## Supplementary Table: Summary of gene alterations and responses

| **Patient** | **Local test** | **Central tissue test** | **Central plasma test** | **Patient group(s)** |
| --- | --- | --- | --- | --- |
| **Gene and alteration** | **g/s/u** | **Gene and alteration** | **AF** | **g/s/u** | **Gene and alteration** | **AF** | **g/s/u** |
| **1** | .. |  | .. |  |  | *ATM* Q2243\*  | 14.23  | s | *ATM* |
| **2** | .. |  | *ATM* loss  | NA | s | .. |  |  | *ATM* |
| **3** | *ATM* V1468D | u | *ATM* V1468D  | 11.39  | u | NA |  |  | *ATM* |
| **4** | .. |  | *ATM* Y2398fs\*1  | 32.53 | s | .. |  |  | *ATM* |
| **5** | .. |  | .. |  |  | *ATM* splice site 2250+2T>C  | 0.69  | s | *ATM* |
| **6** | .. |  | .. |  |  | *ATM* F1445fs\*5*ATM* K1706fs\*7 | 26.1135.91 | sg | *ATM* |
| **7** | .. |  | *ATM* C117fs\*4  | 9.51 | s | .. |  |  | *ATM* |
| **8** | .. |  | *ATM* E834fs\*7  | 46.19 | s | .. |  |  | *ATM* |
| **9** | *ATM* loss | s | .. |  |  | *ATM* rearrangement | NA | s | *ATM* |
| **10** | *ATM* Y959\* | g | .. |  |  | *ATM* Y959\* | 87.28 | g | *ATM* |
| **11** | .. |  | *ATM* L2633\*  | 36.86  | s | *ATM* L2633\* | 7.08 | s | *ATM* |
| **12** | .. |  | *ATM* E1783\* *ATM* E957fs\*12  | 37.622.62  | ss | *ATM* E1783\* ATM E957fs\*12  | 6.82 9.91 | ss | *ATM* |
| **13** | .. |  | *ATM* splice site 902-1G>T  | 52.38  | g | *ATM* splice site 902-1G>T *CHEK2* A537fs\*37 | 53.04 14.25 | gs | *ATM, CHEK2* |
| **14** | .. |  | .. |  |  | *ATM* R3008C | 0.33 | s | *ATM* |
| **15** | *ATM* rearrangement  | s | .. |  |  | *ATM* rearrangement | NA | s | *ATM* |
| **16** | .. |  | .. |  |  | *ATM* Q2942\*  | 0.14  | s | *ATM* |
| **17** | .. |  | .. |  |  | *ATM* I1581fs\*5  | 8.66  | s | *ATM* |
| **18** | .. |  | .. |  |  | *ATM* Q1867fs\*50 *ATM* Q51fs\*5 | 43.115.52  | gs | *ATM* |
| **19** | .. |  | *ATM* splice site 2921+1G>A  | 32.25  | s | *ATM* splice site 2921+1G>A *CHEK2* rearrangement | 19.53NA  | s s | *ATM, CHEK2* |
| **20** | .. |  | .. |  |  | *ATM* Q2269\* *ATM* rearrangement | 1.16NA | ss | *ATM* |
| **21** | .. |  | *ATM* C2930\*  | 46.98 | g | *ATM* C2930\* *ATM* M1T  | 50.49 0.38  | g s | *ATM* |
| **22** | .. |  | .. |  |  | *ATM* R3008C | 0.23 | s | *ATM* |
| **23** | *ATM* K397Rfs\*9  | g | .. |  |  | *ATM* not tested*BRCA2* G1006\* | NA0.18 | NAs | *ATM* |
| **24** | *ATM* I2629fs\*25  | s | .. |  |  | *ATM* I2629fs\*25 *ATM* A235fs\*20*ATM* rearrangement | 7.33 0.29NA | s sg | *ATM* |
| **25** | *ATM* I2629fs\*25 *ATM* loss*CHEK2* loss *FANCA* loss | sssu | .. |  |  | .. |  |  | *ATM, CHEK2,* Other |
| **26** | .. |  | .. |  |  | *ATM* R3008H  | 0.58  | s | *ATM* |
| **27** | .. |  | *ATM* splice site 6348-1G>A  | 24.74  | s | *ATM* splice site 6348-1G>A  | 0.42  | s | *ATM* |
| **28** | .. |  | *ATM* splice site 7630-2A>C *ATM* rearrangement*RAD54L* splice site 767-2A>G | 51.53NA52.02  | gsu | *ATM* splice site 7630-2A>C *ATM* rearrangement*ATM* R3008H*CHEK2* splice site 908+1G>T  | 61.49NA0.150.17 | gsss | *ATM, CHEK2,* Other |
| **29** | .. |  | *ATM* T1871fs\*33  | 36.91  | s | *ATM* T1871fs\*33  | 1.97  | s | *ATM* |
| **30** | *ATM* R805\*  | u | .. |  |  | .. |  |  | *ATM* |
| **31** | .. |  | *ATM* S1799fs\*2 *ATM* L2234fs\*1  | 25.73 25.44  | ss | .. |  |  | *ATM* |
| **32** | .. |  | *ATM* E343fs\*2  | 45.74  | g | .. |  |  | *ATM* |
| **33** | .. |  | ND |  |  | *ATM* Y1252fs\*1  | 0.83 | s | *ATM* |
| **34** | .. |  | .. |  |  | *ATM* W2104\*  | 0.4  | s | *ATM* |
| **35** | .. |  | ND |  |  | *ATM* R23\*  | 0.17  | s | *ATM* |
| **36** | .. |  | *ATM* L312\*  | 34.45 | s | *ATM* L312\*  | 5.35  | s | *ATM* |
| **37** | .. |  | *ATM* loss | NA | s | .. |  |  | *ATM* |
| **38** | .. |  | *ATM* R2443\* | 21.09 | s | *ATM* R2443\*  | 0.21 | s | *ATM* |
| **39** | .. |  | *ATM* Y1475\*  | 65.5  | s | .. |  |  | *ATM* |
| **40** | .. |  | ND |  |  | *ATM* R111\*  | 0.17  | s | *ATM* |
| **41** | .. |  | *ATM* C620fs\*1  | 31.12  | u | .. |  |  | *ATM* |
| **42** | .. |  | *ATM* K673fs\*31  | 49.16  | s | *ATM* K673fs\*31 *CHEK2* R145fs\*9  | 56.240.33  | ss | *ATM, CHEK2* |
| **43** | .. |  | *ATM* splice site 5918+1G>A  | 47.66  | g | *ATM* splice site 5918+1G>A  | 49.17  | g | *ATM* |
| **44** | *ATM* I798fs\*9  | s | .. |  |  | *ATM* I798fs\*9  | 12.45  | s | *ATM* |
| **45** | *ATM* rearrangement  | s | .. |  |  | .. |  |  | *ATM* |
| **46** | .. |  | .. |  |  | *ATM* R1875\* | 0.17 | s | *ATM* |
| **47** | *ATM* V1268\*  | g | .. |  |  | *ATM* V1268\*  | 59.14  | g | *ATM* |
| **48** | .. |  | .. |  |  | *ATM* D2661fs\*9  | 2.11  | s | *ATM* |
| **49** | .. |  | .. |  |  | *ATM* W308\**CHEK2* S39fs\*1 | 0.690.98 | ss | *ATM, CHEK2* |
| **50** | *CDK12* rearrangement | u | .. |  |  | .. |  |  | *CDK12* |
| **51** | .. |  | *CDK12* S251\*  | 25.57  | u | *CDK12* S251\* | 4.51 | u | *CDK12* |
| **52** | .. |  | *CDK12* Y319\*  | 87.36  | u | *CDK12* Y319\*  | 41.66  | u | *CDK12* |
| **53** | *CDK12* Y978Afs\*19  | u | *CDK12* Y978fs\*19  | 61.75 | u | .. |  |  | *CDK12* |
| **54** | *CDK12* rearrangement | u | *CDK12* rearrangement  | NA | u | .. |  |  | *CDK12* |
| **55** | .. |  | *CDK12* Y742\*  | 10.67  | u | *CDK12* Y742\* *CDK12* L427fs\*9  | 38.74 24.86  | uu | *CDK12* |
| **56** | .. |  | *CDK12* splice site 2249-44\_2275del71 *CDK12* M1028fs\*29  | 43.1732.78  | uu | ND |  |  | *CDK12* |
| **57** | .. |  | *CDK12* Q115\* *CDK12* L760fs\*2  | 26.2610.67  | uu | .. |  |  | *CDK12* |
| **58** | *CDK12* rearrangement  | u | *CDK12* rearrangement | NA | u | *CDK12* rearrangement  | NA | u | *CDK12* |
| **59** | *CDK12* S171Rfs\*20  | u | *CDK12* S171fs\*20  | 31.03  | u | *CDK12* S171fs\*20  | 8.3  | u | *CDK12* |
| **60** | .. |  | *CHEK2* V198fs\*7 *CDK12* T971fs\*24  | 53.39 34.1  | gu | *CHEK2* V198fs\*7 *CDK12* T971fs\*24  | 56.67 41.22  | gu  | *CHEK2, CDK12* |
| **61** | *CDK12* V136Sfs*CDK12* splice site 2964-1G>C  | uu | *CDK12* V136fs\*21 *CDK12* splice site 2964-1G>C  | 35.71 27.18 | u u | .. |  |  | *CDK12* |
| **62** | .. |  | *CDK12* S574fs\*12 *CDK12* P683fs\*70  | 13.15 8.2  | uu | *CDK12* S574fs\*12*CHEK2* splice site 592+2T>G  | 2.83 0.18  | u s | *CHEK2, CDK12* |
| **63** | .. |  | *CDK12* P549fs\*61 *CDK12* L123fs\*4  | 46.85 18.52  | uu  | *CDK12* P550fs\*60 *CDK12* L123fs\*4  | 47.17 20.42  | uu | *CDK12* |
| **64** | .. |  | *CDK12* S142fs\*15 *CDK12* S368fs\*62  | 20.09 21.79 | uu  | *CDK12* S142fs\*15 *CDK12* S368fs\*62  | 1.66 1.51  | uu | *CDK12* |
| **65** | .. |  | *CHEK2* T367fs\*15  | 45.16  | g | *CHEK2* T367fs\*15  | 48.84  | g | *CHEK2* |
| **66** | .. |  | *CHEK2* I157T *NBN* K219fs\*16 *FANCA* loss | 96.78 92.18 NA | g gu | *CHEK2* I157T  | 50.21  | g | *CHEK2,* Other |
| **67** | *CHEK2* E127fs\*4*BRIP1* V648fs\*38 | ss | *CHEK2* E127fs\*4 *BRIP1* V648fs\*38  | 46.43 19.85  | ss | *CHEK2* E127fs\*4  | 2.23  | s | *CHEK2,* Other |
| **68** | .. |  | *BRCA2* T2517fs\*7 | 16.02 | s | *CHEK2* splice site 444+1G>A  | 49.09  | g | *CHEK2* |
| **69** | .. |  | *RAD51* E18fs\*10  | 6.46  | u | .. |  |  | Other |
| **70** | *FANCA* rearrangement | u | .. |  |  | .. |  |  | Other |
| **71** | .. |  | *NBN* R714\*  | 6.48  | s | .. |  |  | Other |
| **72** | .. |  | *NBN* K219fs\*16  | 62.1  | g | .. |  |  | Other |
| **73** | .. |  | *NBN* R466fs\*18  | 17.43  | s | .. |  |  | Other |
| **74** | .. |  | ­.. |  |  | *PALB2* splice site 109-2A>G *PALB2* rearrangement | 51.15 NA | gs | Other |
| **75** | .. |  | *RAD51B* rearrangement | NA | u | .. |  |  | Other |
| **76** | .. |  | *PALB2* Q1175\*  | 68.49 | g | .. |  |  | Other |
| **77** | .. |  | *FANCA* V372fs\*42 | 54.33 | u | .. |  |  | Other |
| **78** | .. |  | *BRIP1* R798\* | 47.91 | g | .. |  |  | Other |
| Patients with a PSA response. Patients with both a PSA response and a radiographic response. Cells with 2 dots (..) indicate the test was not performed.Abbreviations: AF, allele frequency; g, germline alteration; s, somatic alteration; NA, not applicable; ND, not detected; u, unknown germline/somatic status.  |