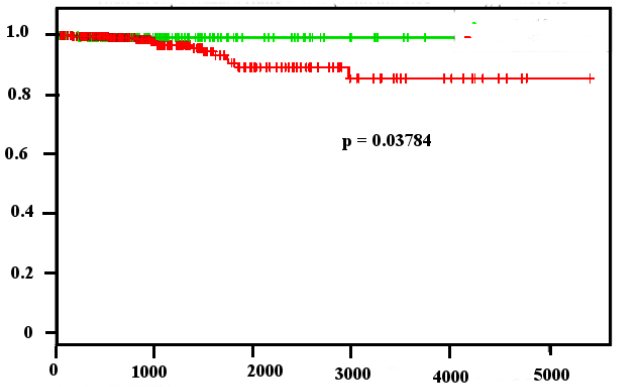

Figure xiiid: THCA Specific Top Lost

Supplementary Figure 3 (i - xiiic): Kaplan-Meier survival analysis plots of multigene cancer biomarkers involved in edgetic perturbations. The x axes indicate the number of days until patient death whereas the y axes indicate the probability of patient survival. In all the Figures, the green lines indicate better survival (longer life-span) after cancer diagnosis while the red lines indicate poor survival (shorter life-span) after cancer diagnosis as a result of the proteins involved in edgetic gains or losses. In all the cases, the proteins involved in edgteic perturbations predicted poor survival of the patients (Log-rank test p-value < 0.05), indicating their importance in cancer monitoring and prognosis. (a) Overall survival predicted from gene signatures involved in edgetic gains across most patients of a cancer type (except for LIHC), (b) Overall survival predicted from gene signatures involved in edgetic losses across most patients of a cancer type, (c) Overall survival predicted from gene signatures involved in edgetic gains across patients showing cancer-specific perturbations, (d) Overall survival predicted from gene signatures involved in edgetic losses across patients showing cancer-specific perturbations. The names of the prominent proteins with multiple perturbations responsible for the above observations can be found in Supplementary File 7.xls (Tables 7a and 7b).