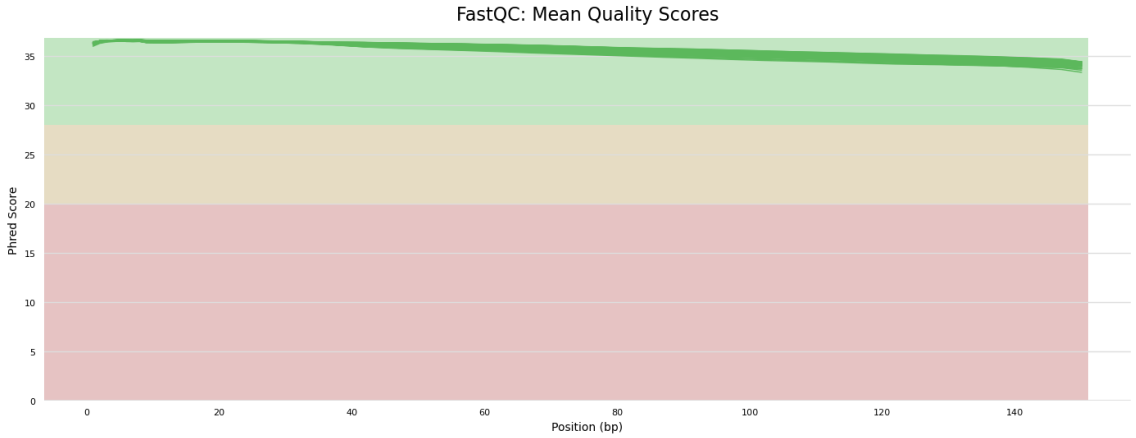
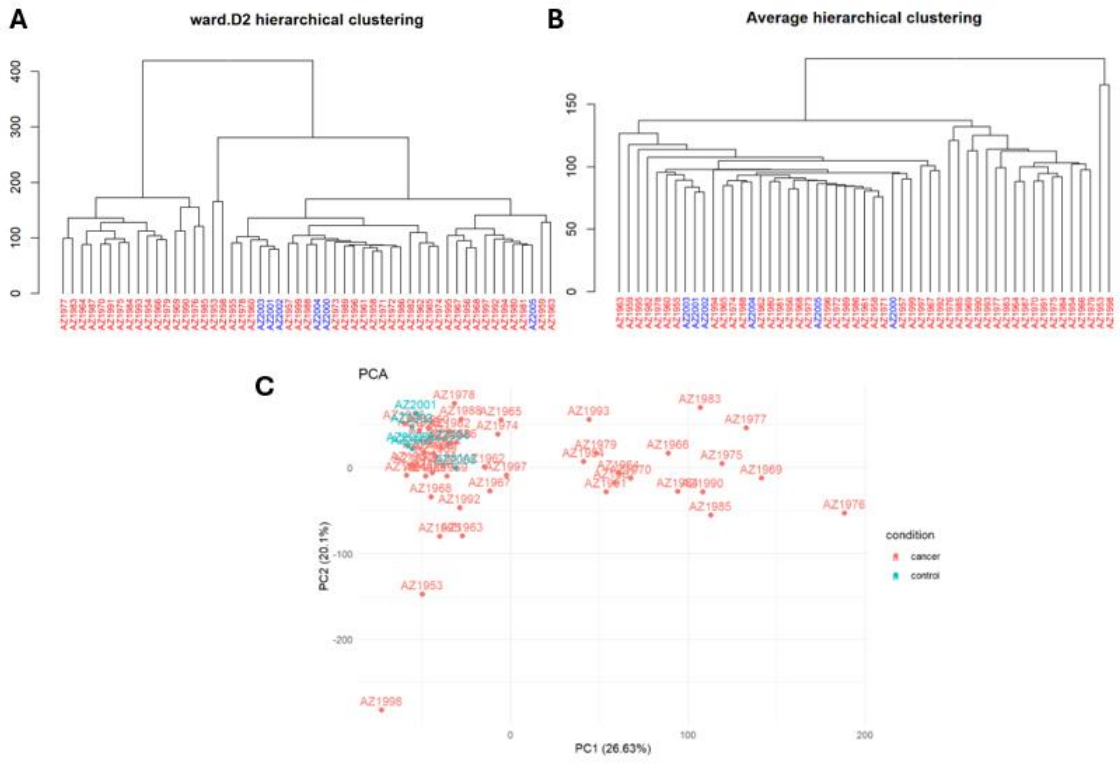
SUPPLEMENTARY MATERIALS

Supplementary Figure 1



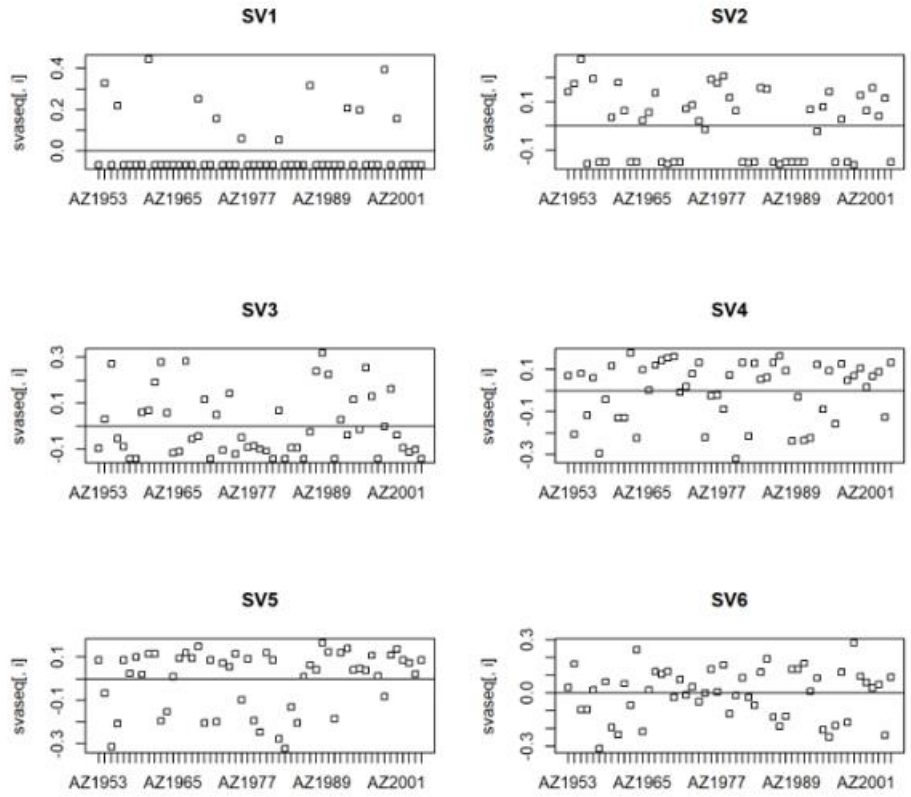
Supplementary Figure 1: Sequence quality histogram. It is displaying the mean quality value across each base position in the read. All bases are located within the green fragment.

Supplementary Figure 2



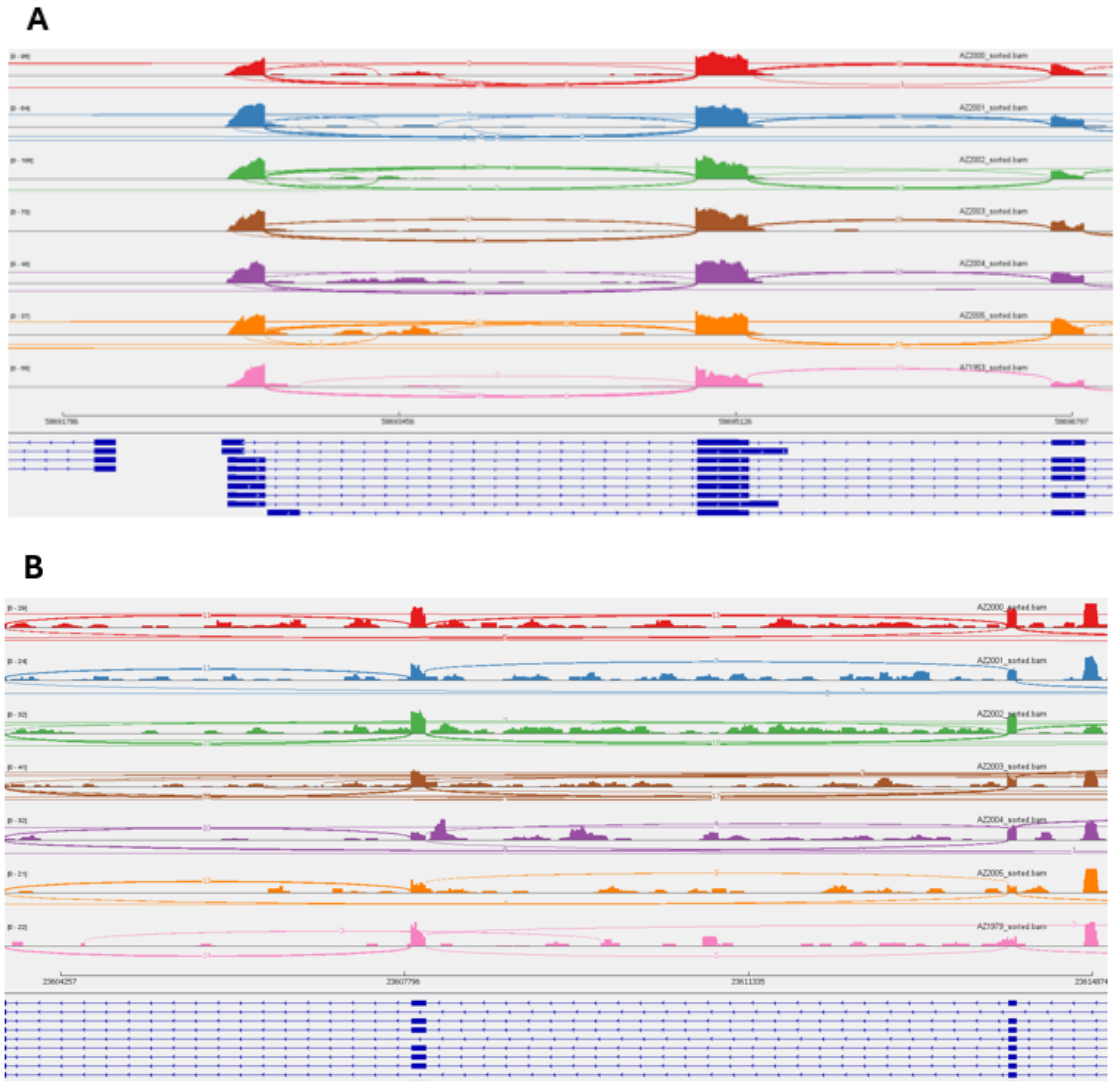
Supplementary Figure 2: Clustering methods. (A, B) Hierarchical clustering of the samples, considering all genes, using the Ward.D2 and average linkage methods. (C) PCA plot representing the first two principal components. In the three plots, “control” cases are coloured in blue and “cancer” cases in red.

Supplementary Figure 3



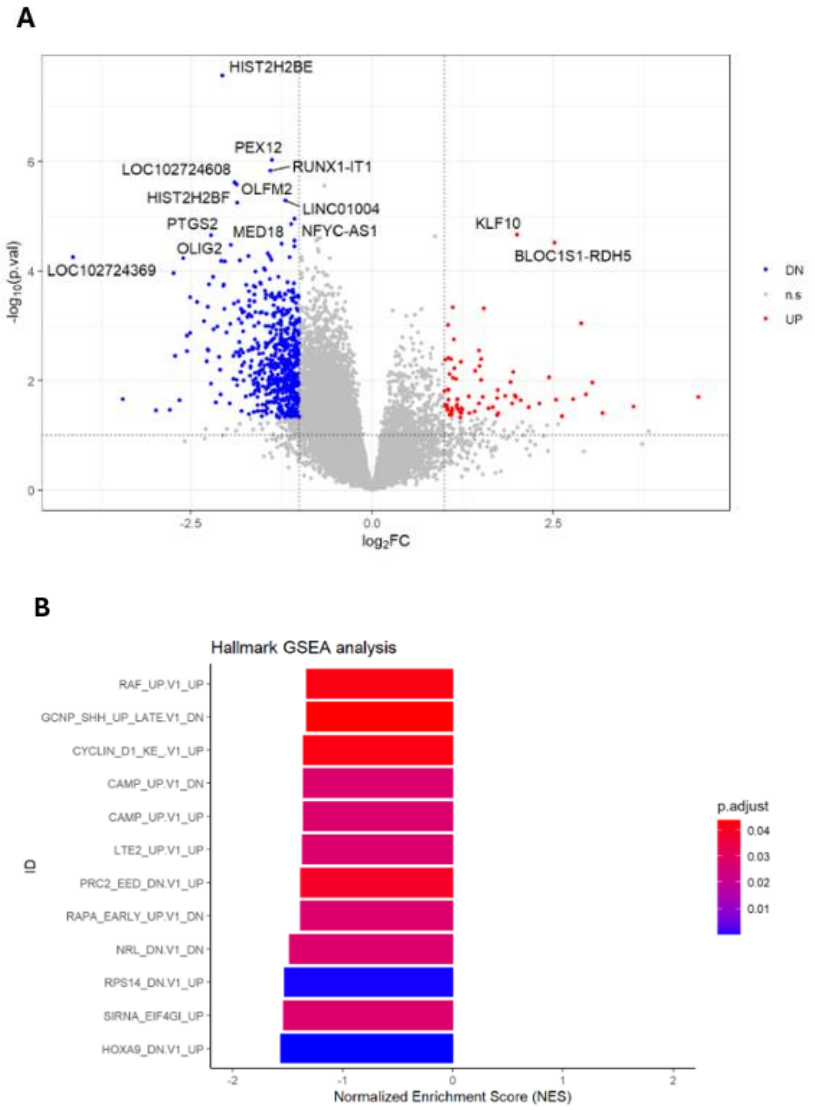
Supplementary Figure 3: Surrogate variables. This plot corresponds to all surrogate variables found in the data when considering the different samples.

Supplementary Figure 4



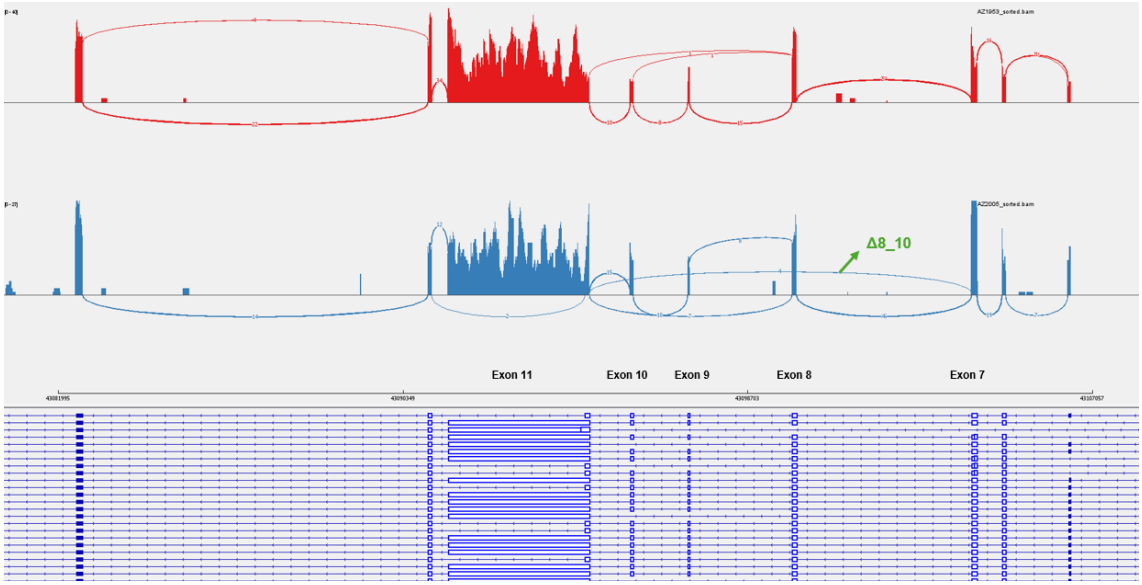
Supplementary Figure 4: IGV visualization. (A) Visualization of a hypothetical case of an AF local event present in the 'cancer' sample AZ1953 (pink) and absent in the rest of the 'control' samples. (B) Visualization of a hypothetical case of a SE local event present in the 'cancer' sample AZ1979 (pink) and absent in the rest of the 'control' samples.

Supplementary Figure 5



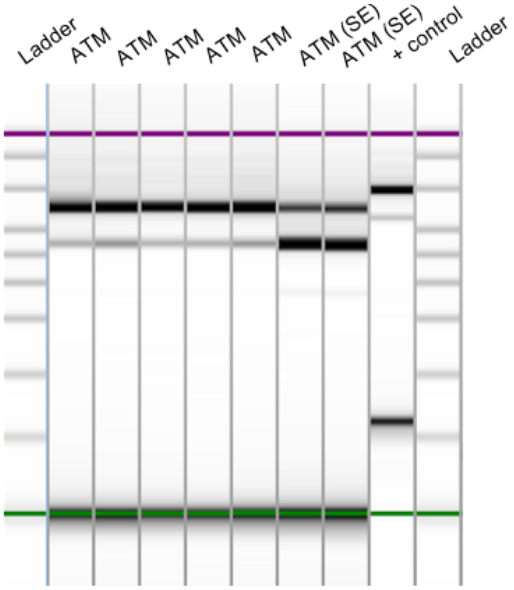
Supplementary Figure 5: Differentially expressed genes and Hallmark analysis. (A) Volcano plot showing the differentially expressed genes after comparing the 47 "cancer" samples against the 6 "control" samples. Down-regulated genes are coloured in blue, not-significant are coloured in grey and up-regulates are coloured in red. (B) Hallmark gene set enrichment analysis (GSEA) selecting the C6 oncogenic signature gene sets from MSigDB. The adjusted p-value for each associated set is represented using a colour scale.

Supplementary Figure 6



Supplementary Figure 6: IGV visualization. Visualization of the deletion in exons 8 to 10 (Δ8_10) is shown for the "cancer" sample AZ1953 (red) and the "control" sample AZ2005 (blue).

Supplementary Figure 7



Supplementary Table 7: **ATM splicing event validation:** Electrophoresis gel showing the full length of the *ATM* gene (upper band) in all lanes except the ladders. Additionally, in the lanes labeled ATM (SE), a lower band corresponding to an exon skipping event for exon 9 of the *ATM* gene can be observed, which validates the results obtained from the FRASER analysis for the AZ1954 sample. A positive control (+ control) for the *ATM* exon skipping event is also included.

Supplementary Table 1

Supplementary Table 1: Percentage of duplications. Table indicating the percentage of duplications observed in each of the samples analyzed.

Supplementary Table 1: Percentage of duplications

Sample ID	% of duplications
AZ1953	39.4
AZ1954	31.5
AZ1955	33.2
AZ1956	35
AZ1957	31.6
AZ1958	38.1
AZ1959	39.7
AZ1960	35.3
AZ1961	35.7
AZ1962	36.8
AZ1963	25
AZ1964	35.2
AZ1965	38.5
AZ1966	32.2
AZ1967	32.3
AZ1968	33.7
AZ1969	46.2
AZ1970	31.2
AZ1971	32.1
AZ1972	30.5
AZ1973	32.1
AZ1974	29.3
AZ1975	33
AZ1976	32.7
AZ1977	30.5
AZ1978	27.8
AZ1979	27.4
AZ1980	29
AZ1981	28.3
AZ1982	34.9
AZ1983	29.8
AZ1984	33.3
AZ1985	31.8
AZ1986	27
AZ1987	30.5
AZ1988	27.4
AZ1989	28.6
AZ1990	34.4
AZ1991	32.3

AZ1992	28.6
AZ1993	28.3
AZ1994	27.9
AZ1995	31.2
AZ1996	29.4
AZ1997	26.4
AZ1998	34.4
AZ1999	32.5
AZ2000	30.2
AZ2001	30.2
AZ2002	31.3
AZ2003	31.1
AZ2004	26.7
AZ2005	28.3