Supplementary Material to:

Westphalen CB, Fine AD, Andre F et al. 2021.

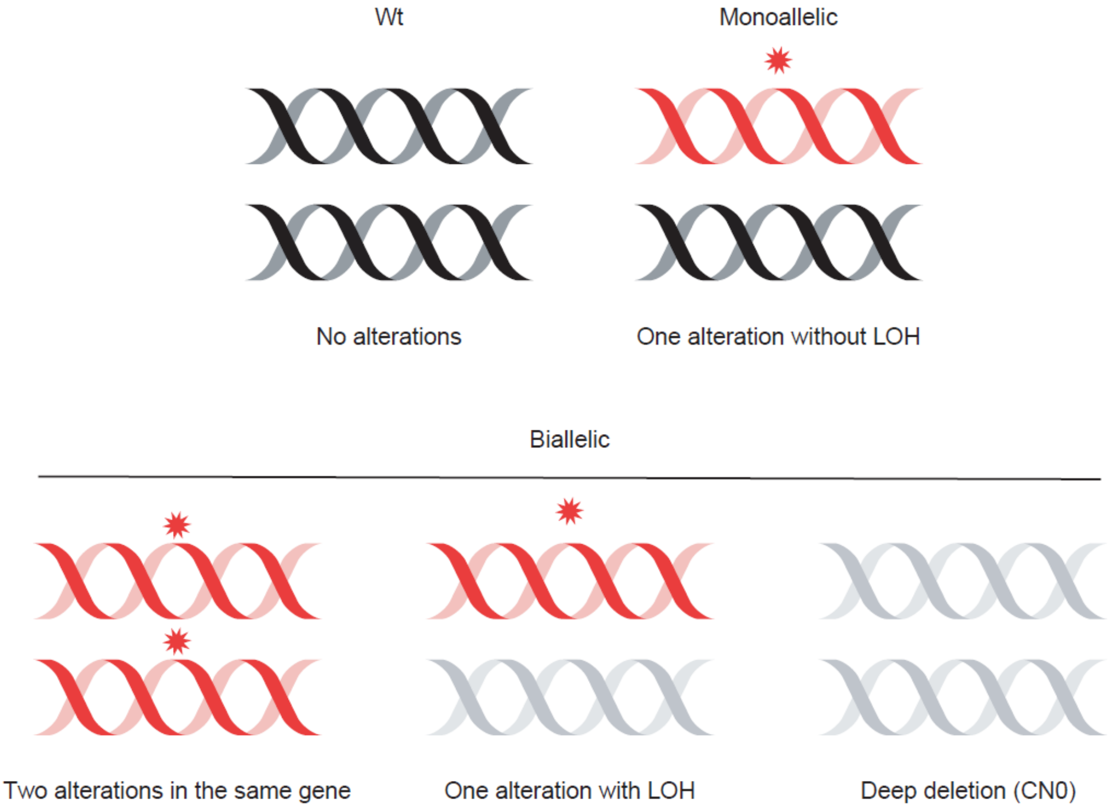
Pan-cancer Analysis of Homologous Recombination Repair-associated Gene Alterations and Genome-wide Loss of Heterozygosity Score

- Supplementary Figures S1-S10
- Supplementary Tables S1-S8

Supplementary Figures

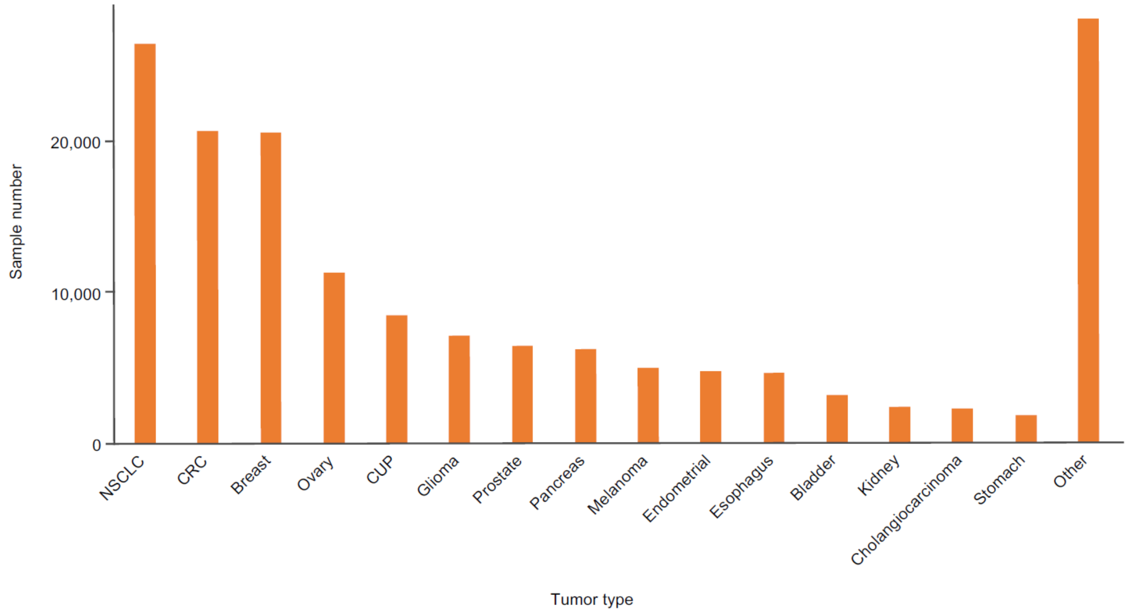
Supplementary Figure 1.

Graphic of biallelic and monoallelic alteration callings. LOH, loss of heterozygosity; wt, wildtype.



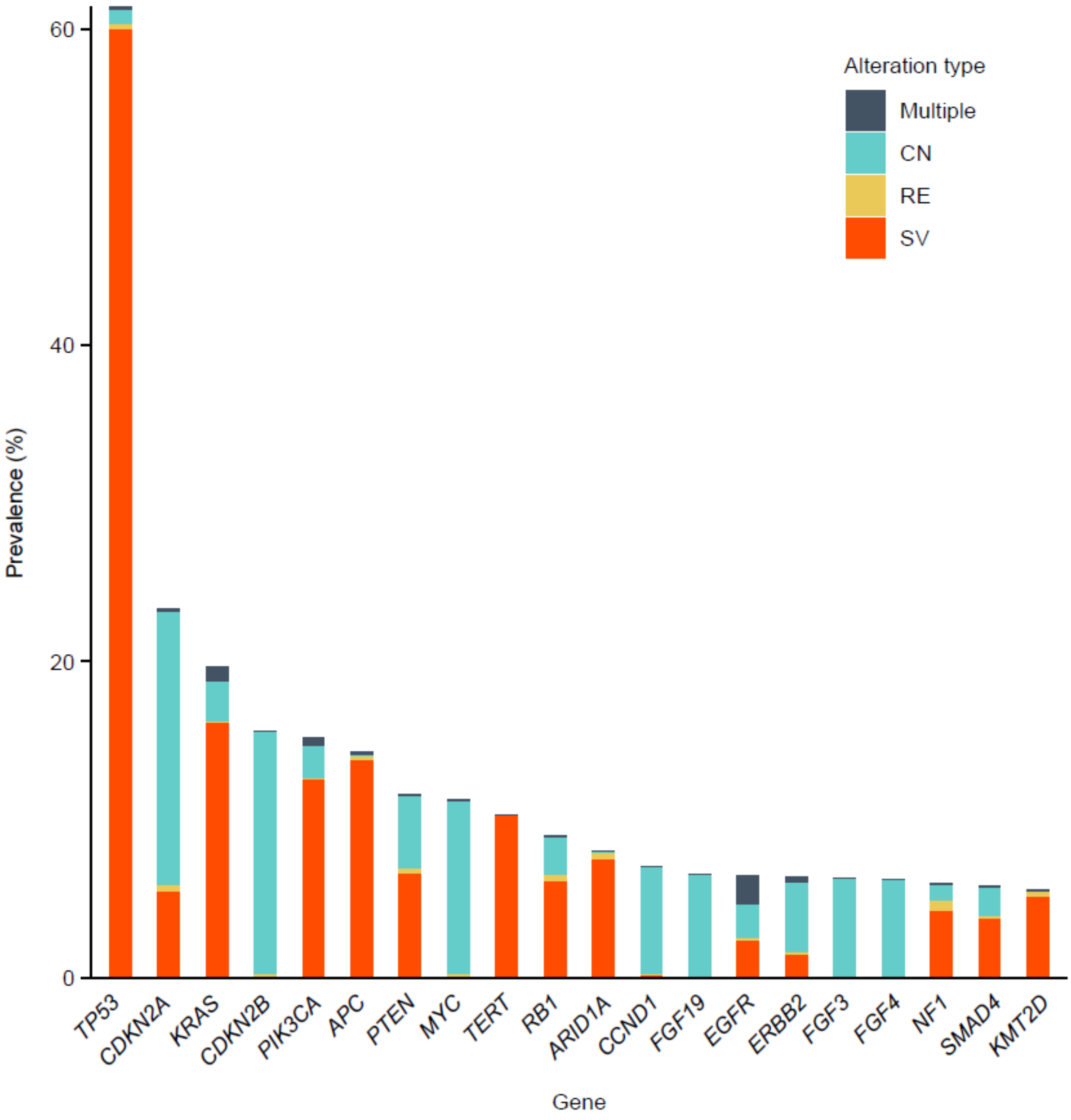
Supplementary Figure 2.

Cancer types represented in the study. CUP, carcinoma-of-unknown-primary-origin.



Supplementary Figure 3.

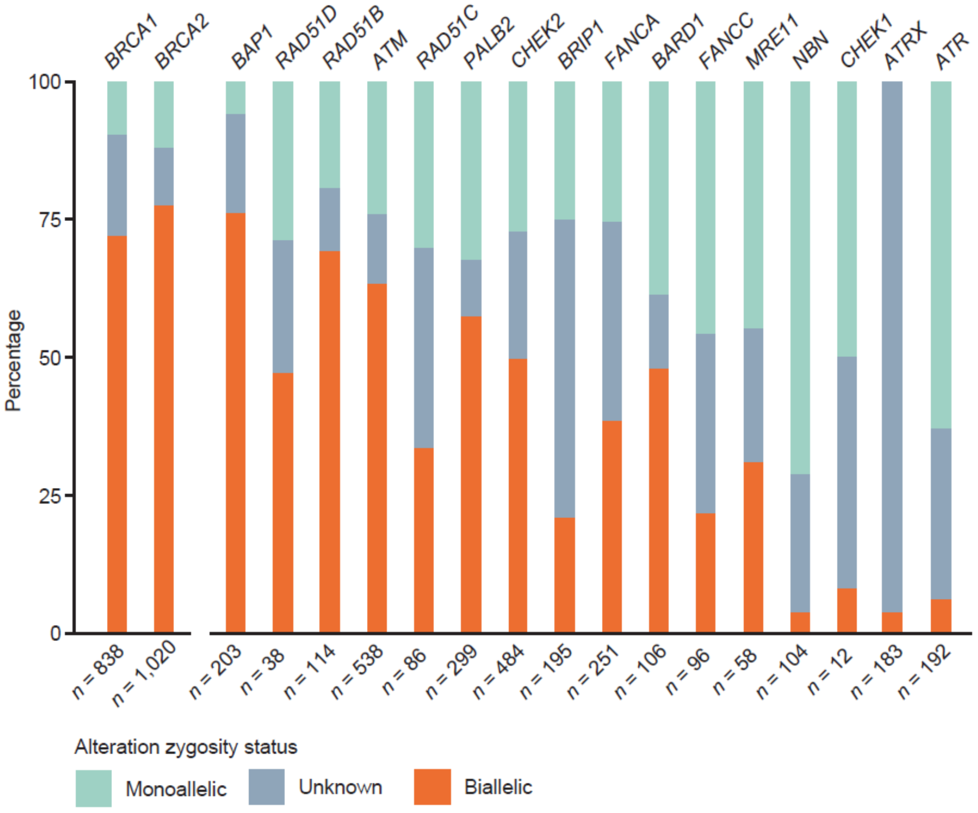
Mutational landscape of the overall cohort. CN, copy number; RE, rearrangement; SV, short variant; the top 20 most frequently altered genes are shown.



Supplementary Figure 4.

Association of HRR-associated gene alterations with biallelic loss in **A,** breast, **B,** ovarian, **C,** pancreatic, **D,** prostate, **E,** bladder, **F,** cholangiocarcinoma, **G,** CRC, **H,** CUP, **I,** endometrial, **J,** esophageal, **K,** glioma, **L,** kidney, **M,** melanoma, **N,** NSCLC, **O,** stomach, and **P,** other cancers. CUP, carcinoma-of-unknown-primary-origin.

A



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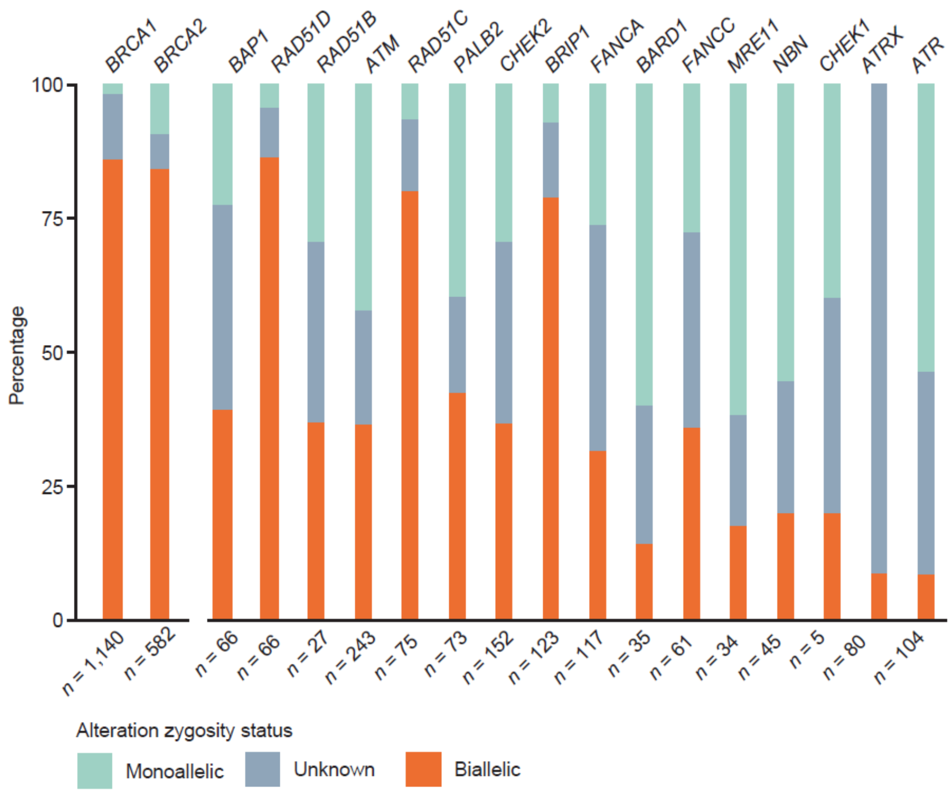
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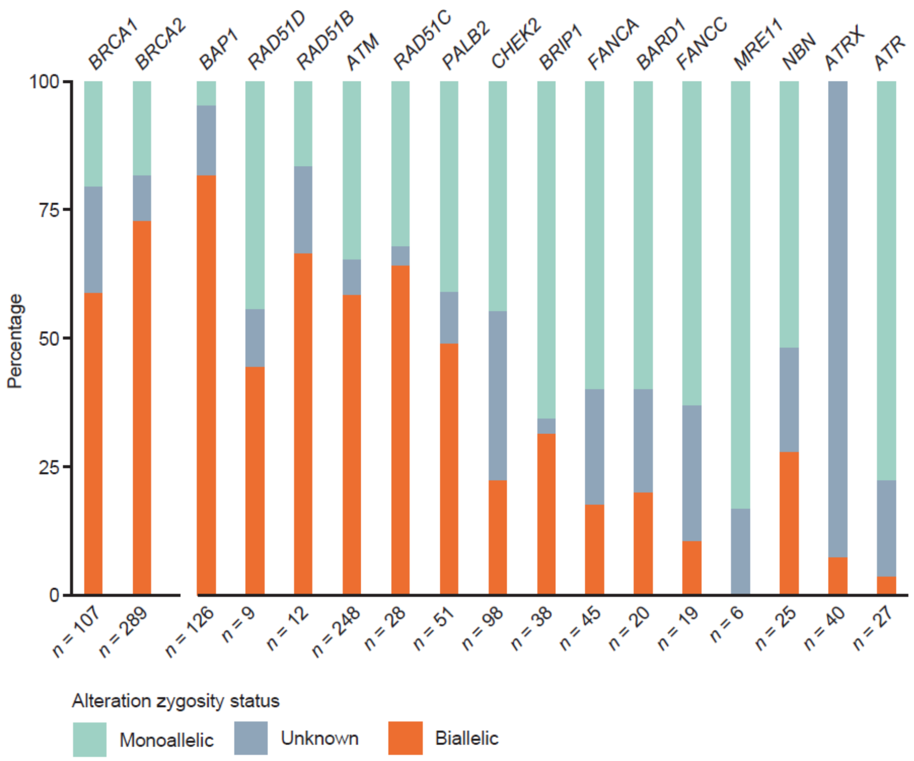
BRCA2
BAP1
RAD51D
RAD51B
ATM
RAD51C
PALB2
CHEK2
BRIP1
FANCA
BARD1
FANCC
MRE11
NBN
CHEK1
ATRX
ATR
100
75
50
25
0
Percentage
n = 1,140
n = 582
n = 66
n = 66
n = 27
n = 243
n = 75
n = 73
n = 152
n = 123
n = 117
n = 35
n = 61
n = 34
n = 45
n = 5
n = 80
n = 104
Alteration zygosity status
Monoallelic
Unknown
Biallelic

C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BRCA2
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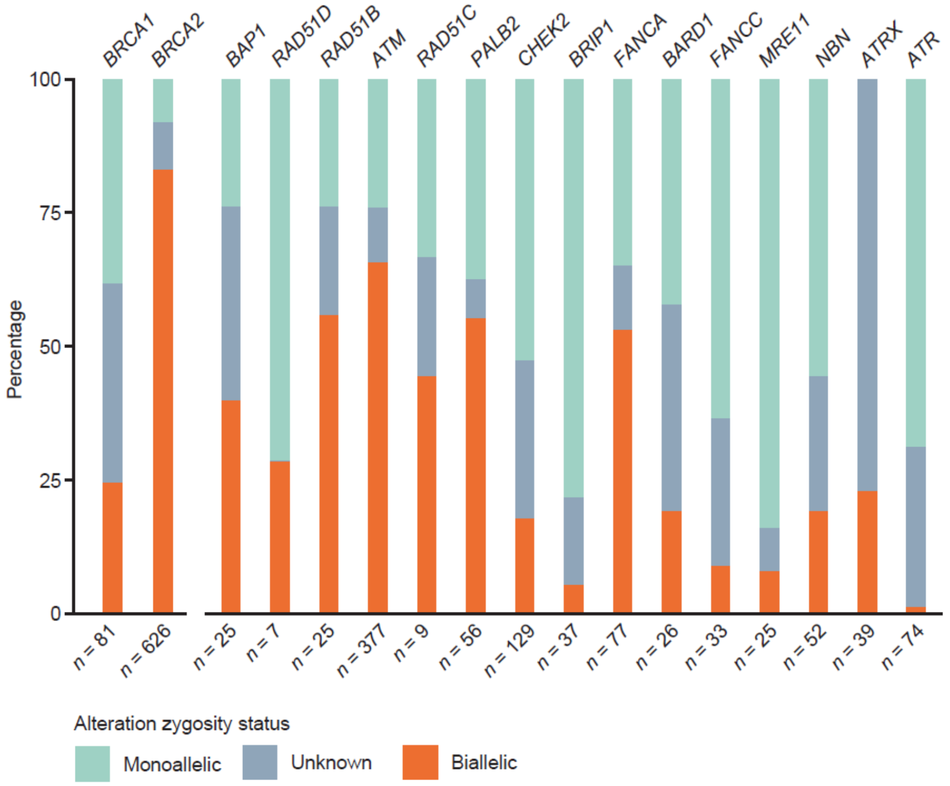
RAD51D
RAD51B
ATM
RAD51C
PALB2
CHEK2
BRIP1
FANCA
BARD1
FANCC
MRE11
NBN
ATRX
ATR
100
75
50
25
0
Percentage
n = 107
n = 289
n = 126
n = 9
n = 12
n = 248
n = 28
n = 51
n = 98
n = 38
n = 45
n = 20
n = 19
n = 6
n = 25
n = 40
n = 27
Alteration zygosity status
Monoallelic
Unknown
Biallelic

D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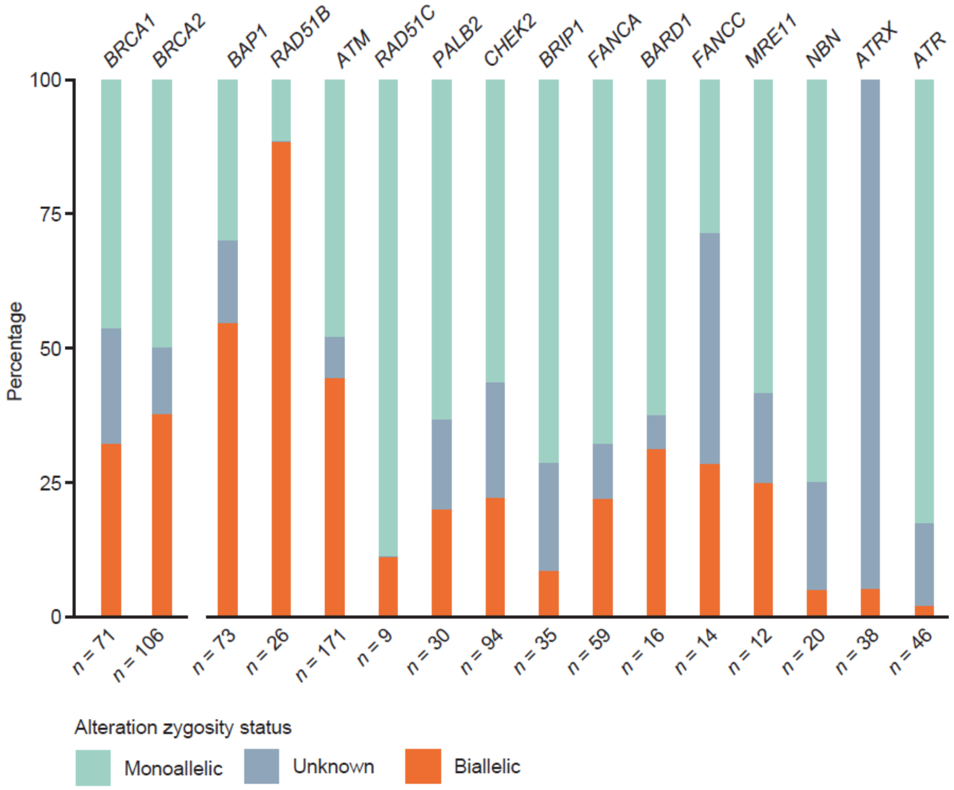
RAD51B
ATM
RAD51C
PALB2
CHEK2
BRIP1
FANCA
BARD1
FANCC
MRE11
NBN
ATRX
ATR
100
75
50
25
0
Percentage
n = 81
n = 626
n = 25
n = 7
n = 25
n = 377
n = 9
n = 56
n = 129
n = 37
n = 77
n = 26
n = 33
n = 25
n = 52
n = 39
n = 74
Alteration zygosity status
Monoallelic
Unknown
Biallelic

E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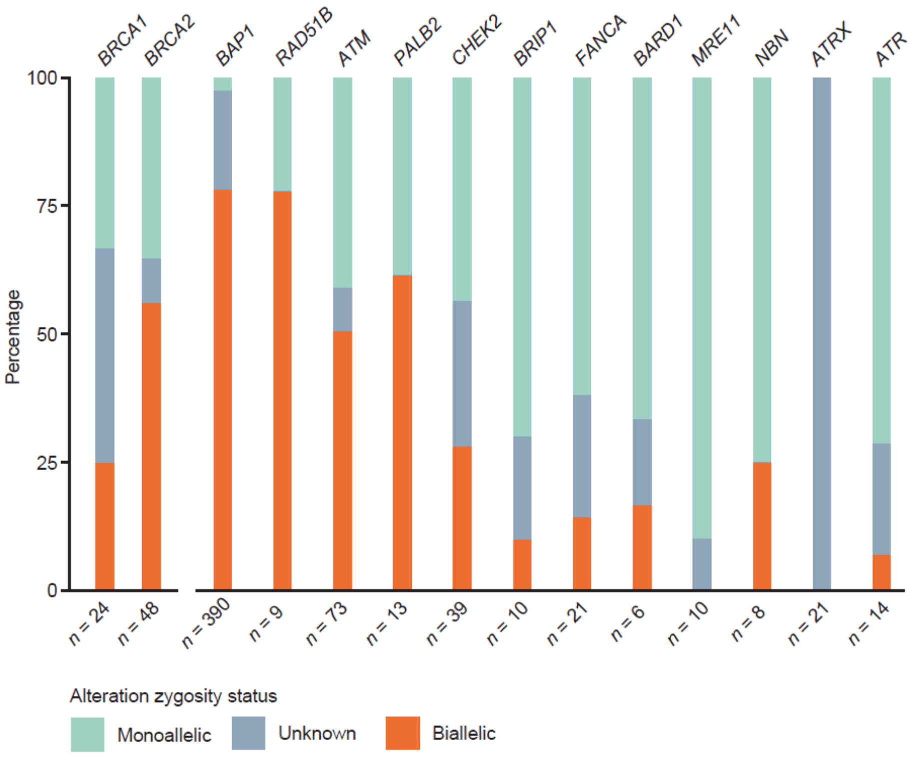
ATM
RAD51C
PALB2
CHEK2
BRIP1
FANCA
BARD1
FANCC
MRE11
NBN
ATRX
ATR
100
75
50
25
0
Percentage
n = 71
n = 106
n = 73
n = 26
n = 171
n = 9
n = 30
n = 94
n = 35
n = 59
n = 16
n = 14
n = 12
n = 20
n = 38
n = 46
Alteration zygosity status
Monoallelic
Unknown
Biallelic

F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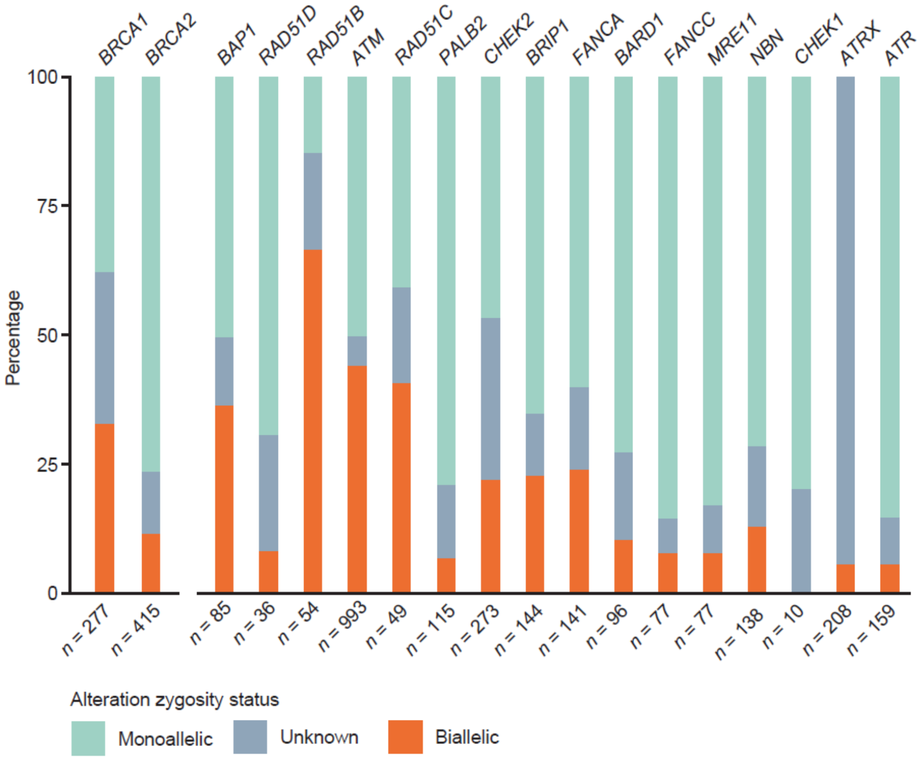
ATM
PALB2
CHEK2
BRIP1
FANCA
BARD1
MRE11
NBN
ATRX
ATR
100
75
50
25
0
Percentage
n = 24
n = 48
n = 390
n = 9
n = 73
n = 13
n = 39
n = 10
n = 21
n = 6
n = 10
n = 8
n = 21
n = 14
Alteration zygosity status
Monoallelic
Unknown
Biallelic

G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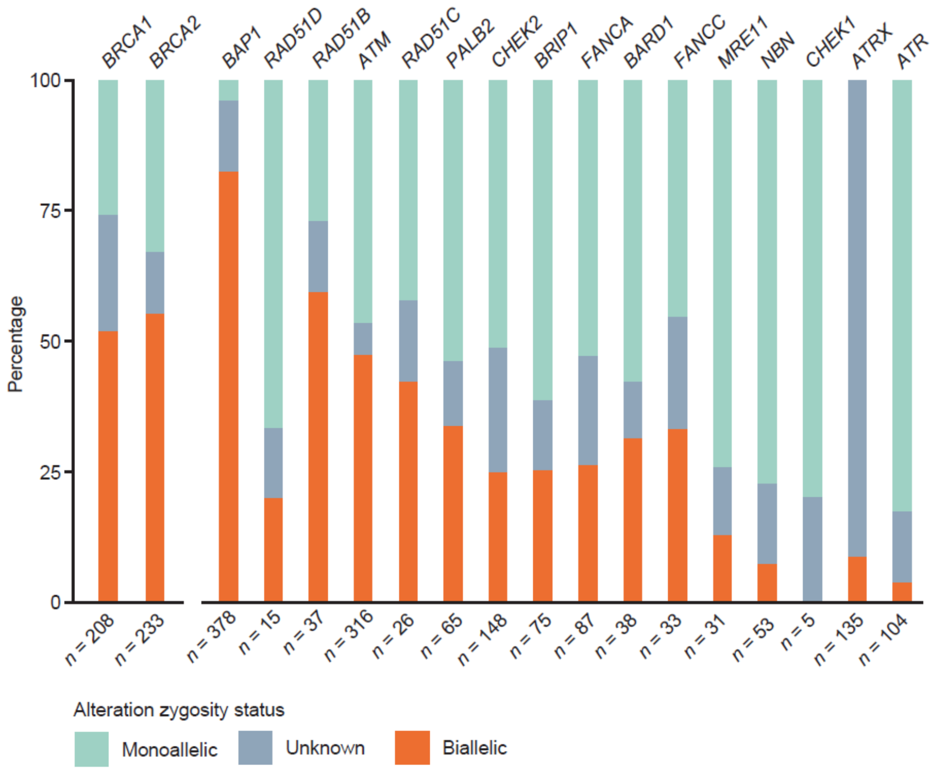
RAD51B
ATM
RAD51C
PALB2
CHEK2
BRIP1
FANCA
BARD1
FANCC
MRE11
NBN
CHEK1
ATRX
ATR
100
75
50
25
0
Percentage
n = 277
n = 415
n = 85
n = 36
n = 54
n = 993
n = 49
n = 115
n = 273
n = 144
n = 141
n = 96
n = 77
n = 77
n = 138
n = 10
n = 208
n = 159
Alteration zygosity status
Monoallelic
Unknown
Biallelic

H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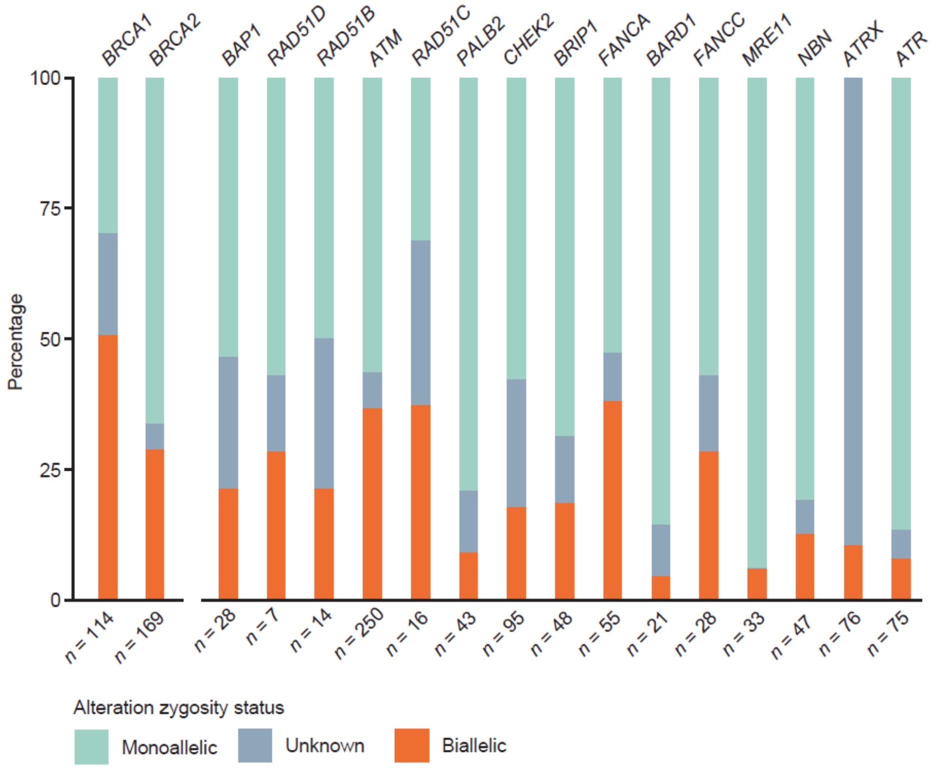
BRCA2
BAP1
RAD51D
RAD51B
ATM
RAD51C
PALB2
CHEK2
BRIP1
FANCA
BARD1
FANCC
MRE11
NBN
CHEK1
ATRX
ATR
100
75
50
25
0
Percentage
n = 208
n = 233
n = 378
n = 15
n = 37
n = 316
n = 26
n = 65
n = 148
n = 75
n = 87
n = 38
n = 33
n = 31
n = 53
n = 5
n = 135
n = 104
Alteration zygosity status
Monoallelic
Unknown
Biallelic

I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BRCA2
BAP1
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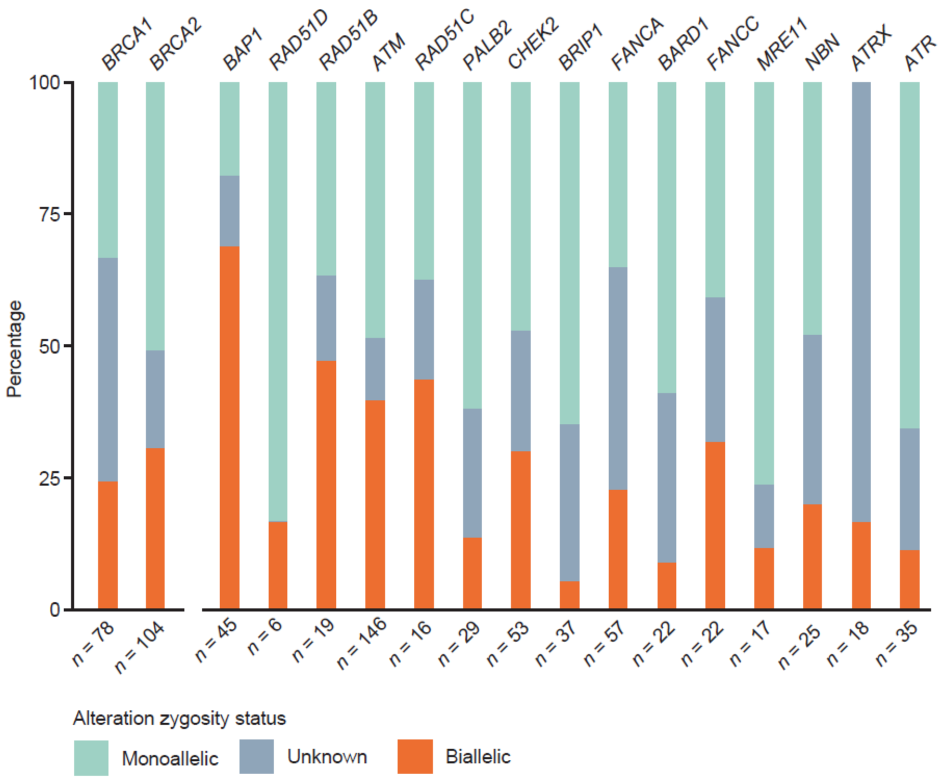
RAD51B
ATM
RAD51C
PALB2
CHEK2
BRIP1
FANCA
BARD1
FANCC
MRE11
NBN
ATRX
ATR
100
75
50
25
0
Percentage
n = 114
n = 169
n = 28
n = 7
n = 14
n = 250
n = 16
n = 43
n = 95
n = 48
n = 55
n = 21
n = 28
n = 33
n = 47
n = 76
n = 75
Alteration zygosity status
Monoallelic
Unknown
Biallelic

J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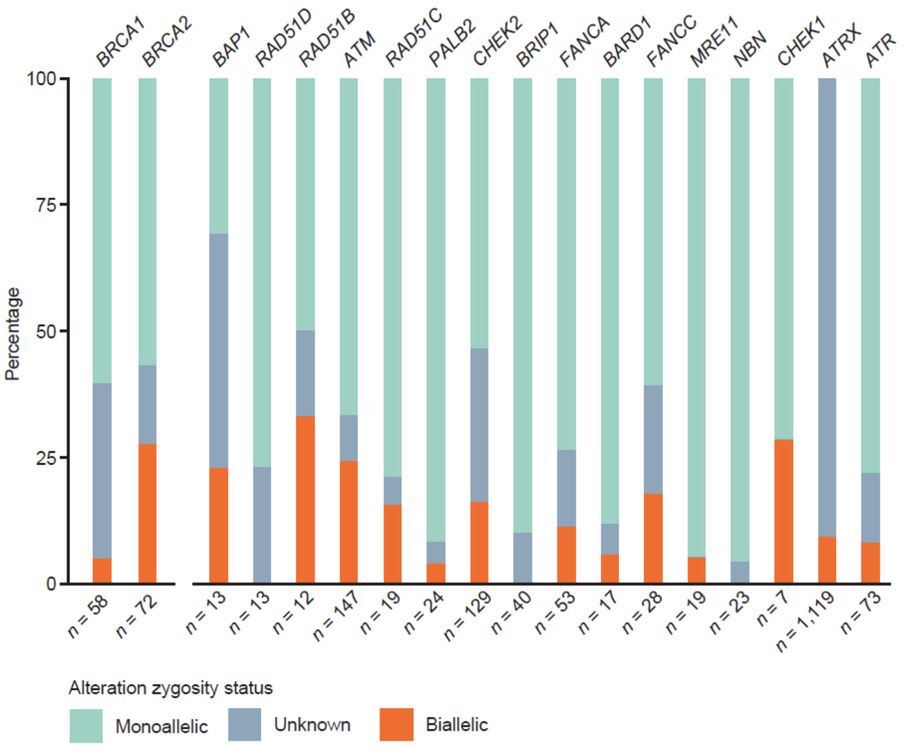
RAD51B
ATM
RAD51C
PALB2
CHEK2
BRIP1
FANCA
BARD1
FANCC
MRE11
NBN
ATRX
ATR
Percentage
100
75
50
25
0
n = 78
n = 104
n = 45
n = 6
n = 19
n = 146
n = 16
n = 29
n = 53
n = 37
n = 57
n = 22
n = 22
n = 17
n = 25
n = 18
n = 35
Alteration zygosity status
Monoallelic
Unknown
Biallelic

K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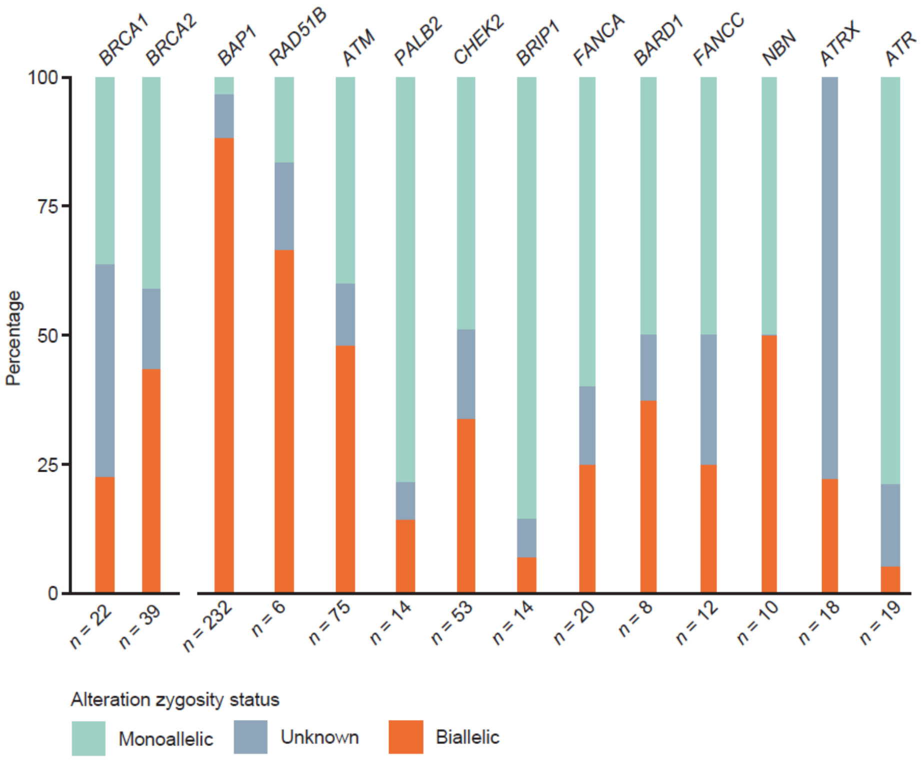
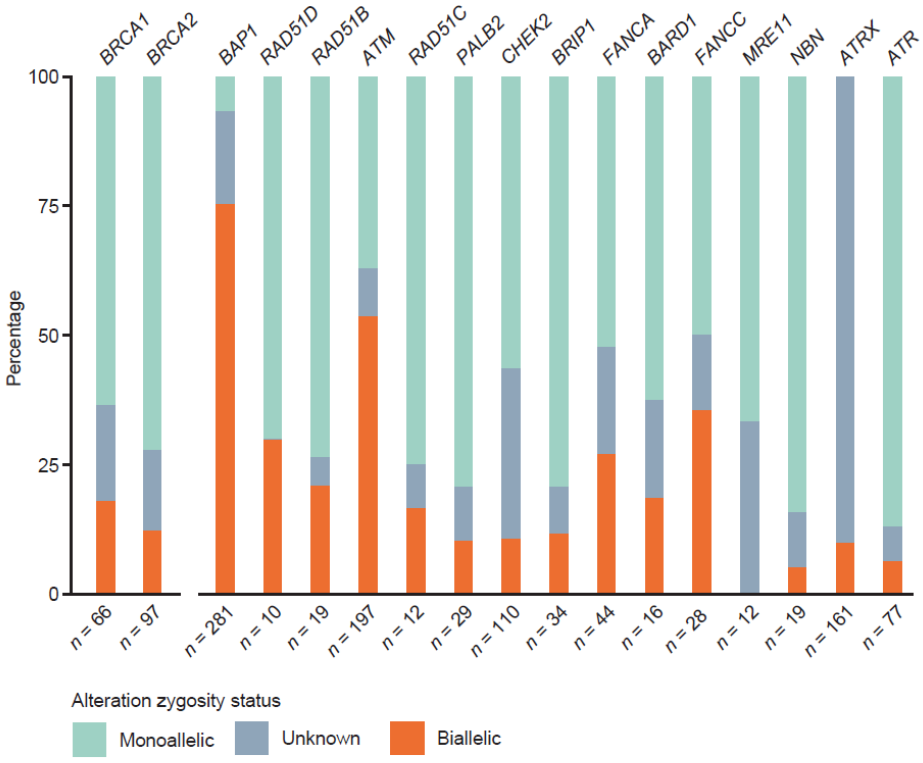
BRCA2
BAP1
RAD51D
RAD51B
ATM
RAD51C
PALB2
CHEK2
BRIP1
FANCA
BARD1
FANCC
MRE11
NBN
CHEK1
ATRX
ATR
Percentage
100
75
50
25
0
n = 58
n = 72
n = 13
n = 13
n = 12
n = 147
n = 19
n = 24
n = 129
n = 40
n = 53
n = 17
n = 28
n = 19
n = 23
n = 7
n = 1,119
n = 73
Alteration zygosity status
Monoallelic
Unknown
Biallelic

L


BRCA1
BRCA2
BAP1
RAD51B
ATM
PALB2
CHEK2
BRIP1
FANCA
BARD1
FANCC
NBN
ATRX
ATR
Percentage
100
75
50
25
0
n = 22
n = 39
n = 232
n = 6
n = 75
n = 14
n = 53
n = 14
n = 20
n = 8
n = 12
n = 10
n = 18
n = 19
Alteration zygosity status
Monoallelic
Unknown
Biallelic

M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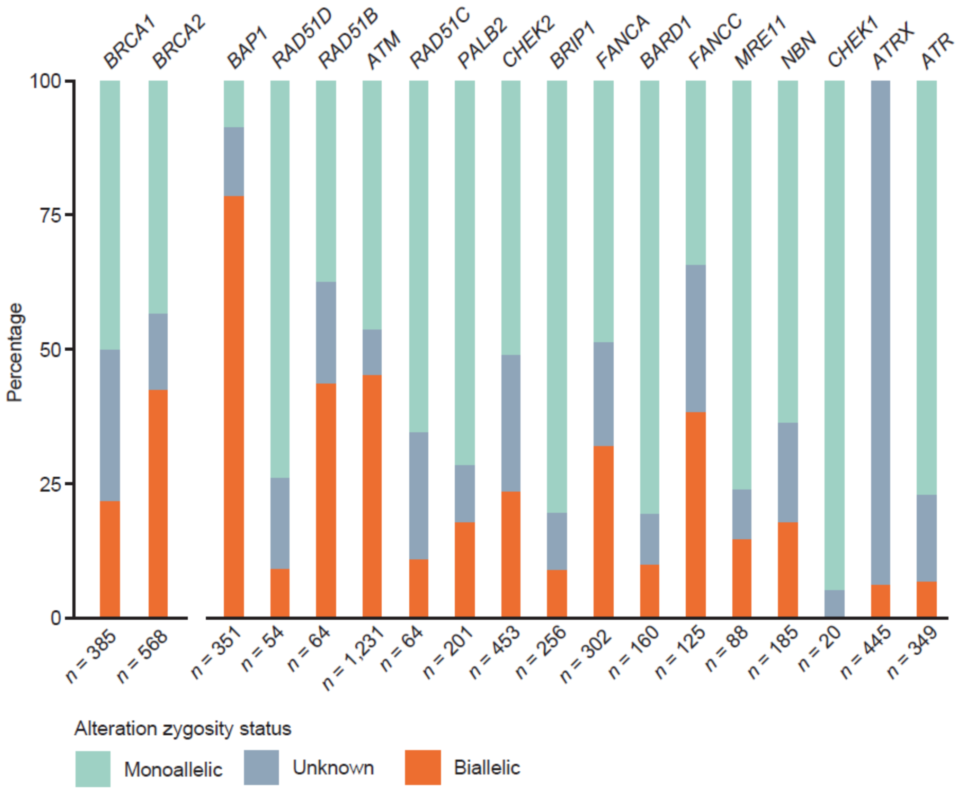
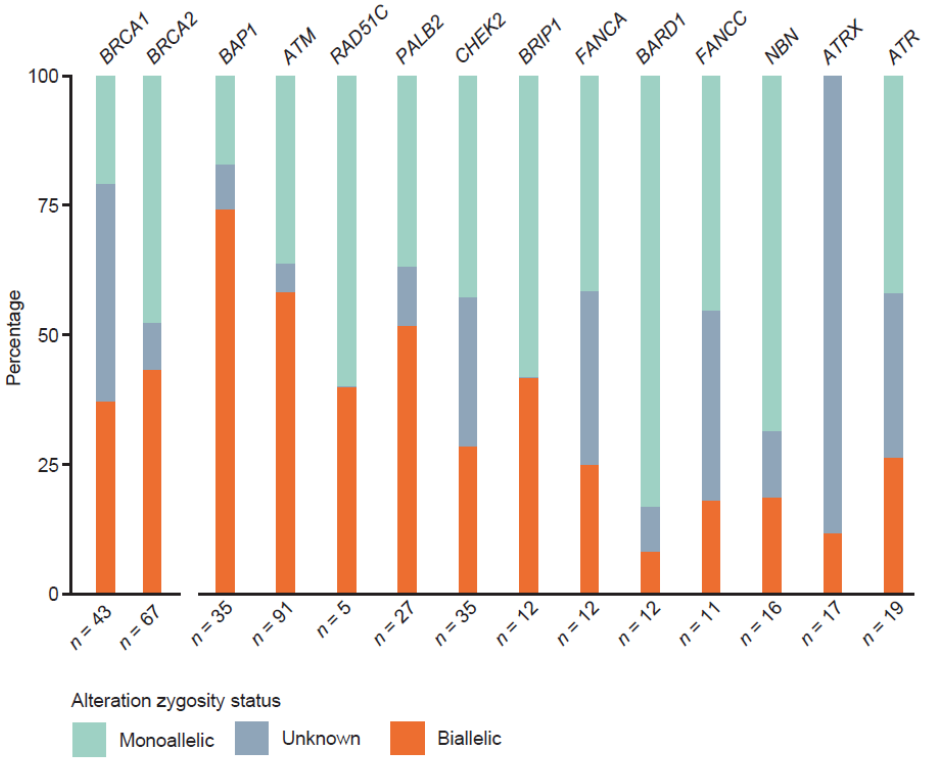
BRCA2
BAP1
RAD51D
RAD51B
ATM
RAD51C
PALB2
CHEK2
BRIP1
FANCA
BARD1
FANCC
MRE11
NBN
ATRX
ATR
Percentage
100
75
50
25
0
n = 66
n = 97
n = 281
n = 10
n = 19
n = 197
n = 12
n = 29
n = 110
n = 34
n = 44
n = 16
n = 28
n = 12
n = 19
n = 161
n = 77
Alteration zygosity status
Monoallelic
Unknown
Biallelic

N


BRCA1
BRCA2
BAP1
RAD51D
RAD51B
ATM
RAD51C
PALB2
CHEK2
BRIP1
FANCA
BARD1
FANCC
MRE11
NBN
CHEK1
ATRX
ATR
100
75
50
25
0
Percentage
n = 385
n = 568
n = 351
n = 54
n = 64
n = 1,231
n = 64
n = 201
n = 453
n = 256
n = 302
n = 160
n = 125
n = 88
n = 185
n = 20
n = 445
n = 349
Alteration zygosity status
Monoallelic
Unknown
Biallelic

O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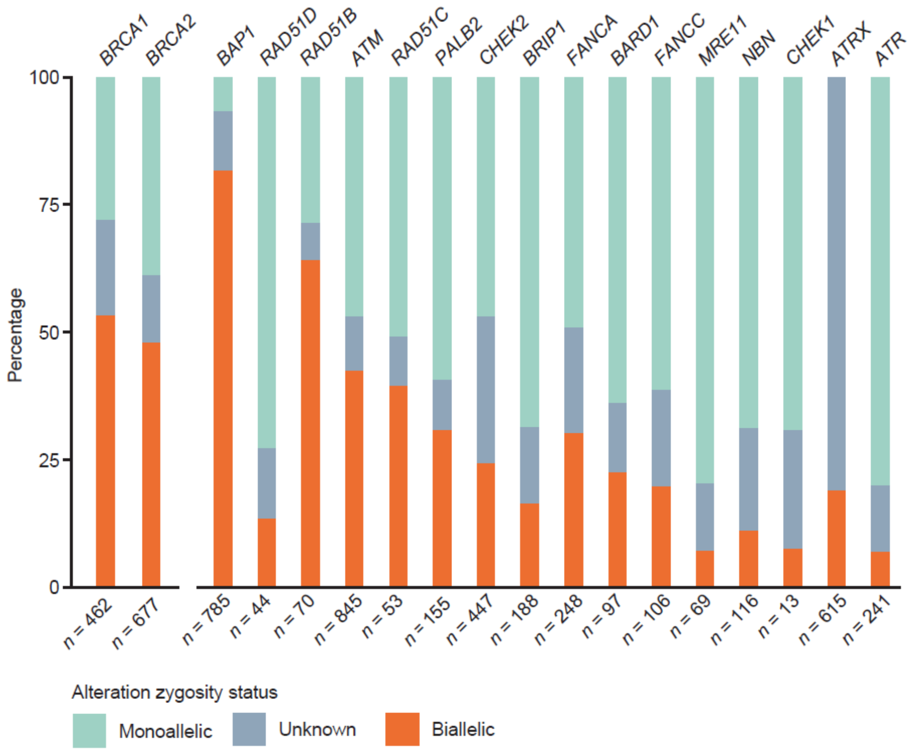
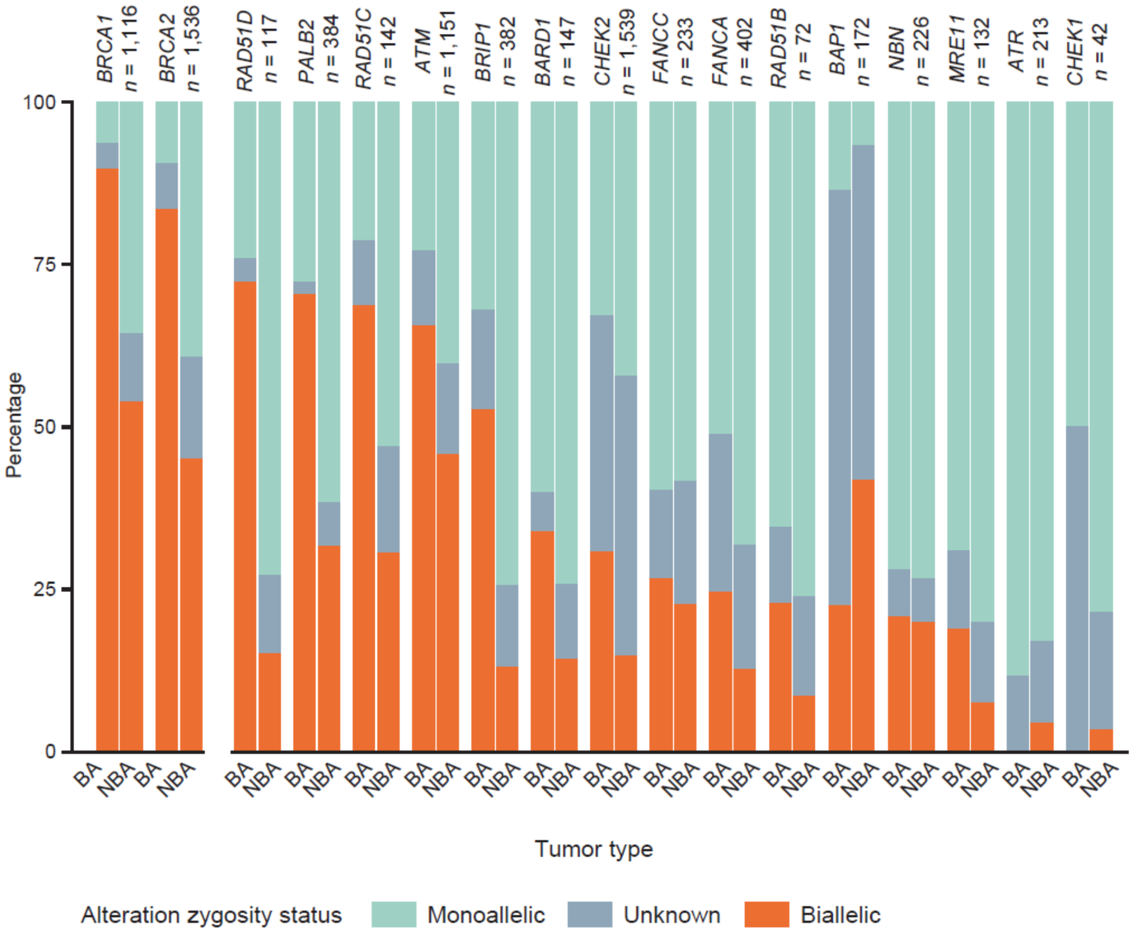
BRCA2
BAP1
ATM
RAD51C
PALB2
CHEK2
BRIP1
FANCA
BARD1
FANCC
NBN
ATRX
ATR
100
75
50
25
0
Percentage
n = 43
n = 67
n = 35
n = 91
n = 5
n = 27
n = 35
n = 12
n = 12
n = 12
n = 11
n = 16
n = 17
n = 19
Alteration zygosity status
Monoallelic
Unknown
Biallelic

P


BRCA1
BRCA2
BAP1
RAD51D
RAD51B
ATM
RAD51C
PALB2
CHEK2
BRIP1
FANCA
BARD1
FANCC
MRE11
NBN
CHEK1
ATRX
ATR
100
75
50
25
0
Percentage
n = 462
n = 677
n = 785
n = 44
n = 70
n = 845
n = 53
n = 155
n = 447
n = 188
n = 248
n = 97
n = 106
n = 69
n = 116
n = 13
n = 615
n = 241
Alteration zygosity status
Monoallelic
Unknown
Biallelic

Supplementary Figure 5.

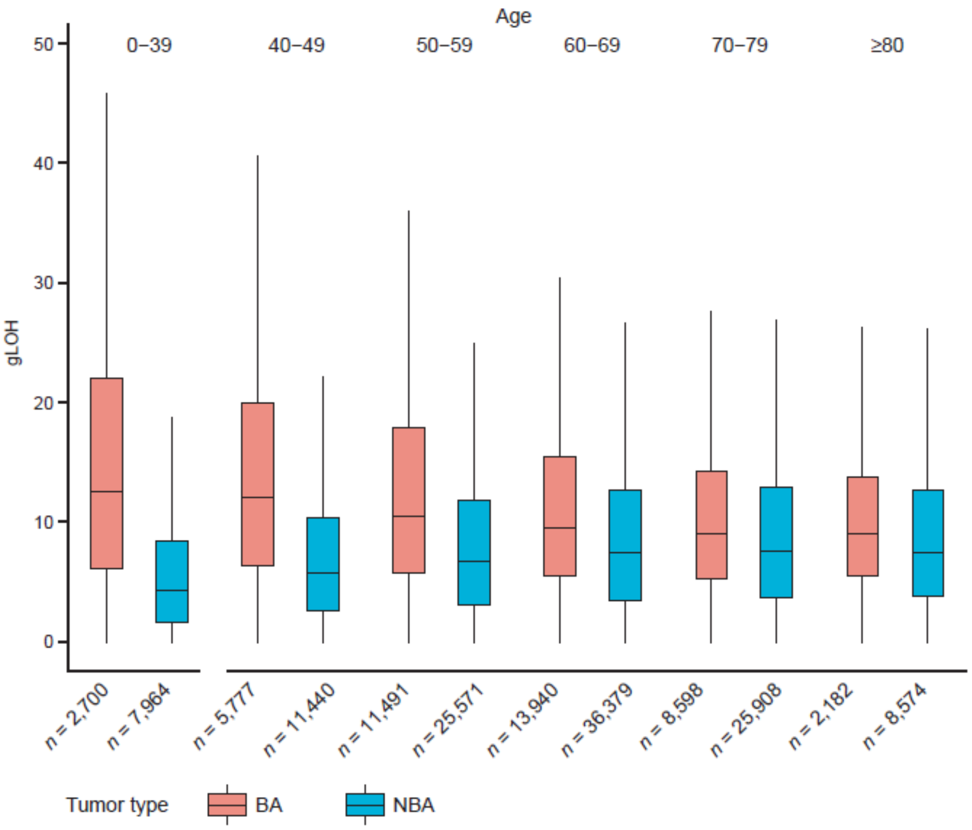
Association of HRR-associated gene alterations of predicted germline origin with biallelic loss.



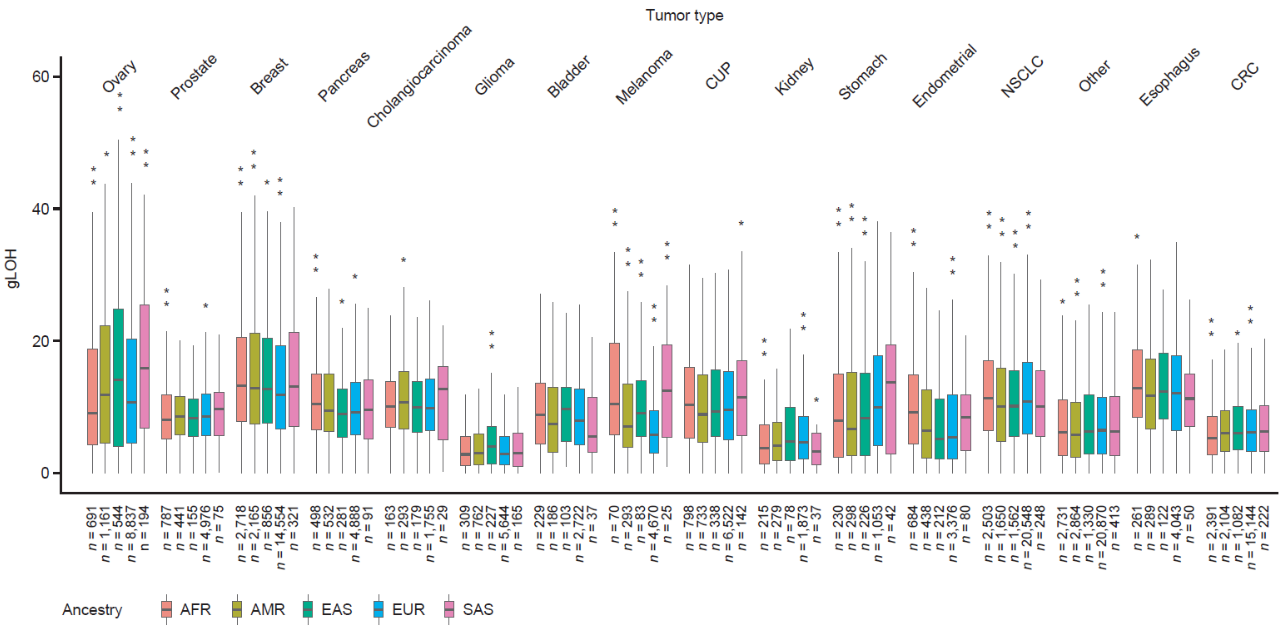
Supplementary Figure 6.

Association of gLOH with **A,** age and **B,** ancestry. AFR, African; AMR, Central and South American; CUP, carcinoma-of-unknown-primary-origin; EAS, East Asian; EUR, European; SAS, South Asian; asterisks denote level of significance after false discovery correction: * = $P < 0.05$; ** = $P < 0.01$.

A



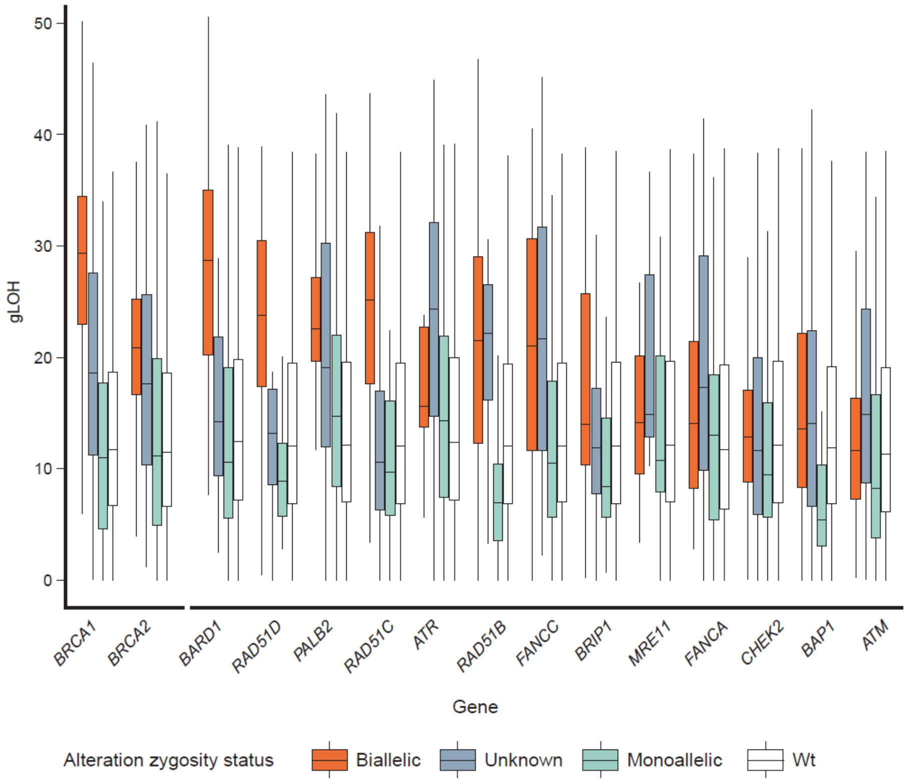
B


Tumor type
gLOH
60
40
20
0
Ovary
Prostate
Breast
Pancreas
Cholangiocarcinoma
Glioma
Bladder
Melanoma
CUP
Kidney
Stomach
Endometrial
NSCLC
Other
Esophagus
CRC
n = 691
n = 1,161
n = 544
n = 8,837
n = 194
n = 787
n = 441
n = 155
n = 4,976
n = 75
n = 2,718
n = 2,165
n = 856
n = 14,554
n = 321
n = 498
n = 532
n = 281
n = 4,888
n = 91
n = 163
n = 293
n = 179
n = 1,755
n = 29
n = 309
n = 762
n = 227
n = 5,644
n = 165
n = 229
n = 186
n = 103
n = 2,722
n = 37
n = 70
n = 293
n = 83
n = 4,670
n = 25
n = 798
n = 733
n = 338
n = 6,522
n = 142
n = 215
n = 279
n = 78
n = 1,873
n = 37
n = 230
n = 298
n = 226
n = 1,053
n = 42
n = 684
n = 438
n = 212
n = 3,376
n = 80
n = 2,503
n = 1,650
n = 1,562
n = 20,548
n = 248
n = 2,731
n = 2,864
n = 1,330
n = 20,870
n = 413
n = 261
n = 289
n = 122
n = 4,043
n = 50
n = 2,391
n = 2,104
n = 1,082
n = 15,144
n = 222
Ancestry
AFR
AMR
EAS
EUR
SAS

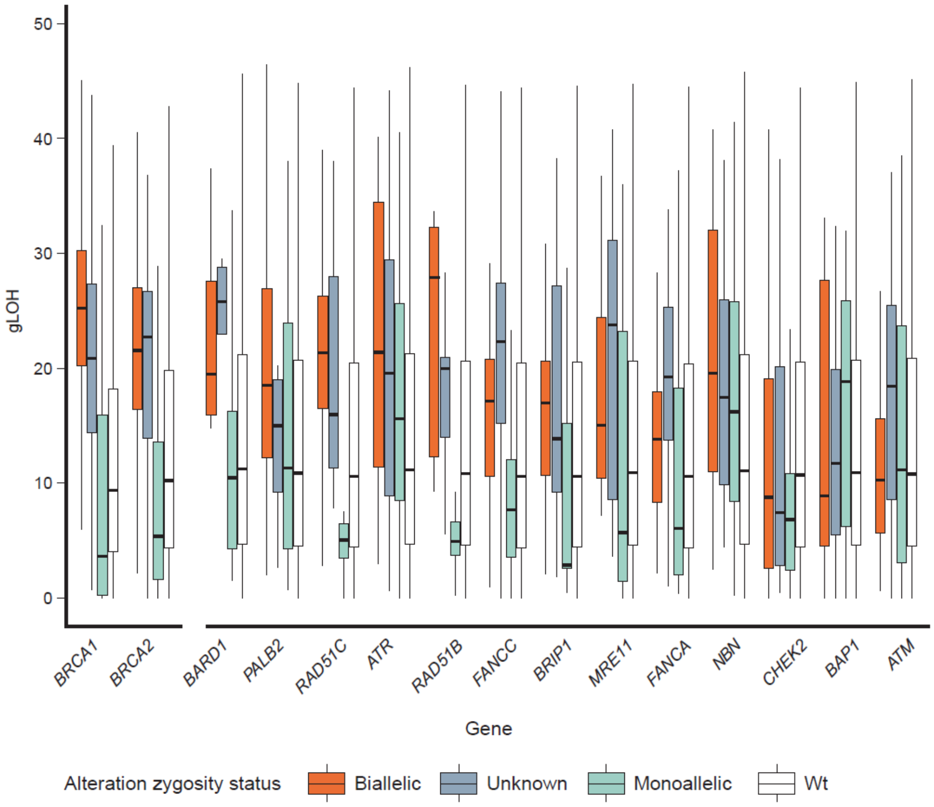
Supplementary Figure 7.

Association of HRR gene alterations with gLOH by cancer type*: **A,** breast, **B,** ovarian, **C,** prostate, **D,** pancreatic, **E,** CRC, and **F,** NSCLC. wt, wild type; * Only genes with at least five assessable alterations in each category (biallelic, BA; monoallelic, NBA) were considered; wt refers to the gene being analyzed; *CHEK1* and *ATRX* had too few samples to be assessable and were therefore excluded.

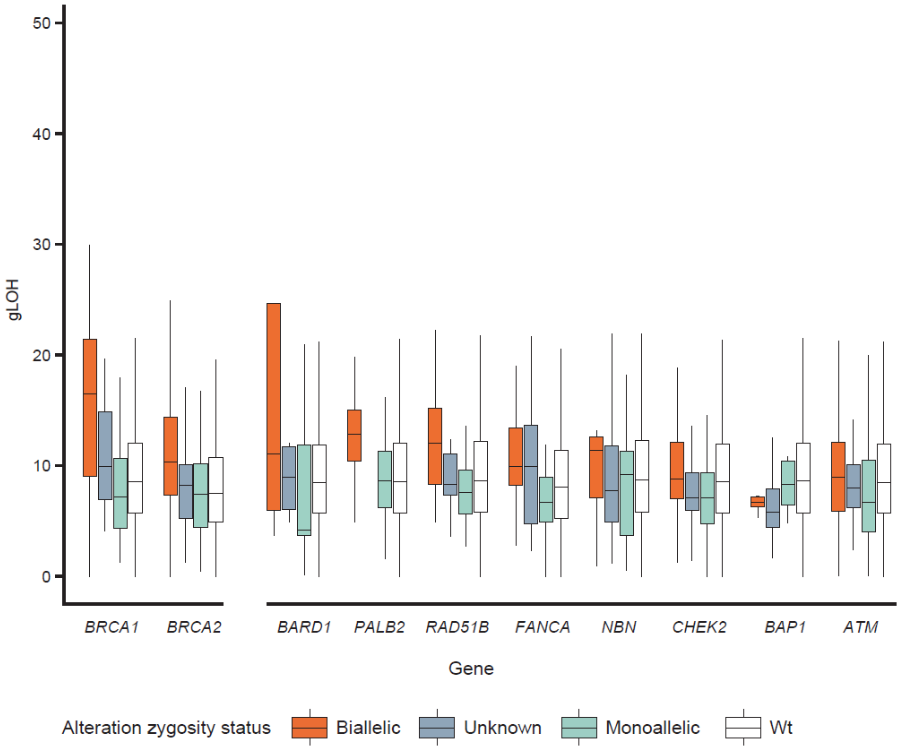
A



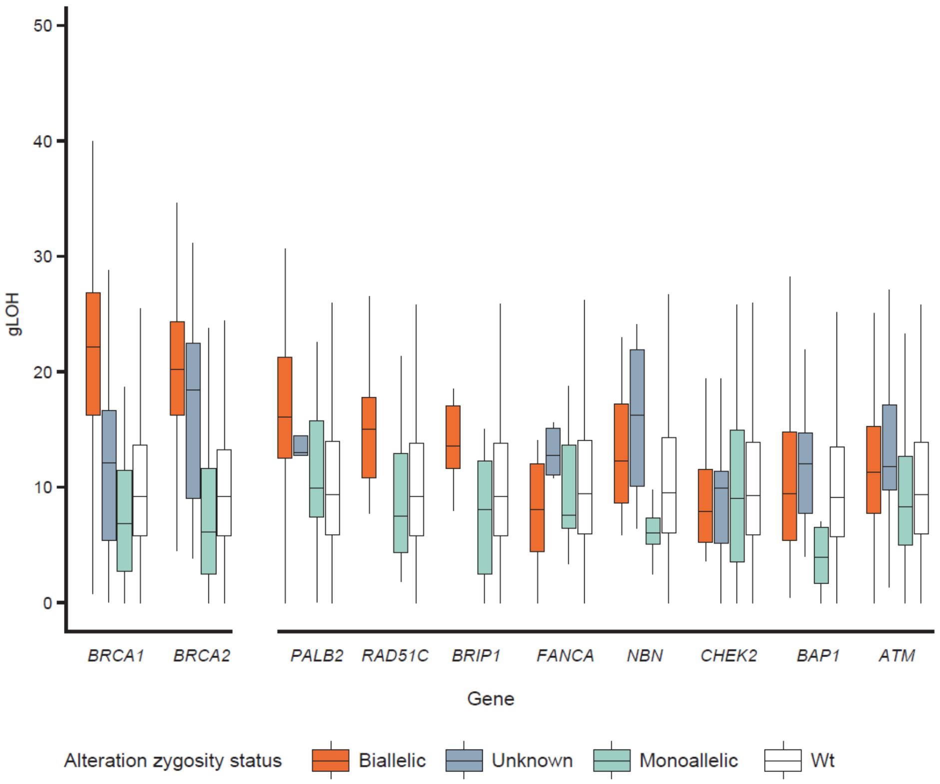
B


50
40
30
20
10
0
gLOH
BRCA1
BRCA2
BARD1
PALB2
RAD51C
ATR
RAD51B
FANCC
BRIP1
MRE11
FANCA
NBN
CHEK2
BAP1
ATM
Gene
Alteration zygosity status
Biallelic
Unknown
Monoallelic
Wt

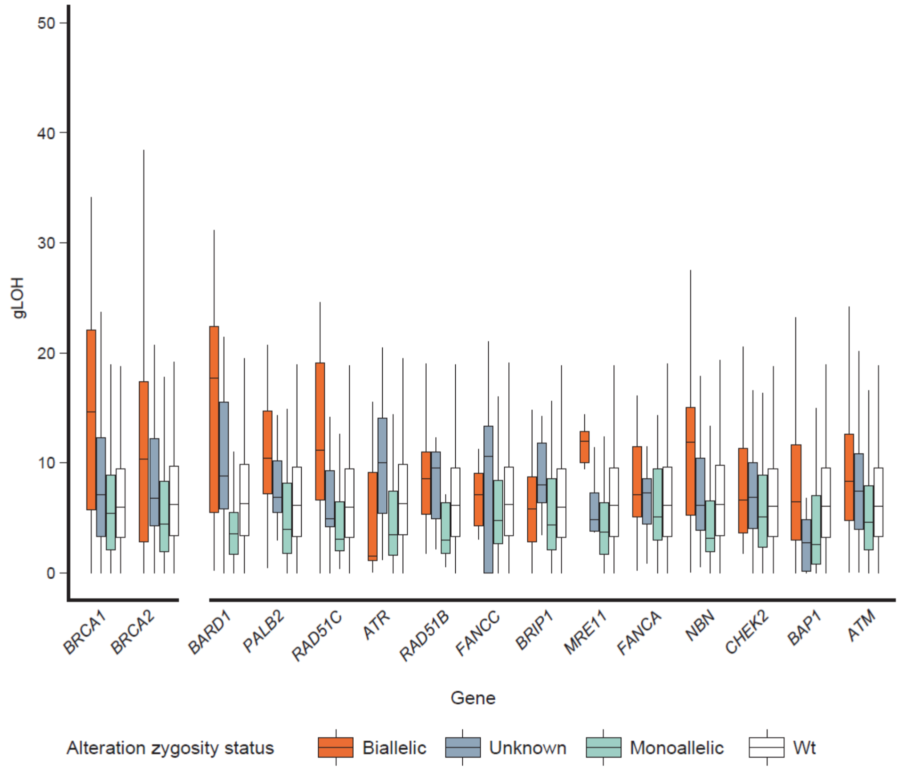
C


50
40
30
20
10
0
gLOH
BRCA1
BRCA2
BARD1
PALB2
RAD51B
FANCA
NBN
CHEK2
BAP1
ATM
Gene
Alteration zygosity status
Biallelic
Unknown
Monoallelic
Wt

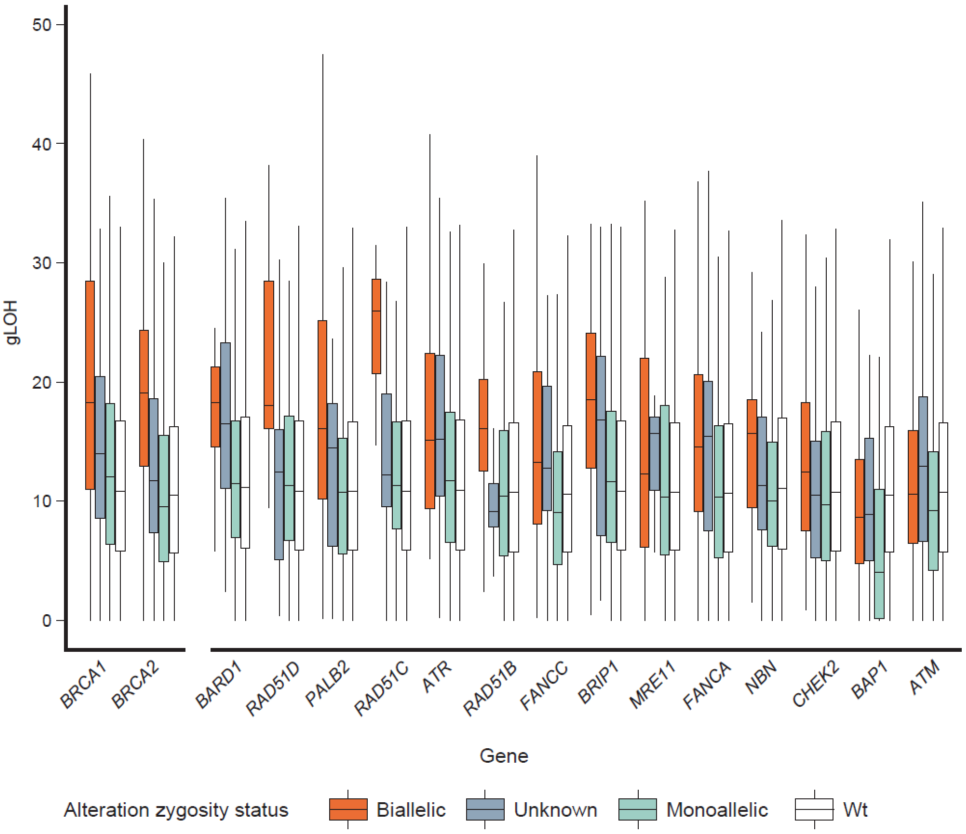
D


gLOH
0
10
20
30
40
50
BRCA1
BRCA2
PALB2
RAD51C
BRIP1
FANCA
NBN
CHEK2
BAP1
ATM
Gene
Alteration zygosity status
Biallelic
Unknown
Monoallelic
Wt

E


gLOH
0
10
20
30
40
50
BRCA1
BRCA2
BARD1
PALB2
RAD51C
ATR
RAD51B
FANCC
BRIP1
MRE11
FANCA
NBN
CHEK2
BAP1
ATM
Gene
Alteration zygosity status
Biallelic
Unknown
Monoallelic
Wt

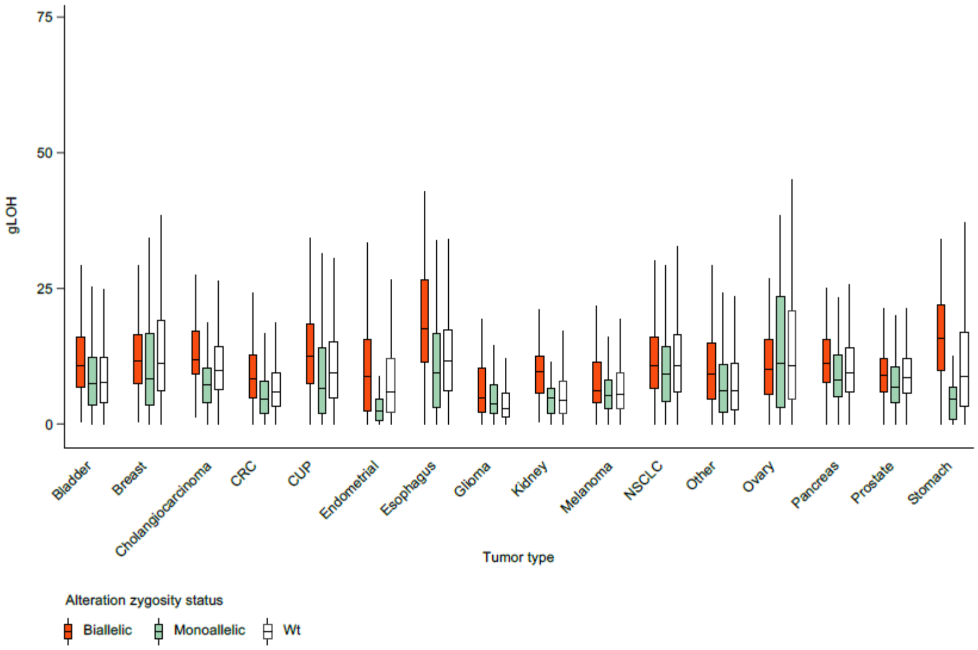
F


gLOH
50
40
30
20
10
0
BRCA1
BRCA2
BARD1
RAD51D
PALB2
RAD51C
ATR
RAD51B
FANCC
BRIP1
MRE11
FANCA
NBN
CHEK2
BAP1
ATM
Gene
Alteration zygosity status
Biallelic
Unknown
Monoallelic
Wt

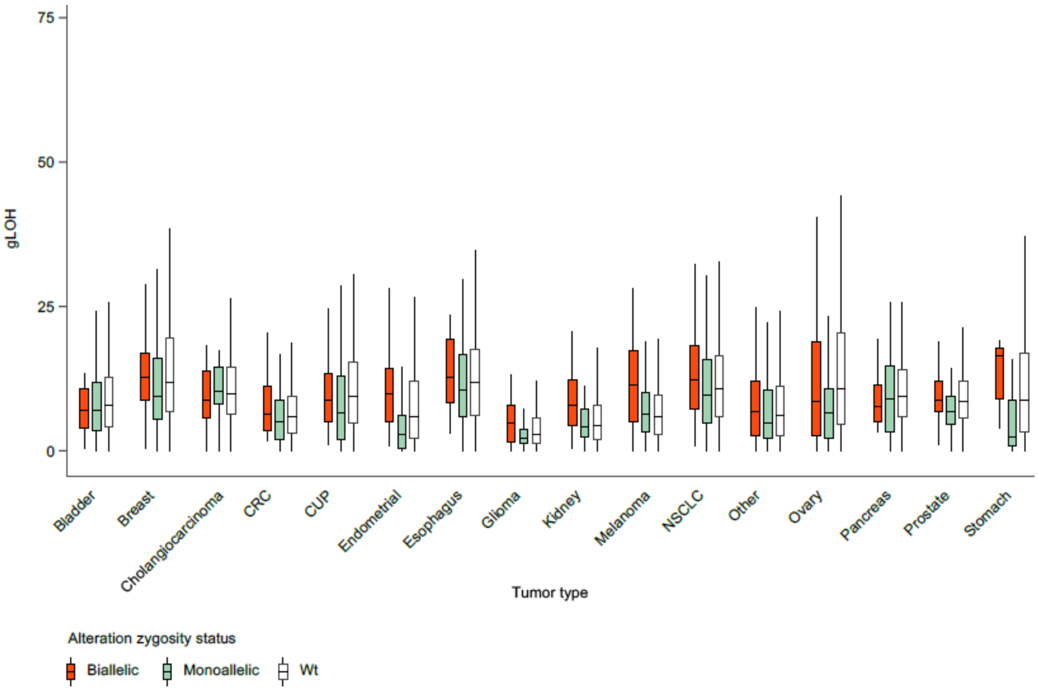
Supplementary Figure 8.

Association between gene alterations and gLOH for: **A,** *ATM*, **B,** *CHEK2*, **C,** *BAP1*, **D,** *CTNNA1*, and **E,** *TP53*. CUP, carcinoma-of-unknown-primary-origin; wt, wild type.

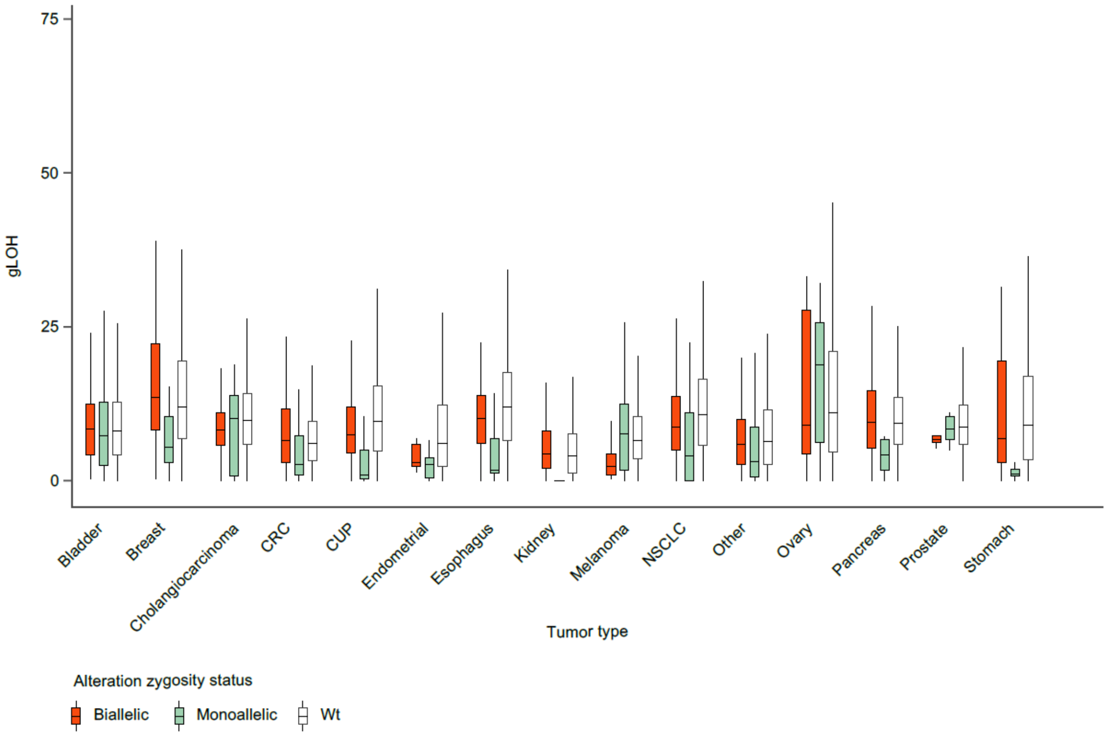
A



B



C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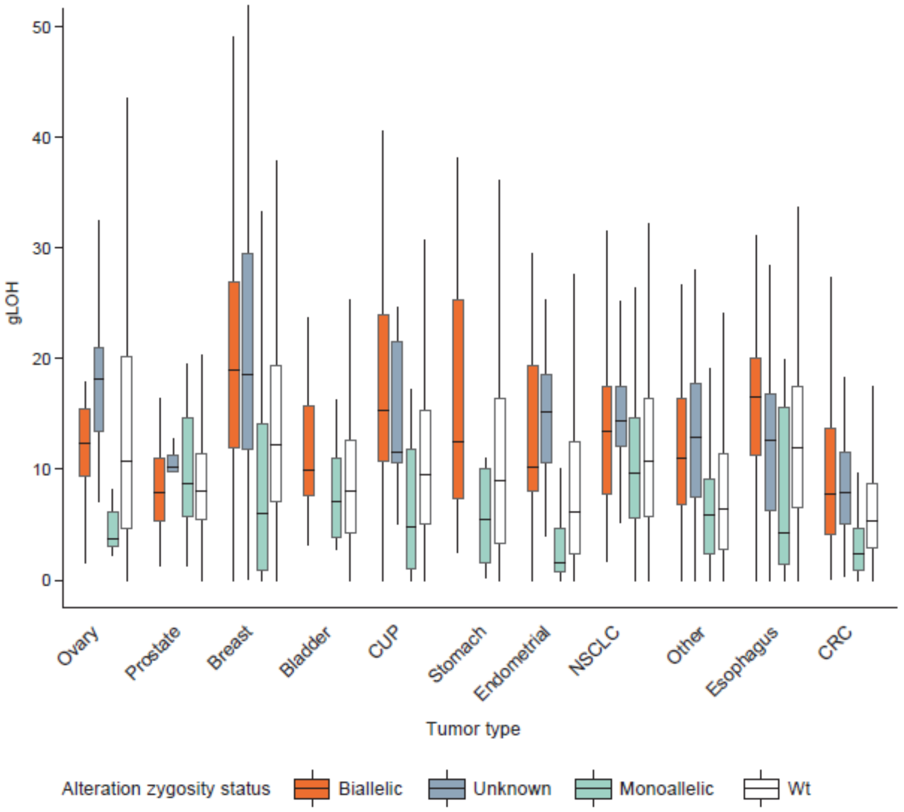
50
25
0
gLOH
Bladder
Breast
Cholangiocarcinoma
CRC
CUP
Endometrial
Esophagus
Kidney
Melanoma
NSCLC
Other
Ovary
Pancreas
Prostate
Stomach
Tumor type
Alteration zygosity status
Biallelic
Monoallelic
Wt

D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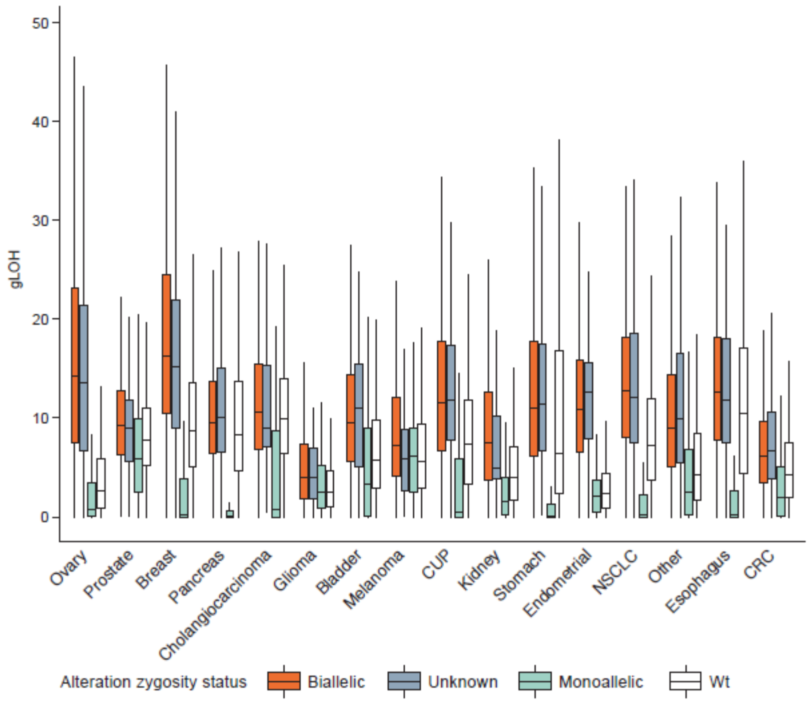
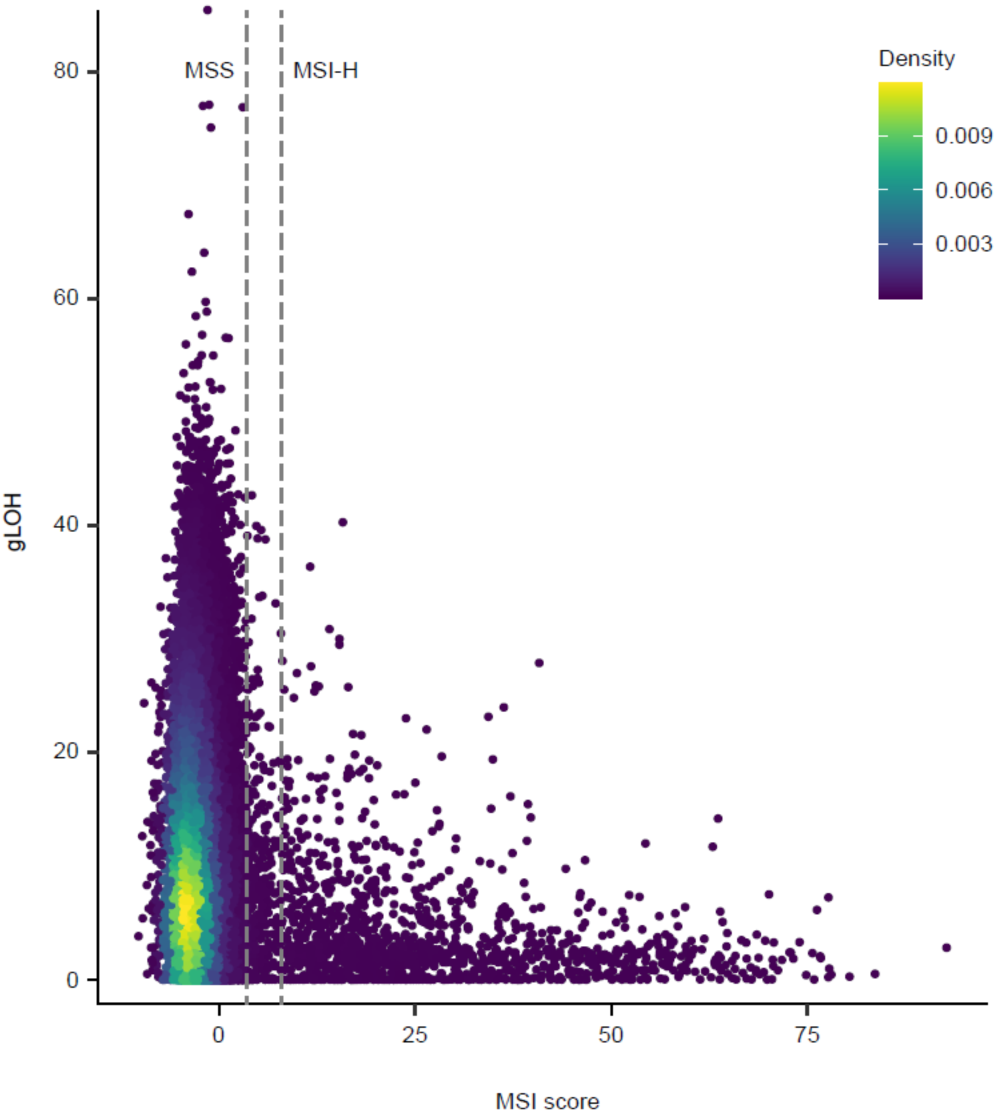
20
10
0
gLOH
Ovary
Prostate
Breast
Bladder
CUP
Stomach
Endometrial
NSCLC
Other
Esophagus
CRC
Tumor type
Alteration zygosity status
Biallelic
Unknown
Monoallelic
Wt

E

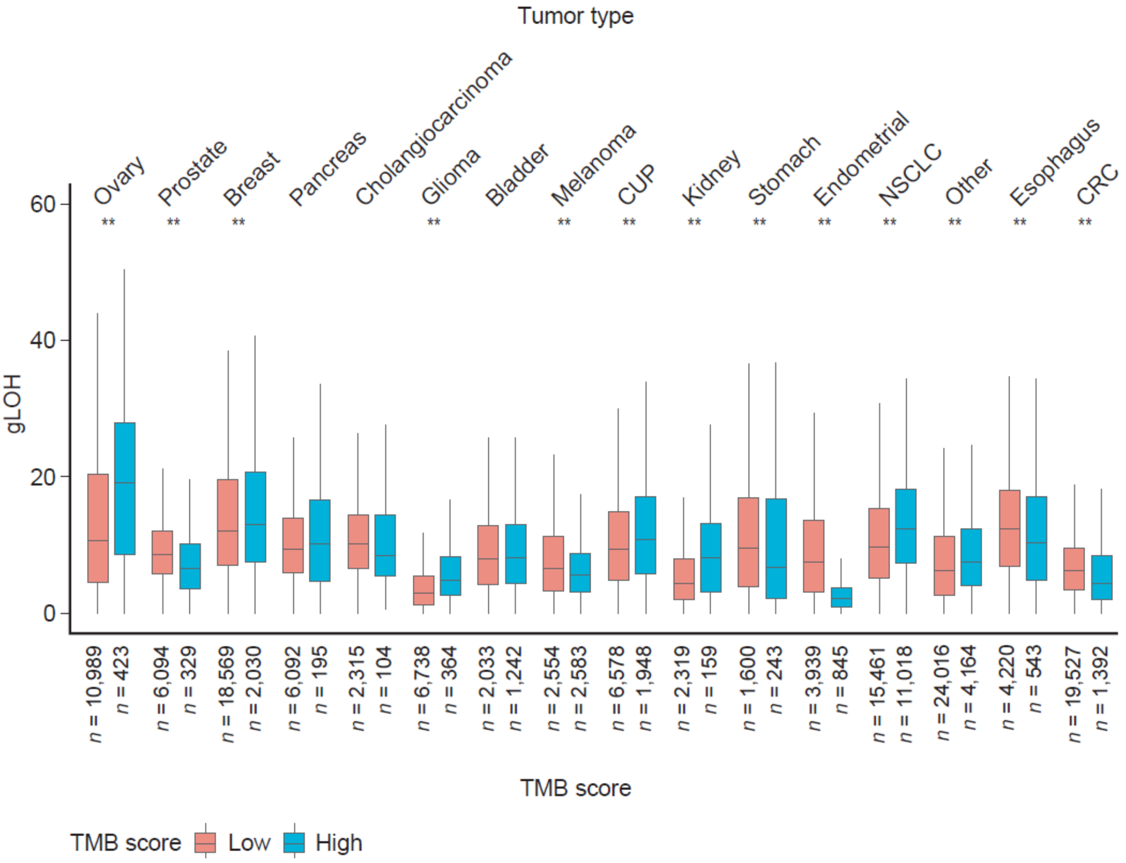

gLOH
50
40
30
20
10
0
Ovary
Prostate
Breast
Pancreas
Cholangiocarcinoma
Glioma
Bladder
Melanoma
CUP
Kidney
Stomach
Endometrial
NSCLC
Other
Esophagus
CRC
Alteration zygosity status
Biallelic
Unknown
Monoallelic
Wt

Supplementary Figure 9. Association of HRR-associated gene alterations and immune checkpoint inhibitor biomarkers: **A,** MSI and **B,** TMB. CUP, carcinoma-of-unknown-primary-origin; MSS, microsatellite stable; asterisks denote level of significance after false discovery correction: * = $P < 0.05$; ** = $P < 0.01$.

A



B


Tumor type
Ovary
Prostate
Breast
Pancreas
Cholangiocarcinoma
Glioma
Bladder
Melanoma
CUP
Kidney
Stomach
Endometrial
NSCLC
Other
Esophagus
CRC
** ** ** ** ** ** ** ** ** ** ** ** ** **
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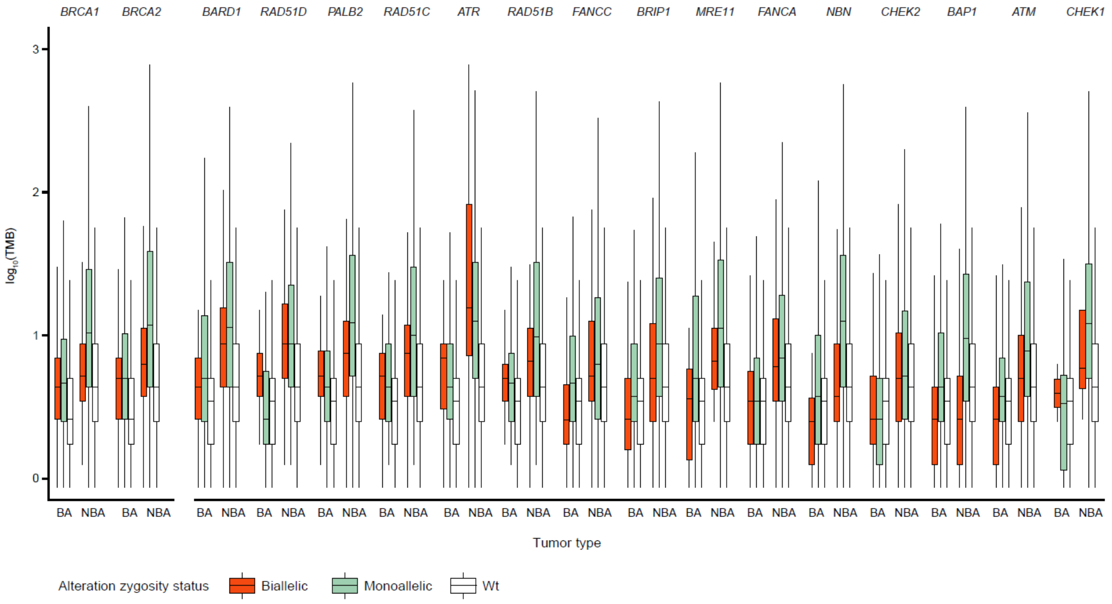
40
20
0
gLOH
n = 10,989
n = 423
n = 6,094
n = 329
n = 18,569
n = 2,030
n = 6,092
n = 195
n = 2,315
n = 104
n = 6,738
n = 364
n = 2,033
n = 1,242
n = 2,554
n = 2,583
n = 6,578
n = 1,948
n = 2,319
n = 159
n = 1,600
n = 243
n = 3,939
n = 845
n = 15,461
n = 11,018
n = 24,016
n = 4,164
n = 4,220
n = 543
n = 19,527
n = 1,392
TMB score
TMB score
Low
High

Supplementary Figure 10. Association of HRR-associated gene alterations with TMB: **A,** MSI and **B,** TMB. wt, wild type; wt refers to the gene being analyzed.



Supplementary Tables

Supplementary Table 1. List of HRR-associated genes in the study.

Gene
BRCA1
BRCA2
PALB2
ATR
ATRX
ATM
BAP1
RAD51B
RAD51C
RAD51D
BRIP1
NBN
CHEK1
CHEK2
FANCA
FANCC
MRE11
BARD1

Supplementary Table 2. Association of alterations and median gLOH for HRR-associated genes in BA and NBA tumor types, stratified by allelic status.

Gene	**Group**	**No. assessable biallelic**	**No. assessable monoallelic**	**No. assessable unknown**	**No. assessable wt**	**Median gLOH biallelic**	**Median gLOH monoallelic**	**Median gLOH unknown**	**Median gLOH wt**	**% change biallelic vs. wt**	***P*-value biallelic vs. wt**
BRCA1	BA	1,666	158	342	42,599	26.4	8.1	18.0	10.1	+162%	0
BRCA2	BA	2,013	283	221	42,248	18.5	7.7	14.2	10.0	+85%	5.6 x 10^{-263}
PALB2	BA	259	168	52	44,286	21.2	12.1	16.9	10.6	+100%	1.4 x 10^{-54}
ATR	BA	23	249	125	44,368	20.9	12.3	18.9	10.8	+93%	3.3 x 10^{-4}
ATRX	BA	26	0	316	44,423	8.6	N/A*	12.4	10.6	-18%	3.9 x 10^{-1}
ATM	BA	823	410	173	43,359	10.4	8.1	12.2	10.2	+1%	4.8 x 10^{-1}
BAP1	BA	294	39	87	44,345	10.7	7.0	12.0	10.4	+2%	1.1 x 10^{-1}
RAD51B	BA	111	38	29	44,587	17.5	6.4	17.8	10.6	+65%	2.3 x 10^{-13}
RAD51C	BA	111	43	44	44,567	20.7	8.6	11.3	10.5	+97%	3.4 x 10^{-23}
RAD51D	BA	81	23	16	44,645	21.7	9.4	13.4	10.5	+107%	7.1 x 10^{-18}
BRIP1	BA	152	112	129	44,372	15.5	8.0	11.8	10.5	+48%	1.1 x 10^{-10}
NBN	BA	30	141	55	44,539	12.5	10.6	13.4	10.8	+15%	1.4 x 10^{-1}
CHEK1	BA	2	12	7	44,744	21.4	12.4	12.1	10.2	+109%	5.1 x 10^{-2}
CHEK2	BA	342	289	232	43,902	11.5	8.2	9.4	10.5	+9%	3.3 x 10^{-2}
FANCA	BA	183	149	158	44,275	12.0	8.3	17.3	10.2	+17%	1.5 x 10^{-3}
FANCC	BA	48	94	67	44,556	17.2	9.8	18.2	10.5	+62%	6.2 x 10^{-5}
MRE11	BA	26	73	24	44,642	13.6	7.1	14.2	10.6	+28%	1.9 x 10^{-2}
BARD1	BA	65	85	37	44,578	25.7	9.8	12.0	10.8	+137%	3.1 x 10^{-19}
TP53	BA	25,480	1,314	1,230	16,741	13.1	0.4	11.8	7.7	+71%	0
CTNNA1	BA	346	54	97	44,268	16.9	7.9	18.1	10.5	+61%	8.0 x 10^{-28}
BRCA1	NBA	672	677	459	114,217	22.0	7.5	11.3	7.3	+201%	7.8 x 10^{-200}
BRCA2	NBA	970	1,300	325	113,430	18.0	5.4	11.4	7.2	+149%	1.6 x 10^{-219}
PALB2	NBA	156	504	85	115,280	16.4	6.9	12.3	7.3	+123%	3.6 x 10^{-32}

ATR	NBA	83	967	161	114,814	8.4	7.2	13.5	7.5	+11%	2.6 x 10^{-1}
ATRX	NBA	310	0	2,561	113,154	7.2	N/A*	7.3	7.3	-1%	3.6 x 10^{-1}
ATM	NBA	2,001	2,172	362	111,490	9.9	6.0	9.0	7.2	+37%	1.2 x 10^{-55}
BAP1	NBA	2,089	234	373	113,329	6.3	3.0	6.4	7.2	-12%	1.0 x 10^{-12}
RAD51B	NBA	188	102	43	115,692	10.9	5.8	9.3	7.3	+49%	2.8 x10^{-13}
RAD51C	NBA	83	149	44	115,749	14.7	6.4	9.8	7.3	+100%	5.6 x 10^{-12}
RAD51D	NBA	23	141	32	115,829	18.9	6.7	10.0	7.3	+157%	3.4 x10^{-7}
BRIP1	NBA	131	646	116	115,132	12.0	7.3	10.9	7.3	+63%	1.5 x 10^{-7}
NBN	NBA	91	463	106	115,365	12.8	6.2	11.4	7.5	+69%	1.4 x 10^{-6}
CHEK1	NBA	4	55	10	115,956	2.6	7.6	11.6	7.2	-63%	1.3 x 10^{-1}
CHEK2	NBA	439	968	522	114,096	9.0	6.2	7.4	7.3	+23%	3.2 x 10^{-6}
FANCA	NBA	305	581	213	114,926	10.6	6.7	9.9	7.2	+45%	1.3 x 10^{-12}
FANCC	NBA	127	261	99	115,538	11.0	5.2	11.4	7.3	+51%	6.5 x 10^{-8}
MRE11	NBA	36	301	37	115,651	11.9	5.5	8.9	7.3	+62%	4.2 x 10^{-3}
BARD1	NBA	77	367	65	115,516	18.3	7.3	12.0	7.5	+142%	3.6 x 10^{-14}
TP53	NBA	62,863	5,206	2,666	45,290	9.2	1.0	9.6	4.9	+88%	0
CTNNA1	NBA	428	255	149	115,193	11.8	5.1	11.8	7.1	+65%	1.3 x 10^{-34}

*X-chromosome gene, so monoallelic status cannot be assessed.

Abbreviations: N/A, not applicable; wt, wild type.

Supplementary Table 3. Association of alterations and median gLOH for HRR-associated genes in breast, ovarian, prostate, pancreatic, CRC, and NSCLC, stratified by allelic status.

Gene	**Group**	**No. assessable biallelic**	**No. assessable monoallelic**	**No. assessable unknown**	**No. assessable wt**	**Median gLOH biallelic**	**Median gLOH monoallelic**	**Median gLOH unknown**	**Median gLOH wt**	**% change biallelic vs. wt**	***P*-value biallelic vs. wt**
BRCA1	Breast	604	82	152	19,776	29.3	10.9	18.6	11.7	+150%	2.3 x 10^{-220}
BRCA2	Breast	791	124	105	19,594	20.9	11.2	17.6	11.5	+81%	1.2 x 10^{-140}
PALB2	Breast	172	97	30	20,315	22.6	14.7	19.0	12.1	+86%	2.2 x 10^{-43}
ATR	Breast	12	121	59	20,422	15.6	14.3	24.3	12.4	+25%	4.0 x 10^{-2}
ATRX	Breast	7	0	176	20,431	22.0	N/A*	13.9	12.1	+81%	1.0 x 10^{-2}
ATM	Breast	341	130	67	20,076	11.6	8.3	14.9	11.3	+2%	4.7 x 10^{-1}
BAP1	Breast	155	12	36	20,411	13.5	5.4	14.1	11.9	+13%	2.5 x 10^{-2}
RAD51B	Breast	79	22	13	20,500	21.5	6.9	22.2	12.0	+78%	5.8 x 10^{-10}
RAD51C	Breast	29	26	31	20,528	25.1	9.7	10.6	12.0	+108%	3.3 x 10^{-7}
RAD51D	Breast	18	11	9	20,576	23.8	8.9	13.2	12.0	+97%	2.0 x 10^{-4}
BRIP1	Breast	41	49	105	20,419	14.0	8.4	11.9	12.0	+16%	2.6 x 10^{-2}
NBN	Breast	4	74	26	20,510	13.4	12.2	14.9	12.5	+7%	4.8 x 10^{-1}
CHEK1	Breast	1	6	5	20,602	22.6	11.5	12.1	11.3	+99%	1.3 x 10^{-1}
CHEK2	Breast	241	132	111	20,130	12.8	9.5	11.6	12.1	+5%	2.0 x 10^{-1}
FANCA	Breast	97	64	90	20,363	14.0	13.0	17.3	11.7	+19%	1.3 x 10^{-2}
FANCC	Breast	21	44	31	20,518	21.0	10.5	21.7	12.1	+74%	1.8 x 10^{-3}
MRE11	Breast	18	26	14	20,556	14.1	10.7	14.9	12.2	+16%	1.8 x 10^{-1}
BARD1	Breast	51	41	14	20,508	28.7	10.5	14.2	12.4	+130%	5.2 x 10^{-16}
TP53	Breast	10,205	627	468	9,314	16.2	0.3	15.2	8.7	+86%	0
CTNNA1	Breast	291	27	71	20,225	18.9	6.0	18.5	12.2	+54%	4.7 x 10^{-23}
BRCA1	Ovary	979	23	138	10,287	25.2	3.6	20.8	9.3	+170%	4.9 x 10^{-291}
BRCA2	Ovary	490	55	37	10,845	21.5	5.4	22.7	10.2	+110%	1.2 x 10^{-86}

PALB2	Ovary	31	29	13	11,354	18.5	11.3	15.0	10.8	+70%	2.2 x 10^{-4}
ATR	Ovary	9	56	39	11,323	21.4	15.6	19.6	11.1	+91%	2.2 x 10^{-2}
ATRX	Ovary	7	0	73	11,347	6.4	N/A*	12.6	10.9	-41%	2.6 x 10^{-2}
ATM	Ovary	89	103	51	11,184	10.3	11.2	18.4	10.8	-4%	2.6 x 10^{-1}
BAP1	Ovary	26	15	25	11,361	8.9	18.8	11.7	10.9	-18%	4.5 x 10^{-1}
RAD51B	Ovary	10	8	9	11,400	27.9	4.9	20.0	10.8	+157%	2.1 x 10^{-3}
RAD51C	Ovary	60	5	10	11,352	21.4	5.0	16.0	10.6	+102%	1.9 x 10^{-12}
RAD51D	Ovary	57	3	6	11,361	21.6	6.5	21.0	10.6	+104%	3.2 x 10^{-11}
BRIP1	Ovary	97	9	17	11,304	17.0	2.8	13.9	10.6	+60%	8.8 x 10^{-6}
NBN	Ovary	9	25	11	11,382	19.6	16.2	17.4	11.1	+76%	4.9 x 10^{-2}
CHEK1	Ovary	1	2	2	11,422	20.1	23.5	25.3	10.8	+86%	2.1 x 10^{-1}
CHEK2	Ovary	56	45	51	11,275	8.8	6.8	7.4	10.7	-18%	5.7 x 10^{-2}
FANCA	Ovary	37	31	49	11,310	13.8	6.1	19.3	10.6	+30%	1.0 x 10^{-1}
FANCC	Ovary	22	17	22	11,366	17.1	7.6	22.3	10.6	+61%	6.8 x 10^{-2}
MRE11	Ovary	6	21	7	11,393	15.0	5.7	23.8	10.9	+37%	1.0 x 10^{-1}
BARD1	Ovary	5	21	9	11,392	19.5	10.4	25.8	11.2	+73%	2.1 x 10^{-2}
TP53	Ovary	8,524	241	266	2,396	14.2	0.8	13.6	2.7	+433%	0
CTNNA1	Ovary	13	7	19	11,388	12.4	3.7	18.2	10.7	+14%	2.8 x 10^{-1}
BRCA1	Prostate	20	31	30	6,353	16.5	7.2	9.9	8.6	+92%	5.4 x 10^{-5}
BRCA2	Prostate	521	51	54	5,808	10.3	7.4	8.2	7.5	+37%	2.2 x 10^{-37}
PALB2	Prostate	31	21	4	6,378	12.8	8.7	5.3	8.5	+50%	1.7 x 10^{-6}
ATR	Prostate	1	51	22	6,360	23.5	7.7	11.5	8.7	+169%	4.5 x 10^{-2}
ATRX	Prostate	9	0	30	6,395	10.0	N/A*	9.8	8.5	+17%	1.2 x 10^{-1}
ATM	Prostate	248	91	38	6,057	9.0	6.7	8.0	8.5	+5%	1.2 x 10^{-1}
BAP1	Prostate	10	6	9	6,409	6.7	8.3	5.8	8.6	-22%	3.4 x 10^{-2}
RAD51B	Prostate	14	6	5	6,409	12.0	7.6	8.3	8.7	+38%	9.3 x 10^{-3}
RAD51C	Prostate	4	3	2	6,425	13.4	10.0	11.3	8.6	+56%	4.7 x 10^{-2}
RAD51D	Prostate	2	5	0	6,427	18.3	4.2	N/A	8.6	+113%	5.1 x 10^{-2}
BRIP1	Prostate	2	29	6	6,397	17.4	8.6	6.6	8.6	+103%	2.4 x 10^{-2}
NBN	Prostate	10	29	13	6,382	11.4	9.2	7.7	8.7	+30%	1.9 x 10^{-1}

CHEK1	Prostate	0	1	0	6,433	N/A	1.5	N/A	8.5	N/A	N/A
CHEK2	Prostate	23	68	38	6,305	8.8	7.1	7.1	8.5	+2%	3.6 x 10^{-1}
FANCA	Prostate	41	27	9	6,357	9.9	6.7	9.9	8.1	+23%	5.2 x 10^{-3}
FANCC	Prostate	3	21	9	6,401	17.1	8.4	14.7	8.7	+97%	2.5 x 10^{-2}
MRE11	Prostate	2	21	2	6,409	11.1	4.6	13.0	8.5	+30%	2.1 x 10^{-1}
BARD1	Prostate	5	11	10	6,408	11.1	4.2	8.9	8.5	+30%	1.9 x 10^{-1}
TP53	Prostate	2,434	170	245	3,585	9.3	5.8	9.0	7.8	+18%	5.1 x 10^{-31}
CTNNA1	Prostate	33	16	5	6,380	7.8	8.7	10.2	8.1	-3%	4.1 x 10^{-1}
BRCA1	Pancreas	63	22	22	6,183	22.2	6.9	12.2	9.2	+141%	3.3 x 10^{-22}
BRCA2	Pancreas	211	53	25	6,001	20.2	6.1	18.4	9.2	+119%	2.7 x 10^{-82}
PALB2	Pancreas	25	21	5	6,239	16.1	10.0	13.0	9.4	+71%	2.5 x 10^{-6}
ATR	Pancreas	1	21	5	6,263	16.5	5.7	13.9	9.7	+70%	1.3 x 10^{-1}
ATRX	Pancreas	3	0	37	6,250	3.5	N/A*	9.1	9.3	-62%	2.2 x 10^{-1}
ATM	Pancreas	145	86	17	6,042	11.3	8.3	11.8	9.4	+20%	1.9 x 10^{-4}
BAP1	Pancreas	103	6	17	6,164	9.4	3.9	12.0	9.2	+3%	3.3 x 10^{-1}
RAD51B	Pancreas	8	2	2	6,278	10.7	13.7	13.7	9.4	+14%	2.5 x 10^{-1}
RAD51C	Pancreas	18	9	1	6,262	15.0	7.5	11.4	9.2	+62%	1.3 x 10^{-4}
RAD51D	Pancreas	4	4	1	6,281	15.6	15.7	5.8	9.2	+68%	1.8 x 10^{-1}
BRIP1	Pancreas	12	25	1	6,252	13.6	8.1	0.0	9.2	+47%	3.0 x 10^{-3}
NBN	Pancreas	7	13	5	6,265	12.3	6.1	16.2	9.6	+28%	1.3 x 10^{-1}
CHEK1	Pancreas	0	3	0	6,287	N/A	12.3	N/A	9.4	N/A	N/A*
CHEK2	Pancreas	22	44	32	6,192	7.9	9.1	9.9	9.3	-14%	1.7 x 10^{-1}
FANCA	Pancreas	8	27	10	6,245	8.1	7.6	12.8	9.5	-14%	1.7 x 10^{-1}
FANCC	Pancreas	2	12	5	6,271	10.7	11.3	10.7	9.3	+15%	4.7 x 10^{-1}
MRE11	Pancreas	0	5	1	6,284	N/A	7.1	6.1	9.3	N/A	N/A*
BARD1	Pancreas	4	12	4	6,270	19.4	9.7	8.1	9.9	+96%	6.3 x 10^{-3}
TP53	Pancreas	4,317	276	251	1,446	9.5	0.1	10.1	8.3	+13%	1.2 x 10^{-11}
CTNNA1	Pancreas	9	4	2	6,275	14.1	11.1	15.9	9.5	+48%	1.3 x 10^{-1}
BRCA1	CRC	91	105	81	20,666	14.6	5.4	7.1	6.0	+144%	4.8 x 10^{-14}
BRCA2	CRC	48	318	49	20,528	10.4	4.4	6.8	6.2	+68%	9.7 x 10^{-4}

PALB2	CRC	8	91	16	20,828	10.4	3.9	6.9	6.1	+71%	3.2×10^{-2}
ATR	CRC	9	136	14	20,784	1.5	3.5	10.0	6.3	-75%	6.5×10^{-2}
ATRX	CRC	12	0	196	20,735	4.3	N/A*	4.5	6.1	-29%	1.2×10^{-1}
ATM	CRC	439	499	55	19,950	8.3	4.6	7.4	6.1	+36%	7.5×10^{-18}
BAP1	CRC	31	43	11	20,858	6.4	2.5	2.7	6.0	+6%	3.4×10^{-1}
RAD51B	CRC	36	8	10	20,889	8.6	2.9	9.5	6.1	+40%	3.0×10^{-3}
RAD51C	CRC	20	20	9	20,894	11.1	3.0	4.9	6.0	+86%	2.0×10^{-3}
RAD51D	CRC	3	25	8	20,907	18.9	5.7	7.9	6.0	+215%	1.5×10^{-2}
BRIP1	CRC	33	94	17	20,799	5.8	4.4	8.0	6.0	-3%	3.0×10^{-1}
NBN	CRC	18	99	21	20,805	11.8	3.1	6.2	6.2	+89%	9.4×10^{-3}
CHEK1	CRC	0	8	2	20,933	N/A	7.6	13.9	6.1	N/A	N/A*
CHEK2	CRC	60	128	85	20,670	6.6	5.0	6.9	6.1	+9%	6.7×10^{-2}
FANCA	CRC	34	85	22	20,802	7.1	5.0	7.3	6.1	+16%	7.0×10^{-2}
FANCC	CRC	6	66	5	20,866	7.1	4.7	10.6	6.2	+14%	3.9×10^{-1}
MRE11	CRC	6	64	7	20,866	11.9	3.7	4.9	6.1	+95%	2.8×10^{-2}
BARD1	CRC	10	70	16	20,847	17.7	3.5	8.8	6.3	+181%	1.1×10^{-2}
TP53	CRC	15,673	605	649	4,016	6.2	1.9	6.7	4.3	+44%	2.1×10^{-120}
CTNNA1	CRC	103	52	29	20,759	7.7	2.4	7.8	5.4	+42%	2.0×10^{-6}
BRCA1	NSCLC	84	193	108	26,126	18.3	12.1	14.0	10.9	+68%	1.0×10^{-12}
BRCA2	NSCLC	242	247	79	25,943	19.2	9.6	11.7	10.5	+81%	9.2×10^{-43}
PALB2	NSCLC	36	144	21	26,310	16.1	10.8	14.5	10.8	+48%	4.9×10^{-5}
ATR	NSCLC	24	269	56	26,162	15.1	11.8	15.2	11.0	+37%	3.0×10^{-3}
ATRX	NSCLC	28	0	417	26,066	10.8	N/A*	12.2	10.8	+0%	1.0×10^{-1}
ATM	NSCLC	559	571	101	25,280	10.7	9.3	13.0	10.8	-1%	1.5×10^{-1}
BAP1	NSCLC	276	31	44	26,160	8.7	4.0	9.0	10.6	-17%	5.7×10^{-5}
RAD51B	NSCLC	28	24	12	26,447	16.2	10.4	9.2	10.8	+49%	2.9×10^{-4}
RAD51C	NSCLC	7	42	15	26,447	26.0	11.4	12.3	10.9	+138%	1.7×10^{-4}
RAD51D	NSCLC	5	40	9	26,457	18.1	11.4	12.5	10.9	+66%	1.4×10^{-2}
BRIP1	NSCLC	23	206	27	26,255	18.5	11.7	16.9	10.9	+70%	1.4×10^{-4}

NBN	NSCLC	33	118	34	26,326	15.7	10.1	11.4	11.1	+41%	8.6 x 10^{-3}
CHEK1	NSCLC	0	19	1	26,491	N/A	9.7	18.8	10.8	N/A	N/A*
CHEK2	NSCLC	107	232	114	26,058	12.5	9.7	10.6	10.8	+15%	7.1 x 10^{-3}
FANCA	NSCLC	97	147	58	26,209	14.6	10.4	15.5	10.7	+36%	1.3 x 10^{-5}
FANCC	NSCLC	48	43	34	26,386	13.3	9.1	12.8	10.6	+24%	3.6 x 10^{-3}
MRE11	NSCLC	13	67	8	26,423	12.3	10.4	15.8	10.8	+13%	2.3 x 10^{-1}
BARD1	NSCLC	16	129	15	26,351	18.3	11.5	16.5	11.2	+63%	4.8 x 10^{-4}
TP53	NSCLC	16,742	1,586	807	7,376	12.7	0.2	12.1	7.2	+76%	0
CTNNA1	NSCLC	63	44	31	26,373	13.4	9.6	14.3	10.7	+25%	8.8 x 10^{-3}

*X-chromosome gene, so monoallelic status cannot be assessed.

Abbreviations: N/A, not applicable; wt, wild type.

Supplementary Table 4. Association of alterations and median gLOH for *ATM* for all tumor types, stratified by allelic status.

Group	**No. assessable biallelic**	**No. assessable monoallelic**	**No. assessable unknown**	**No. assessable wt**	**Median gLOH biallelic**	**Median gLOH monoallelic**	**Median gLOH unknown**	**Median gLOH wt**	**% change biallelic vs. wt**	***P*-value biallelic vs. wt**	**Corrected *P*-value biallelic vs. wt**
Stomach	53	33	5	1,758	15.7	4.7	12.1	8.9	+77%	4.7 x 10^{-6}	1.5 x 10^{-5}
Glioma	36	98	13	6,960	5.0	3.7	5.2	2.9	+69%	2.3 x 10^{-3}	4.0 x 10^{-3}
CUP	150	147	19	8,217	12.5	6.7	12.2	9.4	+33%	2.0 x 10^{-5}	5.5 x 10^{-5}
Cholangiocarcinoma	37	30	6	2,346	11.9	7.3	11.0	9.9	+19%	2.5 x 10^{-3}	4.0 x 10^{-3}
Bladder	76	82	13	3,106	10.8	7.4	13.2	7.7	+39%	9.3 x 10^{-5}	2.1 x 10^{-4}
Breast	341	130	67	20,076	11.6	8.3	14.9	11.3	+2%	4.7 x 10^{-1}	4.7 x 10^{-1}
Esophagus	58	71	17	4,619	17.6	9.4	16.8	11.7	+50%	1.2 x 10^{-6}	6.6 x 10^{-6}
Prostate	248	91	38	6,057	9.0	6.7	8.0	8.5	+5%	1.2 x 10^{-1}	1.5 x 10^{-1}
Kidney	36	30	9	2,407	9.8	4.8	6.8	4.3	+125%	3.4 x 10^{-6}	1.4 x 10^{-5}
Pancreas	145	86	17	6,042	11.3	8.3	11.8	9.4	+20%	1.9 x 10^{-4}	3.8 x 10^{-4}
NSCLC	559	571	101	25,280	10.7	9.3	13.0	10.8	-1%	1.5 x 10^{-1}	1.8 x 10^{-1}
Endometrial	92	141	17	4,540	8.8	2.4	8.6	6.0	+46%	2.1 x 10^{-2}	2.8 x 10^{-2}
Melanoma	106	73	18	4,944	6.3	5.3	5.2	5.5	+13%	9.7 x 10^{-3}	1.4 x 10^{-2}
CRC	439	499	55	19,950	8.3	4.6	7.4	6.1	+36%	7.5 x 10^{-18}	1.2 x 10^{-16}
Ovary	89	103	51	11,184	10.3	11.2	18.4	10.8	-4%	2.6 x 10^{-1}	2.8 x 10^{-1}
Other	359	397	89	27,363	9.3	6.1	8.3	6.1	+52%	4.6 x 10^{-14}	3.7 x 10^{-13}

Abbreviations: CUP, carcinoma-of-unknown-primary-origin; wt, wild type.

Supplementary Table 5. Association of alterations and median gLOH for *CHEK2* for all tumor types, stratified by allelic status.

Group	**No. assessable biallelic**	**No. assessable monoallelic**	**No. assessable unknown**	**No. assessable wt**	**Median gLOH biallelic**	**Median gLOH monoallelic**	**Median gLOH unknown**	**Median gLOH wt**	**% change biallelic vs. wt**	***P*-value biallelic vs. wt**	**Corrected *P*-value biallelic vs. wt**
Stomach	10	15	10	1,814	16.7	2.6	5.1	9.1	+82%	6.1 x 10^{-2}	1.5 x 10^{-1}
Glioma	21	69	39	6,978	5.0	2.3	2.7	2.9	+69%	8.3 x 10^{-2}	1.7 x 10^{-1}
CUP	37	76	35	8,385	8.8	6.7	9.0	9.6	-9%	4.3 x 10^{-1}	4.3 x 10^{-1}
Cholangiocarcinoma	11	17	11	2,380	8.9	10.6	10.3	10.1	-11%	3.3 x 10^{-1}	3.9 x 10^{-1}
Bladder	21	53	20	3,183	7.3	7.1	10.0	8.0	-9%	3.5 x 10^{-1}	3.9 x 10^{-1}
Breast	241	132	111	20,130	12.8	9.5	11.6	12.1	+5%	2.0 x 10^{-1}	3.2 x 10^{-1}
Esophagus	16	25	12	4,712	13.0	10.6	17.1	12.1	+7%	2.4 x 10^{-1}	3.4 x 10^{-1}
Prostate	23	68	38	6,305	8.8	7.1	7.1	8.5	+2%	3.6 x 10^{-1}	3.9 x 10^{-1}
Kidney	18	26	9	2,429	8.2	4.3	6.1	4.5	+80%	7.0 x 10^{-3}	5.2 x 10^{-2}
Pancreas	22	44	32	6,192	7.9	9.1	9.9	9.3	-14%	1.7 x 10^{-1}	3.0 x 10^{-1}
NSCLC	107	232	114	26,058	12.5	9.7	10.6	10.8	+15%	7.1 x 10^{-3}	5.2 x 10^{-2}
Endometrial	17	55	23	4,695	10.0	2.8	4.2	6.0	+65%	3.9 x 10^{-2}	1.5 x 10^{-1}
Melanoma	12	62	36	5,031	11.6	6.5	6.6	6.0	+93%	9.8 x 10^{-3}	5.2 x 10^{-2}
CRC	60	128	85	20,670	6.6	5.0	6.9	6.1	+9%	6.7 x 10^{-2}	1.5 x 10^{-1}
Ovary	56	45	51	11,275	8.8	6.8	7.4	10.7	-18%	5.7 x 10^{-2}	1.5 x 10^{-1}
Other	109	210	128	27,761	7.1	5.0	6.7	6.4	+10%	2.6 x 10^{-1}	3.5 x 10^{-1}

Abbreviations: CUP, carcinoma-of-unknown-primary-origin; wt, wild type.

Supplementary Table 6. Association of alterations and median gLOH for *BAP1* for all tumor types, stratified by allelic status.

Group	**No. assessable biallelic**	**No. assessable monoallelic**	**No. assessable unknown**	**No. assessable wt**	**Median gLOH biallelic**	**Median gLOH monoallelic**	**Median gLOH unknown**	**Median gLOH wt**	**% change biallelic vs. wt**	***P*-value biallelic vs. wt**	**Corrected *P*-value biallelic vs. wt**
Stomach	26	6	3	1,814	6.7	0.6	1.0	8.9	-25%	4.6×10^{-1}	4.9×10^{-1}
Glioma	3	4	6	7,094	11.4	4.0	4.2	3.0	+286%	2.9×10^{-2}	5.7×10^{-2}
CUP	312	15	51	8,155	7.5	0.9	6.5	9.4	-19%	2.4×10^{-5}	1.9×10^{-4}
Cholangiocarcinoma	305	10	75	2,029	8.2	10.0	8.5	9.7	-14%	4.0×10^{-5}	2.1×10^{-4}
Bladder	40	22	11	3,204	8.4	7.2	9.4	8.0	+5%	4.9×10^{-1}	4.9×10^{-1}
Breast	155	12	36	20,411	13.5	5.4	14.1	11.9	+13%	2.5×10^{-2}	5.7×10^{-2}
Esophagus	31	8	6	4,720	9.9	1.6	13.9	11.9	-16%	1.1×10^{-1}	1.7×10^{-1}
Prostate	10	6	9	6,409	6.7	8.3	5.8	8.6	-22%	3.4×10^{-2}	6.0×10^{-2}
Kidney	205	8	19	2,250	4.2	0.0	5.4	3.8	+9%	1.7×10^{-2}	4.6×10^{-2}
Pancreas	103	6	17	6,164	9.4	3.9	12.0	9.2	+3%	3.3×10^{-1}	4.2×10^{-1}
NSCLC	276	31	44	26,160	8.7	4.0	9.0	10.6	-17%	5.7×10^{-5}	2.3×10^{-4}
Endometrial	6	15	7	4,762	2.8	2.5	13.3	6.0	-52%	1.7×10^{-1}	2.4×10^{-1}
Melanoma	212	19	50	4,860	2.4	7.5	2.1	6.3	-61%	1.4×10^{-41}	2.2×10^{-40}
CRC	31	43	11	20,858	6.4	2.5	2.7	6.0	+6%	3.4×10^{-1}	4.2×10^{-1}
Ovary	26	15	25	11,361	8.9	18.8	11.7	10.9	-18%	4.6×10^{-1}	4.9×10^{-1}
Other	642	53	90	27,423	5.7	3.1	5.7	6.2	-8%	3.6×10^{-3}	1.2×10^{-2}

Abbreviations: CUP, carcinoma-of-unknown-primary-origin; wt, wild type.

Supplementary Table 7. Association of alterations and median gLOH for *CTNNA1* for all tumor types, stratified by allelic status.

Group	**No. assessable biallelic**	**No. assessable monoallelic**	**No. assessable unknown**	**No. assessable wt**	**Median gLOH biallelic**	**Median gLOH monoallelic**	**Median gLOH unknown**	**Median gLOH wt**	**% change biallelic vs. wt**	***P*-value biallelic vs. wt**	**Corrected *P*-value biallelic vs. wt**
Stomach	17	9	4	1,819	12.4	5.5	5.9	9.0	+37%	1.1 x 10^{-2}	2.4 x 10^{-2}
Glioma	2	14	2	7,089	9.5	4.8	7.6	3.1	+212%	4.6 x 10^{-1}	4.9 x 10^{-1}
CUP	67	18	9	8,439	15.4	4.8	11.5	9.6	+60%	1.5 x 10^{-9}	1.2 x 10^{-8}
Cholangiocarcinoma	9	3	2	2,405	15.7	13.5	19.0	10.1	+56%	1.5 x 10^{-2}	3.0 x 10^{-2}
Bladder	7	15	3	3,252	9.9	7.1	18.2	8.0	+24%	1.3 x 10^{-1}	1.9 x 10^{-1}
Breast	291	27	71	20,225	18.9	6.0	18.5	12.2	+54%	4.6 x 10^{-23}	7.4 x 10^{-22}
Esophagus	65	15	21	4,664	16.5	4.2	12.6	11.9	+38%	1.5 x 10^{-4}	4.7 x 10^{-4}
Prostate	33	16	5	6,380	7.8	8.7	10.2	8.1	-3%	4.1 x 10^{-1}	4.9 x 10^{-1}
Kidney	0	1	0	2,481	N/A	6.7	N/A	4.6	N/A	N/A	1.0
Pancreas	9	4	2	6,275	14.1	11.1	15.9	9.5	+48%	1.3 x 10^{-1}	1.9 x 10^{-1}
NSCLC	63	44	31	26,373	13.4	9.6	14.3	10.7	+25%	8.8 x 10^{-3}	2.3 x 10^{-2}
Endometrial	8	19	7	4,756	10.2	1.6	15.2	6.1	+65%	5.1 x 10^{-2}	9.1 x 10^{-2}
Melanoma	4	10	3	5,124	7.7	6.4	9.8	5.9	+29%	4.4 x 10^{-1}	4.9 x 10^{-1}
CRC	103	52	29	20,759	7.7	2.4	7.8	5.4	+42%	2.0 x 10^{-6}	8.0 x 10^{-6}
Ovary	13	7	19	11,388	12.4	3.7	18.2	10.7	+14%	2.8 x 10^{-1}	3.7 x 10^{-1}
Other	83	55	38	28,032	11.0	5.9	12.8	6.4	+71%	2.2 x 10^{-8}	1.2 x 10^{-7}

Abbreviations: CUP, carcinoma-of-unknown-primary-origin; N/A, not applicable; wt, wild type.

Supplementary Table 8. Association of alterations and median gLOH for *TP53* for all tumor types, stratified by allelic status.

Group	**No. assessable biallelic**	**No. assessable monoallelic**	**No. assessable unknown**	**No. assessable wt**	**Median gLOH biallelic**	**Median gLOH monoallelic**	**Median gLOH unknown**	**Median gLOH wt**	**% change biallelic vs. wt**	***P*-value biallelic vs. wt**	**Corrected *P*-value biallelic vs. wt**
Stomach	1,057	182	79	531	11.0	0.1	11.3	6.3	+73%	$1.4\text{x}10^{-14}$	$1.7\text{ x }10^{-14}$
Glioma	2,556	393	62	4,096	4.0	2.5	3.9	2.4	+64%	$9.1\text{x}10^{-71}$	$1.8\text{ x }10^{-70}$
CUP	4,719	365	193	3,256	11.5	0.5	11.8	7.3	+58%	$6.8\text{x}10^{-151}$	$1.8\text{ x }10^{-150}$
Cholangiocarcinoma	679	98	50	1,592	10.5	0.8	8.9	9.9	+6%	$1.7\text{x}10^{-3}$	$1.7\text{ x }10^{-3}$
Bladder	1,834	148	70	1,225	9.4	3.3	11.0	5.7	+64%	$1.9\text{x}10^{-53}$	$3.4\text{ x }10^{-53}$
Breast	10,205	627	468	9,314	16.2	0.3	15.2	8.7	+86%	0	0
Esophagus	3,703	331	162	569	12.6	0.2	11.7	10.5	+19%	$3.0\text{x}10^{-9}$	$3.1\text{ x }10^{-9}$
Prostate	2,434	170	245	3,585	9.3	5.8	9.0	7.8	+18%	$5.1\text{x}10^{-31}$	$7.5\text{ x }10^{-31}$
Kidney	499	77	19	1,887	7.5	1.6	4.9	4.0	+84%	$2.5\text{x}10^{-32}$	$4.0\text{ x }10^{-32}$
Pancreas	4,317	276	251	1,446	9.5	0.1	10.1	8.3	+13%	$1.3\text{x}10^{-11}$	$1.4\text{ x }10^{-11}$
NSCLC	16,742	1,586	807	7,376	12.7	0.2	12.1	7.2	+76%	0	0
Endometrial	2,522	229	73	1,966	10.9	2.2	12.6	2.4	+361%	0	0
Melanoma	846	156	37	4,102	7.2	6.1	5.9	5.7	+27%	$1.7\text{x}10^{-17}$	$2.3\text{ x }10^{-17}$
CRC	15,673	605	649	4,016	6.2	1.9	6.7	4.3	+44%	$2.1\text{x}10^{-120}$	$4.9\text{ x }10^{-120}$
Ovary	8,524	241	266	2,396	14.2	0.8	13.6	2.7	+433%	0	0
Other	12,033	1,036	465	14,674	9.0	2.5	9.9	4.3	+108%	0	0

Abbreviations: CUP, carcinoma-of-unknown-primary-origin; wt, wild type.