



Ecl136II		SmaI			
AACCGTCAGATCCGCTAGCGCTACCGGACTCAGATCTCGAG TTGGCAGTCTAGGCGATCGCGTAGCGCTAGTCTAGAGCTC		GGGATCCACCGGTCGCCACCAT CCCTAGGTGGCCAGCGGTGGTA		Loss	Misincorporation
FC					
AACCGTCAGATCCGCTAGCGCTACCGGACTCAGATCTCGAG		GATCCACCGGTCGCCACCAT	0/-2		
AACCGTCAGATCCGCTAGCGCTACCGGACTCAGATCTCGAG		GGGATCCACCGGTCGCCACCAT	0/0		
AACCGTCAGATCCGCTAGCGCTACCGGACTCAGATCTCGAG		GGGATCCACCGGTCGCCACCAT	0/0		
AACCGTCAGATCCGCTAGCGCCACCGG		TCGCCACCAT	-14/-12		
AACCGTCAGATCCGCTAGCGCTACCGGACTCAGATCTCGAG		GGATCCACCGGTCGCCACCAT	0/-1		
AACCGTCAGATCCGCTAGCGCTACCGGACTCAGATCTCGAG		GGGATCCACCGGTCGCCACCAT	0/0		
AACCGTCAGATCCGCTAGCGCTACCGGACTCAGATCTCGAG		GGGATCCACCGGTCGCCACCAT	0/0		
AACCGTCAGATCCGCTAGCGCTACCGGACTCGGATC CACCG		GTGCCACCAT	0/-11	4	
AACCGTCAGATCCGCTAGCGCTACCGGACTCAGATCT TCGAG		TCCACCGGTCGCCACCAT	0/-4	2	
AACCGTCAGATCCGCTAGCGCTACCGGACTCAGATCTCGAG		GGGATCCACCGGTCGCCACCAT	0/0		
AACCGTCAGATCCGCTAGCGCTACCGGACTCAGATCTCGAG		GGGATCCACCGGTCGCCACCAT	0/0		
AACCGTCAGATCCGCTAGCGCTACCGGACTCAGATCTCGAG		GGGATCCACCGGTCGCCACCAT	0/0		
AACCGTCAGATCCGCTAGCGCTACCGGACTCAGATCTCGAG		GGGATCCACCGGTCGCCACCAT	0/0		
AACCGTCAGATCCGCTAGCGCTACCGGACTCAGATCTCGAG		GGGATCCACCGGTCGCCACCAT	0/0		
AACCGTCAGATCCGCTAGCGCTACCGGACTCAGATCTCGAG		GGGATCCACCGGTCGCCACCAT	-6/-11		
FD					
AACCGTCAGATCCGCTAGCGCTACCGGACTCAGATCTCGAG		GGGATCCACCGGTCGCCACCAT	0/0		
AACCGTCAGATCCGCTAGCGCTACCGGACTCAGATCTCGA		GGTCCGCCACCAT	-1/-10		
AACCGTCAGATCCGCTAGCGCTA CTAGATCTC			-8/-35		
AACCGTCAGATCCGCTAGCGCTACCGGACTCAGATCTC		AA GGGATCCACCGGTCGCCACCAT	-3/0	2	
AACCGTCAGATCCGCTAGCGCTACCGGACTCAGATCTCGAG		GGGATCCACCGGTCGCCACCAT	0/0		
AACCGTCAGATCCGCTAGCGCTACCGGACTCAGATCTCGAG		GGGATCCACCGGTCGCCACCAT	0/0		
AACCGTCAGATCCGCTAGCGCTACCGG		TCGCCACCAT	-14/-12		
AACCGTCAGATCCGCTAGCGCTACCGGACTCAGATCTCGAG		GGGATCCACCGGTCGCCACCAT	0/0		
AACCGTCAGATCCGCTAGCGCTACCGGACTCAGATCTCGAG		TCACCGGTCGCCACCAT	0/-4		
AACCGTCAGATCCGCTAGCGCTACCGGACTCAGATCTCG		GGATCCACCGGTCGCCACCAT	-2/-1		
GGC		GAGG	-38/-31	2	
AACCGTCAGATCCGCTAGCGCTACCGGACTCAGATCTCGAG		GGGATCCACCGGTCGCCACCAT	0/0		
AACCGTCAGATCCGCTAGCGCTACCGGACTCAGATCTCGAG		GGGATCCACCGGTCGCCACCAT	0/0		
AACCGTCAGATCCGCTAGCGCTACCGGGATC		CACCGGTCGCCACCAT	-10/-6		
AACCGTCAGATCCGCTAGCGCTACCGGACTCAGATCTCGAG		GGGATCCACCGGTCGCCACCAT	0/0		
FR					
AACCGTCAGATCCGCTAGCGCTACCGGACTCAGATCTCGAG		GGGATCCACCGGTCGCCACCAT	0/0		
AACCGTCAGATCC		ACCGGTCGCCACCAT	-25/-7		
AACCGTCAGATCCGCTAGCG A GGACTCAGATCTCGAG		GGGATCCACCGGTCGCCACCAT	4/0		
AACCGTCAGATCCGCTAGCGCTACCGGACTCAGATCTCGAG		GGGATCCACCGGTCGCCACCAT	0/0		
AACCGTCAGATCCGCTAGCGCTACCGGACTCAGATCTCGAG		GGGATCCACCGGTCGCCACCAT	0/0		
AACCGTCAGATCCGCTAGC		T	-22/-21		
AACCGTCAGATCCGCTAGCGCTACCGGACTCAGATCTCGAG		GGATCCACCGGTCGCCACCAT	0/-1		
AACCGTCAGATCCGCTAGCGCTACCGGACTCAGATCTCGAG		GGGATCCACCGGTCGCCACCAT	0/0		
AACCGTCAGATCCGCTAGCGCTAGCG GAGAGAGCTGTTCAC		GGCGAGGAGCTGTTCACCGGGGGT GT GC CCAT	0/0	39	
AACCGTCAGATCCGCTAGCGCTACCGGACTCAGATCTCGAG		GGGATCCACCGGTCGCCACCAT	0/0		
AACCGTCAGATCCGCTAGCGCTACCGGACTCAGATCTCGAG		GGGATCCACCGGTCGCCACCAT	0/0		
AACCG		GTGCCACCAT	-33/-11		
AACCGTCAGGTCCGCTAGCGCTACCGGACTCAGATCTCGAG		GGGATCCACCGGTCGCCACCAT	0/0		
AACCGTCAGATCCGCTAGCGCTACCGGACTCAGATCTCGAG		GGGATCCACCGGTCGCCACCAT	0/0		
AACCGTCAGATCCGCTAGCGCT a CCGGACTCAGATCTCG		GGGATCCACCGGTCGCCACCAT	-2/0		

Figure S1. Fidelity of DNA damage repair by NHEJ In vivo DNA-ligation assay on FC, FD, and FR cells after transfecting linearized plasmids. Sequence stretches of at the blunt-ended junction. The right columns indicate the number of nucleotide losses and misincorporations, resulting from two independent experiments with minimum seven sequenced clones.

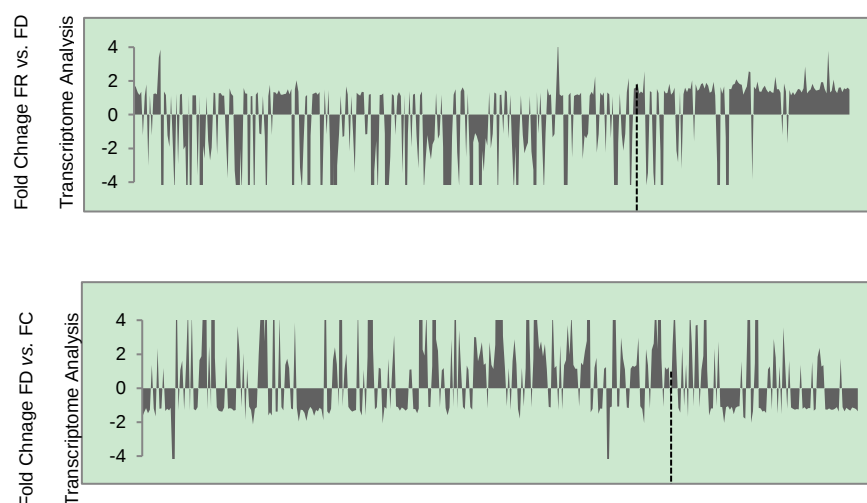


Figure S2 Transcript profile of chromosome 8 genes (A) FR vs. FD; (B) FD vs. FC. The ordinate expresses the fold changes of genes on chromosome 8.

Table S1. Overview of the primers used for qPCR.

Primers qPCR	Sequence 5' - 3'
CDKN1C Fw	CAGTGGACCGAAGTGGACA
CDKN1C Rv	GGGACCGGGACACTAGGC
H2AFY2 Fw	TCCACTGTACATCCCTCAG
H2AFY2 Rv	ATCAAAGTGGGCTGAGATGG
LEF1 Fw	GACGAGATGATCCCCTTCAA
LEF1 Rv	AGGGCTCCTGAGAGGTTTGT
DIRAS3 Fw	TGCCGACCATTGAAAATACC
DIRAS3 Rv	CAGGGTTTCCTTCTTGGTGA
SORBS2 Fw	AAGCACAGCCTGCAAGACCA
SORBS2 Rv	TGGGGTATTGGAGGGTCAGG
SLFN11 Fw	GCCCGATAACCTTCACACTC
SLFN11 Rv	ACCCATTTCTCGTTGTCAG
DCN Fw	GGACCGTTTCAACAGAGAGG
DCN Rv	TCAGAACACTGGACCACTCG
RUNX3 Fw	ACAGCCCCAACTTCCTCTG
RUNX3 Rv	GCTCAGCGGAGTAGTTCTCG
TBX18 Fw	GCGAAAAGGGTTCTTCTGAG
TBX18 Rv	GTGACGCCAGAGGGGAAG
HSPB7 Fw	AGAAGGCCCTGAGCATGTTT
HSPB7 Rv	TGAGAAGTCTCTCACGTCCAC
GALC Fw	GCCAAGCGTTACCATGATTT
GALC Rv	GCAGAGATGGACTCCCAGAG
USP44 Fw	TCCCCACTTCTCAAAGGAAA
USP44 Rv	CATGGCTGGGAAGCAATATC
FAP Fw	TTTTGGCATATGCGGAATTT
FAP Rv	ACGCAGGGTAAGTGGTATCG
KLK5 Fw	AAGGCCCAACCAGCTCTACT

KLK5 Rv	ATTTGACCCCCTGGAACATC
KLK10 Fw	TGTCCTGGTGGACCAGAGTT
KLK10 Rv	TGGTGGTACTTGGGATGGAC
PIM1 Fw	GCTCGGTCTACTCAGGCATC
PIM1 Rv	CCAGTCCAGGAGCCTAATGA
GAPDH Fw	GGAGCGAGATCCCTCCAAAAT
GAPDH Rv	GGCTGTTGTCATACTTCTCATGG
β -ACTIN Fw	CATGTACGTTGCTATCCAGGC
β -ACTIN Rv	CTCCTTAATGTCACGCACGAT



Table S2. Unique SVs in protein coding genes found in FR cells. SVs that affect exonic sequences are shown in bold and cancer related genes are marked in grey.

Chrom 1	start1	end1	Chrom 2	start2	end2	svtype	Event Score	eventSize	gene1	cancerGene1	gene2	cancerGene2	directFusionCandidates	Fragile sites
1	12708095	12708096	1	12711878	12711879	DUP	5	3783	AADACL4_intron2	.	AADACL4_intron3	.	AADACL4_intron2- AADACL4_intron3	
1	12708374	12708375	1	12712048	12712049	DEL	5	3674	AADACL4_intron2	.	AADACL4_intron3	.	AADACL4_intron2- AADACL4_intron3	
1	32389990	32389991	1	32390011	32390012	DUP	5	21	PTP4A2_intron8	.	PTP4A2_intron8	.	.	
1	40034613	40034614	1	40035265	40035266	DEL	3	652	PABPC4_intron6	.	PABPC4_6	.	PABPC4_intron6- PABPC4_6	
1	212459633	212459634	1	212502474	212502475	DEL	5	42841	PPP2R5A_intron2	PPP2R5A	PPP2R5A_intron6	PPP2R5A	PPP2R5A_intron2- PPP2R5A_intron6	
1	212530021	212530022	1	212530289	212530290	DEL	5	268	PPP2R5A_intron15	PPP2R5A	PPP2R5A_intron15	PPP2R5A	.	
1	212530398	212530399	1	212530496	212530497	DEL	3	98	PPP2R5A_15	PPP2R5A	PPP2R5A_intron16	PPP2R5A	PPP2R5A_15- PPP2R5A_intron16	
2	8236260	8236261	2	8236281	8236282	DUP	5	21	AC007464.1_intron1, LINC00299_intron15	.	LINC00299_intron15, AC007464.1_intron1	.	.	
2	12872146	12872147	2	12872126	12872127	DUP	5	20	TRIB2_intron4	.	TRIB2_intron4	.	.	
2	36605475	36605476	2	36605495	36605496	DUP	5	20	CRIM1_intron3	.	CRIM1_intron3	.	.	
2	59610792	59610793	2	59610842	59610843	DEL	5	50	RP11- 444A22.1_intron3, AC007131.2_intron8	.	RP11- 444A22.1_intron3, AC007131.2_intron8	.	.	

2	141566325	141566326	2	142182126	142182127	DEL	5	615801	LRP1B_intron33	LRP1B	LRP1B_intron4	LRP1B	LRP1B_intron33- LRP1B_intron4	FRA2F
2	141648306	141648307	2	142127053	142127054	DEL	5	478747	LRP1B_intron24	LRP1B	LRP1B_intron4	LRP1B	LRP1B_intron24- LRP1B_intron4	FRA2F
2	141913468	141913469	2	142018832	142018833	DEL	5	105364	LRP1B_intron8	LRP1B	LRP1B_intron4	LRP1B	LRP1B_intron8- LRP1B_intron4	FRA2F
2	200661296	200661297	2	200661334	200661335	DEL	5	38	FTCDNL1_intron6	.	FTCDNL1_intron6	.	.	
2	203155429	203155430	2	203155481	203155482	DUP	5	52	NOP58_intron9	.	NOP58_intron9	.	.	FRA2I
2	240694378	240694379	2	240694400	240694401	DUP	5	22	AC093802.1_intron2	.	AC093802.1_intron2	.	.	FRA2J
3	37101746	37101747	3	37101768	37101769	DUP	5	22	LRRFIP2_intron32, MLH1_intron24	MLH1	MLH1_intron24, LRRFIP2_intron32	MLH1	.	
Chrom 1	start1	end1	Chrom 2	start2	end2	svtype	Event Score	eventSize	gene1	cancerGene1	gene2	cancerGene2	directFusionCandidates	Fragile sites
3	50330752	50330753	3	50331420	50331421	INV	5	668	HYAL3_6	.	HYAL3_intron4	.	HYAL3_6- HYAL3_intron4	
3	50330976	50330977	3	50332127	50332128	INV	5	1151	HYAL3_intron5	.	HYAL3_intron4	.	HYAL3_intron5- HYAL3_intron4	
3	58417357	58417358	3	58417601	58417602	DEL	5	244	PDHB_1	PDHB	PDHB_1	PDHB	.	
3	60384818	60384819	3	60578611	60578612	DEL	5	193793	FHIT_intron9	FHIT	FHIT_intron8	FHIT	FHIT_intron9- FHIT_intron8	FRA3B
3	60846107	60846108	3	60851397	60851398	DEL	5	5290	FHIT_intron6	FHIT	FHIT_intron6	FHIT	.	FRA3B
3	60957459	60957460	3	60991335	60991336	DEL	5	33876	FHIT_intron6	FHIT	FHIT_intron6	FHIT	.	FRA3B
3	64641346	64641347	3	64641409	64641410	DEL	5	63	ADAMTS9_5	ADAMTS9	ADAMTS9_5	ADAMTS9	.	
3	131898759	131898760	3	131898779	131898780	DUP	5	20	CPNE4_intron2	.	CPNE4_intron2	.	.	
3	134890706	134890707	3	134890726	134890727	DUP	5	20	EPHB1_intron23	EPHB1	EPHB1_intron23	EPHB1	.	

3	135994735	135994736	3	136002097	136002098	DEL	5	7362	PCCB_intron11	.	PCCB_intron11	.	.	.
3	141211928	141211929	3	141211908	141211909	DUP	5	20	RASA2_intron2	RASA2	RASA2_intron2	RASA2	.	.
3	151151519	151151520	3	151151567	151151568	DEL	5	48	MED12L_48,IGSF10_7	IGSF10,MED12L	MED12L_48,IGSF10_7	IGSF10,MED12L	.	FRA3D
4	8039292	8039293	4	8039317	8039318	DUP	5	25	ABLIM2_intron11	ABLIM2	ABLIM2_intron11	ABLIM2	.	FRA4A
4	68609981	68609982	4	68610001	68610002	DUP	5	20	GNRHR_intron2	.	GNRHR_intron2	.	.	.
4	77146749	77146750	4	77147058	77147059	DEL	5	309	FAM47E_intron3	.	FAM47E_intron3	.	.	.
4	79858845	79858846	4	79858825	79858826	DUP	5	20	PAQR3_intron1	.	PAQR3_intron1	.	.	.
4	144459865	144459866	4	144459938	144459939	DEL	5	73	SMARCA5_intron13	SMARCA5	SMARCA5_13	SMARCA5	SMARCA5_intron13- SMARCA5_13	.
4	144466001	144466002	4	144466625	144466626	DEL	5	624	SMARCA5_intron18	SMARCA5	SMARCA5_18	SMARCA5	SMARCA5_intron18- SMARCA5_18	.
4	144468056	144468057	4	144468534	144468535	DEL	5	478	SMARCA5_20	SMARCA5	SMARCA5_intron21	SMARCA5	SMARCA5_20- SMARCA5_intron21	.
4	150639707	150639708	4	150639885	150639886	DEL	5	178	RP11- 526A4.1_intron10	.	RP11- 526A4.1_intron10	.	.	.
4	170378280	170378281	4	170378366	170378367	DEL	5	86	NEK1_intron26	.	NEK1_intron26	.	.	.
5	21834222	21834223	5	21837527	21837528	DEL	5	3305	CDH12_intron14	CDH12	CDH12_intron14	CDH12	.	FRA5E
5	53366200	53366201	5	53366662	53366663	DUP	3	462	ARL15_intron6	.	ARL15_intron6	.	.	.
5	65111984	65111985	5	65316190	65316191	DUP	5	204206	NLN_intron15	NLN	ERBB2IP_intron9	ERBB2IP	NLN-ERBB2IP	.
Chrom 1	start1	end1	Chrom 2	start2	end2	svtype	Event Score	eventSize	gene1	cancerGene1	gene2	cancerGene2	directFusionCandidates	Fragile sites
5	68470236	68470237	5	68470708	68470709	DEL	5	472	CCNB1_intron6	CCNB1	CCNB1_6	CCNB1	CCNB1_intron6- CCNB1_6	.
5	96086180	96086181	5	96086200	96086201	DUP	5	20	CAST_intron33	.	CAST_intron33	.	.	FRA5D
5	138699739	138699740	5	138699818	138699819	DUP	3	79	PAIP2_intron4	.	PAIP2_intron4	.	.	.

5	141051009	141051010	5	141051029	141051030	DUP	5	20	ARAP3_intron12	ARAP3	ARAP3_intron12	ARAP3	.	
5	161020192	161020193	5	161020250	161020251	DUP	5	58	GABRA6_intron2	GABRA6	GABRA6_intron2	GABRA6	.	
5	175096921	175096922	5	175096941	175096942	DUP	5	20	HRH2_intron2	.	HRH2_intron2	.	.	
6	6157205	6157206	6	6160593	6160594	DEL	5	3388	F13A1_intron15	F13A1	F13A1_intron15	F13A1	.	FRA6B
6	42103048	42103049	6	42104632	42104633	DEL	5	1584	C6orf132_intron1	.	C6orf132_intron1	.	.	
6	69731019	69731020	6	69731040	69731041	DUP	5	21	BAI3_intron14	BAI3	BAI3_intron14	BAI3	.	
6	79767649	79767650	6	79767669	79767670	DEL	5	20	PHIP_intron6	PHIP	PHIP_intron6	PHIP	.	
6	109790036	109790037	6	109790094	109790095	DEL	5	58	ZBTB24_intron5	.	ZBTB24_intron5	.	.	
6	111213647	111213648	6	111213937	111213938	DEL	3	290	AMD1_intron8	.	AMD1_8	.	AMD1_intron8- AMD1_8	FRA6F
6	112086339	112086340	6	112086361	112086362	DUP	5	22	FYN_intron11	FYN	FYN_intron11	FYN	.	FRA6F
6	149907785	149907786	6	149907765	149907766	DUP	5	20	GINM1_intron9	.	GINM1_intron9	.	.	
6	162203926	162203927	6	162333168	162333169	DUP	5	129242	PARK2_intron7	.	PARK2_intron6	.	PARK2_intron7- PARK2_intron6	FRA6E
6	162492756	162492757	6	162492947	162492948	DEL	5	191	PARK2_intron4	.	PARK2_intron4	.	.	FRA6E
7	43478455	43478456	7	43478475	43478476	DUP	5	20	HECW1_14	HECW1	HECW1_14	HECW1	.	FRA7D
7	44366861	44366862	7	44366921	44366922	DEL	5	60	CAMK2B_intron1	CAMK2B	CAMK2B_intron1	CAMK2B	.	FRA7D
7	103516272	103516273	7	103516299	103516300	DEL	5	27	RELN_intron2	RELN	RELN_intron2	RELN	.	FRA7F
7	154601421	154601422	7	154601831	154601832	DEL	5	410	DPP6_intron21	DPP6	DPP6_intron21	DPP6	.	
8	6599777	6599778	8	6599797	6599798	DUP	5	20	AGPAT5_intron8	.	AGPAT5_intron8	.	.	
8	56797793	56797794	8	56797813	56797814	DUP	5	20	LYN_intron2	LYN	LYN_intron2	LYN	.	
8	100455975	100455976	8	100461665	100461666	DEL	5	5690	VPS13B_intron29	.	VPS13B_intron29	.	.	
8	116439758	116439759	7	506861	506862	TRA		NA	TRPS1_intron5	TRPS1	.	.		
9	93374497	93374498	9	93374530	93374531	DEL	5	33	DIRAS2_2	.	DIRAS2_2	.	.	
10	1140984	1140985	10	1140959	1140960	DUP	5	25	WDR37_intron12	.	WDR37_intron12	.	.	
10	44360255	44360256	10	44455497	44455498	DEL	5	95242	LINC00840_intron3	.	.	.	LINC00840-(TRUNC)	FRA10G

Chrom 1	start1	end1	Chrom 2	start2	end2	svtype	Event Score	eventSize	gene1	cancerGene1	gene2	cancerGene2	directFusionCandidates	Fragile sites
10	62684313	62684314	10	62684333	62684334	DUP	5	20	RHOBTB1_intron4	.	RHOBTB1_intron4	.	.	FRA10C
10	75548916	75548917	7	100642024	100642025	TRA	3	NA	ZSWIM8_3	.	MUC12_5	MUC12	ZSWIM8-MUC12	FRA10G
10	83693509	83693510	10	83697736	83697737	DEL	5	4227	NRG3_intron4	NRG3	NRG3_intron4	NRG3	.	
10	95089112	95089113	10	95090994	95090995	DEL	5	1882	MYOF_intron48	.	MYOF_intron47	.	MYOF_intron48- MYOF_intron47	
11	1886893	1886894	11	1886766	1886767	DEL	3	127	LSP1_intron5	.	LSP1_intron5	.	.	
11	6789296	6789297	11	6806935	6806936	INV	2	17639	OR2AG2_1	.	OR2AG1_1	.	OR2AG2-OR2AG1	
11	17162508	17162509	11	17163785	17163786	DEL	5	1277	PIK3C2A_intron11	PIK3C2A	PIK3C2A_intron10	PIK3C2A	PIK3C2A_intron11- PIK3C2A_intron10	FRA11C
11	28983561	28983562	11	28983604	28983605	DUP	5	43	RP11- 115J23.1_intron4	.	RP11- 115J23.1_intron4	.	.	
11	49609140	49609141	11	88769938	88769939	INV	2	39160798	.	.	GRM5_intron3	.	(TRUNC)-GRM5	
11	107300538	107300539	11	107300516	107300517	DUP	5	22	CWF19L2_intron7	.	CWF19L2_intron7	.	.	
11	133242546	133242547	11	133245297	133245298	DEL	5	2751	OPCML-IT1_intron0	OPCML	OPCML-IT1_intron0	OPCML	.	
12	11836662	11836663	12	11836708	11836709	DUP	5	46	ETV6_intron2	ETV6	ETV6_intron2	ETV6	.	
12	48330567	48330568	12	48330587	48330588	DUP	5	20	VDR_intron1	VDR	VDR_intron1	VDR	.	
12	70657435	70657436	12	70663571	70663572	DEL	5	6136	CNOT2_intron3	.	CNOT2_intron3	.	.	
12	98540255	98540256	12	98540234	98540235	DUP	5	21	RP11- 690J15.1_intron2	.	RP11- 690J15.1_intron2	.	.	
12	120932416	120932417	12	120932396	120932397	DUP	5	20	DYNLL1_intron5	.	DYNLL1_intron5	.	.	
12	121768476	121768477	12	121769149	121769150	DEL	5	673	ANAPC5_8	ANAPC5	ANAPC5_8	ANAPC5	.	
12	123754022	123754023	12	123754049	123754050	DUP	5	27	CDK2AP1_intron3	.	CDK2AP1_intron3	.	.	
14	72794968	72794969	14	72794946	72794947	DUP	5	22	RGS6_intron4	.	RGS6_intron4	.	.	

14	85198206	85198207	14	106500730	106500731	DEL	5	21302524	.	.	IGH	IGH	(TRUNC)-IGH	
14	89076092	89076093	14	89075709	89075710	DEL	3	383	ZC3H14_21	.	ZC3H14_21	.	.	
15	50635415	50635416	15	50635435	50635436	DUP	5	20	GABPB1_intron2	.	GABPB1_intron2	.	.	
15	77034164	77034165	15	77034328	77034329	DUP	5	164	SCAPER_intron22	.	SCAPER_intron22	.	.	
16	7229859	7229860	16	7251557	7251558	DEL	5	21698	RBFOX1_intron10	.	RBFOX1_intron10	.	.	
16	7251848	7251849	16	7229582	7229583	DUP	2	22266	RBFOX1_intron10	.	RBFOX1_intron10	.	.	
Chrom			Chrom				Event							Fragile
1	start1	end1	2	start2	end2	svtype	Score	eventSize	gene1	cancerGene1	gene2	cancerGene2	directFusionCandidates	sites
16	63482243	63482244	16	63482318	63482319	DEL	5	75	RP11-368L12.1_intron3	.	RP11-368L12.1_intron3	.	.	
16	66371496	66371497	1	20037267	20037268	TRA	3	NA	.	.	TMCO4_intron16	.	(TRUNC)-TMCO4	
16	78333837	78333838	16	78338614	78338615	DEL	5	4777	WWOX_intron18	WWOX	WWOX_intron18	WWOX	.	FRA16D
16	89373729	89373730	16	89373708	89373709	DUP	5	21	ANKRD11_intron11	.	ANKRD11_intron11	.	.	
17	20741244	20741245	17	22041117	22041118	DEL	2	1299873	CCDC144NL_intron6	.	.	.	CCDC144NL-(TRUNC)	
17	31839731	31839732	17	31839752	31839753	DUP	5	21	ASIC2_intron2	.	ASIC2_intron2	.	.	
17	35636710	35636711	17	35636730	35636731	DUP	5	20	ACACA_intron17	ACACA	ACACA_intron17	ACACA	.	
17	38562747	38562748	17	38562830	38562831	DEL	5	83	TOP2A_intron16	TOP2A	TOP2A_intron16	TOP2A	.	
18	20458898	20458899	18	20458873	20458874	DUP	5	25	RBBP8_intron2	RBBP8	RBBP8_intron2	RBBP8	.	
18	30935269	30935270	18	30935289	30935290	DUP	5	20	CCDC178_intron10	CCDC178	CCDC178_intron10	CCDC178	.	FRA18A
19	4710107	4710108	19	4710084	4710085	DUP	5	23	DPP9_intron10	.	DPP9_intron10	.	.	
19	5695157	5695158	19	5695180	5695181	DUP	5	23	LONP1_intron15	.	LONP1_intron15	.	.	
19	11665070	11665071	19	11664859	11664860	DEL	3	211	ELOF1_6	.	ELOF1_7	.	ELOF1_6-ELOF1_7	
19	42424084	42424085	19	42424258	42424259	DEL	5	174	ARHGEF1_intron31	ARHGEF1	ARHGEF1_intron31	ARHGEF1	.	FRA19A
20	15336088	15336089	20	15336117	15336118	DEL	5	29	MACROD2_intron16	.	MACROD2_intron16	.	.	FRA20B
20	17208410	17208411	20	17208334	17208335	DEL	3	76	PCSK2_intron3	.	PCSK2_intron3	.	.	
20	40906734	40906735	20	40906753	40906754	DEL	5	19	PTPRT_intron14	PTPRT	PTPRT_intron14	PTPRT	.	

21	22903293	22903294	21	22903312	22903313	DUP	5	19	NCAM2_intron23	NCAM2	NCAM2_intron23	NCAM2	.	
21	30787123	30787124	21	30787143	30787144	DUP	5	20	BACH1_intron15	BACH1	BACH1_intron15	BACH1	.	
22	24236763	24236764	22	24236955	24236956	DEL	5	192	MIF_1,AP000350.4_3	.	AP000350.4_3,MIF_2	.	MIF_1-MIF_2	
X	30851678	30851679	X	30852573	30852574	DEL	5	895	TAB3_intron11	TAB3	TAB3_intron10	TAB3	TAB3_intron11- TAB3_intron10	FRA XM
X	69066490	69066491	X	69066516	69066517	DUP	5	26	EDA_intron10	.	EDA_intron10	.	.	
X	107539642	107539643	X	107539662	107539663	DUP	5	20	COL4A6_intron4	COL4A6	COL4A6_intron4	COL4A6	.	
X	123715318	123715319	X	123715340	123715341	DUP	5	22	TENM1_intron11	.	TENM1_intron11	.	.	
X	151420235	151420236	X	151420257	151420258	DUP	5	22	GABRA3_intron6	.	GABRA3_intron6	.	.	
Y	16945610	16945611	Y	16945633	16945634	DUP	5	23	NLGN4Y_intron12	.	NLGN4Y_intron12	.	.	

Chrom: chromosome, **svtype:** structural variation type, **DUP:** duplication, **DEL:** deletion, **INV:** inversion, **TRA:** translocation.

