BI-29. VARIANT ANALYSIS OF PRIMARY AND RECURRENT GLIOBLASTOMA USING ION AMPLISEQ™ COMPREHENSIVE CANCER PANEL AND WHOLE EXOME SEQUENCING
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BACKGROUND: Glioblastoma is the most deadly and frequently occurring adult primary brain tumor. The characterization of genetic variants and molecular signatures in glioblastoma is heavily reliant upon genomic sequencing. The availability of rapid and economical sequencing platforms is necessary for the widespread adoption of high-throughput sequencing in the clinical environment. METHODS: Utilizing patient matched triplet samples consisting of normal blood and snap-frozen primary and recurrent glioblastoma tumor samples from the Ohio Brain Tumor Study, we compared whole exome sequencing data from TCGA to sequencing data obtained from Ion AmpliSeq™ Comprehensive Cancer Panel (CCP). RESULTS: As we anticipated, the number of variants identified from the exome sequencing data (n = 619) was greater than those identified from the Ion AmpliSeq™ CCP data (n = 22). Surprisingly, there were only six variants common across both data sets. In addition, none of the variants from the Ion AmpliSeq™ CCP data were shared across patient samples. CONCLUSIONS: Our pilot results suggest disparities in both the number and category of mutations identified from analysis of data generated from the Ion AmpliSeq™ CCP and whole exome sequencing. Future studies are needed to elucidate the nature of these differences and to determine the clinical relevance of variants that may be associated with glioblastoma recurrence and response to treatment. High-throughput sequencing based cancer panels may be improved by the development of brain tumor specific panels.