**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%5.60.2%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%3.22.7 | *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%5.12.32.42.22.4 | *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* A146TK*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