

Figure 1

Cell Line	ALC1i-1 96h EC50 [μ M]
22Rv1	6.0
BXPC3	24
Capan-1	9.0
DU145	5.4
LnCAP	9.0
MDA MB 231	33
MDA MB 436	4.7
OVCAR3	1.8
PSN1	3.0
SKBR3	20
SUM149PT	4.0
SW620	7.3
T47D	7.0

Cell Line	ALC1i-1 11-day EC50 [μ M]
22Rv1	1
BXPC3	1.8
DU145	6.2
MDA MB 231	3.9
MDA MB 436	0.32
PSN1	0.71
SUM149PT	0.16

Figure 2

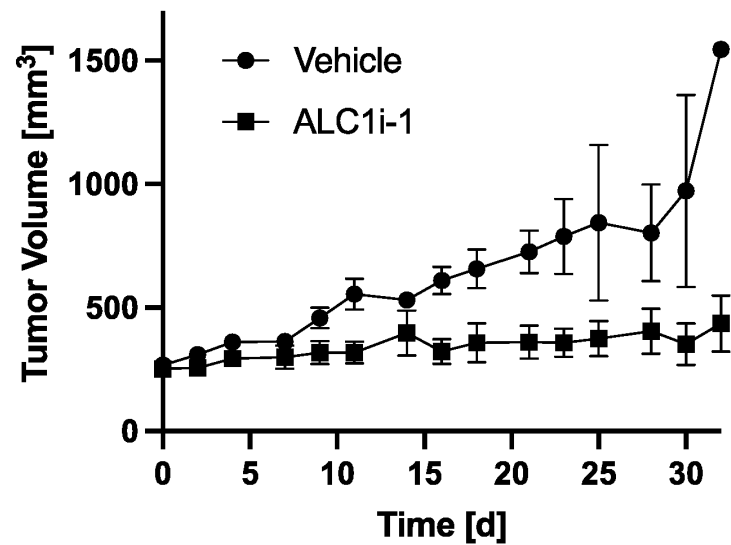


Figure 3

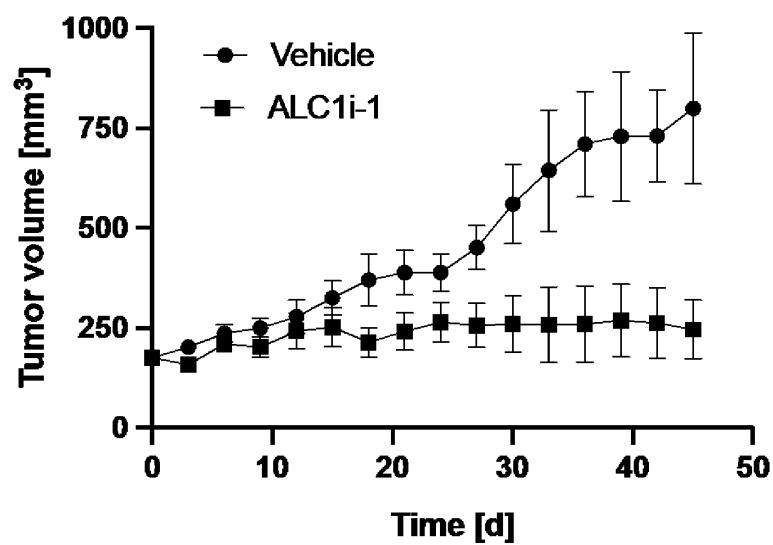


Figure 4

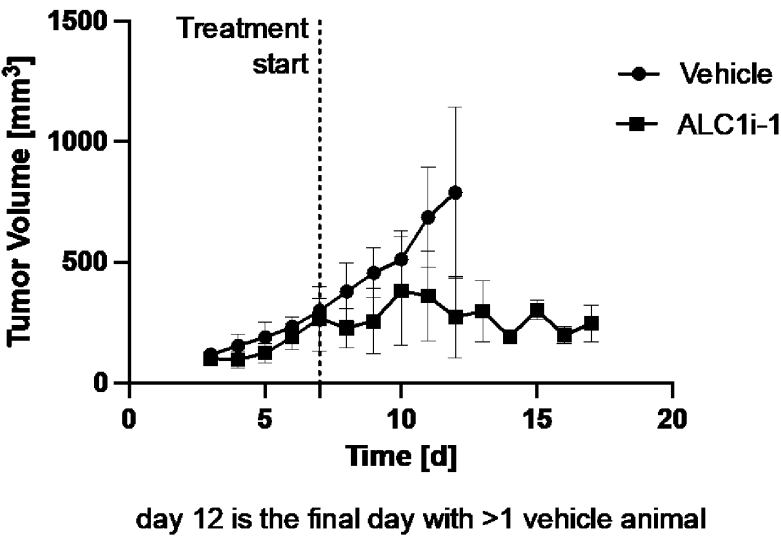


Figure 5

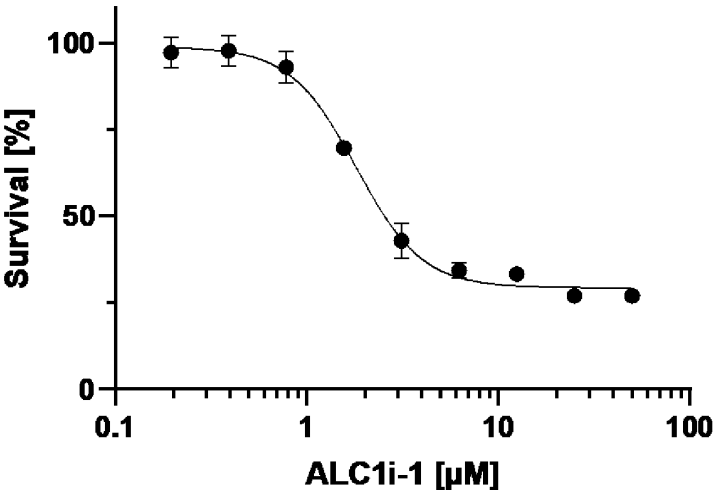


Figure 6

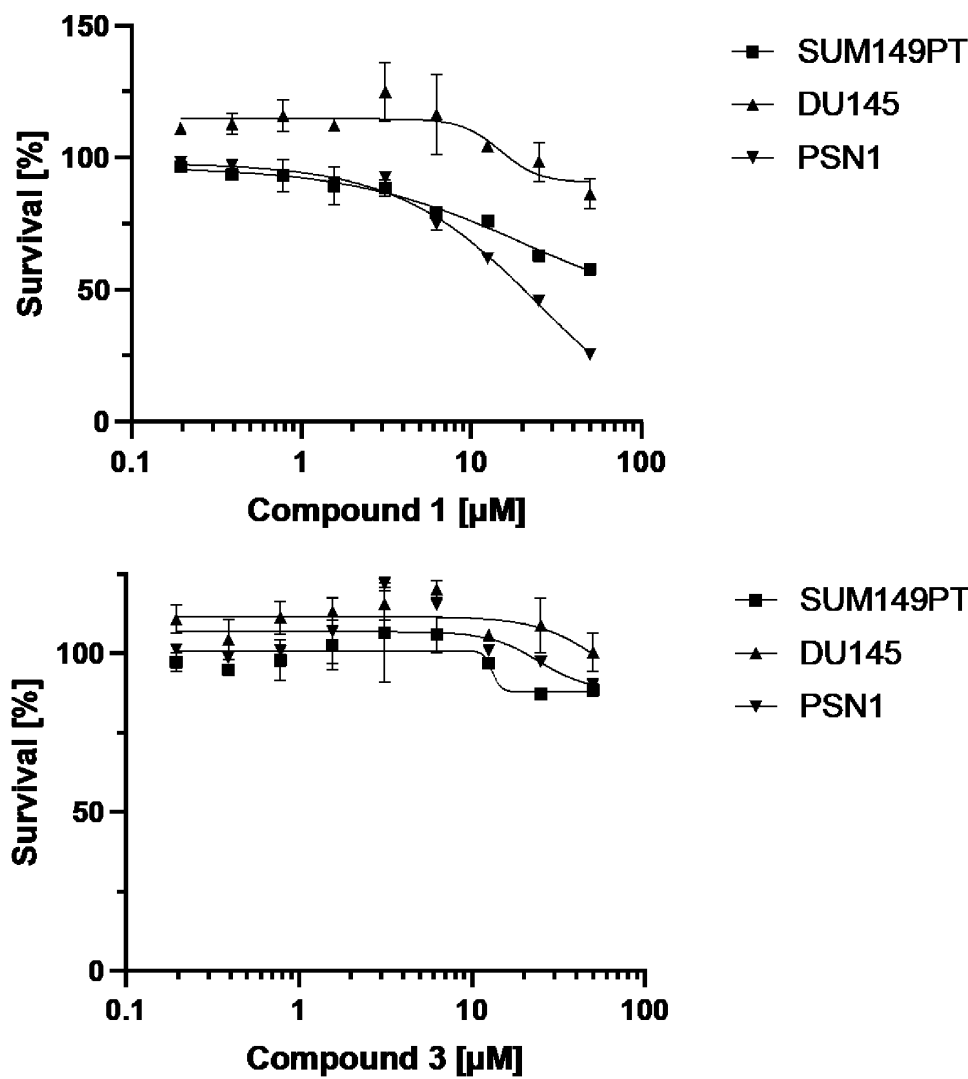


Figure 7

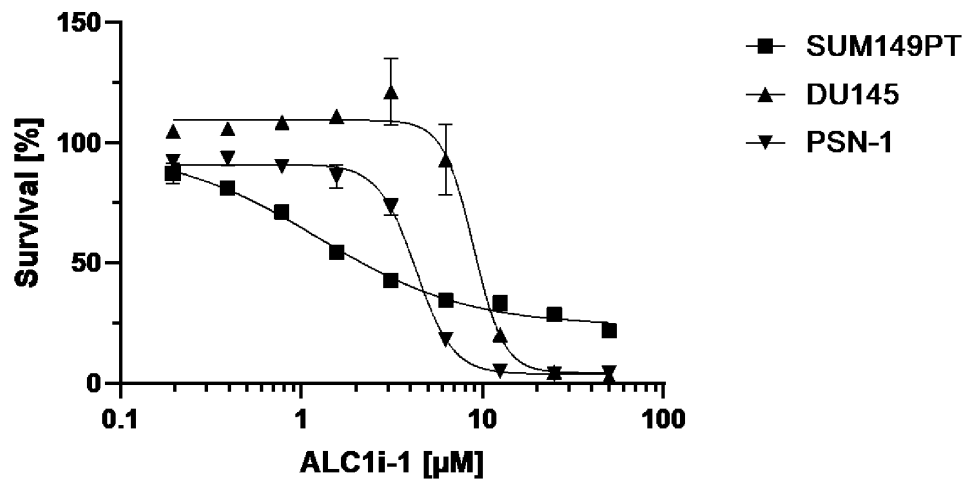


Figure 8

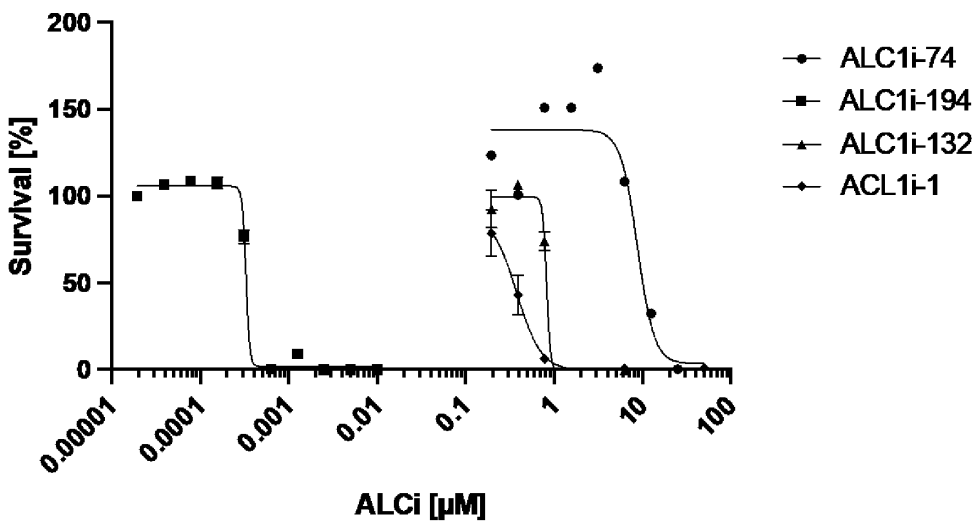


Figure 9

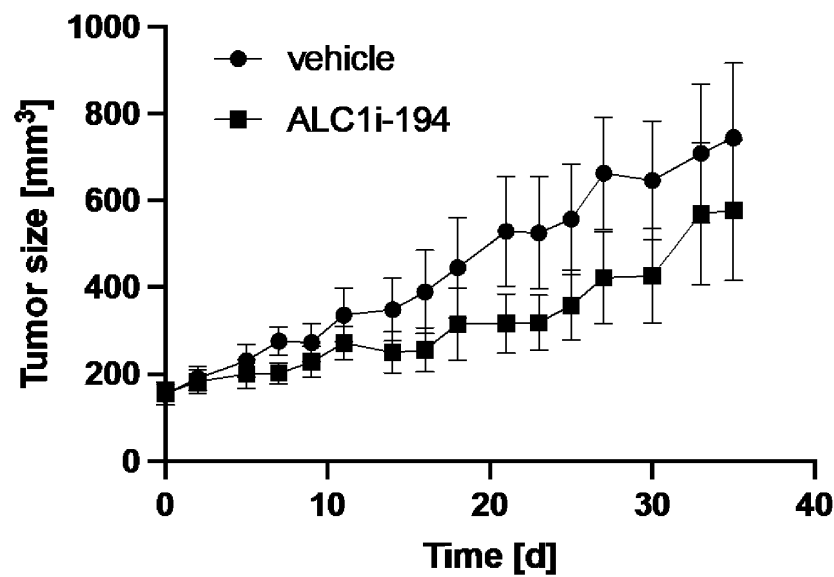


Figure 10

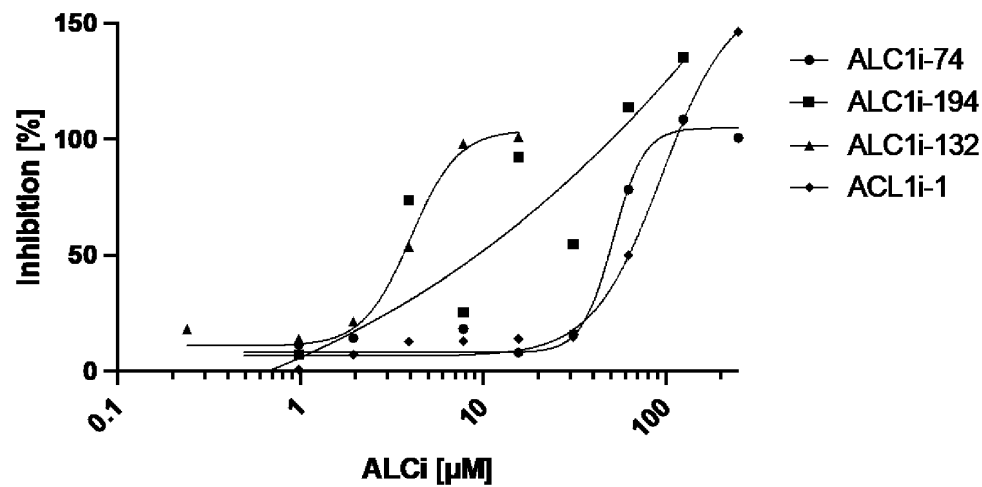


Figure 11

Gene Name (synonyms)	Activity	Chromosome location	Accession number
Base excision repair (BER)			
DNA glycosylases: major altered base released			
UNG	U	12q24.11	NM_080911
SMUG1	U	12q13.13	NM_014311
MBD4	U or T opposite G at CpG sequences	3q21.3	NM_003925
TDG	U, T or ethenoC opposite G	12q23.3	NM_003211
OGG1	8-oxoG opposite C	3p25.3	NM_016821
MUTYH (MYH)	A opposite 8-oxoG	1p34.1	NM_012222
NTHL1 (NTH1)	Ring-saturated or fragmented pyrimidines	16p13.3	NM_002528
MPG	3-meA, ethenoA, hypoxanthine	16p13.3	NM_002434
NEIL1	Removes thymine glycol	15q24.2	NM_024608
NEIL2	Removes oxidative products of pyrimidines	8p23.1	NM_145043
NEIL3	Removes oxidative products of pyrimidines	4q34	NM_018248
Other BER and strand break joining factors			
APEX1 (APE1)	AP endonuclease	14q11.2	NM_001641
APEX2	AP endonuclease	Xp11.21	NM_014481
LIG3	DNA Ligase III	17q12	NM_013975
XRCC1	LIG3 accessory factor	19q13.31	NM_006297
PNKP	Converts some DNA breaks to ligatable ends	19q13.33	NM_007254
APLF	Accessory factor for DNA end-joining	2p13.3	NM_173545
HMCES	Reacts with AP sites	3q21.3	NM_020187
Poly(ADP-ribose) polymerase (PARP) enzymes that bind to DNA			
PARP1 (ADPRT)	Protects strand interruptions	1q42.12	NM_001618
PARP2 (ADPRTL2)	PARP-like enzyme	14q11.2	NM_005484
PARP3 (ADPRTL3)	PARP-like enzyme	3p21.1	NM_001003931
PARG	Poly(ADP-ribose) glycohydrolase	10q11.23	NM_003631
PARPBP	Binds PARP and modulates recombination	12q23.2	NM_001319988
Direct reversal of damage			
MGMT	O6-meG alkyltransferase	10q26.3	NM_002412
ALKBH2 (ABH2)	1-meA dioxygenase	12q24.11	NM_001001655
ALKBH3 (DEPC1)	1-meA dioxygenase	11p11.2	NM_139178
Repair of DNA-protein crosslinks			
TDP1	Removes 3'-tyrosylphosphate and 3'-phosphoglycolate from DNA; human disorder SCAN1	14q32.11	NM_018319
TDP2 (TTRAP)	5'- and 3'-tyrosyl DNA phosphodiesterase	6p22.3	NM_016614
SPRTN (Spartan)	Reads ubiquitylation	1q42.12-q43	NM_032018
Mismatch excision repair (MMR)			

Figure 11 (continued)

MSH2	Mismatch (MSH2-MSH6) and loop (MSH2-MSH3) recognition	2p21	NM_000251
MSH3		5q14.1	NM_002439
MSH6		2p16.3	NM_000179
MLH1	MutL homologs, forming heterodimer	3p22.3	NM_000249
PMS2		7p22.1	NM_000535
MSH4	MutS homologs specialized for meiosis	1p31.1	NM_002440
MSH5		6p21.33	NM_002441
MLH3	MutL homologs of unknown function	14q24.3	NM_014381
<i>PMS1</i>		2q32.2	NM_000534
<i>PMS2P3 (PMS2L3)</i>		7q11.23	NM_005395
HFM1	Helicase in meiotic-crossover formation	1p22.2	NM_001017975
Nucleotide excision repair (NER)			
XPC	Binds DNA distortions	3p25.1	NM_004628
RAD23B		9q31.2	NM_002874
CETN2		Xq28	NM_004344
RAD23A	Substitutes for RAD23B	19p13.13	NM_005053
XPA	Binds damaged DNA in preincision complex	9q22.33	NM_000380
DDB1	Complex defective in xeroderma pigmentosum group E	11q12.2	NM_001923
DDB2 (XPE)		11p11.2	NM_000107
RPA1	Binds DNA in preincision complex	17p13.3	NM_002945
RPA2		1p35.3	NM_002946
RPA3		7p21.3	NM_002947
TFIIH (Catalyzes unwinding in preincision complex)			
ERCC3 (XPB)	3' to 5' DNA helicase	2q14.3	NM_000122
ERCC2 (XPD)	5' to 3' DNA helicase	19q13.32	NM_000400
GTF2H1	Core TFIIH subunit p62	11p15.1	NM_005316
GTF2H2	Core TFIIH subunit p44	5q13.2	NM_001515
GTF2H3	Core TFIIH subunit p34	12q24.31	NM_001516
GTF2H4	Core TFIIH subunit p52	6p21.33	NM_001517
GTF2H5 (TTDA)	Core TFIIH subunit p8	6p25.3	NM_207118
GTF2E2	TFIIIE subunit, mutated in TTD	8p12	NM_002095
CDK7	Kinase subunits of TFIIH	5q13.2	NM_001799
CCNH		5q14.3	NM_001239
MNAT1		14q23.1	NM_002431
ERCC5 (XPG)	3' incision	13q33.1	NM_000123
ERCC1	5' incision DNA binding subunit	19q13.32	NM_001983
ERCC4 (XPF)	5' incision catalytic subunit	16p13.12	NM_005236
LIG1	DNA ligase	19q13.32	NM_000234
NER-related			

Figure 11 (continued)

ERCC8 (CSA)	Cockayne syndrome and UV-Sensitive Syndrome; Needed for transcription-coupled NER	5q12.1	NM_000082
ERCC6 (CSB)		10q11.23	NM_000124
UVSSA (KIAA1530)		4p16.3	NM_020894
XAB2 (HCNP)	Pre-mRNA splicing; Associates with PRPF19, CSA, CSB	19p13.2	NM_020196
MMS19	Iron-sulfur cluster loading and transport	10q24.1	NM_022362
Homologous recombination			
RAD51	Homologous pairing	15q15.1	NM_002875
RAD51B	Rad51 homolog	14q24.1	NM_002877
RAD51D	Rad51 homolog	17q12	NM_002878
HELQ (HEL308)	DNA helicase in RAD51 paralog complex	4q21.23	NM_133636
SWI5	Accessory factor for loading RAD51	9q34.11	NM_001040011
SWSAP1	Shu subunits, RAD51 recruitment	19p13.2	NM_175871
ZSWIM7 (SWS1)		17p12	NM_001042697
SPIDR		8q11.21	NM_001080394
PDS5B		13q13.1	NM_015032
DMC1	Rad51 homolog, meiosis	22q13.1	NM_007068
XRCC2	DNA break and crosslink repair	7q36.1	NM_005431
XRCC3		14q32.33	NM_005432
RAD52	Accessory factors for recombination	12p13.33	NM_134424
RAD54L		1p34.1	NM_003579
RAD54B		8q22.1	NM_012415
BRCA1	Accessory factor for transcription and recombination, E3 Ubiquitin ligase	17q21.31	NM_007294
BARD1	BRCA1-associated	2q35	NM_000465
ABRAXAS1	In BRCA1 A complex	4q21.23	NM_139076
PAXIP1 (PTIP)	MDC1 paralog in 53BP1 pathway	7q36.2	NM_007349
SMC5	Recruit cohesion during HR	9q21.12	NM_015110
SMC6		2p24.2	NM_001142286
SHLD1	Suppressing end-resection	20p12.3	NM_001303477
SHLD2 (FAM35A)		10q23.2	NM_001330112
SHLD3		5q12.3	NM_001365341
SEM1 (SHFM1) (DSS1)	BRCA2 associated	7q21.3	NM_006304
RAD50	ATPase in complex with MRE11A, NBS1	5q23.3	NM_005732
MRE11A	3' exonuclease, defective in ATLD (ataxia-telangiectasia-like disorder)	11q21	NM_005590
NBN (NBS1)	Mutated in Nijmegen breakage syndrome	8q21.3	NM_002485
RBBP8 (CtIP)	Promotes DNA end resection	18q11.2	NM_002894
MUS81	Subunits of structure-specific DNA nuclease	11q13.1	NM_025128
EME1 (MMS4L)		17q21.33	NM_152463
EME2		16p13.3	NM_001257370

Figure 11 (continued)

SLX1A (GIYD1)	Subunit of SLX1-SLX4 structure-specific nuclease, two identical tandem genes in the human genome	16p11.2	NM_001014999
SLX1B (GIYD2)		16p11.2	NM_024044
GEN1	Nuclease cleaving Holliday junctions	2p24.2	NM_182625
Fanconi anemia (Tolerance and repair of DNA crosslinks and other adducts in DNA)			
FANCA	FANCA	16q24.3	NM_000135
FANCB	FANCB	Xp22.31	NM_152633
FANCC	FANCC	9q22.32	NM_000136
BRCA2 (FANCD1)	Cooperation with RAD51, essential function	13q13.1	NM_000059
FANCD2	Target for monoubiquitination	3p25.3	NM_033084
FANCE	FANCE	6p21.31	NM_021922
FANCF	FANCF	11p14.3	NM_022725
FANCG (XRCC9)	FANCG	9p13.3	NM_004629
FANCI (KIAA1794)	target for monoubiquitination	15q26.1	NM_018193
BRIP1 (FANCI)	DNA helicase, BRCA1-interacting	17q23	NM_032043
FANCL	FANCL	2p16.1	NM_018062
FANCM	helicase / translocase	14q21.3	NM_020937
PALB2 (FANCN)	Co-localizes with BRCA2 (FANCD1)	16p12.1	NM_024675
RAD51C (FANCO)	Rad51 homolog , FANCO	17q23.2	NM_002876
SLX4(FANCP)	nuclease subunit / scaffold SLX4 , FANCP	16p13.3	NM_032444
FAAP20 (C1orf86)	FANCA - associated	1p36.33	NM_182533
FAAP24 (C19orf40)	FAAP24	19q13.11	NM_152266
FAAP100	Part of FA core complex	17q25.3	NM_025161
UBE2T (FANCT)	E2 ligase for FANCL	1q32.1	NM_014176
Non-homologous end-joining			
XRCC6 (Ku70)	DNA end binding subunit	22q13.2	NM_001469
XRCC5 (Ku80)	DNA end binding subunit	2q35	NM_021141
PRKDC	DNA-dependent protein kinase catalytic subunit	8q11.21	NM_006904
LIG4	Ligase	13q33.3	NM_002312
XRCC4	Ligase accessory factor	5q14.2	NM_003401
DCLRE1C (Artemis)	Nuclease	10p13	NM_022487
NHEJ1 (XLF, Cernunnos)	End-joining factor	2q35	NM_024782
Modulation of nucleotide pools			
NUDT1 (MTH1)	8-oxoGTPase	7p22.3	NM_002452
DUT	dUTPase	15q21.1	NM_001948
RRM2B (p53R2)	p53-inducible ribonucleotide reductase small subunit 2 homolog	8q22.3	NM_015713
PARK7 (DJ-1)	Guanine glycation repair	1p36.23	NM_007262
DNPH1	Hydrolase for 5-hydroxymethyl deoxyuridine	6p21.1	NM_006443
NUDT15 (MTH2)	Hydrolysis of thiopurines?	13q14.2	NM_018283
NUDT18 (MTH3)	Hydrolysis of 8-hydroxypurine diphosphates	8p21.3	NM_024815
DNA polymerases			

Figure 11 (continued)

POLA1	DNA synthesis at resected ends	Xp22.1-p21.3	NM_001330360
POLB	BER in nuclear DNA	8p11.21	NM_002690
POLD1	Pol delta subunits POLD1 (catalytic subunit), POLD2 (Also subunit of pol zeta), POLD3 (Also subunit of pol zeta), POLD4 (auxiliary subunit)	19q13.33	NM_002691
POLD2		7p13	NM_001127218
POLD3		11q13.4	NM_006591
POLD4		11q13.2	NM_021173
POLE (POLE1)	Pol epsilon subunits	12q24.33	NM_006231
POLE2		14q21.3	NM_002692
POLE3		9q32	NM_017443
POLE4		2p12	NM_019896
REV3L (POLZ)	DNA pol zeta catalytic subunit, essential function	6q21	NM_002912
MAD2L2 (REV7)	DNA pol zeta and shieldin subunit	1p36.22	NM_006341
REV1 (REV1L)	dCMP transferase	2q11.2	NM_016316
POLG	Mitochondrial DNA repair and replication	15q26.1	NM_002693
POLH	xeroderma pigmentosum (XP) variant	6p21.1	NM_006502
POLI (RAD30B)	Lesion bypass	18q21.2	NM_007195
POLQ	TMEJ (alt-EJ)	3q13.33	NM_199420
POLK (DINB1)	Lesion bypass and NER	5q13.3	NM_016218
POLL	Gap-filling during non-homologous end-joining	10q24.32	NM_013274
POLM	Gap filling during non-homologous end-joining	7p13	NM_013284
POLN (POL4P)	Lesion bypass / recombination?	4p16.3	NM_181808
PRIMPOL	Primase and DNA-directed polymerase	4q35.1	NM_152683
DNTT	Terminal transferase	10q24.1	NM_004088
Editing and processing nucleases			
FEN1 (DNase IV)	5' nuclease	11q12.2	NM_004111
FAN1 (MTMR15)	5' nuclease interacting with FANCD2	15q13.2	NM_014967
TREX1	3' exonuclease	3p21.31	NM_033629
TREX2	3' exonuclease	Xq28	NM_080701
EXO1 (HEX1)	5' exonuclease	1q43	NM_003686
APTX (aprataxin)	Processing of DNA single-strand interruptions	9p21.1	NM_175073
SPO11	endonuclease	20q13.32	NM_012444
ENDOV	incision 3' of hypoxanthine and uracil in DNA and inosine in RNA	17q25.3	NM_173627
DNA2	Seckel Syndrome 8	10q21.3	NM_001080449
DCLRE1A (SNM1A)	5'-3' exonuclease, DNA crosslink repair	10q25.3	NM_014881
DCLRE1B (SNM1B)	5' - 3' exonuclease, APOLLO	1p13.2	NM_022836
EXO5	exonuclease	1p34.2	NM_001346946
Ubiquitination and modification			
UBE2A (RAD6A)	Ubiquitin-conjugating enzyme	Xq24-q25	NM_003336
UBE2B (RAD6B)	Ubiquitin-conjugating enzyme	5q31.1	NM_003337

Figure 11 (continued)

RAD18	E3 ubiquitin ligase	3p25.3	NM_020165
SHPRH	E3 ubiquitin ligase, SWI/SNF related, homolog of <i>S. cerevisiae</i> Rad5	6q24.3	NM_001042683
HLTF (SMARCA3)	E3 ubiquitin ligase, SWI/SNF related, homolog of <i>S. cerevisiae</i> Rad5	3q25.1-q26.1	NM_003071
RNF168	E3 ubiquitin ligase for DSB repair; ATM-like and RIDDLE syndrome	3q29	NM_152617
RNF8	E3 ubiquitin ligase for DSB repair	6p21.2	NM_003958
RNF4	E3 ubiquitin ligase	4p16.3	NM_001185009
UBE2V2 (MMS2)	Ubiquitin-conjugating complex	8q11.21	NM_003350
UBE2N (UBC13)		12q22	NM_003348
USP1	Ubiquitin-specific protease for FANCD2, PCNA	1p31.3	NM_003368
WDR48	Necessary for USP1 activity	3p22.2	NM_020839
HERC2	Control of several DNA repair factors	15q13.1	NM_004667
Chromatin Structure and Modification			
H2AX (H2AFX)	Histone, phosphorylated after DNA damage	11q23.3	NM_002105
CHAF1A (CAF1)	Chromatin assembly factor	19p13.3	NM_005483
SETMAR (METNASE)	DNA damage-associated histone methylase and nuclease	3p26	NM_006515
ATRX	Chromatin remodeling, transcription factor	Xq21.1	NM_000489
Genes defective in diseases associated with sensitivity to DNA damaging agents			
BLM	Bloom syndrome helicase	15q26.1	NM_000057
RMI1	In BLM-TOP3A complex	9q21.32	NM_001358291
TOP3A	Topoisomerase IIIa	17p11.2	NM_004618
WRN	Werner syndrome helicase / 3' - exonuclease	8p12	NM_000553
RECQL4	Rothmund-Thompson syndrome	8q24.3	NM_004260
ATM	ataxia telangiectasia	11q22.3	NM_000051
MPLKIP (TTDN1)	non-photosensitive form of trichothiodystrophy	7p14	NM_138701
Other identified genes with known or suspected DNA repair function			
RPA4	Similar to RPA2	Xp21.33	NM_013347
PRPF19 (PSO4)	Pre-mRNA splicing; DNA crosslink repair; binding to SETMAR	11q12.2	NM_014502
RECQL (RECQ1)	DNA helicase	12p12.1	NM_002907
RECQL5	DNA helicase	17q25.1	NM_001003715
RDM1 (RAD52B)	Similar to RAD52	17q12	NM_145654
NABP2 (SSB1)	Single-stranded DNA binding protein (ATM / MRN pathway)	12q13.3	NM_024068
Other conserved DNA damage response genes			
ATR	ATM- and PI-3K-like essential kinase	3q23	NM_001184
ATRIP	ATR-interacting protein	3p21.31	NM_130384
MDC1	Mediator of DNA damage checkpoint	6p21.3	NM_014641
PCNA	Sliding clamp for pol delta and pol epsilon	20p12.3	NM_002592
RAD1	subunits of PCNA-like sensor of damaged DNA	5p13.2	NM_002853
RAD9A		11q13.2	NM_004584

Figure 11 (continued)

HUS1		7p12.3	NM_004507
RAD17 (RAD24)	RFC-like DNA damage sensor	5q13.2	NM_002873
CHEK1	Effector kinases	11q24.2	NM_001274
CHEK2		22q12.1	NM_007194
TP53	Regulation of the cell cycle	17p13.1	NM_000546
TP53BP1 (53BP1)	chromatin-binding checkpoint protein	15q15-q21	NM_001141980
RIF1	suppressor of 5'-end-resection	2q23.3	NM_001177665
TOPBP1	DNA damage checkpoint control	3q22.1	NM_007027
CLK2	S-phase check point and biological clock protein	1q21	NM_003993
PER1	S-phase check point and biological clock protein	17p12	NM_002616

Figure 12

HR-related genes

53BP1	CDKN2B	FGF23	KDM5C	PALB2 (FANCN)	RMI1	TP53
AADAT	CDKN2C	FGF3	KDM6A	PARP1	RMI1 b	TP53BP1
ADM	CEBPA	FGF4	KDR	PARP2	RMI2	TP53I3
AHSA1	CENPA	FGF5	KEAP1	PARP3	RMI2 b	TP63
ALDH3B1	CENPE	FGF6	KEL	PARP4	RNF43	TRAF2
ALDH6A1	CENPJ	FGF9	KIT	PARPBP	ROS1	TRAF7
ALG8	CHAF1A	FGFR1	KLF4	PAX5	RPA1	TRAPPC13
ANLN	CHEK1	FGFR2	KLHL6	PAXX	RPA1 b	TSC1
ARID1a	CHEK2	FGFR3	KMT2A (MLL)	PBRM1	RPA2	TSC2
ARID1b	CIC	FGFR4	KMT2B	PCNA	RPA3	TSHR
ARSD	COL2A1	FH	KMT2C (MLL3)	PDCD1 (PD-1)	RPA4	TTK
ASF1B	COP1	FLCN	KMT2D (MLL2)	PDCD1LG2 (PD-L2)	RPS6KA4	TYRO3
ASPM	CREBBP	FLT1	KNSTRN	PDGFB	RPS6KB1	U2AF1
ATM	CRKL	FLT3	KRAS	PDGFRA	RPS6KB2	VEGFA
ATP10B	CRLF2	FLT4	LATS1	PDGFRB	RPTOR	VHL
ATR	CSF1R	FOXA1	LATS2	PDK1	RSPO1	VTCN1
ATRIP b	CSF3R	FOXL2	LCK	PER1	RSPO2	WRN
ATRX	CTCF	FOXO1	LIG4	PGD	RUNX1	WT1
AURKB	CTLA4	FOXP1	LMO1	PGR	RUNX1T1 (ETO)	XIAP

Figure 12 (continued)

BAP1	CTNNA1	FRS2	LRP1B	PHF6	RYBP	XPO1
BARD1	CTNNB1	FTO	LYN	PHOX2B	SDC4	XRCC2
BBOX1	CUL3	FUBP1	MAD2L2	PIK3C2B	SDHA	XRCC3
BIRC2	CUL4A	FYN	MAGOH	PIK3C2G	SDHAF2	XRCC4
BIRC3	CUL4B	GABRA6	MALT1	PIK3C3	SDHB	XRCC5
BLM	CUX1	GADD45A	MAP2K1 (MEK1)	PIK3CA	SDHC	XRCC6
BMPR1A	CXCR4	GATA1	MAP2K2 (MEK2)	PIK3CB	SDHD	YAP1
BRAF	CYLD	GATA2	MAP2K4	PIK3CD	SESN1	YES1
BRCA1	CYP2C19	GATA3	MAP2K7	PIK3CG	SETBP1	ZFHX3
BRCA1 (FANCS)	DAXX	GATA4	MAP3K1	PIK3R1	SETD2	ZNF217
BRCA2	DCLRE1C	GATA6	MAP3K13	PIK3R2	SF3B1	ZNF703
BRCA2 (FANCD1)	DCUN1D1	GEN1	MAP3K14	PIK3R3	SGK1	ZRSR2
BRD4	DDB1	GID4 (C17orf39)	MAP3K4	PIM1	SH2B3	
BRI3BP	DDR1	GLI1	MAPK1	PLCG1	SH2D1A	
BRIP1	DDR2	GNA11	MAPK3	PLCG2	SHLD1	
BRIP1 (FANCJ)	DDX3X	GNA13	MAPK8	PLK2	SHLD2	
BRIP1 b	DICER1	GNAQ	MAX	PMAIP1	SHPRH	
BTG1	DIS3	GNAS	MCL1	PML	SHQ1	
BTG2	DLL3	GPS2	MDC1	PMS1	SLC34A2	
BTK	DMC1 b	GRIN2A	MDM2	PMS2	SLIT2	
BUB1	DNA2	GRM3	MDM4	PNKP	SLX4	
C10orf119	DNAJB1	GSK3B	MED12	PNRC1	SMAD2	
C10orf73	DNMT1	H1-2	MEF2B	POLA1	SMAD3	
C11orf82	DNMT3A	H2AX	MEN1	POLD1	SMAD4	
C13orf3	DNMT3B	H2BC5	MERTK	POLE	SMARCA2	
C14orf145	DOT1L	H3-3A	MET	POLQ	SMARCA4	
C15orf42	E2F3	H3-3B	MGA	PPARG	SMARCAD1	
C16orf59	EED	H3-4	MGMT	PPM1D	SMARCB1	
C16orf68	EGFL7	H3-5	MITF	PPP1R3A	SMARCD1	
C17orf41	EGFR	H3C1	MLH1	PPP2R1A	SMC1A	
C1orf112	EIF1AX	H3C10	MLH3	PPP2R2A	SMC3	
C1orf54	EIF4A2	H3C11	MPL	PPP4R4	SMC5	
C1QTNF6	EIF4E	H3C12	MRE11	PPP6C	SMC6	
C20orf19	ELF3	H3C13	MRE11A	PRC1	SMO	
C20orf82	ELOC (TCEB1)	H3C2	MRE11A (MRE11)	PRDM1	SNCAIP	
C4orf34	EML4	H3C3	MRN complex	PREX2	SOC51	
C5orf38	EMSY (C11orf30)	H3C4	MSH2	PRG4	SOS1	
C6orf48	ENO1	H3C6	MSH3	PRKAR1A	SOX10	

Figure 12 (continued)

CALR	EP300	H3C7	MSH6	PRKCI	SOX17	
CARD11	EPCAM	H3C8	MST1	PRKDC	SOX2	
CASP8	EPHA2	HDAC2	MST1R	PRKN	SOX9	
CBFB	EPHA3	HDAC9	MTAP	PTCH1	SPEN	
CBL	EPHA5	HELQ	MTOR	PTEN	SPOP	
CBLB	EPHA7	HERC2	MUTYH	PTK2	SRC	
CCDC138	EPHB1	HFM1	MXD4	PTPN11	SRSF2	
CCDC92	ERBB2	HGF	MYB	PTPRB	SSBP1	
CCN6	ERBB3	HLA-A	MYC	PTPRD	STAG2	
CCNA2	ERBB4	HNF1A	MYCL (MYCL1)	PTPRS	STAT3	
CCNB1	ERCC1	HOXB13	MYCN	PTPRT	STAT4	
CCNB1IP1	ERCC2	HRAS	MYD88	QKI	STAT5A	
CCND1	ERCC3	HSD3B1	MYOD1	RAB35	STAT5B	
CCND2	ERCC4	HSP90AA1	NBN	RAC1	STK11	
CCND3	ERCC5	HSP90AB1	NBN (NBS1)	RAD21	STK19	
CCNE1	ERCC6	ICOSLG	NCOA3	RAD50	STK40	
CD274 (PD-L1)	ERG	ID3	NCOR1	RAD51	SUFU	
CD276	ERRFI1	IDH1	NEGR1	RAD51AP1	SUZ12	
CD68	ESR1	IDH2	NF1	RAD51B	SYK	
CD74	ETV1	IFNGR1	NF2	RAD51C	TBC1D4	
CD79A	ETV4	IGF1	NFE2L2	RAD51D	TBX3	
CD79B	ETV5	IGF1R	NFKBIA	RAD52	TCF3 (E2A)	
CD8A	ETV6	IGF2	NHEJ1	RAD54L	TCF7L2	
CDC20	EWSR1	IKBKE	NKX2-1	RAF1	TEK	
CDC27	EXO1	IKZF1	NKX3-1	RARA	TENT5C	
CDC6	EZH2	IL10	NOTCH1	RASA1	TERC	
CDC7	EZR	IL7R	NOTCH2	RB1	TERT	
CDC73	FADD	INHA	NOTCH3	RBM10	TET1	
CDCA2	FANCA	INHBA	NOTCH4	RECQL4	TET2	
CDCA3	FANCC	INO80	NPM1	REL	TFE3	
CDCA5	FANCD2	INPP4A	NRAS	RET	TGFB1	
CDCA7	FANCE	INPP4B	NSD1	REV3L	TGFBR1	
CDCA8	FANCF	INSR	NSD3	RFC1	TGFBR2	
CDH1	FANCG	IRF2	NT5C2	RFC2	TMEM127	
CDK12	FANCI	IRF4	NTRK1	RFC3	TMPRSS2	
CDK2	FANCL	IRS1	NTRK2	RFC4	TNF	
CDK4	FANCM	IRS2	NTRK3	RFC5	TNFAIP3	
CDK6	FAS (TNFRSF6)	JAK1	NUP93	RHEB	TNFRSF14	
CDK8	FAT1	JAK2	NUTM1	RHOA	TOP1	
CDKN1A	FBXW7	JAK3	PAK1	RICTOR	TOP2A	

Figure 12 (continued)

CDKN1B	FGF10	JUN	PAK3	RIF1	TOP3A	
CDKN1C	FGF14	KAT6A (MYST3)	PAK5	RIF1 b	TOP3A b	
CDKN2A	FGF19	KDM5A	PALB2	RIT1	TOPBP1	