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Supplemental Material to:

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Identification of two poorly prognosed ovarian carcinoma subtypes associated with CHEK2 germ-line mutation and non-CHEK2 somatic mutation gene signatures

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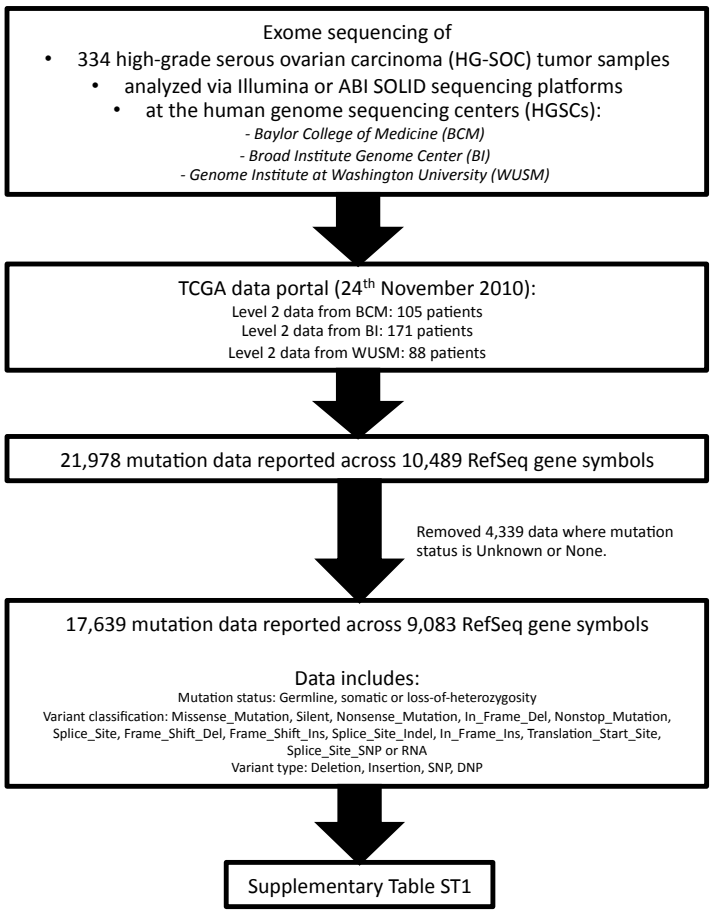
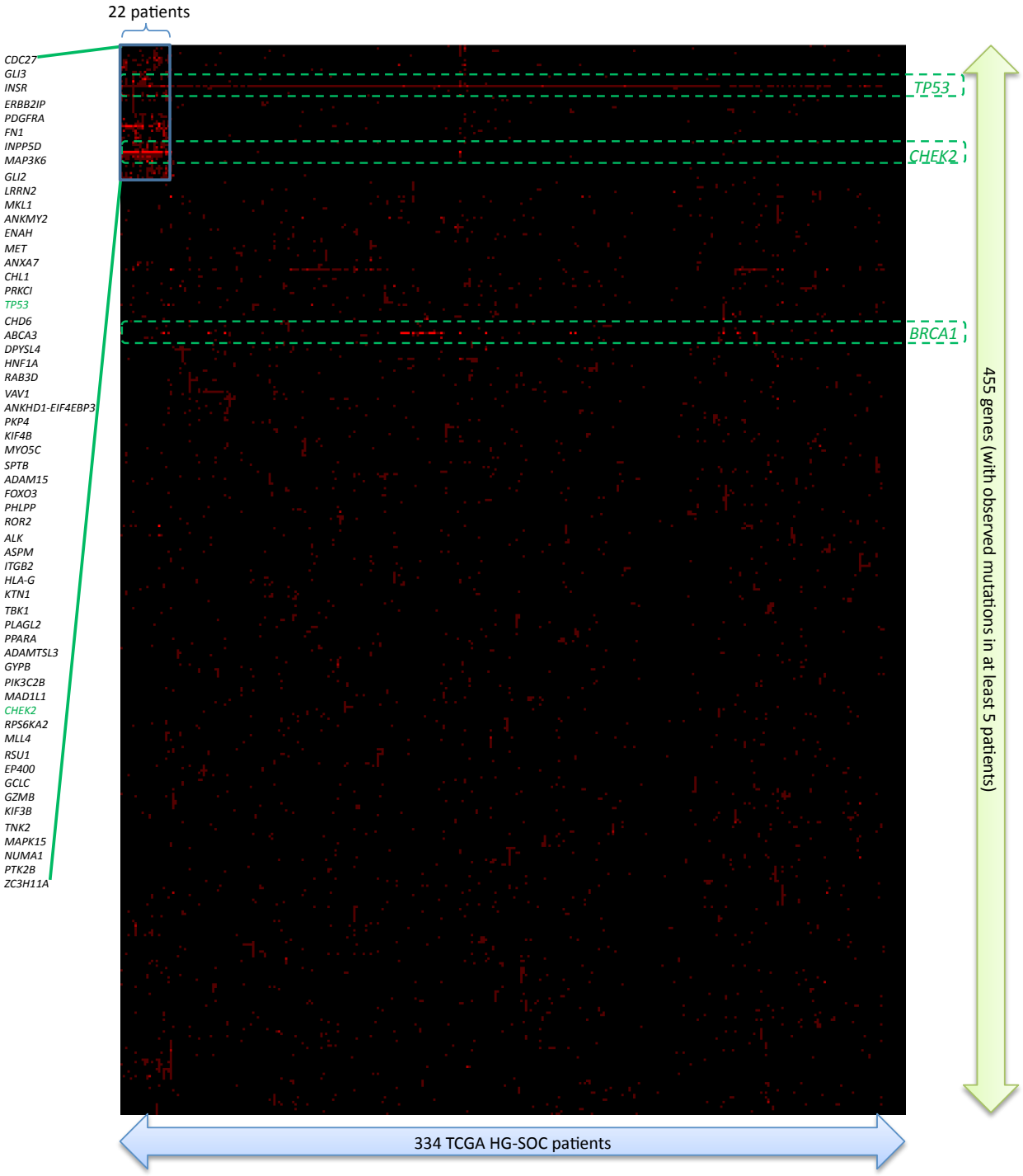
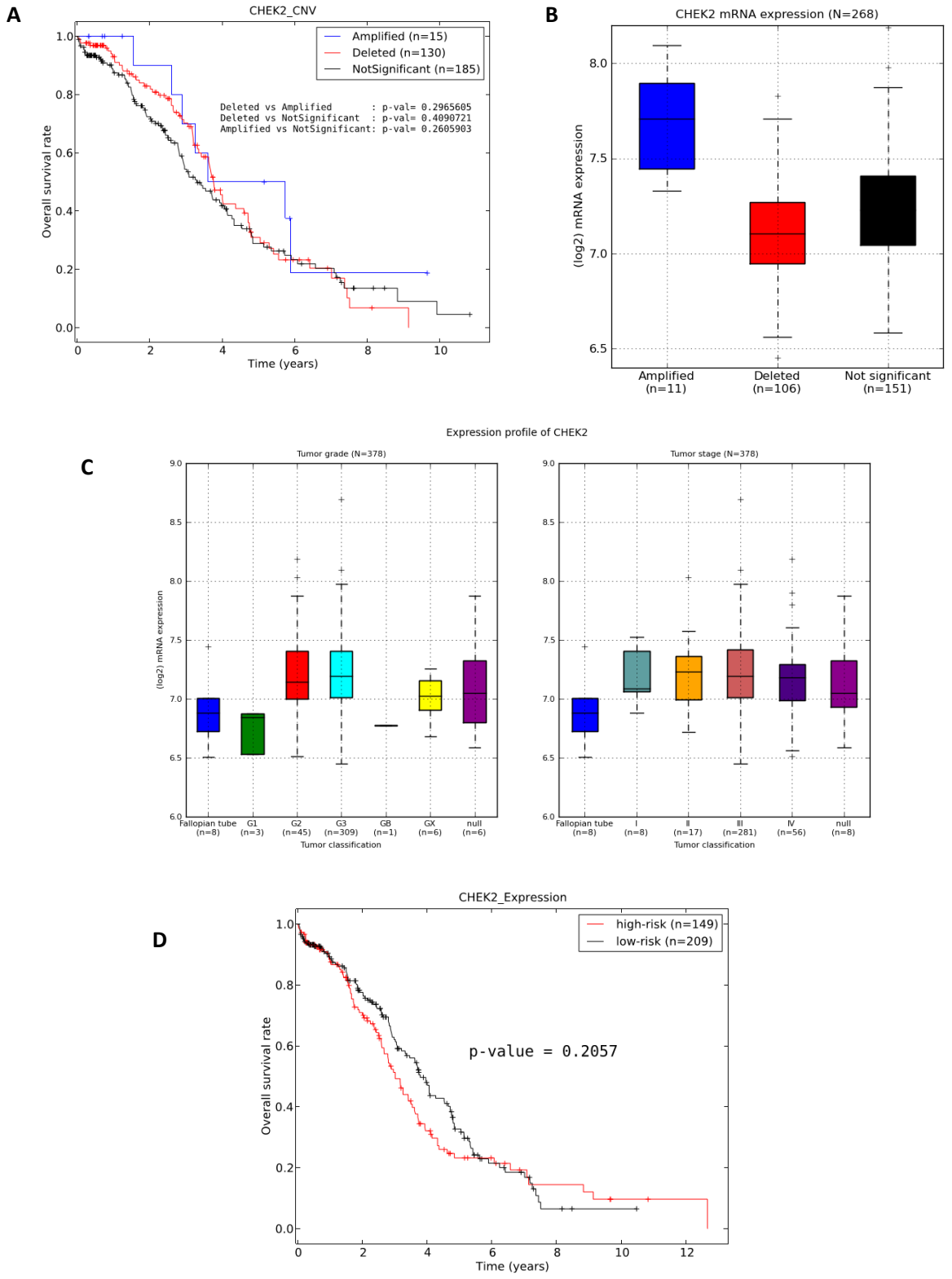


Supplementary Figure SF1: Mutational data of high-grade serous ovarian carcinoma (HG-SOC) downloaded from TCGA data portal.

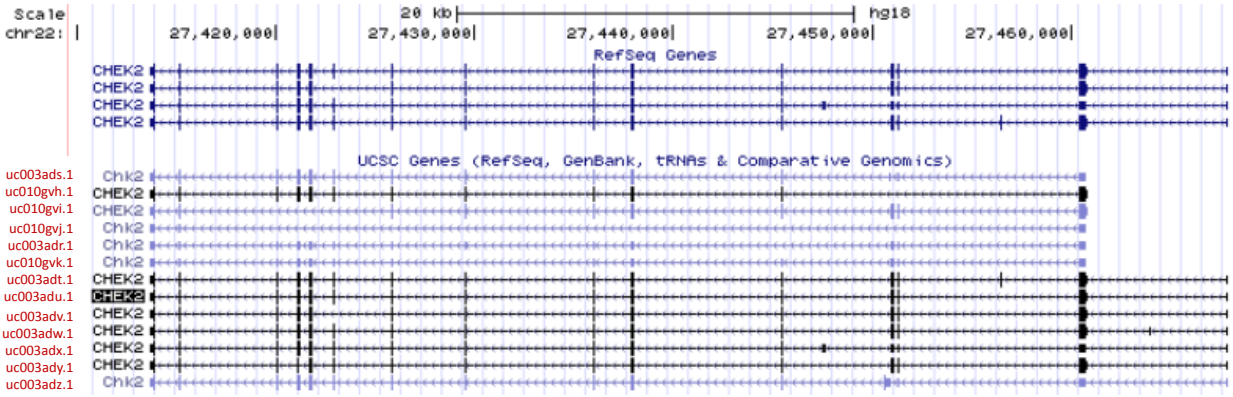


Supplementary Figure SF2: Heatmap of germline, LOH or somatic mutations observed for 455 highly mutated genes (mutated in at least 5 patients) and 334 patients. The intensity of the plot corresponds to the number of mutations (inclusive of silent mutations) observed for that gene and patient.

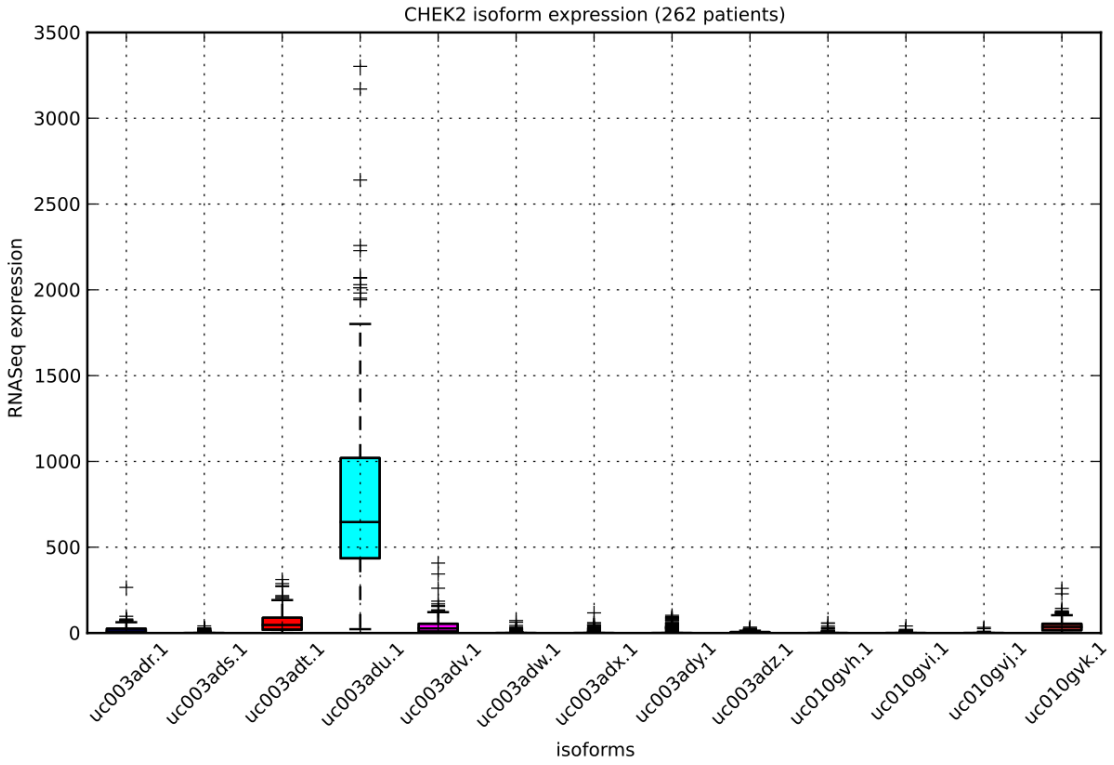


Supplementary Figure SF3: (A) Patient stratification of 330 TCGA HG-SOC patients based on *CHEK2* copy number. **(B)** *CHEK2* expression for samples with *CHEK2* deletion, amplification or insignificant alterations. **(C)** Expression profiles of *CHEK2* mRNA across tumor types for 378 samples. The 378 samples were from 8 fallopian tube samples and 370 HG-SOC samples with tumor grade and stage information. **(D)** Prognostic stratification of 358 HG-SOC patients based on *CHEK2* expression data. 12 HG-SOC patients without survival times and events were excluded from the analysis. High *CHEK2* mRNA expression were associated with higher-risk whereas low *CHEK2* mRNA expression were associated with lower-risk.

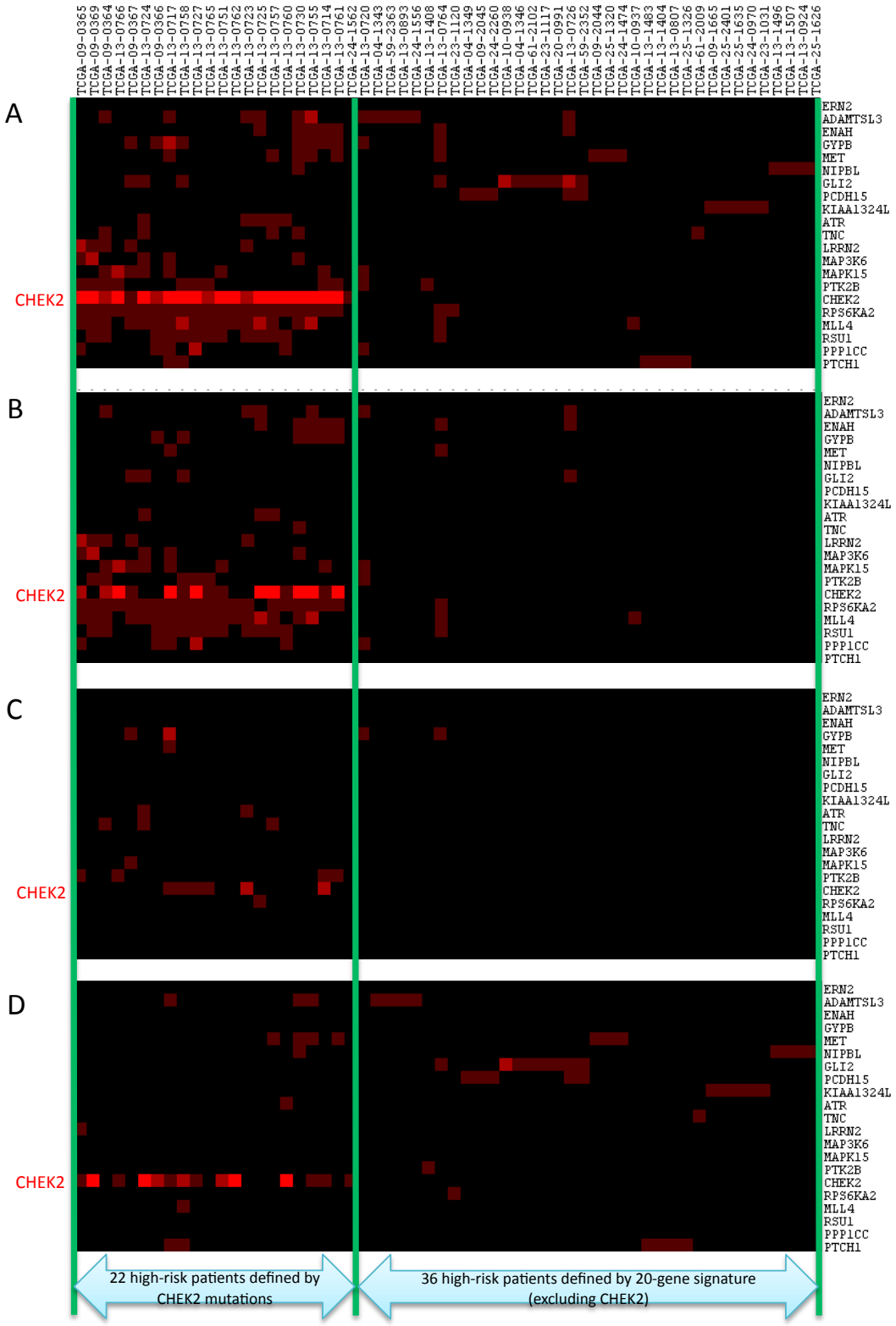
(A)



(B)



Supplementary Figure SF4: (A) Genomic locus of CHEK2 from the UCSC Genome Browser. The intron-exon-UTR structure of individual isoforms are shown. **(B)** RNA-seq expression of the CHEK2 isoforms across 263 high-grade serous ovarian carcinoma patients from the TCGA database.



Supplementary Figure SF5: Cluster of non-silent mutations of the 21 prognostic genes and 58 patients in the poor prognosis subgroup for **(A)** germline, LOH and somatic mutations, **(B)** germline mutations, **(C)** LOH, and **(D)** somatic mutations. Genes and patients were ordered via hierarchical clustering (kendall-tau distance and complete linkage).