**Supplementary Figure Legends**

**Figure S1A.** Recurrent copy number aberrations in treatment naïve glioblastoma. Common chromosomal gains and losses observed in the glioblastoma cohort are highlighted (n =10).

**Figure S1B.** Comprehensive representation of all copy number events in all tumor regions sequenced for the entire study cohort (n = 10). Copy number gains and losses are highlighted in red and blue respectively.

**Figure S2**. Heterogeneity in mutational signatures between tumor sectors. This chart demonstrates the relative proportions of a total of 17 mutational signatures associated with each tumor sector across the 10 glioblastomas sequenced.

**Figure S3**. Subclonal architecture inference for all tumors. The top and middle panels show SciClone-generated tumor coverage versus VAF plots based on SNVs in copy-number neutral, loss of heterozygosity (LOH)-free genomic regions for two distinct tumor sectors. The bottom panels depict the SciClone-generated 2-dimenisonal plot integrating VAF information from two sectors for improved resolution of subclones.

**Figure S4**. Clonal evolution inference for all samples. The left panels show box plots for the VAFs of mutations clusters detected using variants from copy number neutral regions in two distinct sectors (top and bottom). The middle panels show the ClonEvol-generated probable evolutionary relationships between identified subclones in each sector (top and bottom). The right hand panels illustrate the integrated phylogenetic relationships between all subclones in both tumor sectors. All possible predictions generated are shown for each patient.

**Figure S5**. Divergence in VAFs of potentially druggable gene variants between tumor sectors. Representative therapeutic gene variant versus VAF plot highlighting divergent VAFs for the depicted gene variants between sector 1 (S1) and sector 2 (S2) for patient B42.