**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 |