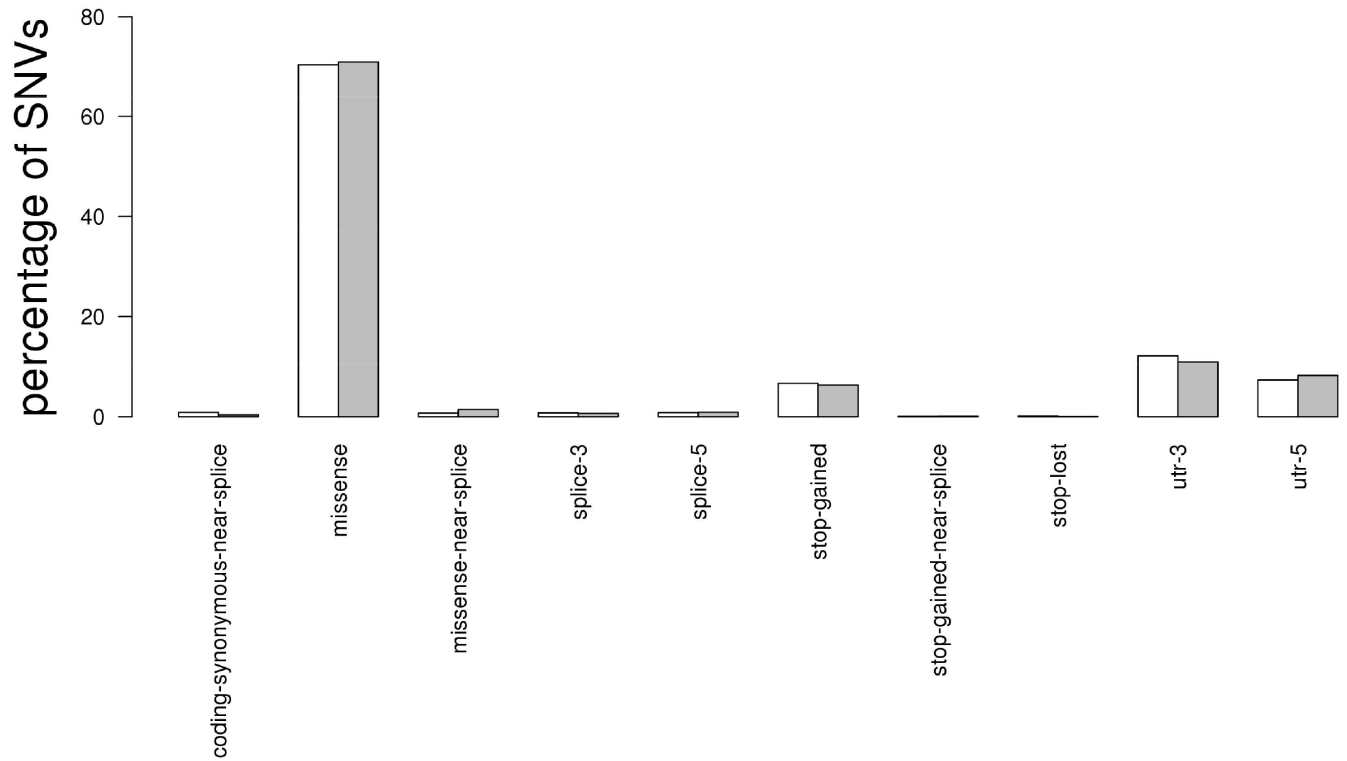
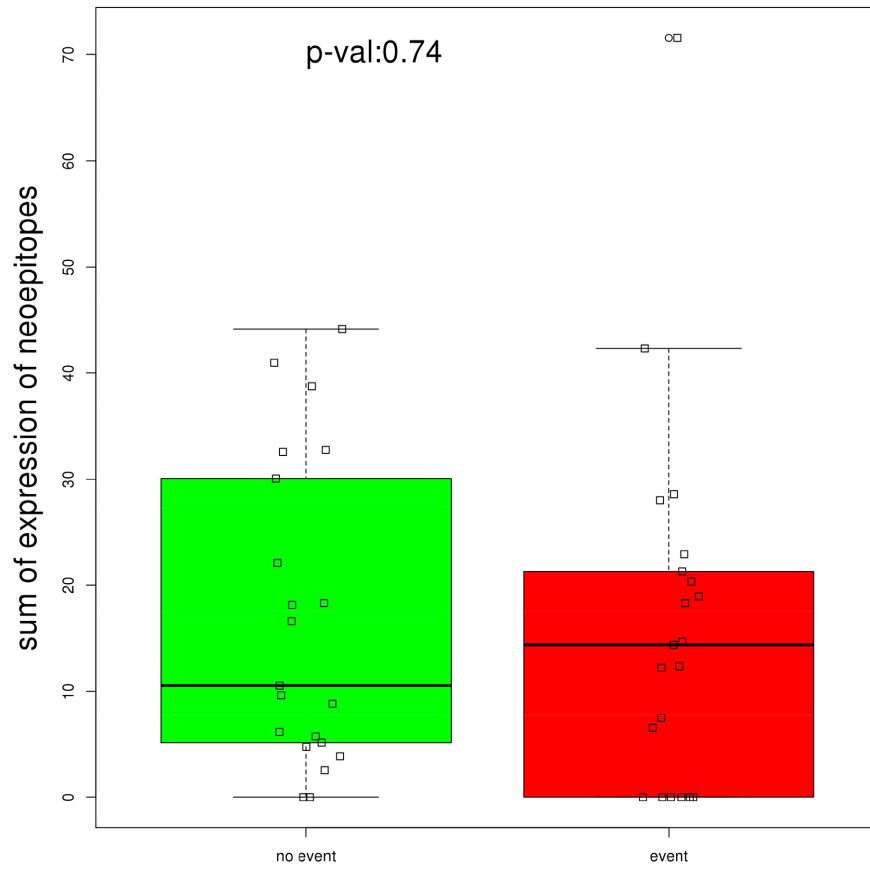


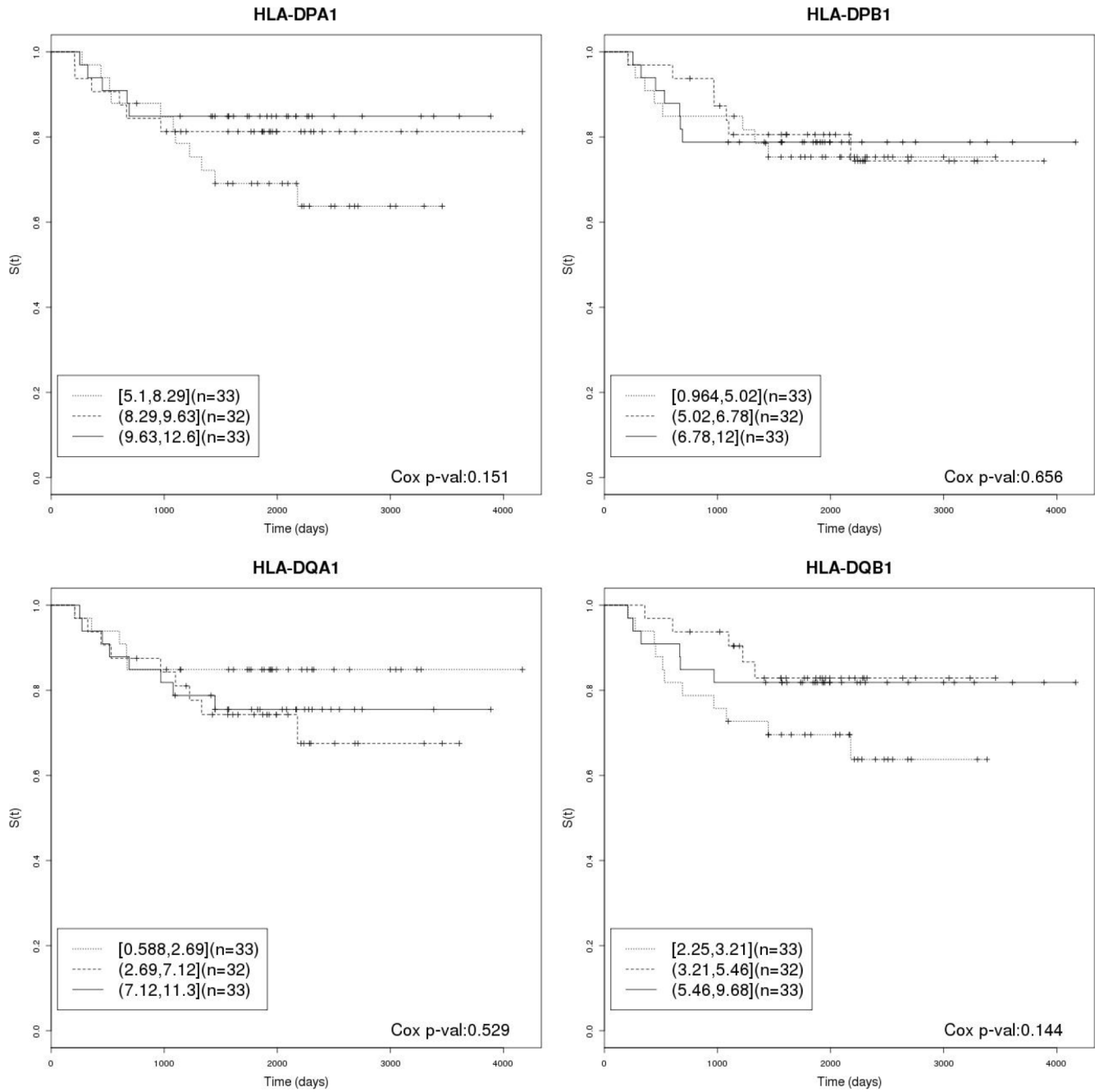
SUPPLEMENTARY FIGURES AND TABLES



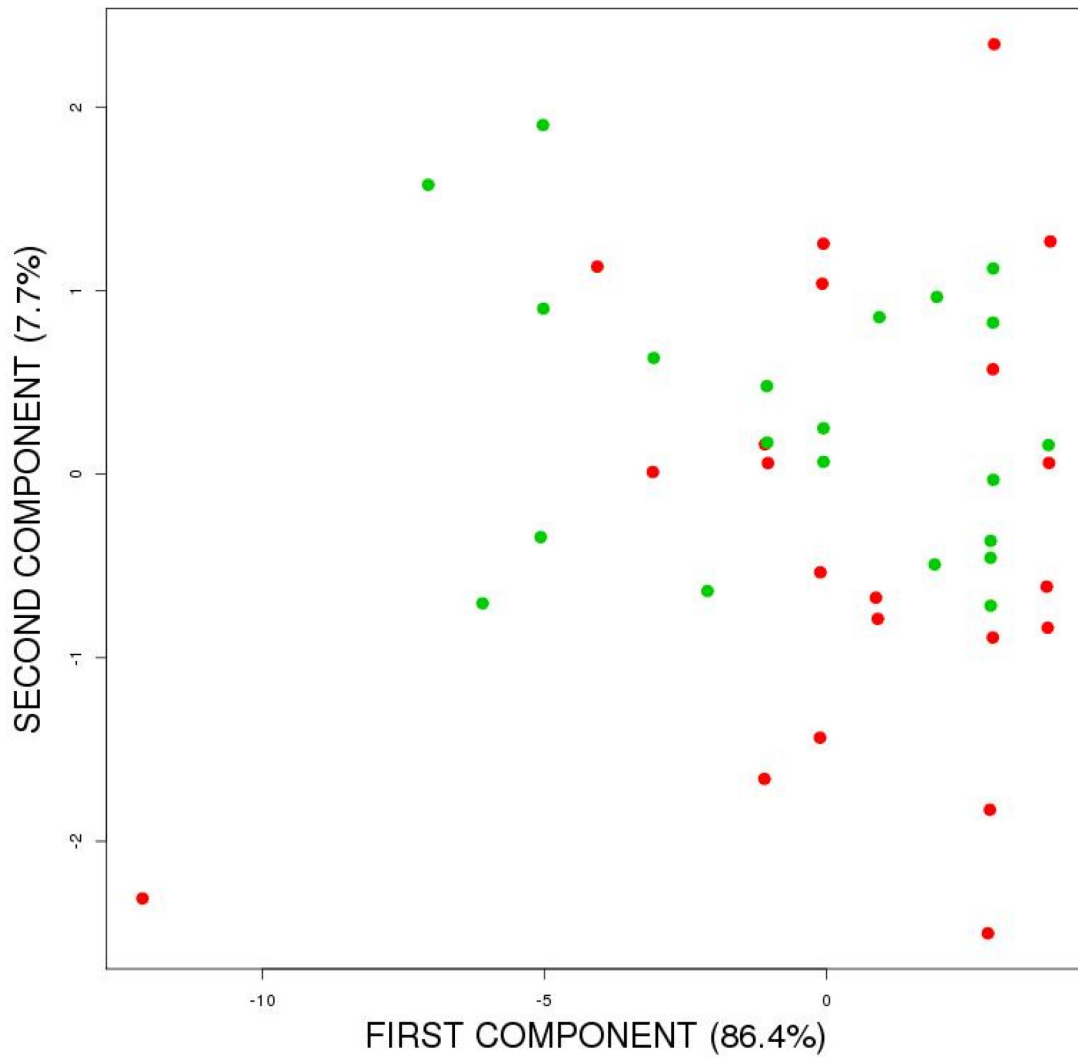
Supplementary Figure 1: Barplot showing the number of mutations in the group of tumors with no event (white) and event (grey), stratifying by type of mutation.



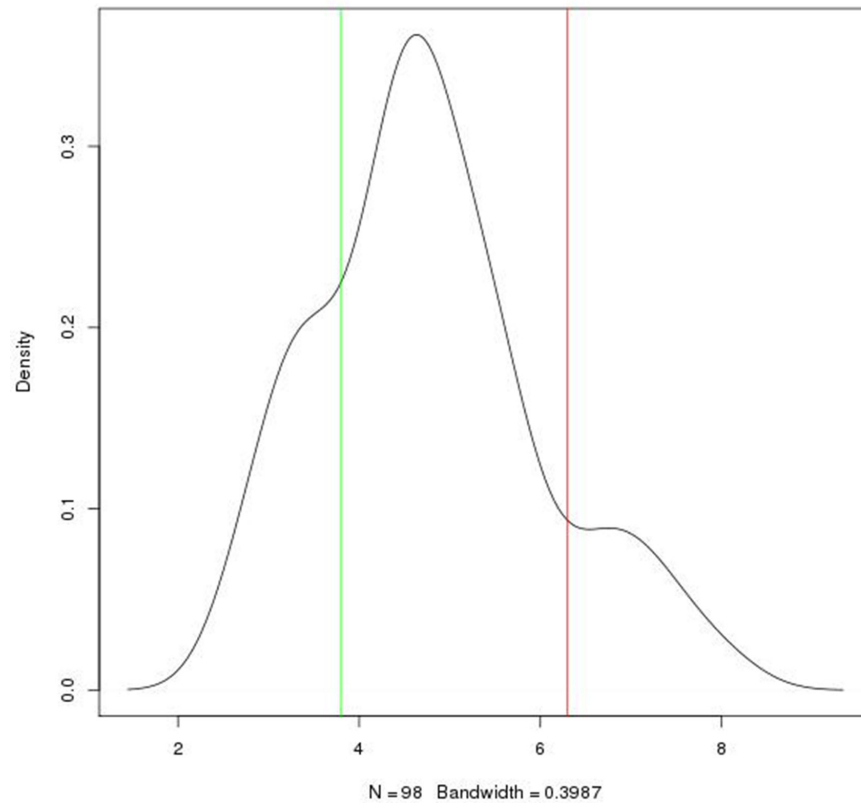
Supplementary Figure 2: Boxplots showing differences in mean of expression levels of genes harboring mutations predicted go generate neoantigens, between good and poor-prognosis group of tumors.



Supplementary Figure 3: Kaplan-Meier curves showing MHC class II genes association with prognosis.



Supplementary Figure 4: PCA scatter plot representing the dispersion of the samples based on number of predicted neopeptides and gene expression levels of HLAs and TAPs. Poor-prognosis tumors (red) and good-prognosis tumors (green) were plotted in 1st and 2nd principal components.



Supplementary Figure 5: Density plot showing *CD8A* level of expression.

Supplementary Table 1: Functional analysis.

See Supplementary File 1

Supplementary Table 2: Baseline characteristics of CRC patients

CRC patients exome sequencing (n=42)	
<i>Gender</i>	
Male	31 (73,8 %)
Female	11 (26,2 %)
<i>Median age (range,years)</i>	70 (43 - 84)
<i>Site</i>	
Right	12 (28,6 %)
Left	30 (71,4 %)
<i>Stage</i>	
II A	38 (90,5 %)
II B	4 (9,5 %)
<i>Recurrence</i>	
No relapse	21 (50 %)
Relapse	21 (50 %)
<i>Recurrence-free median time (range,months)</i>	60,9 (6,8 – 127,8)
