**Supplementary Table 1.** 54 gene panel (ctDNA), identifies potential tumor-related genomic alterations within 54 cancer-related genes including amplifications in *ERBB2, EGFR*, and *MET (*N=34 patients)

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| --- |
| **GENES WITH COMPLETE EXON COVERAGE** |
| *ALK* | *APC* | *AR* | *BRAF* |   18 GENES **3 Copy Number** **Variations in**  **BOLD** |
| *CDKN2A* | ***EGFR*** | ***ERBB2*** | *FBXW7* |
| *KRAS* | ***MET*** | *MYC* | *NOTCH1* |
| *NRAS* | *PIK3CA* | *PTEN* | *PROC* |
| *RB1* | *TP53* |  |  |
|  |
| **GENES WITH CRITICAL EXON COVERAGE** 36 GENES |
| *ABL1* | *AKT1* | *ATM* | *CDH1* | *CSF1R* | *CTNNB1* |
| *ERBB4* | *EZH2* | *FGFR1* | *FGFR2* | *FGFR3* | *FLT3* |
| *GNA11* | *GNAQ* | *GNAS* | *HNF1A* | *HRAS* | *IDH1* |
| *IDH2* | *JAK2* | *JAK3* | *KDR* | *KIT* | *MLH1* |
| *MPL* | *NPM1* | *PDGFRA* | *PTPN11* | *RET* | *SMAD4* |
| *SMARCB1* | *SMO* | *SRC* | *STK11* | *TERT* | *VHL* |