## 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 | 26.11  35.91 | s  g | *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 | 37.6  22.62 | s  s | *ATM* E1783\*  ATM E957fs\*12 | 6.82  9.91 | s  s | *ATM* |
| **13** | .. |  | *ATM* splice site 902-1G>T | 52.38 | g | *ATM* splice site 902-1G>T  *CHEK2* A537fs\*37 | 53.04  14.25 | g  s | *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 | 43.1  15.52 | g  s | *ATM* |
| **19** | .. |  | *ATM* splice site 2921+1G>A | 32.25 | s | *ATM* splice site 2921+1G>A  *CHEK2* rearrangement | 19.53  NA | s  s | *ATM, CHEK2* |
| **20** | .. |  | .. |  |  | *ATM* Q2269\*  *ATM* rearrangement | 1.16  NA | s  s | *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\* | NA  0.18 | NA  s | *ATM* |
| **24** | *ATM* I2629fs\*25 | s | .. |  |  | *ATM* I2629fs\*25  *ATM* A235fs\*20  *ATM* rearrangement | 7.33  0.29  NA | s  s  g | *ATM* |
| **25** | *ATM* I2629fs\*25  *ATM* loss  *CHEK2* loss  *FANCA* loss | s  s  s  u | .. |  |  | .. |  |  | *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 | 51.53  NA  52.02 | g  s  u | *ATM* splice site 7630-2A>C  *ATM* rearrangement  *ATM* R3008H  *CHEK2* splice site 908+1G>T | 61.49  NA  0.15  0.17 | g  s  s  s | *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 | s  s | .. |  |  | *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 | 56.24  0.33 | s  s | *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 | 0.69  0.98 | s  s | *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 | u  u | *CDK12* |
| **56** | .. |  | *CDK12* splice site 2249-44\_2275del71  *CDK12* M1028fs\*29 | 43.17  32.78 | u  u | ND |  |  | *CDK12* |
| **57** | .. |  | *CDK12* Q115\*  *CDK12* L760fs\*2 | 26.26  10.67 | u  u | .. |  |  | *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 | g  u | *CHEK2* V198fs\*7  *CDK12* T971fs\*24 | 56.67  41.22 | g  u | *CHEK2, CDK12* |
| **61** | *CDK12* V136Sfs  *CDK12* splice site 2964-1G>C | u  u | *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 | u  u | *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 | u  u | *CDK12* P550fs\*60  *CDK12* L123fs\*4 | 47.17  20.42 | u  u | *CDK12* |
| **64** | .. |  | *CDK12* S142fs\*15  *CDK12* S368fs\*62 | 20.09 21.79 | u  u | *CDK12* S142fs\*15  *CDK12* S368fs\*62 | 1.66  1.51 | u  u | *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  g  u | *CHEK2* I157T | 50.21 | g | *CHEK2,* Other |
| **67** | *CHEK2* E127fs\*4  *BRIP1* V648fs\*38 | s  s | *CHEK2* E127fs\*4  *BRIP1* V648fs\*38 | 46.43  19.85 | s  s | *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 | g  s | 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. | | | | | | | | | |