**Supplemental Table 4:** Alterations Detected in ctDNA and Tissue NGS\*

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| --- | --- | --- | --- |
| **Patient ID** | **ctDNA** | **% ctDNA/ Copy number\*\*** | **Tissue NGS** |
| 1 | *AKT1* E17K  *TP53* M237I | 1.85%  0.32% | *DNMT3A* splice site 2409-1G>T |
| 2 | *TP53* H178P  *TP53* R273C | 0.4%  0.2% | *CEBPA* Q182\*  *GATA3* \*445fs\*2+ |
| 3 | *BRAF* N581S | 0.2% | *IGF1R* amplification  *GATA3* M401fs\*45+ |
| 4 | *PIK3CA* H1047R  *ESR1* Y537S  *ESR1* D538E  *PIK3CA* amplification  *KRAS* amplification | 26.49%  6.13%  2.72% | *PIK3CA* H1047R  *ESR1* Y537S  *CCND1* amplification  *FGF19* amplification  *FGF3* amplification  *FGF4* amplification |
| 5 | *EGFR* amplification |  | *MCL1* amplification  *ESR1* D538G |
| 6 | No alterations detected |  | *ERBB2* amplification  *ERBB2* S310F  *AKT1* E17K  *PIK3CA* E545K |
| 7 | *PIK3CA* R108H | 0.1% | *ROS1* amplification  *MDM2* amplification  *CDH1* D402fs\*1  *TNFAIP2* rearrangement exon 9 |
| 8 | *ERBB2* G120V  *ERBB2* E109Q  *ERRB2* amplification  *NOTCH1* S94F  *NOTCH1* R1962H | 0.8%  0.8%  5.6  0.2%  0.2% | No tissue NGS available for this patient |
| 9 | *JAK2* V617F  *PIK3CA* E542K  *GNAS* R201H | 33.7%  4.7%  0.6% | *NF1* loss  *PIK3CA* E542K  *CCND1* amplification  *MCL1* amplification  *TP53* splice site 993+1G>A  *CDH1* P744fs\*24  *FGF19* amplification  *FGF3* amplification  *FGF4* amplification |
| 10 | No alterations detected |  | No alterations detected |
| 11 | No alterations detected |  | *RPTOR* amplification  *CDKN2A/B* loss  *CCND1* amplification  *TP53* H168R  *SMAD4* loss  *NKX2-1* amplification  *BCL2L2* amplification  *FGF19* amplification  *FGF3* amplification  *FGF4* amplification  *GATA3* N332fs\*21 |
| 12 | *NFE2L2* R42\* | 0.55% | *CCND1* amplification  *FGF19* amplification  *FGF4* amplification  *FGF3* amplification  *EMSY* amplification  *NFKB1A* amplification – equivocal |
| 13 | *TP53* E286G  *MET* amplification | 24.2% | *TP53* E286G  *RAF1* amplification  *MYC* amplification |
| 14 | No alterations detected |  | No tissue NGS available for this patient |
| 15 | *TP53* R175H | 2.5% | No tissue NGS available for this patient |
| 16 | *PIK3CA* H1047R  *TP53* R213L | 13.5%  3.3% | *PIK3CA* H1047R  *TP53* R213L  *FGFR1* amplification  *MYST3* amplification |
| 17 | *TP53* S127Y  *GNAS* R201C | 4.6%  0.3% | *TP53* S127Y  *PTCH1* T416S |
| 18 | *TP53* Y126C  *TP53* H178P | 3.9%  0.2% | *TP53* Y126C  *PTEN* loss  *GNAS* amplification –equivocal  *CRKL* amplification  *CCND3* amplification  *MYC* amplification  *ARFRP1* amplification – equivocal  *ZNF217* amplification  *CREBBP* S893L  *KDM5A* amplification - equivocal |
| 19 | *EGFR* amplification | CN – 2.7 | *MYC* amplification  *TP53* splice site 993+2T>C  *RB1* loss |
| 20 | No alterations detected |  | No tissue NGS available for this patient |
| 21 | *PIK3CA* E545K  *ERBB2* amplification | 39.5%  9.3X | *PIK3CA* E545K  *CCND1* amplification  *MCL1* amplification  *MDM2* amplification  *C17orf39* amplification  *FGF19* amplification  *FGF3* amplification  *FGF4* amplification  *NOTCH2* truncation intron 31  *ZNF703* amplification |
| 22 | No alterations detected |  | *PIK3CA* E545K  *PTEN* Y177fs\*3  *FGFR1* N546K  *CDH1* T474fs\*9  *STAT4* E388\* |
| 23 | *PTEN* C136R | 0.3% | No tissue NGS available for this patient |
| 24 | *ESR1* D538G  *ARID1A* E1799\*  *TP53* F212V  *TP53* R110L  *FGFR1* amplification  *MYC* amplification  *RAF1* amplification  *ERBB2* amplification | 11.7%  10.2%  4.3%  0.2%  ++  ++  +  + | *ESR1* D538G  *ARID1A* R750\* |
| 25 | No alterations detected |  | No tissue NGS available for this patient |
| 26 | *PIK3CA* E545K  *TP53* F109V  *EGFR* amplification | 48%  44.6%  2.4X | No tissue NGS available for this patient |
| 27 | No alterations detected |  | No tissue NGS available for this patient |
| 28 | No alteration detected |  | No tissue NGS available for this patient |
| 29 | No alterations detected |  | No tissue NGS available for this patient |
| 30 | *Met* amplification  *EGFR* amplification | +  + | *AKT3* amplification  *FLT3* amplification  *GNAS* amplification – equivocal  *SRC* amplification  *CCND1* amplification  *IKBKE* amplification  *MCL1* amplification – equivocal  *MDM2* amplification  *ARFRP1* amplification – equivocal  *CDK8* amplification – equivocal  *FGF19* amplification  *FGF3* amplification  *FGF4* amplification  *GATA3* S437fs\*10+  *MDM4* amplification  *PIK3C2B* amplification  *ZNF217* amplification |
| 31 | No alterations detected |  | *FGFR4* amplification – equivocal  *FLT4* amplification – equivocal  *FANCA* Y843\*  *EMSY* amplification  *ESR1* amplification  *GATA3* H435fs\*12+  *MAP2K4* loss |
| 32 | *TP53* R213\* | 5.1% | *TP53* R213\*  *PTEN* V217fs\*4  *PALB2* Q61\* |
| 33 | *PTEN* Q245\*  *TP53* H179Q  *PIK3CA* E545K  *EGFR* amplification | 59.7%  52.2%  38.3%  3X | *PTEN* Q 245\*  *TP53* H179Q  *PIK3CA* E545K  *MAP2K4* loss |
| 34 | *PIK3CA* H1047L | 5.6% | No tissue NGS available for this patient |
| 35 | *TP53* Y107\* | 2.89% | *TP53* Y107\*  *BRCA2* L2686fs\*11  *ARID1A* A343 A348>A  *GATA3* S390fs\*51+ |
| 36 | No alterations detected |  | *CCND1* amplification – equivocal  *FGF19* amplification – equivocal  *FGF3* amplification – equivocal  *FGF4* amplification – equivocal  *MYST3* amplification |
| 37 | *TP53* C141\* | 0.3% | No tissue NGS available for this patient |
| 38 | *TP53* R175H  *EGFR* amplification  *MET* amplification | 0.3%  3.2  2.7 | *FGFR1* amplification  *PALB2* Q775\*  *MYC* amplification  *APC* A2122\_C2123insA  *ZNF703* amplification |
| 39 | *TP53* V216M  *EGFR* amplification | 40%  2.2 | No tissue NGS available for this patient |
| 40 | *PIK3CA* E545K  *ATM* R3008H  *TP53* F270S | 2.9%  0.6%  0.4% | No tissue NGS available for this patient |
| 41 | No alterations detected |  | *RUNX1* L112fs\*10 |
| 42 | No alterations detected |  | *AKT3* amplification – equivocal  *MYC* amplification – equivocal  *TP53* truncation exon 10  *RB1* loss exons 17-27  *SMAD4* F362fs\*12 |
| 43 | No alterations detected |  | No tissue NGS available for this patient |
| 44 | *RB1* Q504\*  *TP53* H168P  *APC* Q901\*  *TP53* S127F | 0.5%  0.3%  0.3%  0.1% | *AXIN1* R492H  *GATA1* W269\*  *MUTYH* Y165C |
| 45 | No alterations detected |  | *CCND1* amplification  *FGF19* amplification  *FGF3* amplification  *FGF4* amplification  *GATA3* M423fs\*24+ |
| 46 | *TP53* F134V  *PIK3CA* H1047R  *ERBB2* amplification  *BRAF* amplification  *MET* amplification  *FGFR2* amplification  *MYC* amplification | 11.2%  10.78%  5.1  2.3  2.4  2.2  2.4 | *TP53* F134V  *PIK3CA* H1047R  *ERBB2* amplification  *CDK12* rearrangement intron 11  *TOP2A* amplification  *FGFR2* amplification –equivocal  *MYC* amplification |
| 47 | No alterations detected |  | No tissue NGS available for this patient |
| 48 | No alterations detected |  | No tissue NGS available for this patient |
| 49 | *PIK3CA* H1047Q  *PIK3C*A E545K  *RAF1* amplification  *FGFR1* amplification  *MYC* amplification | 1.2%  0.6% | *PIK3CA* Q75E  *CYLD* truncation intron 12  *ZNF703* amplification |
| 50 | *FGFR1* amplification |  | *FGFR1* amplification  *CCND1* amplification  *MEN1* M283fs\*3  *EMSY* amplification  *FGF19* amplification  *FGF3* amplification  *FGF4* amplification  *MYST3* amplification  *ZNF703* amplification |
| 51 | No alterations detected |  | No tissue NGS available for this patient |
| 52 | *TP53* V216L  *TP53* H179Q  *TP53* 211I | 0.5%  0.16%  0.15% | *TP53* splice site 559+1G>T  *GATA3* R399fs\*48+ |
| 53 | *STK11* Q170\*  *ESR1* D538G | 2.94%  2.46% | *STK11* Q170\*  *ESR1* D538G |
| 54 | *PIK3CA* E81K  *PIK3CA* amplification  *ERBB2* amplification | 34.1%  ++  + | No tissue NGS available for this patient |
| 55 | No alterations detected |  | No tissue NGS available for this patient |
| 56 | *IDH2* R140Q | 0.4% | No tissue NGS available for this patient |
| 57 | *TP53* R213Q  *BRAF* amplification  *CDK4* amplification | 0.2%  +++  ++ | *BRAF* amplification  *CDK4* amplification  *MAP2K2* amplification – equivocal  *NRAS* amplification  *MDM2* amplification  *TOP1* amplification  *BCL2L1* amplification – equivocal  *ESR1* L536H  *FRS2* amplification  *KEL* amplification |
| 58 | *TP53* V272L  *TP53* F270L  *FGFR1* amplification | 2.7%  2.7%  + | *TP53* F272L  *TP53* F270L  *FGFR1* amplification  *ZNF703* amplification |
| 59 | *JAK2* V617F  *IDH1* R132G | 21.3%  0.2% | No tissue NGS available for this patient |
| 60 | *TP53* M246V  *TP53* E51\*  *KRAS* G12D | 0.2%  0.2%  0.2% | No tissue NGS available for this patient |
| 61 | *PIK3CA* H1047R  *PIK3CA* E453K  *KRAS* A146T  K*RAS* G12V  *ESR1* D538G | 1.1%  0.2%  0.9%  0.2%  0.2% | No tissue NGS available for this patient |
| 62 | *ESR1* Y537C  *ESR1* D538G  *MYC* amplification | 4.1%  1.8%  + | *ESR1* Y537C  *ESR1* D538G  *MYC* amplification – equivocal  *BRCA2* L240fs\*4  *GATA3* 5115fs\*189 |

\*All data is included in this Table (characterized alterations included; VUS and synonymous alterations excluded); however, when concordance data was calculated in the Results, it was done using only alterations that were detectable in both assays at that time

\*\*% ctDNA listed when available and copy number (CN) listed when available.

\*\*\* For ctDNA copy number descriptions: 1+: greater than 2.12 but equal to less than 2.4 of copy number; 2+: greater than 2.4 but equal to less than 4.0 of copy number; 3+: greater than 4.0