**Supplementary Table 1. Mutation hotspots interrogated by Sequenom.** Sequenom mass-spectrometry genotyping for specific mutations in 8 genes was performed. The assay may not have detected certain mutations if the proportion of tumor cells in the sample studied was less than 10%. Initially, 15 unstained slides of 4 microns each were requested for each tumor sample, and a minimum of 60ng of DNA required for optimal performance of the Sequenom.

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| Clinical Panel | Investigational Panel |
| *BRAF* V600*EGFR* L858*KRAS* G12*KRAS* G13*PIK3CA* R88*PIK3CA* N345*PIK3CA* C420*PIK3CA* E542*PIK3CA* E545*PIK3CA* M1043*PIK3CA* H1047 | *AKT1* E17*BRAF* G469*BRAF* D594*EGFR* E709*EGFR* G719*EGFR* D761*EGFR* L861*EGFR* S768*EGFR* R776*EGFR* T790*EGFR* T854*ERBB2* L775 | *ERBB2* D769*ERBB2* V777*KRAS* Q61*KRAS* K117*KRAS* A146*MAP2K1* Q56*MAP2K1* K57*MAP2K1* D67*NRAS* G12*NRAS* G13*NRAS* Q61 |