

Supplementary Data

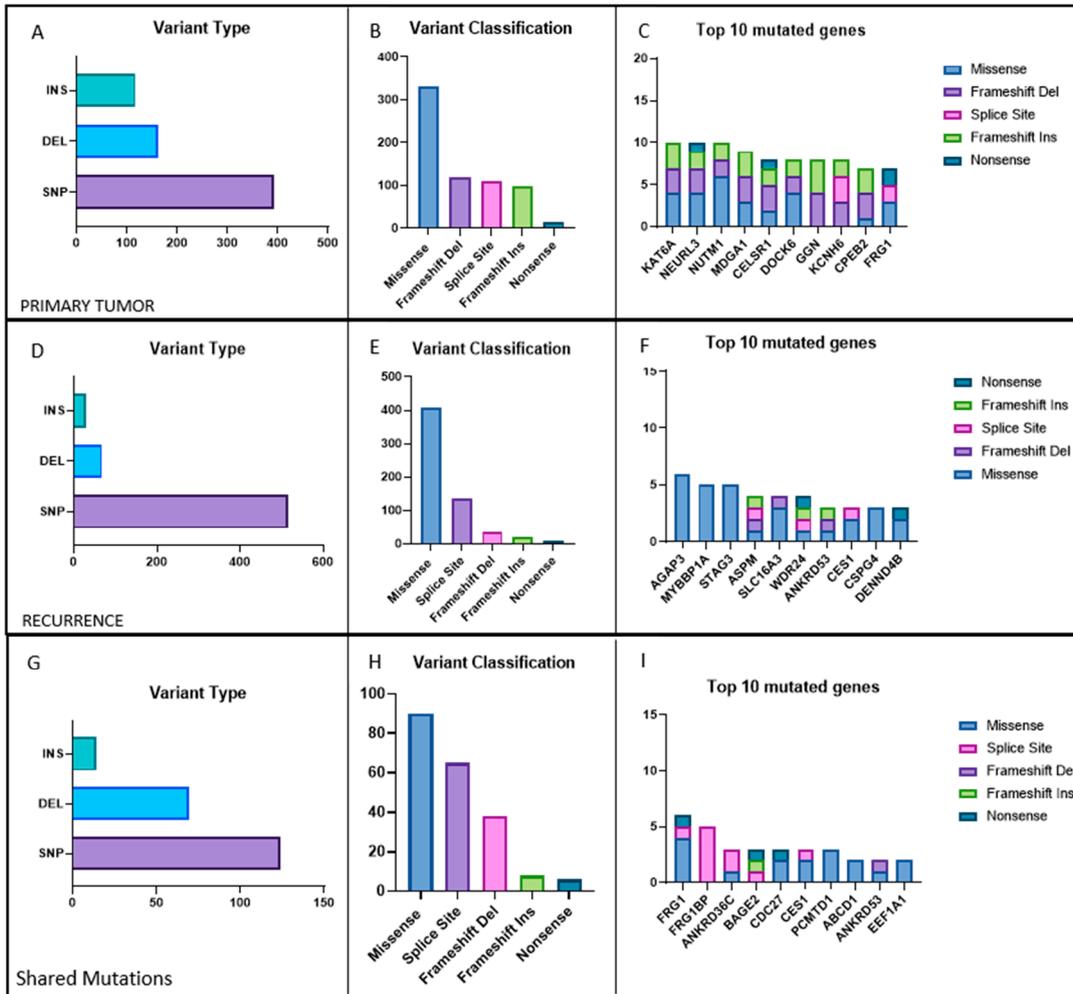


Figure 1S

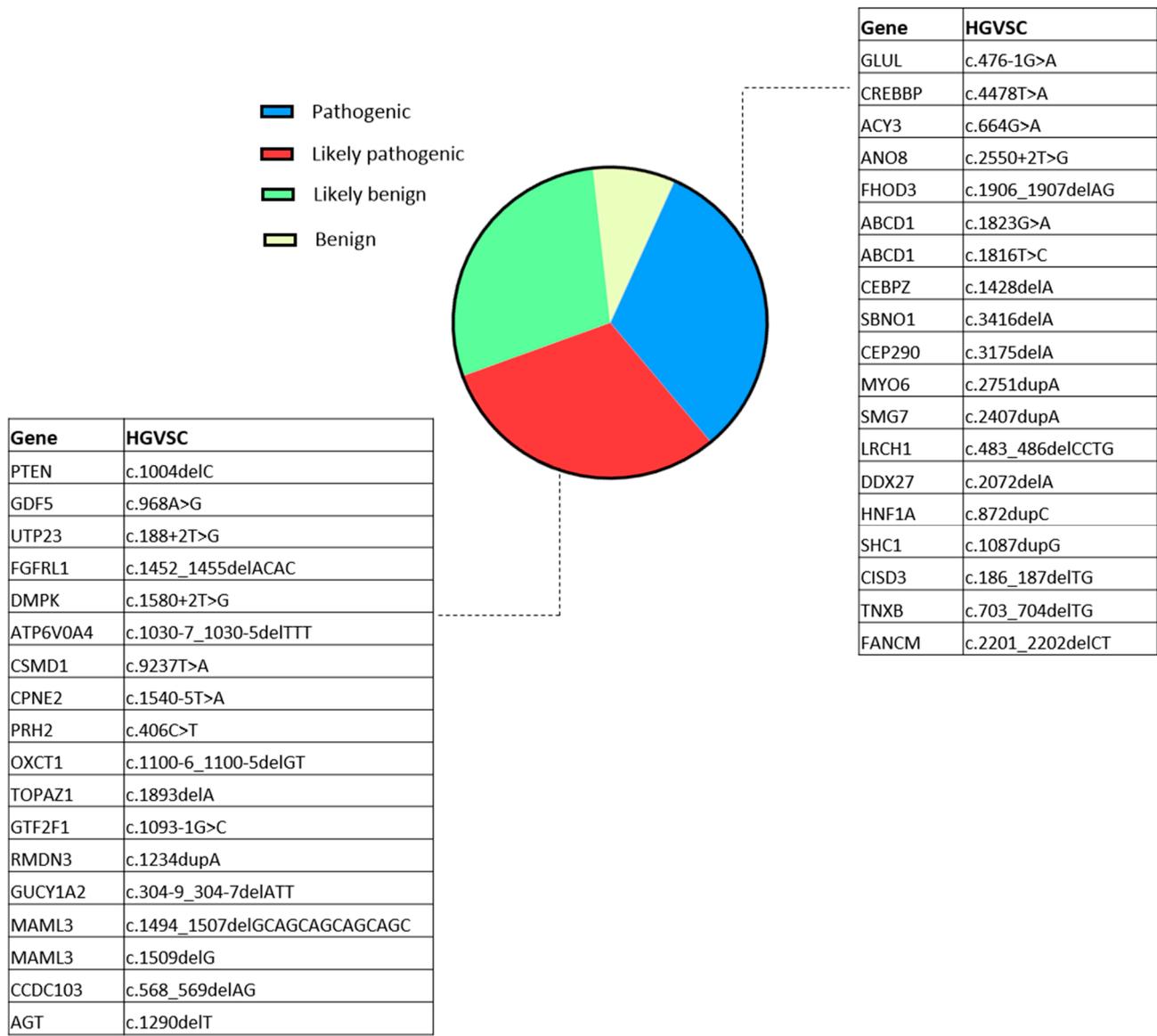


Figure 2S

GBM Driver Genes from IntOGen	Primary tumor	Recurrent tumor	Concurrent Mutations
PTEN			X
NF1			
BRAF			X
AKAP9			X
ARID1A			
CAD			

SOX9*			X
MAP4K3			
WT1*			X
PBMR1			
CSDE1			
PRPF8			
CARM1			

Table 1S

Legenda Supplementary Data

Figure 1S

In Figure 1S, primary (A, B and C) and recurrent tumor (D, E and F) results are shown. In A, for the primary tumor the mutations are classified by type: 392 SNPs, 163 deletions and 117 insertions. While in B the variant classification plot shows the number and classification of the variants, in order of frequency. The same results are shown respectively for the recurrent tumor in D (mutations type plot) and E (mutations classification plot). Specifically, for the recurrent tumor the type of mutations are 515 SNPs, 68 deletions and 29 insertions. In C and F the top 10 mutated genes are reported together with mutations distribution for primary and recurrent tumor respectively. For primary tumor, the 10 most mutated genes are: KAT6A, NEURL3, NUTM1, MDGA1, CELSR1, DOCK6, GGN, KCNH6, CPEB2, and FRG1. For the recurrent tumor, the 10 most mutated genes are: AGAP3, MYBBP1A, STAG3, ASPM, SLC16A3, WDR24, ANKRD53, CES1, CSPG4 and DENND4B. In G and H the variant type and the classification plots are shown. In I the top 10 mutated genes in common between the tissues are reported: FRG1, FRG1BP, ANKRD36C, BAGE2, CDC27, CES1, PCMTD1, ABCD1, ANKRD53 and EEF1A1.

Figure 2S

Pie chart showing the 210 shared variants' classification. In blue the 18 classified as "pathogenic" are shown and are reported in the table above. In red the 19 the classified as "likely pathogenic" are shown and reported in the table below.

Table 1S

Analysis with IntOGene framework: from the Cancer Genome Atlas, 75 mutational cancer drivers were detected in the GBM project. 13/75 driver genes were present and distributed mainly in the primary tumor.

In particular: *NF1*, *BRAF*, *CAD*, *MAP4K3*, *PBMR1*, *CSDE1*, *PRPF8* mutated only in the primary tumor, *ARID1A* and *CARM1* were exclusively mutated in the recurrent tumor, and *PTEN*, *AKAP9*, *SOX9*, *WT1* and *BRAF* were altered in both the primary and recurrent tumors with the same mutation (except for *SOX9* and *WT1* with a different mutation). * For each gene the same mutations were present in primary and recurrent tumors except for *SOX9* and *WT1*