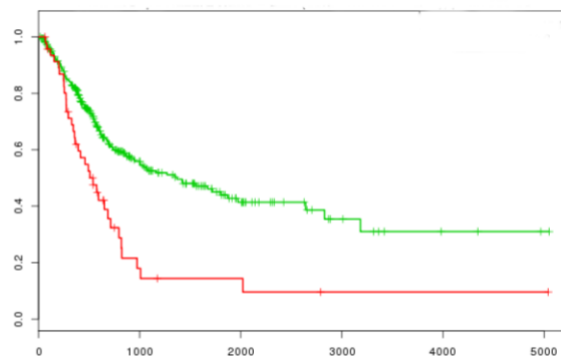
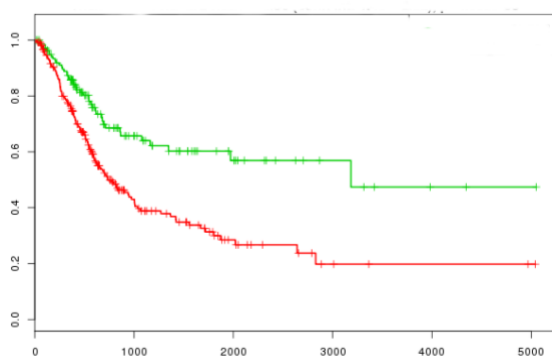


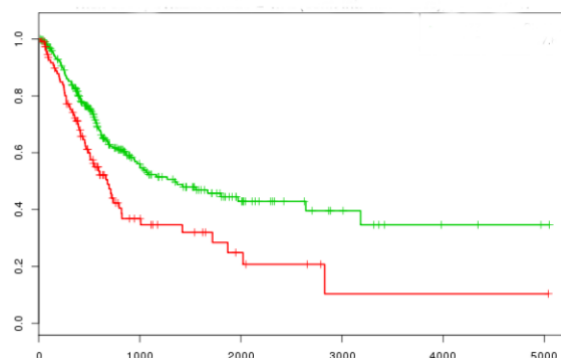
BLCA (a)



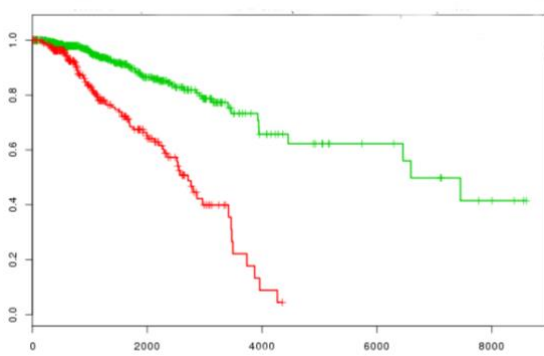
BLCA (b)



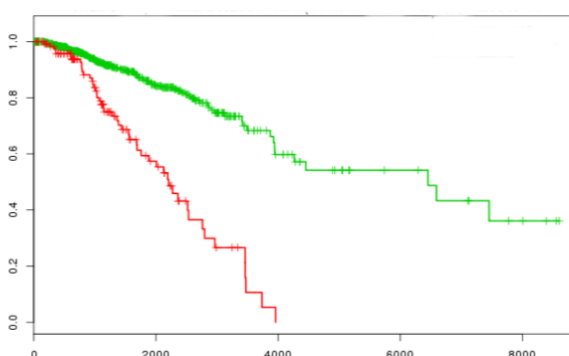
BLCA (c)



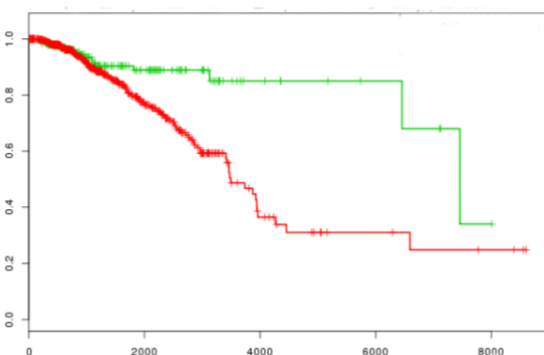
BLCA (d)



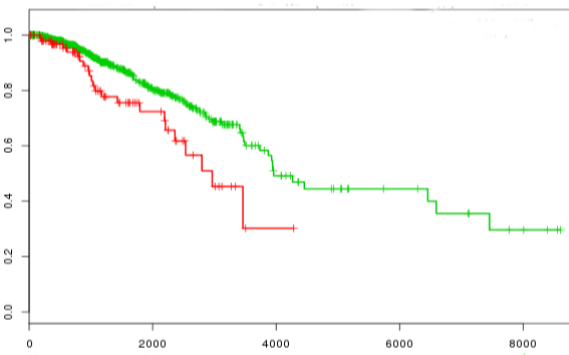
BRCA (a)



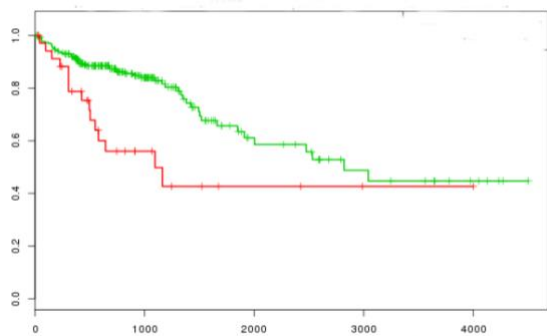
BRCA (b)



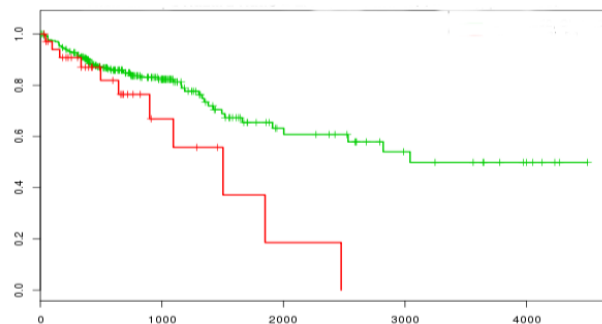
BRCA (c)



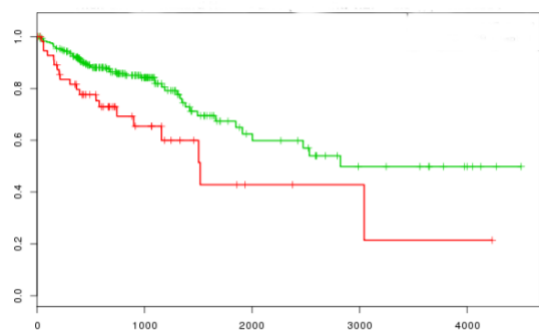
BRCA (d)



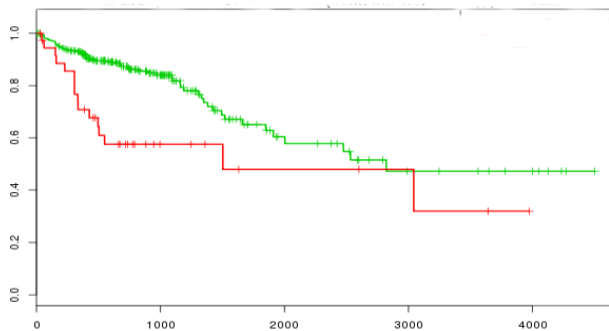
COAD (a)



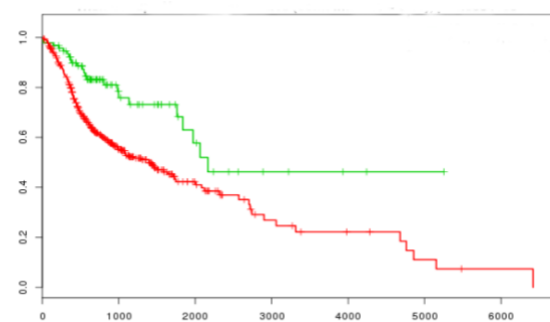
COAD (b)



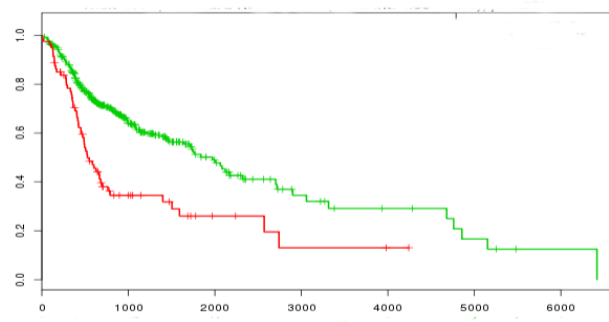
COAD (c)



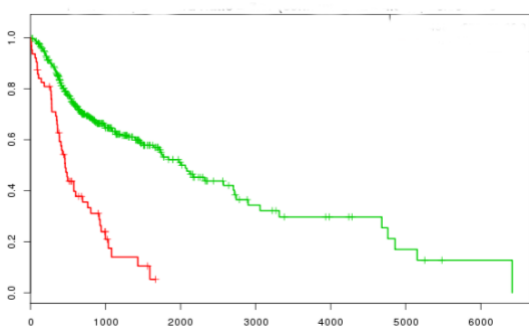
COAD (d)



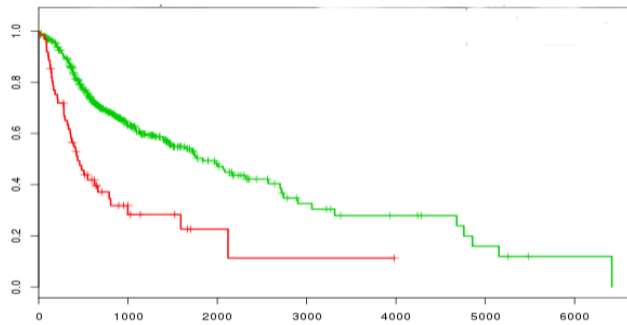
HNSC (a)



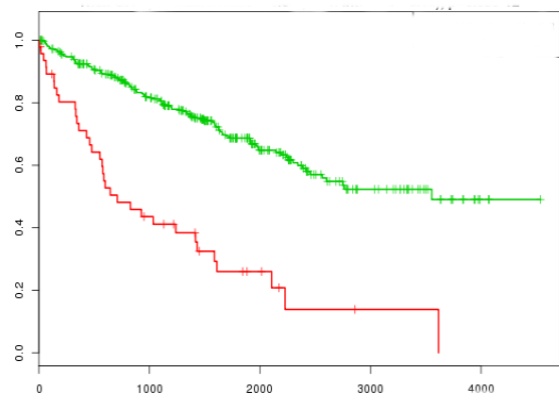
HNSC (b)



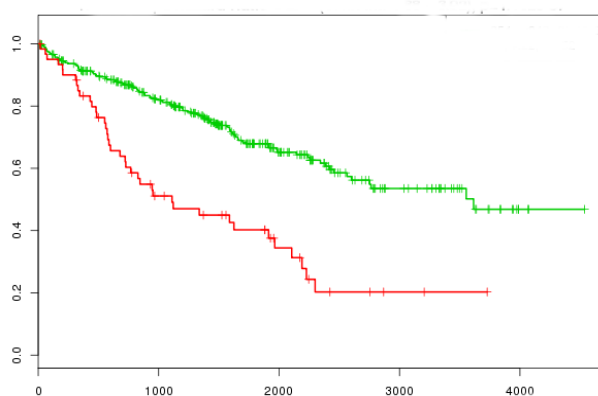
HNSC (c)



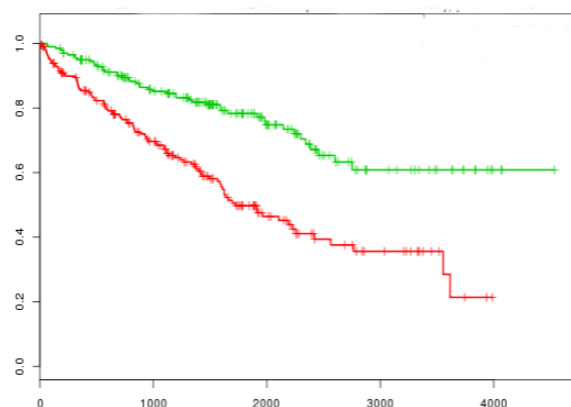
HNSC (d)



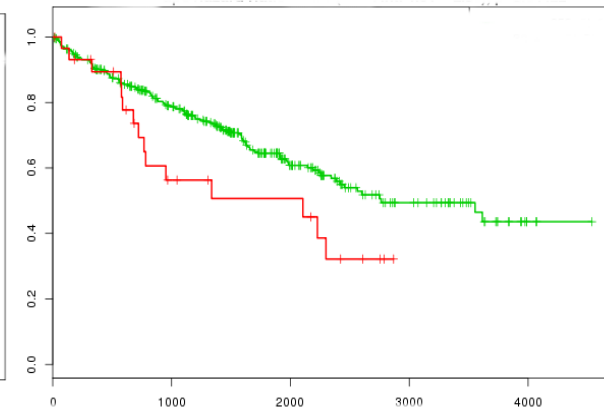
KIRC (a)



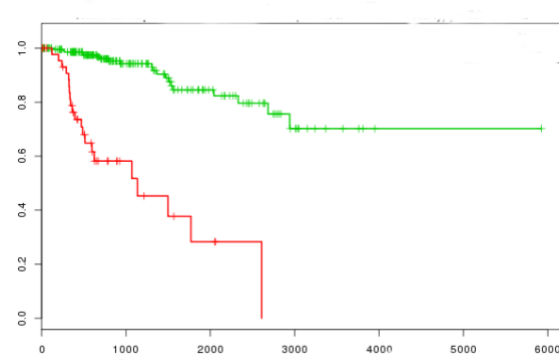
KIRC (b)



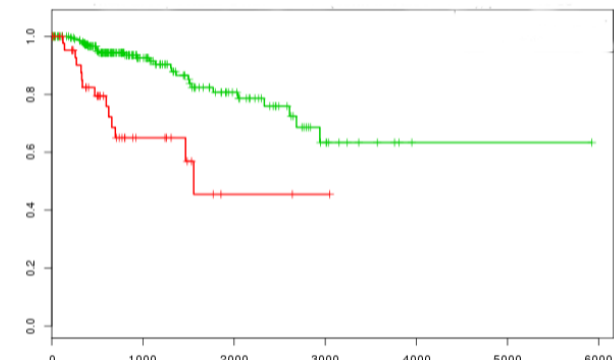
KIRC (c)



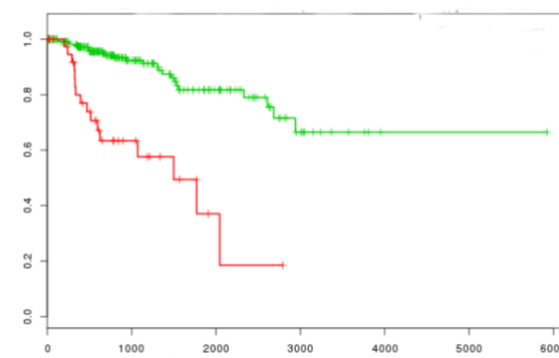
KIRC (d)



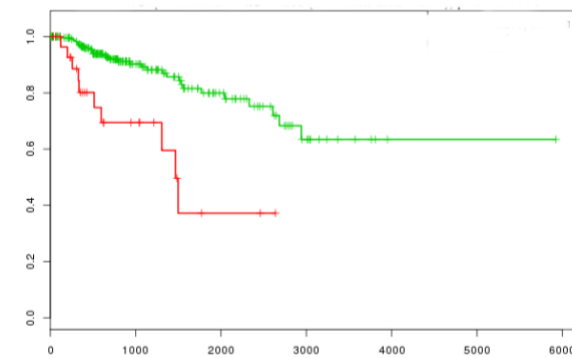
KIRP (a)



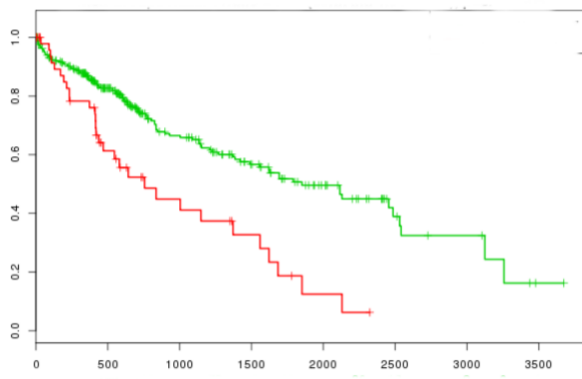
KIRP (b)



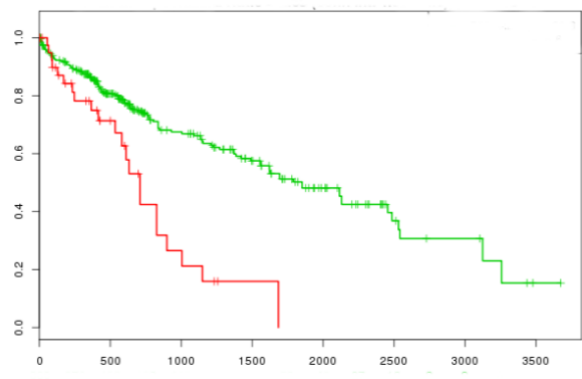
KIRP (c)



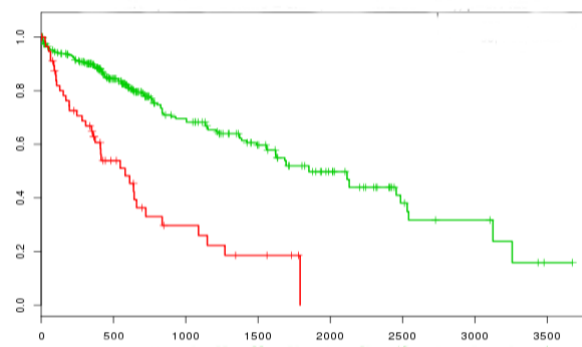
KIRP (d)



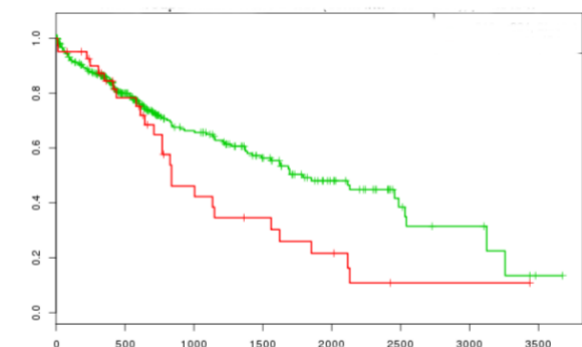
LIHC (a)



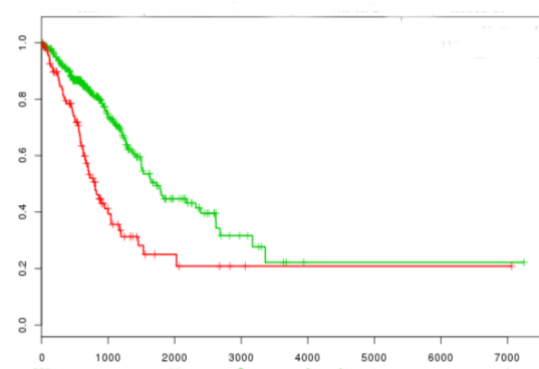
LIHC (b)



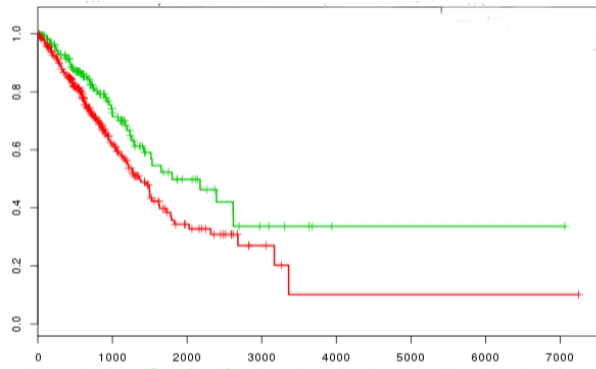
LIHC (c)



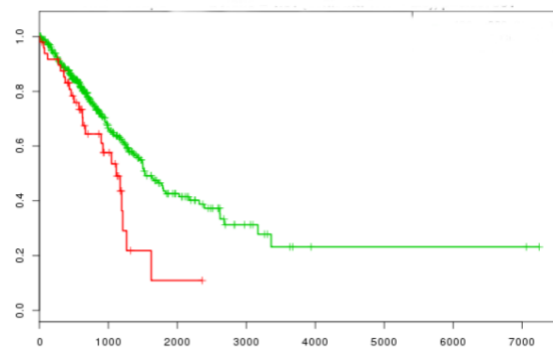
LIHC (d)



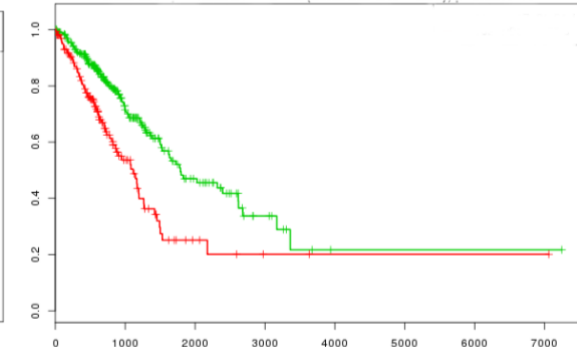
LUAD (a)



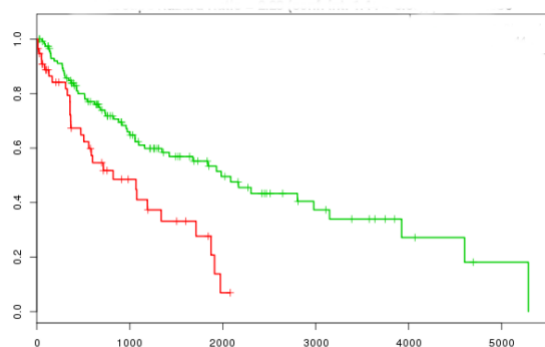
LUAD (b)



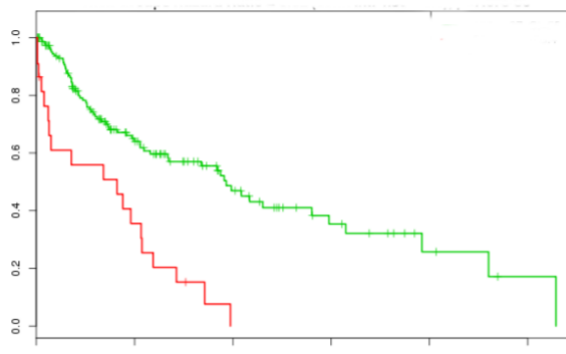
LUAD (c)



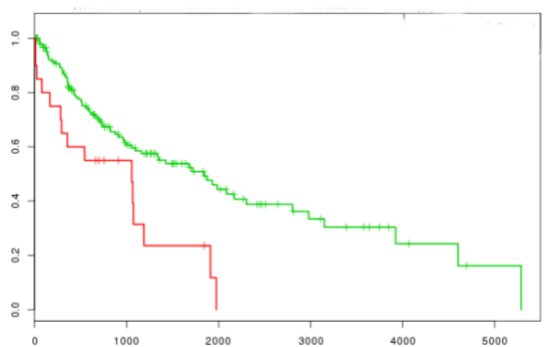
LUAD (d)



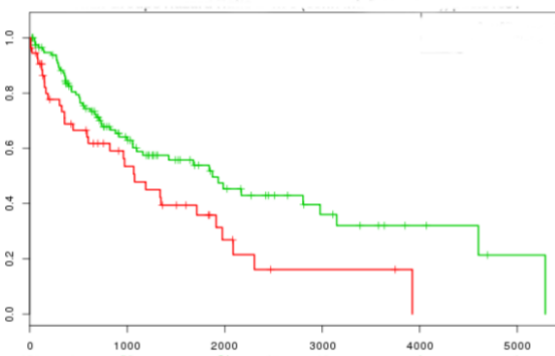
LUSC (a)



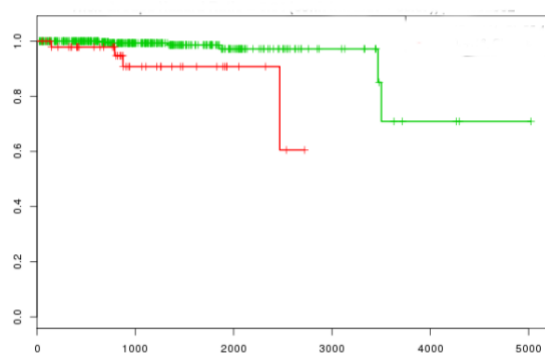
LUSC (b)



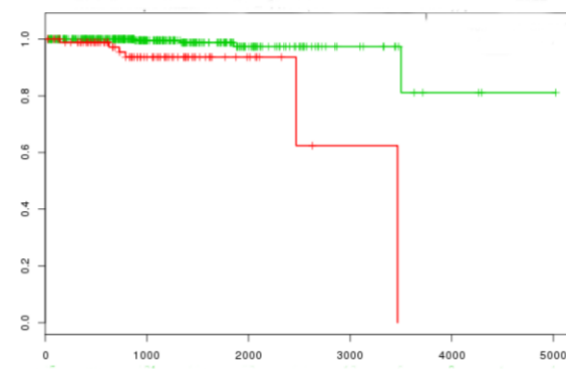
LUSC (c)



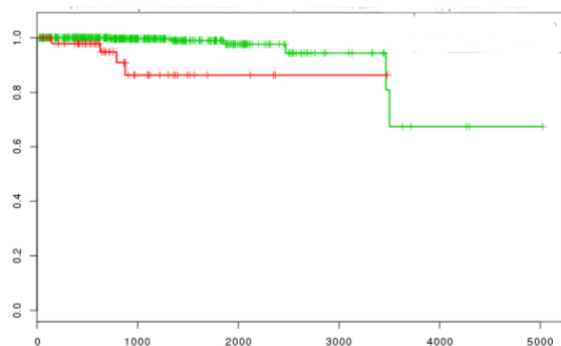
LUSC (d)



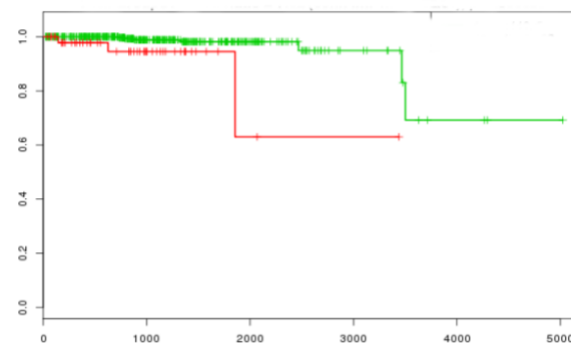
PRAD (a)



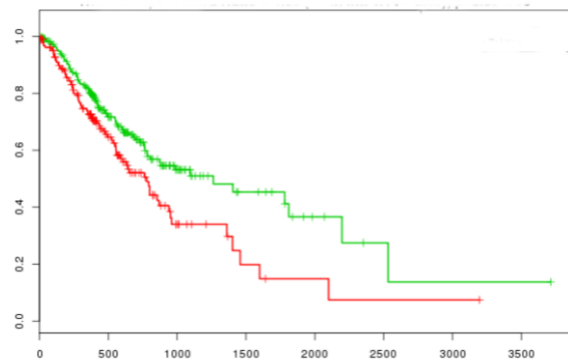
PRAD (b)



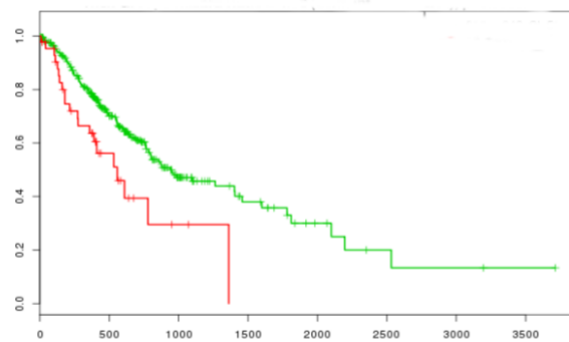
PRAD (c)



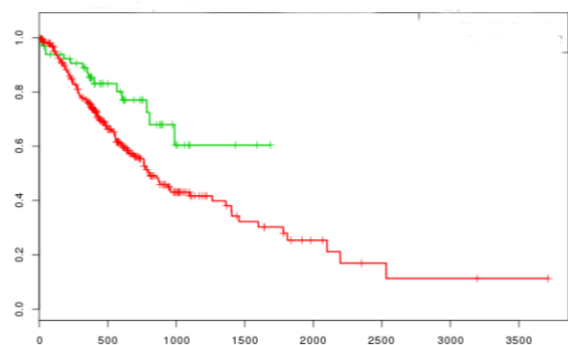
PRAD (d)



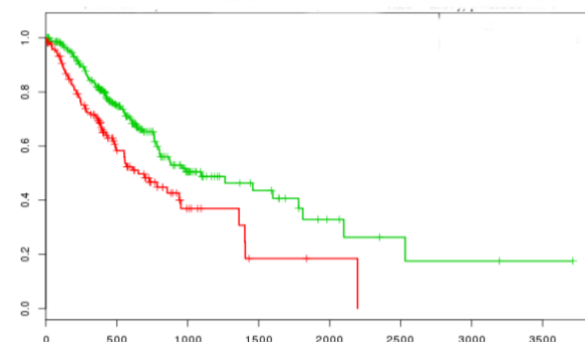
STES (a)



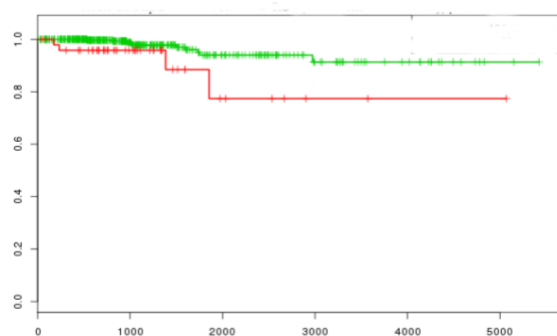
STES (b)



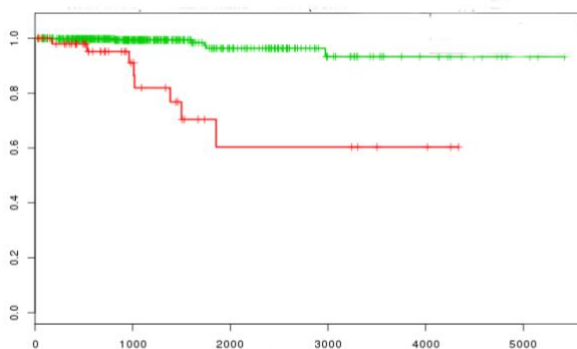
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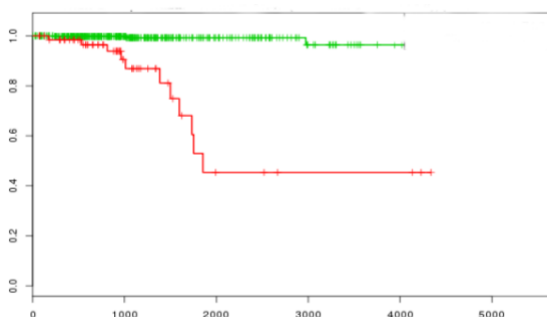
STES (d)



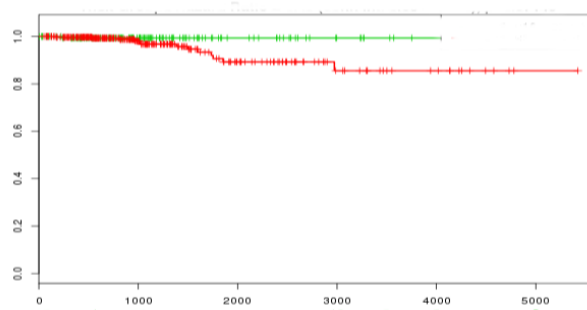
THCA (a)



THCA (b)



THCA (c)



THCA (d)

**Supplementary Figure 2:** 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 edgetic perturbations predicted poor survival of the patients (Logrank test  $p\text{-value} < 0.05$ ), 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, (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 multigene signatures responsible for the above observations can be found in Supplementary File 7.xls (Tables 7a and 7b).