BARD1 germline variants induce haploinsufficiency and DNA repair defects in neuroblastoma

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Supplemental Methods

Cell culture

IMR-5 and RPE1 cells were obtained from the Children's Hospital of Philadelphia (CHOP) cell line bank. RPE1 cells are a human retinal pigment epithelium cell line immortalized through the retroviral insertion of human telomerase reverse transcriptase (hTERT) and were originally a kind gift from the laboratory of Dr. Michael Hogarty. Cell lines were cultured in RPMI containing 10% FBS and 2 mM L-Glutamine at 37°C under 5% CO_2. Cells were regularly tested for the presence of mycoplasma and genotyped to confirm cell identity using short tandem repeat (STR) typing.

Generation of isogenic cell models

IMR-5 and hTERT RPE1 cells were electroporated using a Lonza 4D-Nucleofector X-unit™ with 1.6 µg pU6-(BbsI)_CBh-Cas9-T2A-mCherry, into which one of four guide RNA sequences (R112*, R150*, E287fs, Q564*; **Supplemental Table 2**) had been cloned, and 0.4 µg single-stranded donor oligonucleotides containing the desired *BARD1* mutation and a synonymous PAM-ablating mutation. The pU6-(BbsI)_CBh-Cas9-T2A-mCherry plasmid was a gift from Ralf Kuehn (Addgene plasmid # 64324; http://n2t.net/addgene:64324; RRID:Addgene_64324).[1] Following electroporation, cells were transferred to media containing 5 µM L755507 (Selleck Chemicals) to enhance homology-directed repair efficiency.[2] Two days later, single mCherry-positive cells were sorted into 96-well plates using a BD FACSJazz cell sorter. Genomic DNA from single cell clones was extracted using the Qiagen DNeasy Blood and Tissue kit and the *BARD1* DNA was PCR amplified and Sanger sequenced to screen for the desired *BARD1* mutation. Heterozygous *BARD1* variants were confirmed using the PolyPeakParser program.[3] Clones that did not integrate a *BARD1* variant at either allele were also propagated for use as non-targeted control clones.

Quantitative RT-PCR

Total RNA was isolated from exponentially growing neuroblastoma cells utilizing RNeasy mini kits (Qiagen) and mRNAs were converted to cDNA using the SuperScript III system (ThermoFisher Scientific). Taqman® gene expression assays (Thermo Fischer Scientific) were used to quantitate *BARD1* (Hs00184427_m1 [*BARD1* exon 1-2 boundary] and Hs00957655_m1 [*BARD1* exon 9-10 boundary]), *BRCA1* (Hs00183233_m1),

and *HPRT1* (Hs99999909_m1) on an Applied Biosystems 7900HT Sequence Detection System using standard cycling conditions. Relative transcript abundance was determined by the $2^{-\Delta\Delta Ct}$ method using *HPRT1* as an internal control.

Immunofluorescence

RPE1 *BARD1*$^{+/mut}$ and wild-type cells were seeded on poly-L-lysine coated coverslips (Electron Microscopy Sciences) and treated with 4 μM cisplatin or vehicle. Twenty-four hours after treatment, cells were fixed with 4% paraformaldehyde, stained with primary antibody (RAD51, Abcam ab88572, 1:100 or Phospho-Histone H2A.X (Ser139) (20E3), Cell Signaling Technology #9718, 1:800) followed by a secondary Alexa 488 or Alexa 555 antibody. Cells were mounted with ProLong gold with DAPI (Thermo Fisher Scientific, #P36931) and visualized with a Leica DM5000B microscope and photographed with a Leica DFC365 FX camera. RAD51 and γ-H2AX foci were quantified using Focinator v2.0 software and ImageJ.[4]

mClover-LMNA assay

IMR-5 *BARD1*$^{+/mut}$ and wild-type cells were co-transfected with 1.6 μg pX330-LMNA-gRNA1 and 0.4 μg pCR2.1 Clover-LMNA using the Lonza 4D-Nucleofector X-unit™ system. The mClover-LMNA reagents were a kind gift form the laboratory of Graham Dellaire. After 3 days, cells were fixed in 2% paraformaldehyde and analyzed on a CytoFLEX-LX flow cytometer to quantitate clover-positive cells.

Cytotoxicity studies

IMR-5 and RPE1 *BARD1*$^{+/mut}$ cells and paired wild-type cells were plated on Day 1 in a 96-well plate. On Day 2, serial dilutions of olaparib (Selleck Chemicals, DMSO) or cisplatin (Selleck Chemicals, H_2O) were added. After 4 days, cell viability was determined using a CellTiter-Glo® Assay (Promega) in a GloMax (Promega) plate reader according to the manufacturer's instructions. Luminescence values were normalized to vehicle treated wells and data were analyzed and graphed in GraphPad Prism software and a log (inhibitor) vs. response nonlinear regression model was used to calculate IC_{50}s.

In vivo IMR5 *BARD1*$^{+/mut}$ xenograft efficacy studies

In vivo murine xenograft efficacy studies were designed to assess the efficacy of olaparib in IMR5 *BARD1*$^{+/mut}$ isogenic cell line derived xenograft models. IMR5 *BARD1*$^{+/mut}$ isogenic cell lines were expanded *in vitro* and 5 x 10^6 cells were mixed with Matrigel (Corning, cat# 354234) and injected into the flanks of CB17-SCID mice (Taconic Farms, Germantown NY). When the tumors reached a size of 1-1.5 cm^3, they were serially passaged into study CB17-SCID mice. When tumors reached enrollment size (0.15 cm^3-0.3 cm^3), mice were then randomly enrolled into 2 treatment cohorts (Olaparib or vehicle; n=10 per cohort), using a rolling enrollment to ensure almost identical tumor sizes across treatment cohorts. Olaparib was dosed intraperitoneally at 20mg/kg once daily for 28 days. Tumor sizes were measured at least twice weekly using calipers and tumor volumes were calculated as: volume = ((diameter1/2 + diameter2/2)3*0.5236)/1000. Mice weights were also measured at least twice weekly, and mice were monitored daily for signs of any clinical toxicity. Mice were sacrificed when tumor burden reached 2 cm^3 or they showed any signs of distress including excessive weight loss. All *in vivo* animal studies were performed according to Children's Hospital of Philadelphia (CHOP) policies in the Department of Veterinary Research (DVR) and were conducted according to an approved IACUC Protocol (#0006430). Up to 5 mice were maintained in cages under barrier conditions in a pathogen-free facility fully accredited by the Association for Assessment and Accreditation of Laboratory Animal Care (AAALAC).

Quantification and statistical analysis

Differences between groups were presented as the mean ± SEM as noted in the figure legends. Experimental sample numbers (n) are indicated in the figures, figure legends and results section. All statistical analysis was done with GraphPad Prism and p-values < 0.05 were considered statistically significant. RAD51 and γ-H2AX foci were quantified using Focinator v2.0 software and ImageJ.[4]

Whole-genome sequencing of IMR-5 cells

All code is available on GitHub (https://github.com/diskin-lab-chop/nbl-bard1), except when a public pipeline is referenced. After 20 passages, genomic DNA was extracted from three IMR-5 *BARD1*$^{+/mut}$ clonal cell lines and one non-targeted control clone using the Qiagen Blood and Tissue kit and then treated with RNase to digest RNA. DNA integrity was assessed by pulse-field gel electrophoresis. Libraries were prepared with a 1%

PhiX spike-in, fragmented, and sequenced on an Illumina HiSeq 10X using S2 chemistry with 150 bp paired-end reads to at least 30X mean coverage. Separately, DNA from WT parental IMR-5 cells (prior to 20 passages) was isolated and sequenced with similar methods, and this parental sample served as the "normal" control for filtering variant calls from the *BARD1*$^{+/mut}$ and non-targeted control clones. FASTQ files were aligned against hg19 (b37 reference from the Broad Institute) with BWA-MEM 0.7.17[5] using the public Seven Bridges Genomics workflow "Whole Genome Sequencing - BWA + GATK 4.0 (with Metrics)" on CAVATICA (https://www.cavatica.org/, app ID: admin/sbg-public-data/whole-genome-sequencing-bwa-gatk-4-0, revision 41). After alignment, BAM files were randomly downsampled with Picard DownsampleSam to achieve 50x mean coverage, or 1.1 billion aligned reads, for each of the three *BARD1*$^{+/mut}$ clones and the non-targeted control clone. Only chromosomes 1-22, X, and Y were considered for subsequent analyses.

Copy number analysis

Copy number segmentation profiles were generated with Control-FREEC v11.5[6] using a public Seven Bridges workflow on CAVATICA (app ID: admin/sbg-public-data/control-freec-11-5, revision 4) with default settings. The parental IMR-5 cell line (described above) was used as the normal control for paired analysis. Segments containing less than 5 genomic bins (approximately 5.6 kb) were removed. Segments overlapping 50% or more with the ENCODE hg19 blacklist[7] or segmental duplications (as defined by the UCSC Genome Browser[8], considering only those with >95% identity) were removed. Copy number ratio thresholds for gain and loss were set at 1.2 and 0.8, respectively. Breakpoint analysis was performed with the *svpluscnv* R package (https://github.com/ccbiolab/svpluscnv)[9], based on methods developed by Lopez *et al*.[10] Double-strand breaks were quantified by counting regions where the fold change between any two adjacent segments was greater than 1.2 or less than 0.8 (*fc.pct*=0.2).

Structural variant (SV) analysis

SVs were called with Delly v0.7.9[11] in paired mode, using the parental IMR-5 cell line as the normal control. SVs were filtered for the default PASS criteria at the dataset and individual levels and required to have at least 5 reads supporting the alternate allele (considering both split-read and paired-read support). SVs with one or more breakpoints falling within the ENCODE blacklist or segmental duplications (described above) were

removed. Stringent filtering (shown in **Figure 3B-D, Supplemental Figure 2B-C**) considered only precise SVs supported by split reads, whereas relaxed filtering (shown in **Supplemental Figure 3A-E**) included both precise and imprecise SVs.

Single-nucleotide variant (SNV) and indel analysis

SNVs and indels were called with MuTect2[12] from GATK v4.1.3.0, again using parental IMR-5 as the normal control. The read orientation bias filter was applied. Variants flagged by FilterMutectCalls for any reason except "clustered_events" were removed. Di- and tri-nucleotide polymorphism calls were removed. For all figures except the mutational signature analysis, variants were required to have at least 5 reads supporting the alternate allele.

Mutational signature analysis

The above filtered variant calls were used as input to the deconstructSigs v. 1.9.0 R package to perform mutational signature analysis using the following signature sets: COSMIC v2 SBS and COSMIC v3.2 SBS (https://cancer.sanger.ac.uk/signatures/). The v3.2 COSMIC mutational signatures were down-sampled to remove signatures driven by therapy, environmental exposures, and/or sequencing artifacts, along with SBS39 due to the high similarity to SBS3, while maintaining other neuroblastoma-specific[13] and biologically relevant signatures. Our analysis code can be found on GitHub (https://github.com/diskin-lab-chop/nbl-bard1).

Supplemental Data

Supplemental Table 1. Characteristics of neuroblastoma-associated germline *BARD1* variants.

USI	Age at diagnosis (Days)	Sex	*MYCN*	Risk group	Variant	Exon	Cell line models	Other cancers associated with germline *BARD1* variant
PATZRU	833	Male	NA	High	c.159-1G>T (splice site)	2		Breast[14]
PAHYWC	704	Male	Amp	High	c.C334T; p.R112*	3	IMR-5 x 2	Breast[14, 15]
PARSEA	1779	Male	NA	High	c.448C>T; p.R150*	4	IMR-5	Breast[14, 16] Ovarian[17]
PATHJZ	340	Female	NA	Intermediate	c.860_861del; p.E287fs	4	IMR-5 x 3	-
PASGEE	1825	Male	NA	High	c.1677+1G>T (splice donor)	7		-
PASFDU	758	Female	NA	High	c.C1690T; p. Q564*	8	RPE1	Breast[14, 16, 18-22] Ovarian[16, 19, 23, 24] Endometrial[25] Colorectal[22, 26]
PATGWT	591	Male	Amp	High	c.1921C>T; p.R641*	10		Breast[21, 27, 28] Pancreatic[29]
PASCIX	1660	Male	NA	High	c.1935_1954dup; p.Glu652fs	10		Breast[16, 30, 31]

Amp., *MYCN* amplified tumor; NA, *MYCN* non-amplified tumor.

Supplemental Table 2. Guide RNAs and repair template oligonucleotides used to generate *BARD1* isogenic. cell lines.

Variant	Guide RNA	Single-stranded repair oligonucleotide	Notes
c.C334T; p.R112*	CTTGAAGATAAATAGACAAC GTTGTCTATTTATCTTCAAG	ACTGATGAATTTAACTAAGAGAGATAGGGATAGTT CTTACCTGACAGCTCATTG TCATGTAGCAAATTTC*A*AAGCTTACTACAAAGTTGA ATCATGCTGTC*G*AGTTGTC TATTTATCTTCAAGTCTTGTATCCAGGCCGGG	
c.C448T; p.R150*	ATCTGACTTTCTTACTTCGA TCGAAGTAAGAAAGTCAGAT	GCATCTTTTTTTATTGCAGGCTGGGTTTGCACTGA AGCTTTACTCACAACATAT CTGACTTTCTTACTTC*A*AGG*AGA*AAACCACATTTTA ATTGAATTCTTCTTGTTTC CTGCATCATTAAACAAACTTTTCCTAGGTTTA	
c.860_861del; p.E287fs	AGTCTCCAGACACTAAGAGC GCTCTTAGTGTCTGGAGACT	GGCTCCTTGACAGAATCTGAATGTTTTGGAAGTTT AACTGAAGTCTCTTTACCA TTGGCTGAGCAAATAG__TCTCCAGACACTAAGAG CAG*A*AATGAAGTAGTGACT CCTGAGAAGGTCTGCAAAAATTATCTTACATC	Utilzed for E287 #1
		TAGATGTAAGATAATTTTTGCAGACCTTCTCAGGA GTCACTACTTCATTC*T*[a]TGC TCTTAGTGTCTGGAGA__CTATTTGCTCAGCCAAT GGTAAAGAGACTTCAGTT AAACTTCCAAAACATTCAGATTCTGTCAAGGAGCC	Utilized for E287 #2,3
c.C1960T; p.Q564*	TATATTAACAGATGAACACT AGTGTTCATCTGTTAATATA	TCACTGAGCATTTTCTGTTGTTCTGAAGACAGCCC ACTGCCTATAAGTACAAGA GGTCCATCCCTACGCT*AT*CCAGTGTTCATCTGTTA ATATAAAAGGAGATACCAGTGTTAAAAACATTAGA CGACTAGACAAAGACAT	

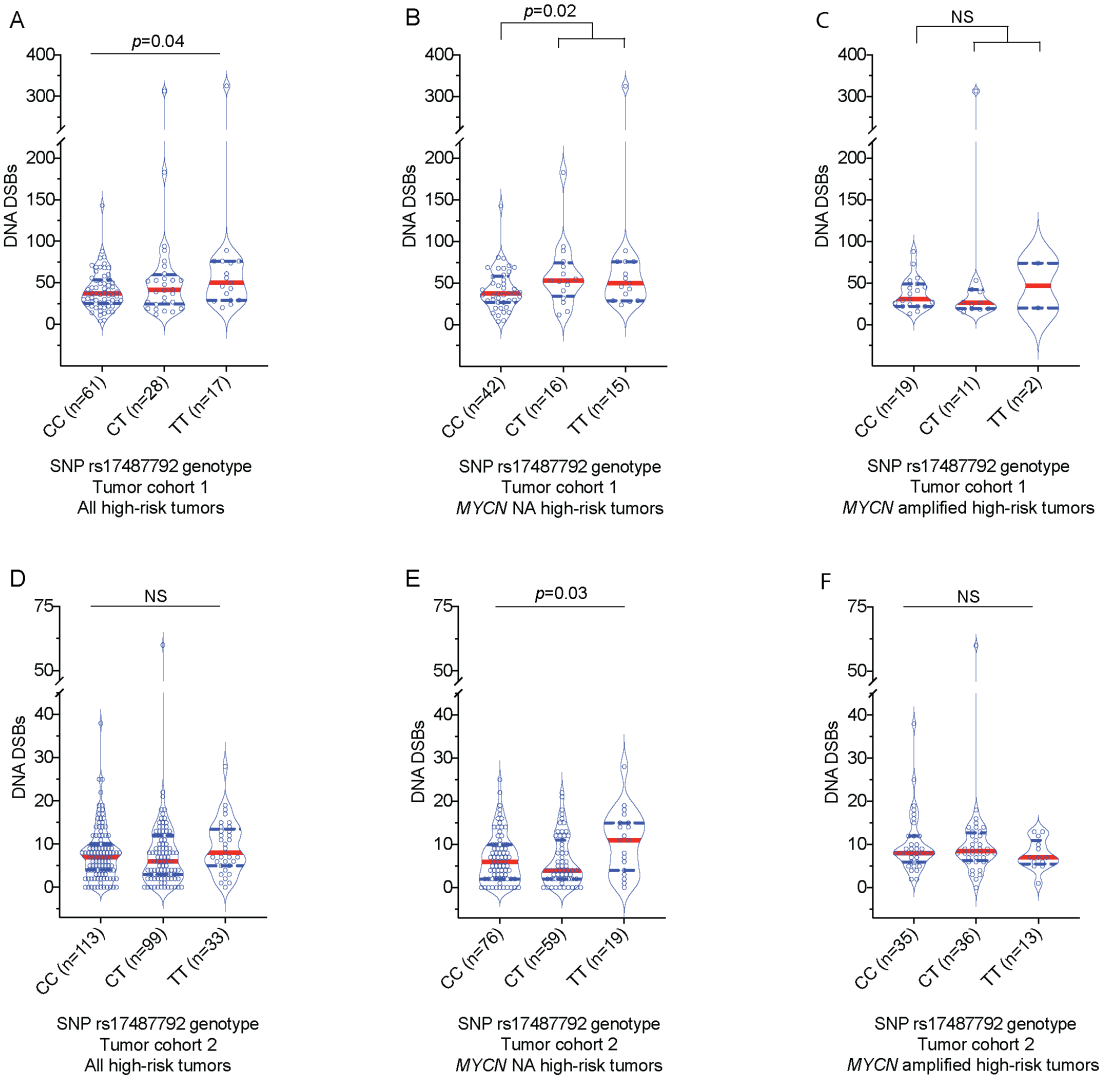
[a]This PAM variant is non-synonymous, but occurs after the frameshift at codon 287 and subsequent truncating variant at codon 291
Double underline, Pathogenic variant; *Italic*: Protospacer adjacent motif (PAM) variant.

Supplemental Table 3. Possible CRISPR off-target sites evaluated via Sanger sequencing.

Guide RNA	Type	Forward Primer	Reverse Primer	CFD Score
R112*	Intergenic	ACCTCACATGTGCTAAGGATGT	GTGATTTTCCTTACGAAGTGCTGA	0.90
	Exon (RP6)	AGGTCTTACTCCCAAAACATGTCA	ACATGCAAAGTAAACACTTGCA	0.13
	Exon (RP11)	AGCTTTTACACATGCTGAGACT	CACACACACAAACACCACACA	0.07
R150*	Intergenic	AGGGCAAGACAAGACTGCAA	CTTGGCTGGAAGGAGCATGA	0.41
	Exon (EPAS1)	TGGTTCTCTGGCCATTTCCC	CAAATGTGAGGTGCTGCCAC	0.14
E287fs	Intergenic	GCATTTTAGCATGGTGTCTATGGT	ACGTATCAACAAATAGCATTCACT	0.67
	Exon (CCR9)	TGTTATCGGGTAGCTGCCTG	GATGCAACTCTCCCTGGGAC	0.41
	Exon (LL22NC03)	TCCTGTCGTGTCTGTTTCGG	GAGCCACAGGTGAGAGTGAC	0.05
Q564*	Intergenic	TCATTGAACTGCATACAAGTGCT	ATTGAAAACTGGATATTCTCTGCTT	0.36
	Exon (RP11)	CCTGGGACTCGAACCGTATG	GTACAACCTGGTGTGGAGGG	0.33
	Exon (UBE2G1)	AAAGCCACCTCGTTCAGTGT	ACTTCCCTTCCTCTGTCGGA	0.04

Supplemental Figures and Figure Legends

Supplemental Figure 1



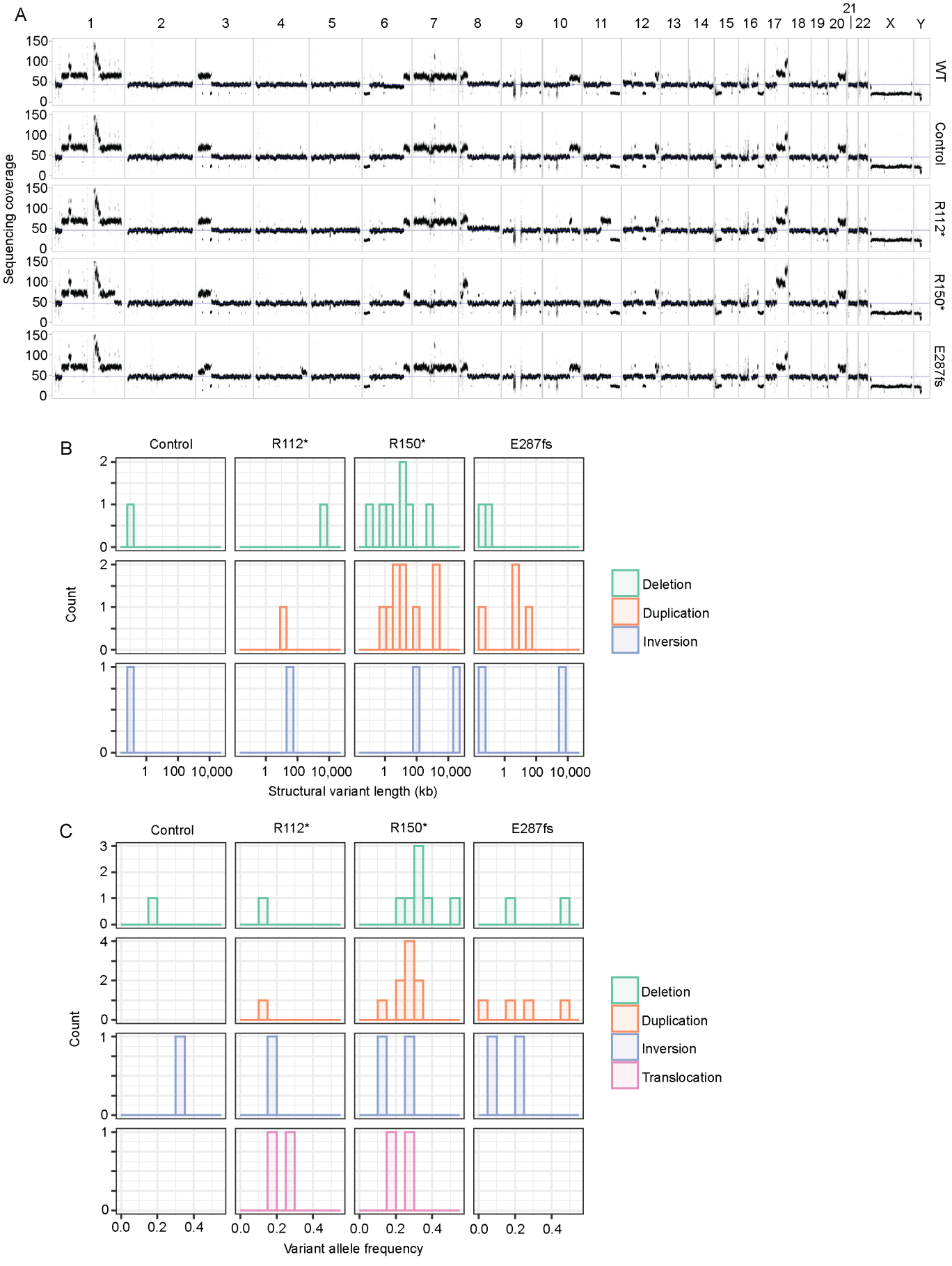
Supplemental Figure 1. Common *BARD1* germline risk variants correlate with genome-wide deficiencies in DNA repair in high-risk *MYCN* non-amplified primary neuroblastomas.

(**A**-**F**) Violin plots depicting the number of DNA DSBs in neuroblastoma tumors from only high-risk patients with different germline SNP rs174877792 genotypes. Panels **A**, **B** and **C** depict DNA DSBs in all high-risk tumors, high-risk tumors without *MYCN* amplification and high-risk tumors with *MYCN* amplification in tumor cohort 1, respectively. Panels **D**, **E** and **F** depict DNA DSBs in all high-risk tumors, high-risk tumors without *MYCN* amplification and high-risk tumors with *MYCN* amplification in tumor cohort 2, respectively. Red dotted line denotes median and blue dotted lines denotes quartiles.

MYCN NA, *MYCN* non-amplified.

Associated with **Figure 1**.

Supplemental Figure 2



Supplemental Figure 2. *BARD1*$^{+/mut}$ neuroblastoma IMR-5 clonal cell lines exhibit genome-wide genomic instability.

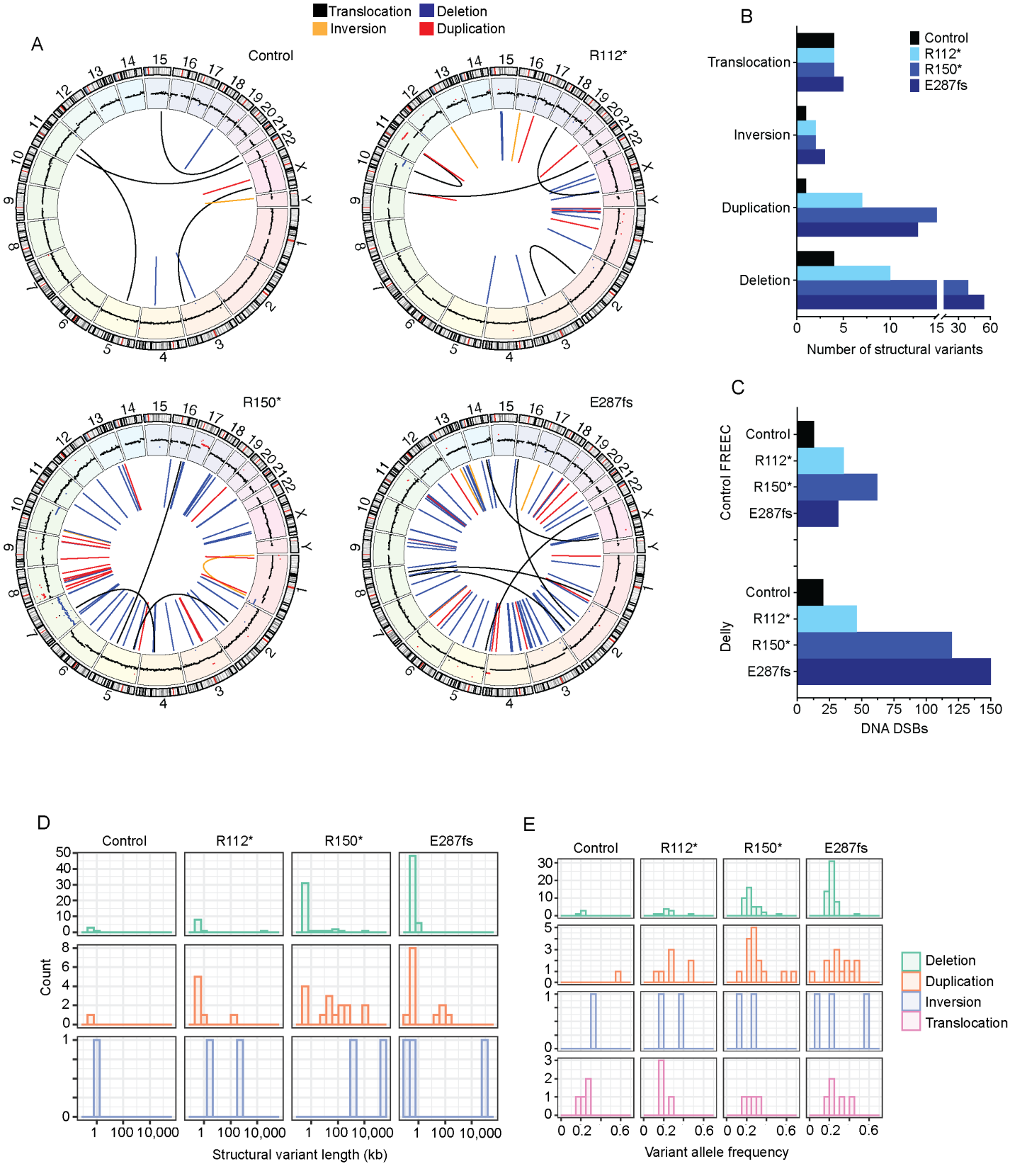
(**A**) Whole-genome sequencing coverage for WT parental cells, a non-targeted control clone and *BARD1*$^{+/mut}$ isogenic IMR-5 cells.

(**B**) Histograms showing length of structural variants in control and *BARD1*$^{+/mut}$ isogenic IMR-5 cells.

(**C**) Histograms showing allele frequency of structural variants in control and *BARD1*$^{+/mut}$ isogenic IMR-5 cells.

Associated with **Figure 3**.

Supplemental Figure 3



Supplemental Figure 3. Structural variant analysis with relaxed filtering confirms increased genome instability in *BARD1*$^{+/mut}$ neuroblastoma IMR-5 clonal cell lines.

(**A**) Circos plots depicting identified structural variants in control and *BARD1*$^{+/mut}$ isogenic IMR-5 models using less stringent filtering parameters.

(**B**) Counts of structural variants in control and *BARD1*$^{+/mut}$ isogenic IMR-5 cells using less stringent filtering parameters.

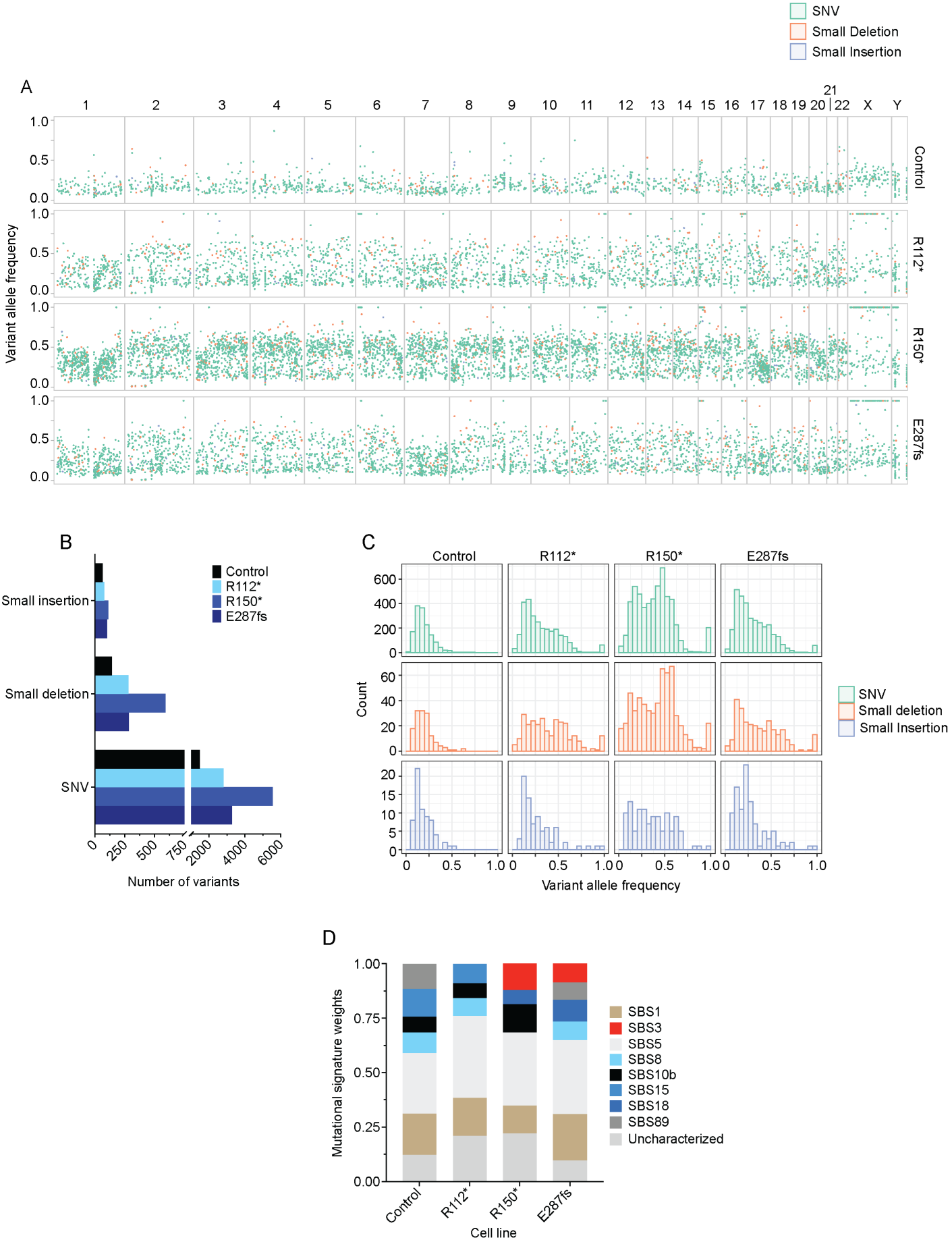
(**C**) Counts of DNA DSBs in control and BARD1$^{+/mut}$ IMR-5 cells, quantified from the Control-FREEC copy number (**top**) and the Delly structural variant data (**bottom**) using less stringent filtering parameters.

(**D**) Histograms showing length of structural variants in control and *BARD1*$^{+/mut}$ isogenic IMR-5 cells using less stringent filtering parameters.

(**E**) Histograms showing allele frequency of structural variants in control and *BARD1*$^{+/mut}$ IMR-5 isogenic cells using less stringent filtering parameters.

Associated with **Figure 3**.

Supplemental Figure 4



Supplemental Figure 4. IMR-5 *BARD1*$^{+/mut}$ isogenic cells acquired more SNVs and indels than the non-targeted control clone.

(**A**) Variant allele frequency distribution across the genome for SNVs and indels acquired in control clone and *BARD1*$^{+/mut}$ isogenic IMR-5 cells relative to WT parental IMR-5 cells.

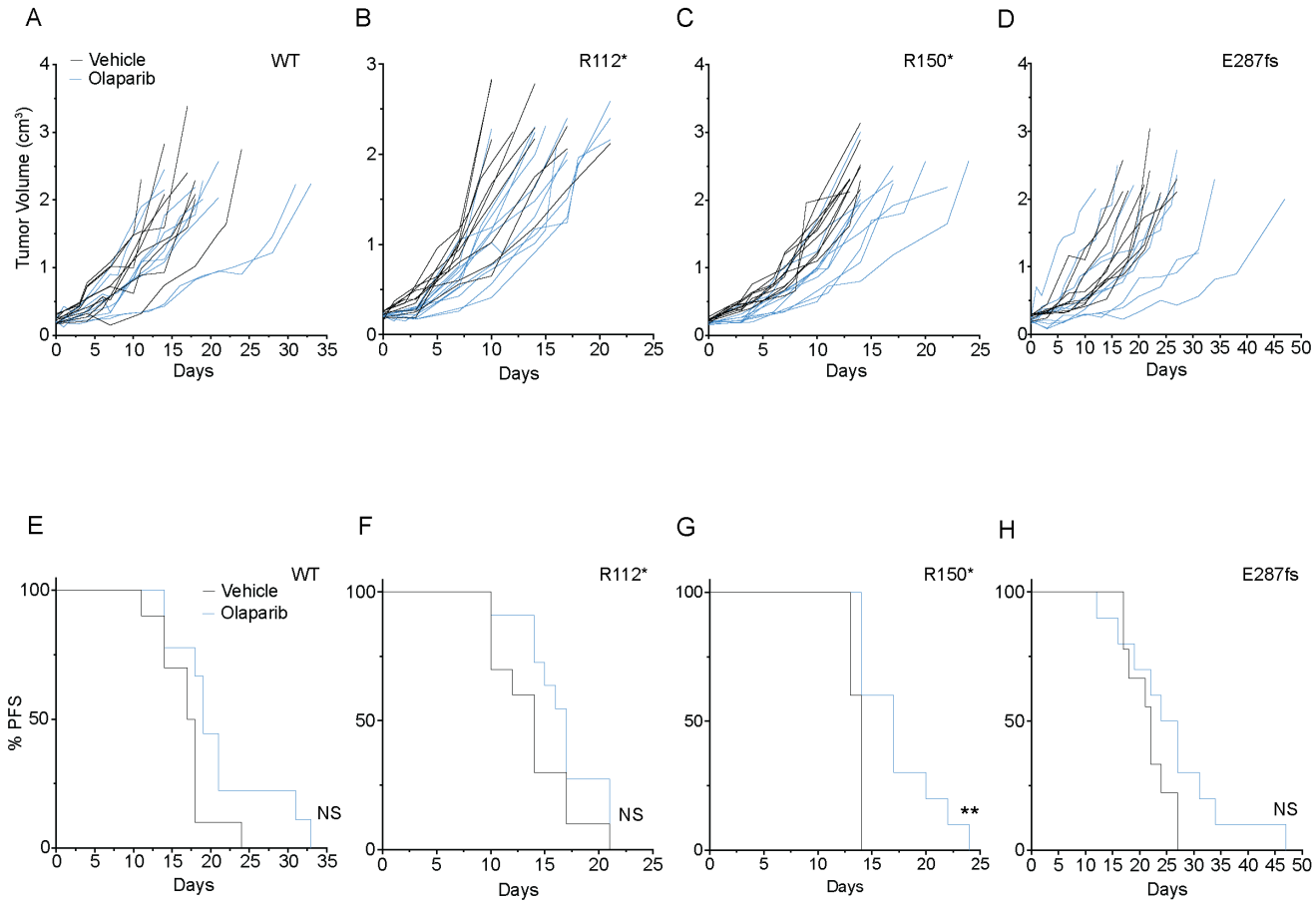
(**B**) Count of SNVs and indels identified in control and *BARD1*$^{+/mut}$ isogenic IMR-5 cells.

(**C**) Histograms showing allele frequency of SNVs and indels identified in control and *BARD1*$^{+/mut}$ isogenic IMR-5 models.

(**D**) Plot of mutational signature weights in non-targeted control and *BARD1*$^{+/mut}$ IMR-5 cells using COSMIC mutational signatures (v3.2).

Associated with **Figure 3**.

Supplemental Figure 5



Supplemental Figure 5. IMR-5 and RPE1 *BARD1*$^{+/mut}$ models show increased sensitivity to olaparib and cisplatin.

(**A**-**D**) Individual tumor growth curves of WT and *BARD1*$^{+/mut}$ IMR-5 xenografts treated with daily olaparib or vehicle [WT IMR-5 (**A**), *BARD1*$^{+/R112*}$ (**B**), *BARD1*$^{+/R150*}$ (**C**), *BARD1*$^{+/E287fs}$ (**D**)].

(**E**-**H**) Progression-free survival of mice with WT and *BARD1*$^{+/mut}$ IMR-5 xenografts treated with daily olaparib or vehicle [WT IMR-5 (**E**), *BARD1*$^{+/R112*}$ (**F**), *BARD1*$^{+/R150*}$ (**G**), *BARD1*$^{+/E287fs}$ (**H**)].

***P* < 0.01; NS, not significant.

Associated with **Figure 4**.

Supplemental References

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