

Patient Number	Toxicity Score	D90 prostate	V100 prostate	VR100 rectum	gammaH2AX sum of ranks for monocytes & lymphocytes (Olive et al.)	ATM chr11:107598768-107745035 Total number of variants (coding)	107599043
1	1	165	96.8	0.00	39	26 (1)	G>GA
2	0	176	97.0	0.17	49	26 (1)	G>GA
3	0	165	95.8	0.79	9	26 (1)	G>GA
4	6	128	86.9	0.23	9	26 (1)	G>GA
5	0	166	94.4	0.00	11	28 (2)	G>A
6	3	172	96.6	0.33	25	30 (2)	G>A
7	7	176	96.9	0.17	48	25 (1)	G>A
8	5	182	97.9	0.03	11	18 (1)	G>GA
9	9	113	78.3	0.03	58	24 (2)	G>GA
10	7	152	93.0	0.98	6	5 (1)	reference
11	4	141	89.0	0.81	57	23 (2)	G>GA
12	0	151	93.2	0.84	26	24 (1)	G>A
13	0	130	84.1	0.01	65	27 (1)	no_data
14	0	143	89.8	0.46	35	26 (1)	no_data
15	0	146	91.3	0.16	27	21 (1)	no_data
16	0	146	90.6	0.94	44	17 (1)	no_data
17	4	130	84.4	1.48	61	26 (2)	G>A
18	3	146	90.9	0.05	11	9 (1)	reference
19	7	183	97.9	0.89	14	18 (1)	no_data
20	0	183	99.0	0.26	61	21 (1)	no_data
21	4	148	91.4	0.81	50	22 (1)	G>A
22	0	151	93.2	0.34	60	27 (1)	G>A
23	10	136	88.2	0.07	49	30 (2)	G>A
24	1	131	85.7	0.00	61	23 (1)	G>A
25	0	155	93.5	0.20	22	26 (2)	G>GA
26	5	170	97.9	0.26	65	24 (1)	G>A
27	0	142	89.0	0.00	29	23 (1)	G>A
28	0	166	96.0	1.20	69	28 (2)	G>A
29	0	154	93.1	1.54	63	4 (1)	reference
30	10	167	97.0	0.10		29 (1)	G>A
31	1	128	85.2	1.46	38	24 (1)	G>GA
32	4	164	95.4	0.90	51	28 (1)	G>GA
33	0	157	93.7	1.50	69	26 (1)	G>GA
34	13	136	87.6	3.80	74	5 (2)	reference
35	4	160	95.2	3.20	61	24 (1)	G>GA

36	11	150	92.5	1.20
37	5	148	91.7	0.06
38	4	142	88.5	0.35
39	0	154	96.1	0.20
43	3	147	91.0	0.31
44	0	152	92.3	0.70

43
47
40
26
18
39

23 (1)	G>GA
23 (1)	G>A
6 (2)	reference
5 (3)	reference
26 (1)	G>GA
29 (3)	G>A
ENSG00000149311, ENST00000278616 5'-4519	

107603527-107603528	107603670-107603671	107603786	107611536	107619716	107626842	107629509	107629532-107629535
no_data	het_delAA	reference	reference	reference	reference	no_data	no_data
reference	reference	reference	reference	reference	reference	no_data	no_data
no_data	het_delAA	reference	reference	A>AG	reference	no_data	no_data
no_data	het_delAA	reference	reference	reference	reference	no_data	no_data
no_data	het_delAA	reference	no_data	reference	reference	G>A	no_data
no_data	het_delAA	reference	reference	reference	reference	G>A	no_data
het_insT	het_delAA	reference	reference	A>AG	reference	no_data	no_data
no_data	het_delAA	reference	reference	reference	reference	no_data	no_data
no_data	het_delAA	reference	reference	A>AG	reference	G>GA	no_data
reference	reference	reference	reference	reference	reference	reference	reference
no_data	het_delAA	reference	reference	reference	reference	G>GA	no_data
no_data	delAA	reference	reference	reference	reference	G>A	no_data
no_data	het_delAA	reference	reference	reference	reference	G>GA	no_data
no_data	delAA	reference	reference	reference	reference	G>A	het_delTATT
no_data	het_delAA	reference	reference	A>AG	reference	no_data	no_data
no_data	no_data	reference	reference	reference	reference	no_data	no_data
no_data	delAA	reference	reference	A>AG	reference	G>GA	no_data
reference	reference	reference	reference	reference	reference	reference	reference
no_data	het_delAA	reference	reference	reference	reference	no_data	no_data
het_insT	het_delAA	reference	reference	reference	reference	no_data	no_data
no_data	het_delAA	reference	reference	A>AG	reference	G>A	no_data
no_data	delAA	reference	A>AG	reference	reference	G>A	no_data
no_data	het_delAA	reference	A>AG	reference	reference	G>A	no_data
no_data	delAA	reference	reference	A>AG	reference	G>A	no_data
reference	reference	reference	reference	reference	reference	G>GA	no_data
no_data	delAA	reference	reference	A>AG	reference	G>A	no_data
no_data	delAA	reference	reference	reference	reference	G>A	no_data
no_data	no_data	reference	reference	A>AG	reference	G>A	no_data
reference	reference	reference	reference	reference	reference	reference	reference
no_data	delAA	reference	A>AG	reference	reference	G>A	no_data
no_data	het_delAA	reference	reference	reference	reference	no_data	no_data
no_data	het_delAA	reference	reference	A>AG	reference	no_data	no_data
no_data	het_delAA	reference	reference	reference	reference	no_data	no_data
reference	reference	reference	reference	reference	reference	no_data	no_data
no_data	no_data	reference	reference	reference	reference	G>GA	no_data

no_data	het_delAA	reference	reference	A>AG	reference	G>GA	no_data
no_data	delAA	reference	no_data	reference	reference	G>A	no_data
reference	reference	reference	reference	reference	A>AC_p.L480LF	reference	reference
reference	reference	C>CG_p.S49SC	no_data	no_data	reference	reference	reference
no_data	het_delAA	reference	reference	A>AG	reference	G>GA	no_data
no_data	delAA	reference	reference	reference	reference	G>A	no_data
5'-35	IVS2+36	146	IVS4-71	IVS5-174	1440	IVS12-242	IVS12-219

107629696	107629971	107632498	107633583	107634867	107642985	107648666	107655418	107655419	107655577-107655579
no_data	reference	T>C	reference	A>AG	T>TA	reference	reference	reference	reference
no_data	reference	T>C	reference	A>AG	T>TA	reference	het_delT	het_delT	no_data
no_data	reference	T>C	reference	A>AG	T>TA	reference	reference	reference	reference
no_data	reference	T>C	reference	A>AG	T>TA	reference	reference	reference	reference
no_data	reference	no_data	reference	A>AG	T>A	reference	het_delT	no_data	no_data
no_data	reference	no_data	reference	A>G	T>TA	reference	het_delT	het_delT	no_data
no_data	reference	no_data	reference	A>AG	T>TA	reference	no_data	no_data	no_data
no_data	reference	no_data	reference	A>AG	no_data	reference	reference	reference	reference
no_data	reference	no_data	reference	A>AG	no_data	C>CG_p.P1054PR	reference	reference	reference
reference	reference	no_data	no_data	reference	no_data	reference	no_data	no_data	no_data
no_data	reference	no_data	reference	A>AG	no_data	reference	reference	reference	reference
T>TG	reference	no_data	reference	A>G	T>A	reference	reference	reference	reference
no_data	reference	no_data	reference	A>AG	T>TA	reference	reference	reference	reference
no_data	reference	T>C	reference	A>G	T>A	reference	no_data	no_data	het_delCAT
no_data	reference	no_data	reference	A>AG	T>TA	reference	no_data	no_data	no_data
no_data	reference	no_data	reference	A>AG	no_data	reference	no_data	no_data	no_data
no_data	reference	T>C	reference	A>AG	T>TA	C>CG_p.P1054PR	reference	reference	reference
reference	reference	no_data	reference	reference	reference	reference	reference	reference	reference
no_data	reference	no_data	reference	A>AG	no_data	reference	reference	reference	reference
no_data	no_data	no_data	reference	A>AG	no_data	reference	reference	reference	reference
no_data	reference	no_data	reference	A>G	T>TA	reference	het_delT	het_delT	no_data
T>TG	no_data	no_data	reference	A>G	T>A	reference	reference	reference	reference
no_data	reference	no_data	reference	A>G	T>A	reference	het_delT	het_delT	no_data
no_data	reference	no_data	reference	A>G	T>A	reference	reference	reference	reference
no_data	reference	no_data	reference	A>AG	T>TA	reference	het_delT	het_delT	no_data
no_data	reference	no_data	reference	A>G	T>A	reference	reference	reference	reference
no_data	reference	no_data	reference	A>G	T>A	reference	reference	reference	reference
no_data	reference	no_data	reference	A>G	T>A	reference	reference	reference	reference
no_data	reference	T>C	reference	A>G	T>A	reference	het_delT	het_delT	no_data
reference	reference	T>C	reference	reference	reference	reference	reference	reference	reference
T>TG	reference	T>C	reference	A>G	T>A	reference	reference	reference	reference
no_data	reference	T>C	reference	A>AG	T>TA	reference	reference	reference	reference
no_data	reference	T>C	reference	A>AG	T>TA	reference	reference	reference	reference
no_data	reference	T>C	reference	A>AG	T>TA	reference	reference	reference	reference
no_data	reference	T>C	reference	reference	reference	reference	reference	reference	reference
no_data	reference	T>C	reference	A>AG	T>TA	reference	reference	reference	reference

no_data	reference	no_data	reference	A>AG	reference	reference	reference	reference	reference
no_data	reference	no_data	reference	no_data	T>TA	reference	no_data	no_data	no_data
reference	reference	no_data	reference	reference	no_data	reference	reference	reference	reference
reference	reference	no_data	reference	reference	no_data	reference	no_data	no_data	no_data
no_data	reference	T>C	reference	A>AG	T>TA	reference	reference	reference	reference
T>TG	T>TC_p.S707SP	T>C	A>AG	A>G	T>A	reference	reference	reference	reference
IVS12-55	2119	IVS14+220	IVS15+39	IVS15-56	IVS16-123	3161	IVS22-10	IVS22-9	IVS23+31

107656913-107656914	107656916-107656918	107656919-107656920	107658490	107660115	107663344	107664566	107666033
no_data	no_data	het_insA	reference	no_data	T>TC	G>GA	reference
no_data	no_data	het_insA	reference	reference	T>TC	G>GA	reference
no_data	no_data	het_insA	reference	reference	T>TC	G>GA	reference
no_data	no_data	het_insA	reference	reference	T>TC	G>GA	reference
no_data	no_data	no_data	reference	A>AC	T>C	G>A	reference
no_data	no_data	het_insA	reference	A>AC	T>C	G>A	reference
no_data	no_data	het_insA	reference	reference	T>TC	G>GA	reference
no_data	het_insAAA	het_insA	reference	reference	no_data	G>GA	reference
no_data	no_data	no_data	reference	reference	T>TC	G>GA	reference
no_data	no_data	no_data	reference	reference	reference	reference	reference
reference	reference	reference	reference	reference	T>TC	G>GA	reference
no_data	no_data	no_data	reference	reference	T>C	G>A	reference
no_data	no_data	het_insA	reference	A>AC	T>TC	G>GA	reference
no_data	no_data	no_data	reference	reference	T>C	G>A	reference
no_data	no_data	het_insA	reference	reference	T>TC	G>GA	reference
no_data	no_data	het_insA	reference	no_data	no_data	G>GA	reference
reference	reference	reference	reference	reference	T>C	G>A	reference
no_data	no_data	no_data	reference	reference	T>TC	reference	reference
no_data	no_data	het_insA	reference	reference	T>TC	G>GA	reference
reference	reference	reference	reference	A>AC	T>TC	G>GA	reference
no_data	no_data	no_data	reference	reference	T>C	G>A	reference
no_data	no_data	no_data	reference	reference	T>C	G>A	reference
no_data	no_data	no_data	reference	A>AC	T>C	G>A	reference
no_data	no_data	no_data	reference	reference	T>C	G>A	reference
no_data	no_data	no_data	reference	reference	T>TC	G>GA	reference
no_data	no_data	no_data	reference	reference	T>C	G>A	reference
no_data	no_data	no_data	reference	reference	T>C	G>A	reference
no_data	no_data	no_data	reference	A>AC	T>C	G>A	reference
no_data	no_data	no_data	reference	reference	reference	reference	reference
no_data	no_data	no_data	reference	reference	T>C	G>A	reference
no_data	no_data	no_data	reference	no_data	T>TC	G>GA	reference
het_insA	no_data	no_data	reference	reference	T>TC	G>GA	reference
no_data	no_data	het_insA	reference	reference	T>TC	G>GA	C>CT
reference	reference	reference	reference	reference	reference	reference	reference
no_data	no_data	no_data	reference	A>AC	T>TC	G>GA	reference

reference	reference	reference	reference	reference	T>TC	G>GA	reference
no_data	no_data	no_data	reference	reference	T>C	G>A	reference
no_data	no_data	no_data	reference	reference	no_data	reference	reference
reference	reference	reference	reference	reference	reference	reference	reference
reference	reference	reference	reference	reference	T>TC	G>GA	reference
no_data	no_data	no_data	A>AC	reference	T>C	G>A	reference
IVS23-19	IVS23-16	IVS23-13	IVS24-157	IVS25-49	IVS26-193	IVS27-348	IVS29+294

107668697	107668940	107668943	107669347	107675481	107680597	107680672	107680673	107688139
no_data	no_data	A>AG	reference	G>GA	no_data	no_data	no_data	no_data
no_data	no_data	A>AG	reference	G>GA	no_data	no_data	no_data	no_data
no_data	no_data	A>AG	reference	G>GA	reference	reference	reference	no_data
no_data	no_data	A>AG	reference	G>GA	reference	reference	reference	no_data
no_data	no_data	A>G	reference	G>A	no_data	G>GA_p.D1853DN	no_data	no_data
no_data	no_data	A>G	reference	G>GA	no_data	G>GA_p.D1853DN	no_data	no_data
no_data	no_data	A>AG	reference	G>GA	reference	reference	reference	no_data
no_data	no_data	A>AG	reference	G>GA	no_data	no_data	no_data	no_data
no_data	no_data	A>AG	reference	G>GA	reference	reference	reference	no_data
reference	reference	reference	reference	reference	no_data	no_data	no_data	no_data
no_data	no_data	A>AG	T>TC_p.V1570VA	G>GA	reference	reference	reference	no_data
no_data	no_data	A>G	reference	G>A	reference	reference	reference	no_data
no_data	no_data	A>AG	reference	G>GA	no_data	no_data	no_data	no_data
no_data	no_data	A>G	reference	G>A	no_data	no_data	no_data	no_data
no_data	no_data	A>AG	reference	G>GA	reference	reference	reference	no_data
no_data	no_data	A>AG	reference	G>GA	reference	reference	reference	no_data
no_data	no_data	A>G	reference	G>A	reference	reference	reference	no_data
reference	reference	reference	reference	G>GA	reference	reference	reference	no_data
no_data	no_data	no_data	reference	G>GA	no_data	no_data	no_data	no_data
no_data	no_data	A>AG	no_data	reference	no_data	no_data	no_data	no_data
no_data	no_data	A>G	reference	G>A	no_data	no_data	no_data	no_data
no_data	no_data	A>G	reference	G>A	no_data	no_data	no_data	T>TA
no_data	no_data	A>G	reference	G>A	no_data	G>GA_p.D1853DN	no_data	no_data
no_data	no_data	A>G	reference	G>A	reference	reference	reference	no_data
no_data	no_data	A>AG	reference	G>GA	no_data	G>GA_p.D1853DN	no_data	no_data
no_data	no_data	A>G	reference	G>A	reference	reference	reference	no_data
no_data	no_data	A>G	reference	G>A	reference	reference	reference	no_data
no_data	no_data	A>G	reference	G>A	reference	reference	reference	no_data
no_data	no_data	A>G	reference	G>A	no_data	G>GA_p.D1853DN	no_data	no_data
reference	reference	reference	reference	reference	reference	reference	reference	no_data
no_data	A>G	A>G	reference	G>A	reference	reference	reference	no_data
no_data	no_data	A>AG	reference	G>GA	reference	reference	reference	no_data
no_data	no_data	A>AG	reference	G>GA	G>GC	no_data	no_data	no_data
no_data	no_data	A>AG	reference	G>GA	reference	reference	reference	no_data
C>CT_p.P1526PP	no_data	no_data	reference	reference	reference	reference	reference	no_data
no_data	no_data	no_data	reference	G>GA	reference	reference	reference	no_data

no_data	no_data	A>AG	reference	G>GA	no_data	no_data	no_data	no_data
no_data	no_data	A>G	reference	G>A	no_data	no_data	no_data	no_data
reference	reference	reference	reference	reference	no_data	no_data	no_data	no_data
C>CT_p.P1526PP	no_data	no_data	reference	reference	no_data	no_data	no_data	no_data
no_data	no_data	A>AG	reference	G>GA	reference	reference	reference	no_data
no_data	no_data	A>G	reference	G>A	no_data	no_data	A>AT_p.D1853DV	no_data
4578	IVS30+209	IVS30+212	4709	IVS33-170	IVS36-15	5557	5558	IVS39-209

[illegible]

A>G_p.N1983S	het_delCT	het_delCT	no_data	no_data	het_delATT	het_delATT
A>G_p.N1983S	no_data	delCT	no_data	no_data	delATT	delATT
A>G_p.N1983S	no_data	no_data	no_data	no_data	reference	reference
A>G_p.N1983S	no_data	no_data	no_data	no_data	reference	reference
A>G_p.N1983S	het_delCT	het_delCT	no_data	no_data	het_delATT	het_delATT
A>G_p.N1983S	no_data	delCT	no_data	no_data	no_data	delATT
5948	IVS40+188	IVS40+190	IVS40+193	IVS40+218	IVS46-72	IVS46-60

077003761	107705352	107705392	107707982	107708979	107710091	107710156	107710157	107723406	107729825	107729907	107730683
reference	T>TG	no_data	reference	G>A	C>CT	no_data	het_delT	T>TC	no_data	G>A	no_data
reference	T>TG	G>GA	reference	G>A	no_data	no_data	no_data	T>TC	no_data	G>A	no_data
reference	T>TG	no_data	reference	G>A	no_data	no_data	het_delT	T>TC	no_data	G>A	no_data
reference	T>TG	no_data	reference	no_data	C>CT	no_data	het_delT	T>TC	no_data	G>A	no_data
reference	T>G	G>GA	reference	G>A	C>CT	no_data	delT	T>C	no_data	G>A	no_data
reference	T>G	G>GA	reference	G>A	C>CT	delT	no_data	T>TC	no_data	G>A	no_data
reference	T>TG	no_data	reference	G>A	C>CT	no_data	delT	T>TC	no_data	G>A	no_data
reference	T>TG	no_data	reference	G>A	no_data	no_data	het_delT	T>TC	no_data	G>A	no_data
reference	T>TG	no_data	reference	G>A	no_data	no_data	delT	T>TC	no_data	G>A	no_data
reference	reference	reference	reference	no_data	reference	reference	reference	T>TC	no_data	G>A	no_data
reference	T>TG	no_data	reference	no_data	C>T	no_data	het_delT	T>TC	no_data	G>A	no_data
reference	T>G	no_data	reference	G>A	C>T	no_data	delT	T>C	no_data	G>A	no_data
reference	T>TG	no_data	reference	G>A	C>CT	no_data	het_delT	T>TC	no_data	G>A	no_data
reference	T>G	no_data	reference	G>A	C>T	no_data	delT	T>C	no_data	G>A	no_data
reference	T>TG	no_data	no_data	G>A	no_data	no_data	no_data	T>TC	no_data	G>A	no_data
reference	T>TG	no_data	reference	G>A	no_data	no_data	het_delT	T>TC	no_data	G>A	no_data
reference	T>G	no_data	reference	G>A	C>CT	no_data	delT	T>TC	no_data	G>A	no_data
reference	reference	reference	reference	G>A	reference	reference	reference	T>TC	no_data	G>A	no_data
reference	T>TG	no_data	reference	G>A	no_data	no_data	no_data	T>TC	no_data	G>A	no_data
reference	T>TG	no_data	reference	G>A	C>CT	no_data	het_delT	T>TC	no_data	G>A	no_data
reference	T>G	no_data	reference	G>A	no_data	no_data	delT	no_data	no_data	G>A	no_data
reference	T>G	no_data	reference	G>A	C>T	no_data	delT	T>C	A>AC	G>A	no_data
reference	T>G	G>GA	reference	G>A	C>CT	no_data	delT	T>C	A>AC	G>A	no_data
reference	T>G	no_data	reference	no_data	C>CT	no_data	delT	T>C	no_data	G>A	no_data
reference	T>TG	no_data	reference	G>A	no_data	no_data	het_delT	T>TC	no_data	G>A	no_data
reference	T>G	no_data	reference	G>A	C>CT	no_data	delT	T>C	no_data	G>A	no_data
reference	T>G	no_data	reference	G>A	C>T	no_data	delT	T>C	no_data	G>A	no_data
reference	T>G	G>GA	reference	G>A	no_data	no_data	delT	T>C	no_data	G>A	no_data
reference	reference	reference	reference	G>A	reference	reference	reference	reference	no_data	G>A	reference
reference	T>G	no_data	reference	G>A	C>T	no_data	delT	T>C	A>AC	G>A	no_data
reference	T>TG	no_data	reference	G>A	no_data	no_data	no_data	T>TC	no_data	G>A	no_data
reference	T>TG	no_data	G>GT	G>A	no_data	no_data	het_delT	T>TC	no_data	G>A	no_data
reference	T>TG	no_data	reference	G>A	no_data	het_delT	no_data	T>TC	no_data	G>A	no_data
reference	reference	reference	reference	G>A	reference	reference	reference	reference	no_data	G>A	no_data
reference	T>TG	no_data	reference	G>A	C>CT	no_data	het_delT	T>TC	no_data	G>A	no_data

reference	T>TG	no_data	reference	G>A	no_data	no_data	het_delT	no_data	no_data	G>A	no_data
no_data	T>G	no_data	reference	G>A	C>T	no_data	delT	no_data	no_data	G>A	G>GA
G>GT	reference	reference	reference	no_data	reference	reference	reference	reference	no_data	G>A	reference
reference	reference	reference	reference	G>A	reference	reference	reference	reference	no_data	G>A	reference
reference	T>TG	no_data	reference	G>A	no_data	no_data	het_delT	T>TC	no_data	G>A	no_data
reference	T>G	no_data	reference	G>A	C>T	no_data	delT	no_data	no_data	G>A	no_data
IVS48+65	IVS49+176	IVS49+216	IVS52+7	IVS53+141	IVS54+185	IVS54+250	IVS54+251	IVS59+103	IVS60+7	IVS60+89	IVS60-65

BRCA1 chr17:38448839-38531993

107730693	107730871	107741993	107741996	107743049	107743125	107744838	Total number of variants (coding)	38449934	38450800
C>CT	A>AG	G>GT	no_data	C>CT	no_data	G>GT	31 (1)	G>A	C>A
C>CT	A>AG	G>GT	no_data	C>CT	no_data	G>GT	3 (0)	reference	reference
C>CT	A>AG	G>GT	no_data	C>CT	no_data	G>GT	0 (0)	reference	reference
C>CT	A>AG	G>GT	T>TC	C>CT	no_data	G>GT	2 (0)	reference	reference
C>T	A>G	G>T	no_data	C>T	no_data	G>T	23 (1)	G>A	C>CA
C>T	A>G	G>GT	no_data	C>CT	no_data	G>T	27 (1)	reference	C>CA
C>CT	A>AG	no_data	no_data	C>CT	no_data	G>GT	2 (0)	reference	reference
C>CT	A>AG	no_data	no_data	reference	reference	G>GT	31 (1)	G>A	C>A
C>CT	A>AG	G>GT	no_data	C>CT	no_data	G>GT	18 (1)	no_data	C>CA
no_data	A>AG	no_data	no_data	reference	reference	reference	0 (0)	no_data	reference
C>CT	A>AG	no_data	no_data	C>CT	no_data	G>GT	0 (0)	reference	reference
C>T	A>G	G>T	no_data	C>T	no_data	G>T	6 (0)	reference	reference
C>CT	A>AG	G>GT	no_data	C>CT	C>CT	G>GT	0 (0)	no_data	reference
C>CT	A>AG	G>T	T>TC	C>T	no_data	G>T	0 (0)	no_data	reference
C>CT	A>AG	G>GT	no_data	no_data	no_data	G>GT	19 (1)	no_data	C>CA
no_data	no_data	G>GT	T>TC	no_data	no_data	G>GT	1 (0)	no_data	reference
C>T	A>G	no_data	no_data	C>T	no_data	G>T	29 (1)	G>GA	C>CA
C>CT	A>AG	reference	reference	reference	reference	reference	29 (1)	G>GA	C>CA
C>CT	A>AG	no_data	no_data	C>CT	no_data	no_data	32 (1)	G>GA	C>CA
C>CT	A>AG	no_data	no_data	C>CT	no_data	no_data	0 (0)	no_data	reference
no_data	no_data	G>GT	no_data	C>CT	no_data	G>GT	21 (1)	no_data	C>A
C>T	A>G	G>T	no_data	C>T	no_data	G>T	22 (1)	no_data	C>A
C>T	A>G	G>T	no_data	C>T	no_data	G>T	0 (0)	reference	reference
C>T	A>G	G>T	no_data	C>T	no_data	G>T	1 (0)	no_data	reference
C>CT	A>AG	G>GT	no_data	C>CT	no_data	G>GT	11 (0)	no_data	C>CA
C>T	A>G	G>T	no_data	C>T	no_data	G>T	4 (0)	no_data	reference
C>T	A>G	G>T	no_data	C>T	no_data	G>T	29 (1)	G>GA	C>CA
C>T	A>G	G>T	no_data	C>T	no_data	G>T	3 (0)	reference	reference
reference	reference	reference	reference	reference	reference	reference	28 (1)	G>GA	C>CA
C>T	A>G	G>T	T>TC	C>T	no_data	G>T	18 (1)	G>GA	no_data
C>CT	A>AG	G>GT	T>TC	C>CT	no_data	G>GT	18 (1)	no_data	C>A
C>CT	A>AG	G>GT	no_data	C>CT	no_data	G>GT	1 (0)	reference	reference
C>CT	A>AG	G>GT	no_data	C>CT	no_data	G>GT	25 (1)	no_data	C>CA
no_data	no_data	reference	reference	reference	reference	reference	0 (0)	reference	reference
C>CT	A>AG	G>GT	no_data	C>CT	no_data	G>GT	0 (0)	reference	reference

C>CT	A>AG	G>GT	no_data	C>CT	no_data	G>GT	20 (1)	no_data	C>CA
C>T	A>G	no_data	no_data	C>T	no_data	G>T	0 (0)	no_data	reference
reference	reference	G>GT	no_data	reference	reference	reference	28 (1)	G>GA	C>CA
reference	reference	no_data	no_data	reference	reference	reference	0 (0)	reference	reference
C>CT	A>AG	G>GT	no_data	C>CT	no_data	G>GT	30 (1)	G>GA	C>CA
C>T	A>G	G>T	T>TC	C>T	no_data	G>T	28 (1)	G>GA	C>CA
IVS60-55	IVS61+59	3'+548	3'+551	3'+1604	3'+1680	3'+3393			

[illegible]

T>TC	no_data	no_data	no_data	no_data	no_data	no_data	no_data	C>CT	T>TC	no_data	no_data	T>TC
reference	no_data	no_data	no_data	no_data	no_data	reference	reference	reference	reference	reference	reference	reference
T>TC	reference	C>CT	no_data	G>GT	no_data	G>GT	no_data	C>CT	T>TC	no_data	no_data	T>TC
reference	reference	reference	reference	reference	reference	reference	reference	reference	reference	reference	reference	reference
T>TC	T>TC	C>CT	no_data	no_data	T>TC	reference	reference	reference	T>TC	no_data	A>AG	T>TC
T>TC	reference	C>CT	no_data	G>GT	no_data	G>GT	no_data	C>CT	T>TC	no_data	no_data	T>TC

[illegible]

G>GC	A>AT	het_delGTTGG	C>CT	A>AG	no_data	T>TG	T>TC	no_data	T>TC	no_data	no_data
reference	reference	reference	reference	reference	reference	reference	reference	reference	reference	no_data	no_data
G>GC	A>AT	no_data	C>CT	A>AG	no_data	T>TG	T>TC	no_data	T>TC	G>GA	no_data
reference	reference	reference	reference	reference	reference	reference	reference	reference	reference	reference	reference
G>GC	A>AT	no_data	no_data	A>AG	G>GT	T>TG	T>TC	no_data	T>TC	G>GA	no_data
G>GC	A>AT	het_delGTTGG	no_data	A>AG	no_data	T>TG	T>TC	no_data	T>TC	G>GA	no_data

[illegible]

A>AG_p.M299MV	G>GA	no_data	reference	reference	no_data	no_data	het_insCCT		no_data	reference
reference	reference	reference	no_data	no_data	no_data	reference	reference		reference	reference
A>AG_p.M299MV	G>GA	no_data	reference	reference	reference	no_data	het_insCCT		no_data	no_data
reference	reference	reference	reference	reference	reference	reference	reference		reference	reference
A>AG_p.M299MV	G>GA	C>CT	reference	reference	reference	C>CT	het_insCCT		no_data	no_data
A>AG_p.M299MV	G>GA	no_data	reference	reference	reference	no_data	het_insCCT		no_data	no_data

38501690	38502890	38502895	38502896	38505172	38505457	38510660	38529773	38529874	38530713	Total number of variants (coding)
C>T	delA	no_data	delA	T>A	no_data	T>C	A>G	T>C	G>C	13 (3)
no_data	reference	reference	reference	no_data	G>A	reference	reference	reference	reference	14 (4)
reference	reference	reference	reference	reference	reference	reference	reference	reference	reference	14 (4)
reference	reference	reference	reference	no_data	G>A	reference	reference	reference	reference	14 (3)
C>CT	het_delA	no_data	no_data	no_data	no_data	T>TC	no_data	no_data	G>GC	2 (0)
C>CT	het_delA	no_data	het_delA	T>TA	no_data	T>TC	no_data	no_data	G>GC	7 (2)
reference	reference	reference	reference	no_data	G>GA	reference	reference	reference	reference	11 (1)
C>T	delA	no_data	no_data	T>A	no_data	T>C	A>G	T>C	G>C	11 (1)
no_data	no_data	no_data	no_data	no_data	no_data	no_data	A>AG	T>TC	G>GC	14 (4)
no_data	reference	reference	reference	no_data	no_data	reference	reference	reference	reference	15 (4)
no_data	reference	reference	reference	no_data	no_data	reference	reference	reference	reference	18 (4)
no_data	reference	reference	reference	no_data	no_data	T>TC	reference	reference	G>GC	14 (2)
no_data	reference	reference	reference	no_data	no_data	no_data	reference	reference	reference	12 (2)
no_data	reference	reference	reference	no_data	no_data	reference	reference	reference	reference	7 (0)
no_data	no_data	no_data	no_data	no_data	no_data	T>TC	A>AG	T>TC	G>GC	11 (2)
reference	reference	reference	reference	no_data	G>GA	reference	reference	reference	reference	15 (4)
C>CT	het_delA	het_delA	het_delA	T>TA	no_data	T>TC	A>AG	T>TC	G>GC	6 (2)
C>CT	het_delA	no_data	het_delA	T>TA	no_data	T>TC	A>AG	T>TC	G>GC	15 (3)
C>CT	het_delA	no_data	het_delA	T>TA	G>GA	T>TC	A>AG	T>TC	G>GC	5 (0)
no_data	reference	reference	reference	no_data	no_data	no_data	reference	reference	reference	15 (3)
no_data	no_data	no_data	delA	no_data	no_data	no_data	A>G	T>C	G>C	9 (1)
no_data	no_data	no_data	delA	no_data	no_data	T>C	A>G	T>C	G>C	10 (2)
reference	reference	reference	reference	reference	reference	reference	reference	reference	reference	1 (0)
reference	reference	reference	reference	no_data	G>GA	reference	reference	reference	reference	16 (4)
C>CT	no_data	no_data	no_data	no_data	no_data	no_data	no_data	no_data	G>GC	11 (1)
reference	reference	reference	reference	no_data	G>GA	reference	reference	reference	reference	14 (4)
C>CT	het_delA	no_data	het_delA	T>TA	G>GA	T>TC	A>AG	T>TC	G>GC	4 (0)
reference	reference	reference	reference	no_data	G>A	reference	reference	reference	reference	5 (0)
C>CT	het_delA	no_data	het_delA	T>TA	no_data	T>TC	A>AG	T>TC	G>GC	12 (2)
C>CT	no_data	no_data	no_data	no_data	no_data	no_data	A>AG	T>TC	G>GC	4 (0)
no_data	delA	no_data	no_data	no_data	no_data	T>C	no_data	no_data	G>C	14 (4)
reference	reference	reference	reference	no_data	no_data	reference	reference	reference	reference	11 (1)
C>CT	het_delA	het_delA	het_delA	no_data	no_data	T>TC	A>AG	T>TC	G>GC	10 (1)
reference	reference	reference	reference	no_data	no_data	no_data	reference	reference	reference	15 (4)
reference	reference	reference	reference	no_data	no_data	reference	reference	reference	reference	16 (4)

reference	no_data	no_data	no_data	no_data	no_data	T>TC	A>AG	T>TC	G>GC	1 (0)
reference	no_data	no_data	no_data	no_data	no_data	reference	reference	reference	reference	4 (0)
C>CT	het_delA	no_data	het_delA	T>TA	no_data	T>TC	A>AG	T>TC	G>GC	10 (1)
reference	reference	reference	reference	reference	reference	reference	reference	reference	reference	9 (1)
C>CT	het_delA	no_data	het_delA	T>TA	no_data	T>TC	A>AG	T>TC	G>GC	1 (0)
C>CT	het_delA	no_data	het_delA	T>TA	no_data	T>TC	A>AG	T>TC	G>GC	12 (2)

[illegible]

reference	reference	reference	reference	reference
no_data	no_data	no_data	no_data	no_data
reference	reference	reference	reference	reference
no_data	no_data	no_data	no_data	no_data
reference	reference	reference	reference	reference
reference	reference	reference	reference	reference

reference
no_data
reference
no_data
reference
reference

reference	reference
no_data	no_data
reference	reference
no_data	no_data
reference	reference
reference	reference

reference	reference
reference	reference
reference	reference
reference	reference
reference	reference

[illegible]

reference	reference	reference	reference	reference	reference	no_data	no_data	T>C	no_data	no_data	reference	reference
reference	reference	reference	reference	reference	C>CG	no_data	C>CT	T>C	G>GA	no_data	reference	reference
reference	reference	reference	reference	reference	C>CG	no_data	C>T	T>C	G>A	no_data	reference	reference
reference	reference	reference	reference	reference	C>G	no_data	C>T	T>C	G>A	no_data	reference	no_data
reference	reference	reference	reference	reference	reference	no_data	no_data	T>C	no_data	no_data	reference	no_data
reference	reference	reference	reference	reference	C>CG	no_data	C>CT	T>C	G>GA	no_data	reference	G>GT

[illegible]

reference	reference	reference	reference	reference	reference	reference	reference	reference	reference
reference	reference	reference	reference	reference	reference	reference	reference	reference	reference
no_data	no_data	reference	T>TA	no_data	A>AC_p.R156RR	A>AT	G>GA	no_data	reference
no_data	no_data	reference	T>TA	no_data	A>AC_p.R156RR	A>AT	G>GA	no_data	reference
reference	reference	reference	reference	reference	reference	reference	reference	reference	reference
no_data	no_data	G>GA_p.D312DN	T>TA	C>CT	A>AC_p.R156RR	A>AT	G>GA	no_data	reference

H2AFX chr11:118468793-118472386

50565020	50565097	50565782	50565828	Total number of variants (coding)	118469787	118470258	118470494	118470635	118471119
reference	reference	C>CG	no_data	1 (0)	G>A	reference	reference	reference	reference
reference	reference	C>CG	no_data	4 (0)	G>A	C>CT	C>CT	A>AT	reference
reference	reference	reference	reference	4 (0)	G>A	C>CT	C>CT	A>AT	reference
reference	reference	C>G	no_data	1 (0)	G>A	reference	reference	reference	reference
reference	reference	reference	reference	1 (0)	G>A	reference	no_data	no_data	reference
reference	reference	reference	reference	4 (1)	G>A	C>CT	C>CT	no_data	C>CT_p.L66LL
reference	reference	C>CG	no_data	3 (0)	G>A	C>CT	C>CT	no_data	reference
no_data	T>TC	C>CG	no_data	1 (0)	G>A	reference	reference	reference	reference
reference	reference	reference	reference	1 (0)	G>A	reference	reference	reference	reference
reference	reference	C>G	no_data	4 (0)	G>A	C>CT	C>CT	A>AT	reference
reference	reference	C>G	no_data	4 (0)	G>A	C>CT	C>CT	A>AT	reference
reference	reference	C>G	no_data	1 (0)	G>A	reference	reference	reference	reference
reference	reference	C>CG	no_data	2 (0)	no_data	no_data	C>CT	A>AT	reference
G>GA	no_data	reference	reference	1 (0)	G>A	no_data	reference	reference	reference
reference	reference	C>CG	no_data	4 (0)	G>A	C>CT	C>CT	A>AT	reference
reference	reference	C>G	no_data	1 (0)	G>A	reference	no_data	no_data	reference
reference	reference	reference	reference	4 (0)	G>A	C>T	C>CT	A>AT	reference
reference	reference	C>CG	no_data	1 (0)	G>A	reference	reference	reference	reference
no_data	no_data	C>CG	no_data	1 (0)	G>A	reference	reference	reference	reference
reference	reference	C>CG	no_data	1 (0)	G>A	no_data	reference	reference	reference
reference	reference	C>CG	no_data	3 (0)	G>A	C>CT	C>CT	no_data	reference
reference	reference	C>CG	no_data	3 (0)	G>A	C>CT	C>CT	no_data	reference
reference	reference	reference	reference	4 (0)	G>A	C>CT	C>CT	A>AT	reference
reference	reference	C>G	no_data	4 (0)	G>A	C>CT	C>CT	A>AT	reference
reference	reference	C>G	no_data	2 (0)	no_data	no_data	C>CT	A>AT	reference
no_data	T>TC	no_data	no_data	4 (0)	G>A	C>CT	C>CT	A>AT	reference
reference	reference	no_data	no_data	4 (0)	G>A	C>CT	C>CT	A>AT	reference
reference	reference	no_data	no_data	4 (0)	G>A	C>CT	C>CT	A>AT	reference
reference	reference	C>CG	no_data	1 (0)	G>A	C>CT	C>CT	A>AT	reference
reference	reference	reference	reference	4 (0)	G>A	reference	reference	reference	reference
reference	reference	C>CG	no_data	1 (0)	G>A	C>CT	C>CT	A>AT	reference
reference	reference	C>CG	no_data	2 (0)	G>A	reference	no_data	no_data	reference
reference	reference	C>CG	no_data	2 (0)	G>A	C>CT	no_data	no_data	reference
reference	reference	C>CG	no_data	2 (0)	G>A	C>CT	no_data	no_data	reference
reference	reference	C>CG	no_data	2 (0)	G>A	C>T	no_data	no_data	reference
reference	reference	C>G	no_data	1 (0)	G>A	reference	no_data	no_data	reference

reference	reference	reference	reference	4 (0)	G>A	C>CT	C>CT	A>AT	reference
reference	reference	reference	reference	4 (0)	G>A	C>T	C>T	A>T	reference
reference	reference	C>CG	A>AC	4 (0)	G>A	C>CT	C>CT	A>AT	reference
reference	reference	C>CG	no_data	1 (0)	G>A	reference	reference	reference	reference
reference	reference	reference	reference	1 (0)	G>A	reference	no_data	no_data	reference
reference	reference	C>CG	no_data	4 (0)	G>A	C>T	C>T	A>T	reference

LIG4 chr13:107656790-107666882

Total number of variants (coding)	107658205	107658280-107658284	107658879	107659299	107659914	107660726
4 (2)	reference	reference	reference	reference	reference	reference
1 (0)	A>G	no_data	reference	reference	reference	reference
4 (0)	A>AG	no_data	reference	reference	reference	reference
1 (1)	reference	reference	reference	reference	reference	reference
1 (1)	no_data	no_data	reference	reference	T>TC_p.D568DD	reference
5 (1)	no_data	no_data	reference	reference	reference	reference
2 (0)	reference	reference	reference	reference	reference	reference
2 (1)	no_data	no_data	reference	reference	T>TC_p.D568DD	reference
4 (1)	no_data	no_data	reference	reference	T>TC_p.D568DD	reference
5 (1)	no_data	het_delCTTA	reference	reference	T>TC_p.D568DD	reference
1 (0)	reference	reference	reference	reference	reference	reference
3 (0)	reference	reference	reference	reference	reference	reference
3 (0)	reference	reference	reference	reference	reference	no_data
0 (0)	reference	reference	reference	reference	reference	no_data
0 (0)	reference	reference	reference	reference	reference	reference
3 (0)	no_data	no_data	reference	reference	reference	reference
2 (1)	A>AG	no_data	reference	reference	reference	reference
2 (1)	no_data	het_delCTTA	reference	reference	T>TC_p.D568DD	reference
3 (1)	no_data	het_delCTTA	reference	reference	T>TC_p.D568DD	reference
1 (1)	no_data	no_data	no_data	reference	T>TC_p.D568DD	reference
2 (1)	no_data	het_delCTTA	reference	reference	T>TC_p.D568DD	reference
3 (1)	A>AG	het_delCTTA	reference	reference	T>TC_p.D568DD	reference
1 (1)	no_data	no_data	reference	reference	reference	T>TC_p.Y298YH
1 (1)	reference	reference	reference	reference	reference	reference
3 (0)	no_data	no_data	reference	reference	reference	no_data
3 (0)	reference	reference	reference	reference	reference	reference
1 (1)	reference	reference	reference	reference	reference	reference
1 (0)	A>AG	no_data	reference	reference	reference	reference
6 (2)	A>AG	no_data	het_delC	reference	reference	reference
1 (1)	no_data	no_data	reference	reference	T>TC_p.D568DD	reference
4 (1)	no_data	no_data	reference	A>AG_p.Q773QQ	reference	no_data
1 (1)	no_data	no_data	reference	reference	reference	reference
0 (0)	reference	reference	reference	reference	reference	reference
2 (1)	reference	reference	reference	reference	reference	reference
1 (1)	reference	reference	reference	reference	reference	reference

2 (0)	reference	reference	reference	reference	reference	reference
1 (0)	A>AG	no_data	reference	reference	reference	reference
3 (2)	no_data	het_delCTTA	reference	reference	T>TC_p.D568DD	reference
1 (0)	reference	reference	reference	reference	reference	reference
3 (2)	no_data	het_delCTTA	reference	reference	T>TC_p.D568DD	reference
4 (0)	A>AG	no_data	reference	reference	reference	reference

107661333	107661592	107661610	107664749	107664828	107665217	107665795-107665796	107665798-107665799
reference	C>CT_p.T9TI	C>CT_p.A3AV	G>GA	no_data	G>C	reference	reference
reference	reference	reference	reference	reference	reference	reference	reference
reference	reference	reference	reference	reference	reference	no_data	delTT
reference	C>T_p.T9I	no_data	reference	reference	reference	reference	reference
reference	no_data	no_data	reference	reference	reference	reference	reference
reference	C>CT_p.T9TI	no_data	reference	reference	reference	no_data	no_data
reference	no_data	no_data	G>GA	no_data	G>GC	reference	reference
reference	no_data	no_data	no_data	no_data	G>GC	reference	reference
reference	reference	reference	reference	reference	reference	delTT	no_data
reference	no_data	no_data	reference	reference	reference	no_data	delTT
reference	no_data	no_data	no_data	G>GA	no_data	reference	reference
reference	reference	reference	reference	reference	reference	no_data	delTT
no_data	no_data	no_data	reference	reference	reference	no_data	delTT
no_data	no_data	no_data	reference	reference	reference	no_data	no_data
reference	no_data	no_data	reference	reference	reference	no_data	no_data
reference	reference	reference	reference	reference	reference	no_data	delTT
reference	C>CT_p.T9TI	no_data	reference	reference	reference	reference	reference
reference	reference	reference	reference	reference	reference	reference	reference
reference	reference	reference	no_data	no_data	G>GC	no_data	no_data
reference	no_data	no_data	reference	reference	reference	no_data	no_data
reference	no_data	no_data	reference	reference	reference	no_data	no_data
reference	no_data	no_data	reference	reference	reference	reference	reference
reference	no_data	no_data	reference	reference	reference	no_data	no_data
G>GA_p.E95EE	no_data	no_data	reference	reference	reference	no_data	no_data
no_data	no_data	no_data	no_data	no_data	no_data	no_data	delTT
reference	reference	reference	reference	reference	reference	no_data	delTT
reference	C>CT_p.T9TI	no_data	reference	reference	reference	reference	reference
reference	reference	reference	reference	reference	reference	reference	reference
reference	C>CT_p.T9TI	C>CT_p.A3AV	G>GA	no_data	G>GC	reference	reference
no_data	no_data	no_data	reference	reference	reference	no_data	no_data
reference	no_data	no_data	reference	reference	reference	no_data	delTT
reference	C>CT_p.T9TI	no_data	reference	reference	reference	no_data	no_data
reference	reference	reference	reference	reference	reference	no_data	no_data
reference	C>CT_p.T9TI	no_data	no_data	no_data	G>GC	reference	reference
reference	C>CT_p.T9TI	no_data	no_data	no_data	no_data	no_data	no_data

reference	no_data	no_data	reference	reference	reference	no_data	no_data
reference	no_data	no_data	reference	reference	reference	no_data	no_data
reference	C>CT_p.T9TI	no_data	reference	reference	reference	no_data	no_data
reference	no_data	no_data	no_data	no_data	G>GC	no_data	no_data
reference	C>CT_p.T9TI	no_data	reference	reference	reference	no_data	no_data
reference	reference	reference	reference	reference	reference	no_data	delTT

MDC1 chr6:30774563-30794009							
107665800-107665801	107665802	107665805	107665929-107665931	107665933	Total number of variants (coding)	30776050	30776138
reference	reference	reference	reference	reference	2 (0)	reference	reference
reference	reference	reference	reference	reference	2 (0)	reference	reference
no_data	C>G	G>A	no_data	no_data	4 (1)	reference	reference
reference	reference	reference	reference	reference	4 (2)	reference	reference
reference	reference	reference	reference	reference	2 (0)	reference	reference
het_delTT	C>CG	G>GA	het_insC	no_data	4 (1)	reference	reference
reference	reference	reference	reference	reference	2 (0)	reference	reference
reference	reference	reference	reference	reference	5 (2)	reference	reference
no_data	C>G	G>A	no_data	no_data	2 (0)	no_data	no_data
no_data	C>G	G>A	no_data	no_data	3 (1)	reference	reference
reference	reference	reference	reference	reference	2 (0)	reference	reference
no_data	C>G	G>A	no_data	no_data	2 (0)	reference	reference
no_data	C>G	G>A	no_data	no_data	2 (0)	reference	reference
no_data	no_data	no_data	no_data	no_data	3 (0)	reference	reference
no_data	no_data	no_data	no_data	no_data	3 (1)	reference	reference
no_data	C>G	G>A	no_data	no_data	2 (0)	reference	reference
reference	reference	reference	reference	reference	4 (1)	reference	reference
reference	reference	reference	reference	reference	3 (1)	reference	reference
no_data	no_data	no_data	no_data	no_data	4 (1)	reference	reference
no_data	no_data	no_data	no_data	no_data	3 (1)	reference	reference
no_data	no_data	no_data	no_data	no_data	3 (1)	reference	reference
reference	reference	reference	reference	reference	4 (2)	reference	reference
no_data	no_data	no_data	no_data	no_data	4 (2)	reference	reference
no_data	no_data	no_data	no_data	no_data	2 (0)	reference	reference
no_data	C>G	G>A	no_data	no_data	3 (1)	reference	reference
no_data	C>G	G>A	no_data	no_data	2 (1)	no_data	no_data
reference	reference	reference	reference	reference	2 (0)	no_data	no_data
reference	reference	reference	reference	reference	3 (1)	reference	reference
reference	reference	reference	reference	reference	6 (2)	G>GC	no_data
no_data	no_data	no_data	no_data	no_data	4 (1)	reference	reference
no_data	C>G	G>A	no_data	no_data	2 (0)	reference	reference
no_data	no_data	no_data	no_data	no_data	3 (1)	reference	reference
no_data	no_data	no_data	no_data	no_data	19 (10)	no_data	G>GA
reference	reference	reference	reference	reference	4 (1)	reference	reference
no_data	no_data	no_data	no_data	no_data	2 (0)	reference	reference

no_data	no_data	G>A	no_data	951dupC	3 (0)	reference	reference
no_data	no_data	no_data	no_data	no_data	2 (0)	reference	reference
no_data	no_data	no_data	no_data	no_data	8 (3)	reference	reference
no_data	no_data	no_data	no_data	no_data	3 (0)	reference	reference
no_data	no_data	no_data	no_data	no_data	11 (5)	reference	reference
no_data	C>G	G>A	no_data	no_data	3 (0)	reference	reference

[illegible]

no_data	G>GA	reference	reference	reference	reference	reference	no_data
reference	reference	reference	reference	reference	reference	reference	reference
no_data	G>GA	reference	reference	reference	reference	reference	no_data
no_data	G>GA	reference	reference	reference	reference	reference	reference
no_data	G>GA	C>CT	T>TG_p.D1855DE	T>TA_p.V1791VE	C>CG_p.P1745PR	no_data	reference
no_data	G>A	reference	reference	reference	reference	reference	no_data

[illegible]

no_data	no_data	reference	reference	reference	reference	reference
reference	reference	reference	reference	reference	reference	reference
no_data	no_data	T>TC_p.M1316MT	reference	reference	reference	reference
reference	reference	reference	reference	no_data	no_data	no_data
reference	reference	reference	reference	no_data	no_data	no_data
no_data	no_data	reference	reference	reference	reference	reference

30783584	30783903	30783969	30784025	30787607	30788541	30788587	30788777
reference	reference	reference	reference	A>T	reference	reference	reference
reference	reference	reference	reference	A>T	reference	reference	reference
reference	reference	reference	reference	A>T	no_data	no_data	no_data
reference	reference	reference	reference	A>T	reference	reference	reference
reference	reference	reference	reference	A>T	reference	reference	reference
reference	reference	reference	reference	A>T	no_data	no_data	no_data
reference	reference	reference	no_data	A>AT	reference	reference	reference
reference	reference	reference	reference	A>AT	reference	reference	reference
reference	reference	reference	reference	A>T	reference	reference	reference
no_data	no_data	A>AC_p.Q789QP	no_data	A>T	reference	reference	reference
reference	reference	reference	reference	A>AT	reference	reference	reference
reference	reference	reference	reference	A>T	reference	reference	reference
reference	reference	reference	reference	A>AT	reference	reference	reference
reference	reference	reference	reference	A>T	reference	reference	reference
no_data	no_data	no_data	no_data	A>T	no_data	no_data	no_data
reference	reference	reference	reference	A>AT	reference	reference	reference
no_data	no_data	no_data	no_data	A>T	no_data	no_data	no_data
reference	reference	reference	reference	A>T	reference	reference	reference
reference	reference	reference	reference	A>T	no_data	no_data	no_data
no_data	A>AG_p.D811DG	no_data	no_data	A>T	reference	reference	reference
reference	reference	reference	reference	A>AT	reference	reference	reference
reference	reference	reference	reference	A>T	no_data	no_data	no_data
reference	reference	reference	reference	A>T	no_data	no_data	C>CT_p.S307SS
reference	reference	reference	reference	A>T	reference	reference	reference
reference	reference	reference	reference	A>T	no_data	no_data	no_data
reference	reference	reference	reference	A>AT	reference	reference	reference
reference	reference	reference	reference	A>AT	reference	reference	reference
reference	reference	reference	reference	A>T	no_data	no_data	no_data
A>AC_p.R917RS	no_data	no_data	no_data	A>T	no_data	no_data	no_data
reference	reference	reference	reference	A>T	no_data	no_data	no_data
reference	reference	reference	reference	A>AT	reference	reference	reference
reference	reference	reference	reference	A>AT	no_data	no_data	no_data
reference	reference	reference	G>GC_p.T770TT	A>T	reference	reference	reference
reference	reference	reference	reference	A>T	reference	reference	reference
no_data	no_data	no_data	no_data	A>AT	reference	reference	reference

reference	reference	reference	reference	A>T	reference	reference	reference
reference	reference	reference	reference	A>T	reference	reference	reference
reference	reference	reference	reference	A>T	C>CT_p.P386PL	G>GA_p.E371EK	reference
reference	reference	reference	reference	A>T	reference	reference	reference
reference	reference	reference	G>GC_p.T770TT	A>T	reference	reference	reference
reference	reference	reference	reference	A>T	reference	reference	reference

[illegible]

reference	reference	reference	reference	reference	no_data	no_data	no_data	no_data	no_data	T>C
reference	reference	reference	reference	reference	no_data	no_data	no_data	no_data	no_data	T>C
reference	reference	reference	reference	reference	no_data	T>TC	no_data	G>GT	no_data	T>C
reference	reference	reference	reference	reference	reference	reference	reference	no_data	no_data	T>C
reference	no_data	A>AG	C>CT_p.R179RC	no_data	no_data	T>TC	no_data	no_data	no_data	T>C
reference	reference	reference	reference	reference	no_data	no_data	no_data	no_data	no_data	T>C

MRE11A chr11:93789113-93867687 Total

number of variants (coding)	93790438	93792428	93810133-93810135	93818773	93819914	93836908	93837216	93843001	93848996
2 (0)	reference	reference	reference	no_data	reference	reference	reference	reference	T>C
7 (0)	T>TC	reference	reference	T>TC	T>TG	A>AG	no_data	reference	reference
7 (0)	T>TC	reference	reference	T>TC	T>TG	A>AG	no_data	reference	reference
8 (0)	reference	reference	reference	T>TC	reference	A>AG	C>CT	reference	T>TC
2 (0)	T>TC	no_data	reference	no_data	reference	no_data	no_data	no_data	no_data
3 (0)	reference	no_data	no_data	T>TC	reference	reference	reference	G>GA	T>TC
1 (0)	T>C	no_data	reference	no_data	reference	reference	reference	reference	reference
2 (0)	T>TC	no_data	reference	no_data	reference	reference	reference	reference	reference
3 (0)	T>TC	reference	reference	no_data	reference	no_data	no_data	no_data	T>TC
1 (0)	T>C	no_data	reference	no_data	reference	reference	reference	no_data	reference
4 (0)	T>TC	no_data	reference	T>TC	reference	no_data	C>CT	reference	reference
3 (0)	T>TC	no_data	reference	no_data	reference	no_data	no_data	reference	T>TC
3 (0)	T>TC	no_data	reference	no_data	no_data	no_data	no_data	no_data	T>TC
1 (0)	reference	no_data	reference	no_data	reference	no_data	no_data	no_data	T>C
1 (0)	T>C	no_data	reference	no_data	reference	no_data	no_data	reference	reference
5 (0)	T>TC	reference	no_data	T>TC	reference	reference	reference	G>GA	reference
3 (0)	reference	no_data	reference	T>TC	reference	reference	reference	reference	T>TC
2 (0)	T>TC	reference	reference	no_data	reference	reference	reference	reference	T>TC
7 (0)	reference	C>CT	reference	T>TC	T>TG	no_data	no_data	reference	T>TC
3 (0)	reference	no_data	no_data	T>TC	reference	A>AG	no_data	no_data	T>TC
1 (0)	reference	no_data	reference	reference	reference	reference	reference	reference	T>C
7 (0)	reference	no_data	het_delCT	T>C	reference	A>AG	C>CT	G>GA	T>TC
1 (0)	T>C	no_data	reference	no_data	reference	reference	reference	reference	no_data
3 (0)	T>TC	C>CT	reference	no_data	reference	reference	reference	reference	T>TC
0 (0)	no_data	no_data	no_data	no_data	no_data	no_data	no_data	no_data	no_data
6 (0)	reference	reference	reference	T>C	reference	A>G	C>T	reference	reference
8 (0)	T>TC	reference	reference	T>TC	reference	A>AG	C>CT	reference	T>TC
6 (0)	reference	reference	reference	T>C	T>G	A>G	no_data	reference	reference
7 (0)	T>TC	reference	reference	T>TC	reference	A>AG	C>CT	reference	reference
6 (0)	T>TC	reference	no_data	T>TC	no_data	A>AG	no_data	reference	reference
3 (0)	reference	no_data	reference	no_data	no_data	no_data	no_data	reference	no_data
2 (0)	reference	no_data	reference	no_data	reference	no_data	no_data	reference	T>C
6 (0)	reference	reference	reference	T>TC	reference	A>AG	C>CT	reference	no_data
6 (0)	reference	reference	reference	T>TC	reference	A>AG	C>CT	reference	reference
7 (0)	reference	no_data	no_data	T>TC	no_data	A>G	C>T	no_data	T>TC

5 (0)	T>TC	no_data	reference	T>TC	reference	A>AG	C>CT	reference	reference
3 (0)	T>TC	no_data	reference	reference	reference	reference	reference	no_data	T>TC
6 (0)	T>TC	reference	reference	T>TC	reference	A>AG	no_data	reference	reference
7 (0)	reference	reference	no_data	T>C	reference	A>AG	C>CT	G>GA	reference
7 (0)	reference	reference	no_data	T>C	reference	A>AG	C>CT	G>GA	reference
9 (0)	T>TC	reference	reference	T>TC	reference	A>AG	C>CT	reference	T>TC

RAD50 chr5:131919528-132008497

93852640	93865455	93865568	93866600	93866690	93866773	Total number of variants (coding)	131920878	131943112	131943178
reference	reference	reference	C>CT	no_data	no_data	2 (0)	G>A	no_data	no_data
reference	C>CT	C>CT	no_data	no_data	C>CA	2 (0)	G>A	reference	reference
reference	C>CT	C>CT	no_data	no_data	C>CA	2 (0)	G>A	no_data	no_data
reference	C>CT	C>CT	C>CT	no_data	C>CA	2 (0)	G>A	reference	reference
reference	no_data	no_data	no_data	no_data	C>CA	9 (0)	G>A	G>GA	no_data
reference	no_data	no_data	reference	reference	reference	8 (0)	G>A	G>GA	A>AG
reference	reference	reference	reference	reference	reference	8 (1)	G>A	G>GA	no_data
reference	reference	reference	C>CT	no_data	no_data	2 (0)	G>A	reference	reference
C>CT	no_data	no_data	reference	reference	reference	2 (0)	G>A	reference	reference
reference	no_data	no_data	no_data	no_data	no_data	2 (0)	G>A	no_data	no_data
reference	no_data	no_data	no_data	no_data	C>CA	2 (0)	G>A	no_data	no_data
reference	no_data	no_data	C>CT	no_data	no_data	4 (0)	G>A	reference	reference
reference	no_data	no_data	C>CT	no_data	no_data	2 (0)	G>A	reference	reference
no_data	no_data	no_data	reference	reference	reference	3 (0)	G>A	reference	reference
reference	no_data	no_data	no_data	no_data	no_data	8 (0)	G>A	G>GA	no_data
reference	C>CT	C>CT	no_data	no_data	no_data	2 (0)	G>A	reference	reference
reference	reference	reference	C>T	no_data	no_data	8 (0)	G>A	G>GA	no_data
reference	reference	reference	reference	reference	reference	3 (1)	G>A	no_data	no_data
reference	C>CT	C>CT	no_data	no_data	C>CA	2 (0)	G>A	reference	reference
no_data	no_data	no_data	no_data	no_data	no_data	2 (0)	G>A	reference	reference
reference	no_data	no_data	reference	reference	reference	2 (0)	G>A	reference	reference
reference	no_data	no_data	no_data	no_data	C>CA	2 (0)	G>A	reference	reference
reference	reference	reference	reference	reference	reference	2 (0)	G>A	reference	reference
reference	reference	reference	no_data	no_data	no_data	6 (0)	G>A	G>GA	no_data
no_data	no_data	no_data	no_data	no_data	no_data	1 (0)	G>A	reference	reference
reference	C>T	C>T	no_data	no_data	C>A	1 (0)	G>A	reference	reference
reference	C>CT	C>CT	no_data	no_data	C>CA	3 (0)	G>A	reference	reference
reference	C>T	C>T	no_data	no_data	C>A	2 (0)	G>A	reference	reference
reference	C>CT	C>CT	no_data	no_data	C>CA	1 (0)	G>A	reference	reference
reference	C>CT	C>CT	no_data	no_data	C>CA	3 (0)	G>A	reference	reference
reference	C>T	C>T	no_data	no_data	C>A	2 (0)	G>A	no_data	no_data
reference	reference	reference	C>CT	no_data	no_data	2 (0)	G>A	no_data	no_data
reference	C>CT	C>CT	no_data	no_data	C>CA	6 (0)	G>A	reference	reference
reference	C>CT	C>CT	no_data	no_data	C>CA	2 (0)	G>A	no_data	no_data
reference	C>CT	C>CT	no_data	no_data	C>CA	10 (0)	G>A	G>GA	no_data

reference	no_data	no_data	no_data	no_data	C>CA	2 (0)	G>A	reference	reference
reference	no_data	no_data	C>CT	no_data	no_data	2 (0)	G>A	reference	reference
no_data	C>CT	no_data	C>CT	no_data	C>CA	2 (0)	G>A	no_data	no_data
reference	C>T	C>T	no_data	no_data	C>CA	6 (0)	G>A	G>GA	no_data
reference	C>T	C>T	no_data	no_data	C>CA	2 (0)	G>A	reference	reference
reference	C>CT	C>CT	no_data	G>GA	C>CA	2 (0)	G>A	reference	reference

[illegible]

reference	reference	reference	reference	no_data	C>T	reference	reference	reference	reference	reference
reference	reference	reference	reference	no_data	C>T	reference	reference	reference	reference	reference
no_data	reference	reference	reference	no_data	C>T	reference	reference	reference	reference	reference
T>TC	no_data	reference	G>GA	no_data	no_data	reference	reference	no_data	T>TC	T>TA
reference	no_data	reference	reference	no_data	C>T	reference	reference	reference	reference	reference
reference	reference	reference	reference	no_data	C>T	reference	reference	reference	reference	reference

132005895	132007387	132007550-132007551	132007552-132007553
reference	reference	reference	reference
reference	reference	reference	reference
reference	reference	reference	reference
reference	reference	reference	reference
reference	no_data	reference	reference
reference	no_data	reference	reference
reference	no_data	no_data	no_data
reference	reference	reference	reference
reference	reference	reference	reference
reference	reference	reference	reference
reference	reference	reference	reference
reference	no_data	het_delCA	het_delCA
reference	reference	reference	reference
reference	reference	reference	reference
reference	reference	reference	reference
reference	reference	reference	reference
reference	no_data	het_delCA	no_data
C>CT_p.I1293II	reference	reference	reference
reference	reference	reference	reference
reference	reference	reference	reference
reference	no_data	reference	reference
reference	reference	reference	reference
reference	reference	reference	reference
reference	reference	reference	reference
reference	reference	reference	reference
reference	reference	reference	reference
reference	reference	reference	reference
reference	reference	reference	reference
reference	reference	reference	reference
reference	reference	reference	reference
reference	reference	reference	reference
reference	C>CA	reference	reference
reference	reference	reference	reference
reference	reference	reference	reference
reference	no_data	het_delCA	het_delCA
reference	reference	reference	reference
reference	no_data	het_delCA	no_data

reference
reference
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Toxicity and Dosimetry data						Total variants			
Patient #	Toxicity Score	Prostate D90 (Gy)	Prostate V100 (%)	Rectal VR100 (cm ³)	gammaH2AX sum of ranks for monocytes & lymphocytes (Olive et al.)	ATM	BRCA1	ERCC2	H2AFX
2	0	176	97.0	0.17	49	26	3	14	4
3	0	165	95.8	0.79	9	26	0	14	4
5	0	166	94.4	0.00	11	28	23	2	1
12	0	151	93.2	0.84	26	24	6	14	1
13	0	130	84.1	0.01	65	27	0	12	2
14	0	143	89.8	0.46	35	26	0	7	1
15	0	146	91.3	0.16	27	21	19	11	4
16	0	146	90.6	0.94	44	17	1	15	1
20	0	183	99.0	0.26	61	21	0	15	1
22	0	151	93.2	0.34	60	27	22	10	3
25	0	155	93.5	0.20	22	26	11	11	2
27	0	142	89.0	0.00	29	23	29	4	4
28	0	166	96.0	1.20	69	28	3	5	4
29	0	154	93.1	1.54	63	4	28	12	1
33	0	157	93.7	1.50	69	26	25	10	2
39	0	154	96.1	0.20	26	5	0	9	1
44	0	152	92.3	0.70	39	29	28	12	4
1	1	165	96.8	0.00	39	26	31	13	1
24	1	131	85.7	0.00	61	23	1	16	4
31	1	128	85.2	1.46	38	24	18	14	1
6	3	172	96.6	0.33	25	30	27	7	4
18	3	146	90.9	0.05	11	9	29	15	1
43	3	147	91.0	0.31	18	26	30	1	1
11	4	141	89.0	0.81	57	23	0	18	4
17	4	130	84.4	1.48	61	26	29	6	4
21	4	148	91.4	0.81	50	22	21	9	3
32	4	164	95.4	0.90	51	28	1	11	2
35	4	160	95.2	3.20	61	24	0	16	1
38	4	142	88.5	0.35	40	6	28	10	4
8	5	182	97.9	0.03	11	18	31	11	1
26	5	170	97.9	0.26	65	24	4	14	4
37	5	148	91.7	0.06	47	23	0	4	4
4	6	128	86.9	0.23	9	26	2	14	1
7	7	176	96.9	0.17	48	25	2	11	3

10	7	152	93.0	0.98	6	5	0	15	4
19	7	183	97.9	0.89	14	18	32	5	1
9	9	113	78.3	0.03	58	24	18	14	1
23	10	136	88.2	0.07	49	30	0	1	4
30	10	167	97.0	0.10		29	18	4	4
36	11	150	92.5	1.20	43	23	20	1	4
34	13	136	87.6	3.80	74	5	0	15	2

				Coding variants								Non-conservative variants			
LIG4	MDC1	MRE11A	RAD50	ATM	BRCA1	ERCC2	H2AFX	LIG4	MDC1	MRE11A	RAD50	ATM	BRCA1	ERCC2	H2AFX
1	2	7	2	1	0	4	0	0	0	0	0	0	0	0	0
4	4	7	2	1	0	4	0	0	1	0	0	0	0	0	0
1	2	2	9	2	1	0	0	1	0	0	0	0	1	0	0
3	2	3	4	1	0	2	0	0	0	0	0	0	0	0	0
3	2	3	2	1	0	2	0	0	0	0	0	0	0	0	0
0	3	1	3	1	0	0	0	0	0	0	0	0	0	0	0
0	3	1	8	1	1	2	0	0	1	0	0	0	1	0	0
3	2	5	2	1	0	4	0	0	0	0	0	0	0	0	0
1	3	3	2	1	0	3	0	1	1	0	0	0	0	0	0
2	4	7	2	1	1	2	0	1	2	0	0	0	1	0	0
3	3	0	1	2	0	1	0	0	1	0	0	0	0	0	0
1	2	8	3	1	1	0	0	1	0	0	0	0	1	0	0
1	3	6	2	2	0	0	0	0	1	0	0	0	0	0	0
6	6	7	1	1	1	2	0	2	2	0	0	0	1	0	0
0	19	6	6	1	1	1	0	0	10	0	0	0	1	0	0
1	3	7	6	3	0	1	0	0	0	0	0	1	0	0	0
4	3	9	2	3	1	2	0	0	0	0	0	2	1	0	0
4	2	2	2	1	1	3	0	2	0	0	0	0	1	0	0
1	2	3	6	1	0	4	0	1	0	0	0	0	0	0	0
4	2	3	2	1	1	4	0	1	0	0	0	0	1	0	0
5	4	3	8	2	1	2	1	1	1	0	0	0	1	0	0
1	3	2	3	1	1	3	0	1	1	0	1	0	1	0	0
2	11	7	2	1	1	0	0	2	5	0	0	0	1	0	0
1	2	4	2	2	0	4	0	0	0	0	0	0	0	0	0
2	4	3	8	2	1	2	0	1	1	0	0	1	1	0	0
1	3	1	2	1	1	1	0	1	1	0	0	0	1	0	0
1	3	2	2	1	0	1	0	1	1	0	0	0	0	0	0
1	2	7	10	1	0	4	0	1	0	0	0	0	0	0	0
2	8	6	2	2	1	1	0	2	3	0	0	0	1	0	0
2	5	2	2	1	1	1	0	1	2	0	0	0	1	0	0
3	2	6	1	1	0	4	0	0	1	0	0	0	0	0	0
1	2	3	2	1	0	0	0	0	0	0	0	0	0	0	0
1	4	8	2	1	0	3	0	1	2	0	0	0	0	0	0
2	2	1	8	1	0	1	0	0	0	0	1	0	0	0	0

4	3	1	2		1	0	4	0	1	1	0	0		0	0	0	0
2	4	7	2		1	1	0	0	1	1	0	0		0	1	0	0
4	2	3	2		2	1	4	0	1	0	0	0		1	1	0	0
1	4	1	2		2	0	0	0	1	2	0	0		0	1	0	0
1	4	6	3		1	1	0	0	1	1	0	0		0	1	0	0
2	3	5	2		1	1	0	0	0	0	0	0		0	0	0	0
2	4	6	2		2	0	4	0	1	1	0	0		0	0	0	0

				Missense variants									
LIG4	MDC1	MRE11A	RAD50	ATM	BRCA1	ERCC2	H2AFX	LIG4	MDC1	MRE11A	RAD50		
0	0	0	0	1	1	2	0	0	0	0	0		
0	0	0	0	1	0	2	0	0	1	0	0		
0	0	0	0	2	4	0	0	0	0	0	0		
0	0	0	0	1	1	2	0	0	0	0	0		
0	0	0	0	1	0	2	0	0	0	0	0		
0	0	0	0	1	0	0	0	0	0	0	0		
0	0	0	0	1	5	1	0	0	1	0	0		
0	0	0	0	1	0	4	0	0	0	0	0		
0	1	0	0	1	0	2	0	0	1	0	0		
0	1	0	0	1	5	1	0	0	2	0	0		
0	0	0	0	2	2	1	0	0	1	0	0		
1	0	0	0	1	4	0	0	1	0	0	0		
0	0	0	0	2	2	0	0	0	1	0	0		
2	1	0	0	1	4	1	0	2	2	0	0		
0	5	0	0	1	3	0	0	0	7	0	0		
0	0	0	0	2	0	0	0	0	0	0	0		
0	0	0	0	3	4	1	0	0	0	0	0		
2	0	0	0	1	5	1	0	2	0	0	0		
0	0	0	0	1	0	3	0	0	0	0	0		
0	0	0	0	1	2	2	0	0	0	0	0		
1	0	0	0	2	4	1	0	1	1	0	0		
0	0	0	0	1	5	1	0	0	0	0	0		
1	3	0	0	1	6	0	0	1	4	0	0		
0	0	0	0	2	0	3	0	0	0	0	0		
1	0	0	0	2	5	1	0	1	1	0	0		
0	0	0	0	1	4	0	0	0	0	0	0		
1	0	0	0	1	1	0	0	1	1	0	0		
1	0	0	0	1	0	4	0	1	0	0	0		
1	2	0	0	2	4	0	0	1	3	0	0		
0	0	0	0	1	5	0	0	0	1	0	0		
0	0	0	0	1	2	2	0	0	0	0	0		
0	0	0	0	1	0	0	0	0	0	0	0		
1	1	0	0	1	1	2	0	1	1	0	0		
0	0	0	0	1	1	0	0	0	0	0	1		

0	1	0	0		1	0	4	0	0	1	0	0	
0	0	0	0		1	6	0	0	0	1	0	0	
0	0	0	0		2	3	2	0	0	0	0	0	
0	0	0	0		2	3	0	0	1	1	0	0	
0	0	0	0		1	3	0	0	0	1	0	0	
0	0	0	0		1	0	0	0	0	0	0	0	
1	0	0	0		1	0	4	0	1	0	0	0	

Residual gammaH2AX (Olive et al.)		Toxicity score breakdown				
Monocyte score	Lymphocyte score	IPSS Normalized Score (0=Yes, 1=No)	Pre-implant IPSS	Max Late IPSS	RTOG Score	Max Late Urinary RTOG
0.70	0.49	0	6	4	0	0
0.48	0.16	0	4	8	0	0
0.40	0.24	0	5	6	0	0
0.74	0.21	0	6	8	0	0
0.84	0.58	0	2	5	0	0
0.76	0.27	0	16	21	0	0
0.60	0.29	0	4	6	0	0
0.90	0.27	0	2	4	0	0
1.01	0.41	0	3	5	0	0
1.26	0.34	0	1	7	0	0
0.75	0.13	0	6	10	0	0
0.72	0.27	0	11	6	0	0
1.01	0.52	0	7	9	0	0
1.31	0.36	0	2	7	0	0
0.92	0.56	0	6	12	0	0
0.56	0.29	0	7	12	0	0
0.55	0.42	0	7	12	0	0
0.62	0.4	0	13	11	1	1
1.14	0.37	0	3	5	1	0
1.00	0.21	0	8	14	1	1
0.53	0.6	0	19	15	3	2
0.50	0.18	0	7	16	3	0
0.51	0.21	1	1	15	2	1
1.04	0.37	1	4	24	3	2
0.75	0.46	0	6	24	4	2
0.73	0.47	0	6	13	4	2
0.74	0.46	1	2	17	3	2
0.76	0.64	0	5	6	2	1
0.75	0.31	1	3	22	3	2
0.37	0.25	1	5	23	4	2
1.21	0.41	1	4	22	2	1
0.85	0.32	1	5	17	4	2
0.43	0.19	1	5	11	2	1
0.77	0.37	1	4	16	3	2

	0.46	0.07	1	9	24	6	2
	0.40	0.26	0	9	14	5	3
	0.84	0.43	0	9	14	6	1
	0.86	0.33	1	21	33	8	2
			0	5	5	8	3
	0.66	0.41	1	0	24	10	2
	1.21	0.55	0	12	20	10	3

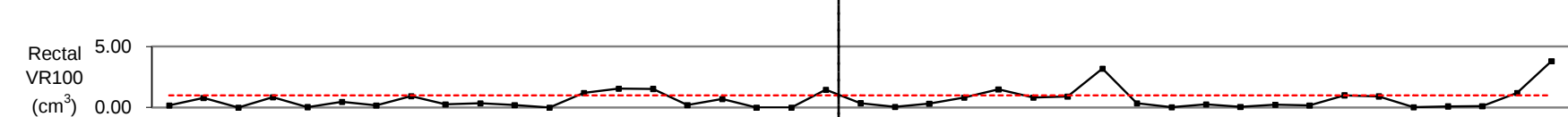
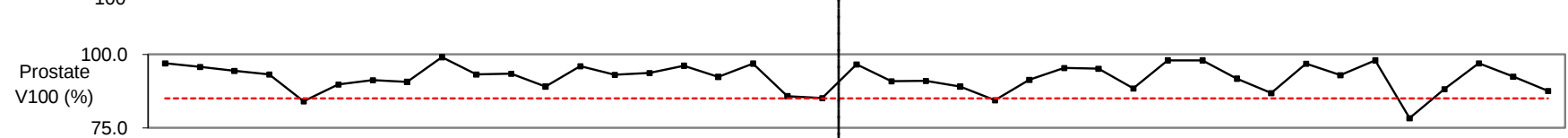
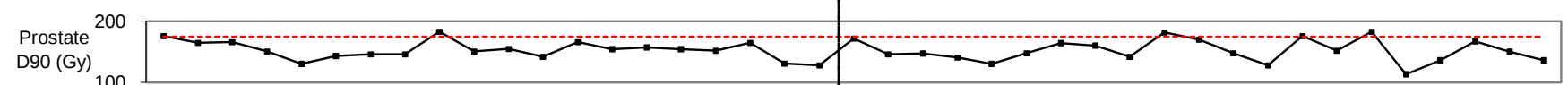
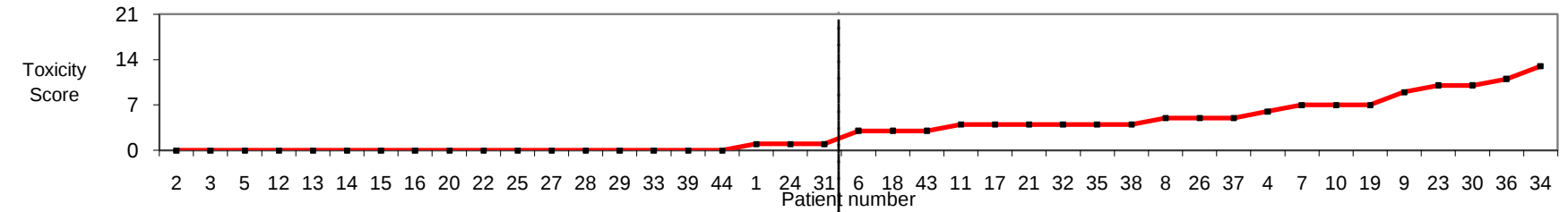
Max Late Rectal RTOG	Acute Urinary Retention >3 weeks (1=Yes, 0=No)	Potency Score	Potency at Implant	Post Implant Potency	Additional clinical data	
					Hormones	Tumor Stage
0	0	0	Normal	NNN	Yes	1C
0	0	0	Impotent	IIIIIII	Yes	2A
0	0	0	Impotent	IIPIIIIIIIIP	Yes	2B
0	0	0	Normal	NNNNNNNNNN	No	1C
0	0	0	Normal	NNNNNNNN	Yes	2B
0	0	0	Normal	NINNNNNNNNN	No	2A
0	0	0	Normal	INNNNN	Yes	1C
0	0	0	Normal	NNNNNNNN	Yes	1C
0	0	0	Partial	NNNNNNNN	Yes	2A
0	0	0	Normal	IIIIIIIIII	No	2A
0	0	0	Partial	NNNNNNIIIN	No	1C
0	0	0	Normal	NNNNNNNN	Yes	1C
0	0	0	Impotent	NIIII	Yes	2A
0	0	0	Normal	IINNINN	Yes	1C
0	0	0	Partial	NNNNNNNN	Yes	1C
0	0	0	Normal	NNNNNN	No	2A
0	0	0	Normal	NNNNNNNN	Yes	1C
0	0	0	Partial	INNNNINNNNN	Yes	2B
1	0	0	Normal	NNNNNN	Yes	2A
0	0	0	Partial	IINNNNNNN	Yes	1C
0	0	0	Normal	INNNNNNI	Yes	1C
2	0	0	Normal	INNNNNNN	Yes	2A
1	0	0	Normal	NNNNNN	Yes	1C
0	0	0	Partial	NNNNNNNNNN	No	2A
1	0	0	Impotent	IIIIINII	Yes	2A
1	0	0	Normal	IPNPNNNNNNNN	Yes	1C
0	0	0	Normal	IINNNNN	No	1C
1	0	2	Normal	NNIIIIII	Yes	1C
0	0	0	Normal	IINNNNNNN	Yes	1C
1	0	0	Normal	NNNIINNN	No	1C
1	0	2	Partial	IIIIIIIIII	Yes	1C
1	0	0	Normal	NNNIINN	No	1C
1	0	3	Normal	IIIIII	Yes	1C
0	0	3	Normal	IIIIIIIIII	Yes	1C

2	0	0	Normal	NNNNNNNNNNNN	Yes	1C
0	0	2	Partial	IIIIIIIIII	No	2A
3	0	3	Normal	IIIIIIIIII	Yes	2A
3	1	0	Impotent	IIIII	No	2A
2	0	2	Partial	IIIIII	Yes	1C
4	0	0	Normal	NNN	Yes	1C
3	0	3	Normal	IINIIII	Yes	2B

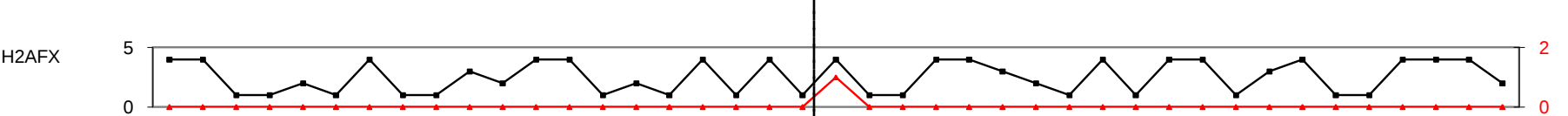
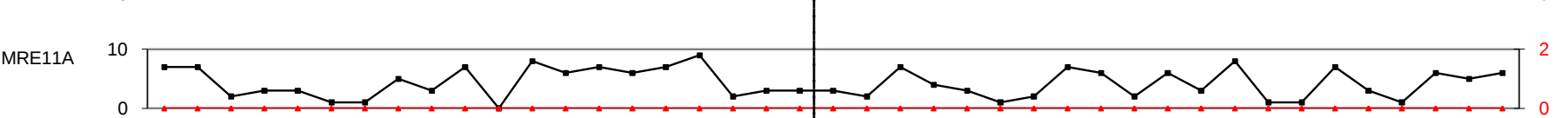
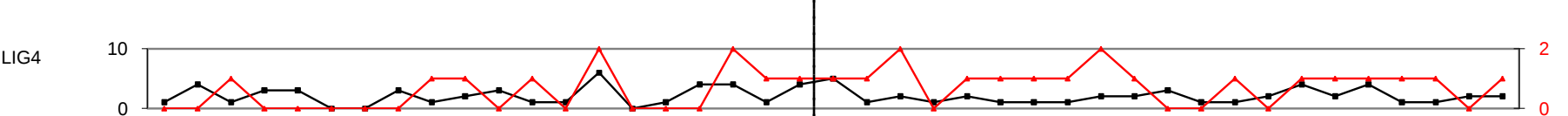
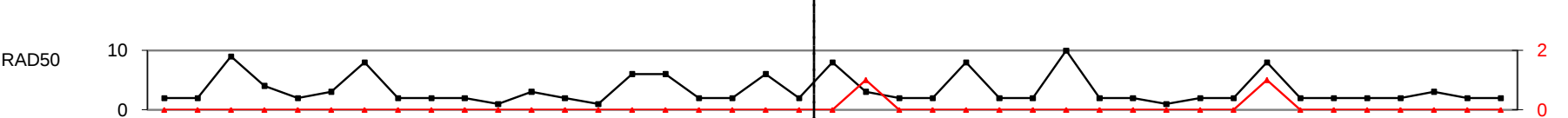
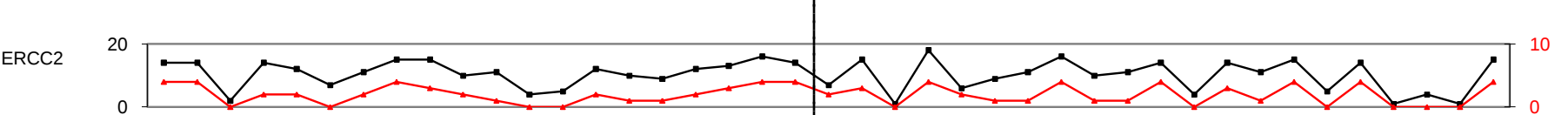
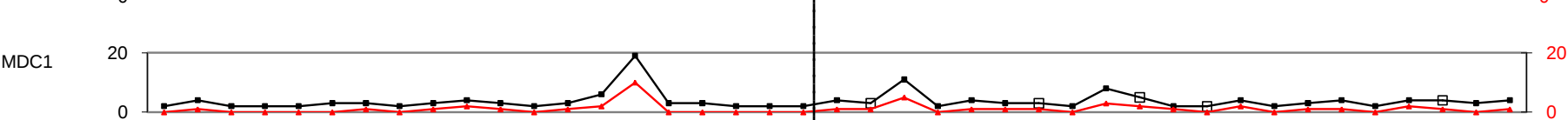
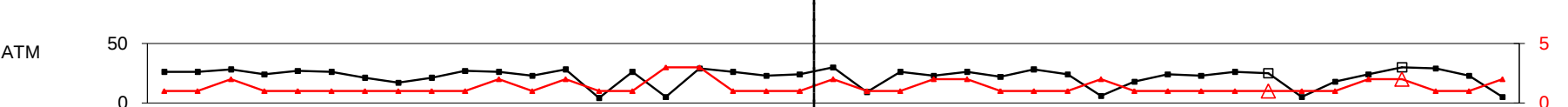
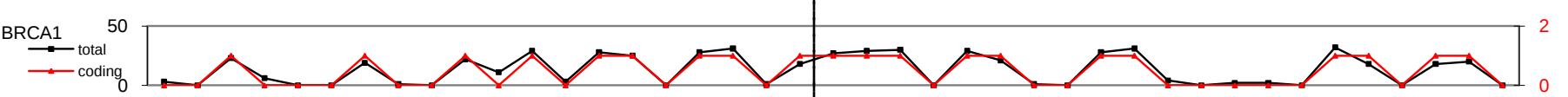
Planning Ultrasound Target Volume (PUTV)	Gleason Score	Age at Implant	PSA at last follow up
32.240	6	69	0.05
33.539	6	76	0.04
28.332	6	70	0.84
21.774	5	49	0.02
40.100	7	75	0.02
32.081	6	71	8.80
50.499	6	70	0.11
29.928	6	51	5.70
49.457	6	72	5.68
37.022	6	62	0.02
39.334	5	53	0.04
37.095	6	56	0.02
46.107	6	74	0.04
30.791	5	60	0.10
19.740	7	68	0.17
39.075	6	63	0.05
38.158	7	59	0.02
35.187	6	62	0.05
28.525	7	64	0.03
22.864	5	66	0.02
29.138	7	62	0.02
19.196	7	51	0.02
26.486	6	65	0.02
38.417	6	66	0.03
32.200	6	71	0.02
27.600	4	69	0.03
37.177	6	62	0.29
51.781	6	72	0.03
39.470	6	61	0.04
38.442	6	61	0.02
48.610	7	76	0.03
40.777	6	64	0.02
32.265	3	60	0.02
33.642	6	71	0.02

35.378	6	58	0.04
47.332	6	68	0.18
26.939	5	62	0.03
33.177	6	75	0.01
31.517	7	70	0.01
35.400	6	57	0.43
47.859	6	76	0.06

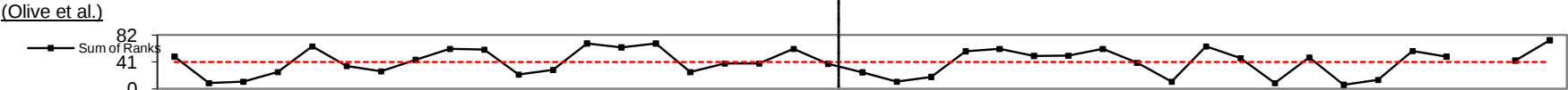
Clinical data



Count of variants



Residual gammaH2AX



Gene name (HGNC symbol)	Amplicon Coordinates (Build 36, hg18)	Amplicon Size (bp)	Forward Primer Sequence (preceded by TGTAACGAGGCCAGT)	Reverse Primer Sequence (preceded by CAGGAACAGCTATGAC)
ATM	chr11:107598633-107599269	673	AGAGAAAGAAAGGCGCCGAAAT	CAGGAAAGATGGAGTGAGGAGAGG
ATM	chr11:107603376-107603752	413	TGCCTTTGACCAGAATGTGCC	CAGGATCTCGAATCAGGCGCT
ATM	chr11:107603731-107604317	623	AAGCGCCTGATTTCGAGATCCT	TTGCCACTCCTGTCCAGCAA
ATM	chr11:107604897-107605533	696	GAAGATTAAGAGCTTTGCAGACCAGA	TGAGTGCAGTGGTGTTCACACGA
ATM	chr11:107611462-107612041	616	GGGCCATAATTTGCCAATTTCTTC	CACTGTCAACTCCTTGACGATGGA
ATM	chr11:107619639-107620264	642	GTAATGTTTCTGCGACCTGGCTCT	TCTCCCCCTTGAAAACCTCACGTA
ATM	chr11:107620495-107621149	655	GAGGGAGAGCTAACAGAAGTGGTCTC	CAGAATCTGCTACCACTGCTTCAAA
ATM	chr11:107622743-107623339	633	TCAAGGATCTTGTCAGAAGAGGCA	TCGAATCATTAGGGTTAGGGTCACCT
ATM	chr11:107624617-107625197	581	TTGTCATGGCAATCACATATCCCT	GGATGGTCTCAATCTCCTGACCTT
ATM	chr11:107626456-107627005	586	TTCCTGCCAATTTAGGAAGTAGGACA	AAGGTCTGCAGGCTGACCCAG
ATM	chr11:107626771-107627347	613	CGATGCCTTACGGAAGTTGCAT	GGTGCTGATATCCCATCACCCCTACA
ATM	chr11:107626771-107627347	613	CGATGCCTTACGGAAGTTGCAT	GGTGCTGATATCCCATCACCCCT
ATM	chr11:107627451-107627964	550	TCGGACACCAGGTCTTATTCCTTC	GAAGAATTGGAGGCACTTCTGTGCT
ATM	chr11:107627694-107628152	495	TGCCAGGCACTGTCCTGATAGA	CAGAAGCAATCAGGCATAAAGACACA
ATM	chr11:107628448-107628999	588	GGAGAGCAGACCTCCGAATGG	AAACAACCTCTTCCCTGGCTAACAG
ATM	chr11:107629396-107629940	581	TGCTCTTTACTTCCTCTGCTTGGTGA	TCCCAGAAGACAGCGATCCAG
ATM	chr11:107629739-107630115	413	ACTTCTTGAAGTGAACACCACCAA	GAGCCCTTTACTGCCACTTTGC
ATM	chr11:107631926-107632547	683	CTGCTTGCCATCAGGAGATACTT	AGCAAACCACCATGGCACTGTAT
ATM	chr11:107633181-107633775	645	TCTGTCACTGGTATGATTTGCAAGAA	ACACCAACCAGTGATCAATTCCCT
ATM	chr11:107634624-107635232	665	TTCCTCCTTTTTGGTGTAAGTGGG	TGCTAAGGGTGCTACTGAACAAGG
ATM	chr11:107642881-107643523	680	CACCACCACACCCAGCTAATTTT	ATGCCTGGCCTGGTTTTATTTCTT
ATM	chr11:107644298-107644874	613	TGGCTGTTGTGCCCTTCTCTT	GGCAAGGTTCCAACCTCAAACACA
ATM	chr11:107646917-107647546	631	CACTGCACCCGGCCTATGTTTAT	CGGTTTAGAAAGCCAAGCCTTAAA
ATM	chr11:107648447-107649065	691	TGGAAACTTACTTGATTTAGGCATC	ACACACCTCACTCGAGTCAACCAC
ATM	chr11:107655136-107655728	629	TGGCTAGTTTGAGTTCAGTGCTGTTT	TGATTGACCCATTGTGACCCA
ATM	chr11:107656736-107657326	627	TGTCAGTGCTTGTGATTTAGCAAAGG	GCCTTGTAAGTGTCTTAAATGGA
ATM	chr11:107658394-107659040	659	AACCAAATGTTGGAACTCTTAGCA	GTCAGATAGCTGGTTGTTGGCACA
ATM	chr11:107659900-107660587	688	AGGGAGACAACACGACATAACCAA	CACTAAAGTGTCAAGATTCTGTTCTCA
ATM	chr11:107660210-107660595	422	TTTGATGAGGTGAAGTCCATTGC	CCAATCAGAGGGAGACAACACGA
ATM	chr11:107663213-107663837	697	TTGGTTGGCAGAAAAATTACCAGG	TGTGGGGAGACTATGGTAAAAGAGGA
ATM	chr11:107664461-107664977	553	TGCCCTACTGTGCTGGGCATA	GGCAAATGTTGCTTTAATCATATGC
ATM	chr11:107664618-107665256	648	CTGAGGCTCATTTATTGAACTGCC	TGACACTTTAGTGATATATTAGCTCAGGGAA
ATM	chr11:107665244-107665844	601	GCGGACAGAGTGAGTCTTTGTCTC	CACATATCACCATGCCCGACTAAT
ATM	chr11:107665667-107666232	602	TGGCTTAGGAGGAGCTTGGGC	TTTCCCAGGCAAGTAGCGCA
ATM	chr11:107668363-107668981	688	TGGAAGCTTAGAGCTGCCTATTCTG	ACGTTGCGAACTGCTATCCCTAGT
ATM	chr11:107669092-107669688	656	TGAAAACACAGAACTAAAAGCTGGG	GGGAATTGCAGTTGCAGTGATTAG
ATM	chr11:107670611-107671220	640	AGGTAGCAGTGAGCCTTGATAGCG	TGGGTTTAGAGAAATCATCTGGCA
ATM	chr11:107672937-107673608	687	TTGTGCTTCTGTTTGTGATTTTGC	ACTCACATTATTCCGCCAATACA
ATM	chr11:107675388-107676039	653	CCACGCCTGGCTAATTTTGTATTT	AGGGACCTTGTCTGGAATGTTTAC
ATM	chr11:107677372-107677965	594	CCCTCCCCCAAAAATCAACTACTA	TGCCTGACACATATTGAAAGCTCA
ATM	chr11:107678599-107679179	651	GTTTTTGCCATACCACTCTGCCTC	CAAGGCACCCCTTAGAACTCCTCT

ATM	chr11:107680465-107681075	675	TTTAGCAGTATGTTGAGTTTATGGCAGA	TTGTGGCAAACCTCCAAAAAGTT
ATM	chr11:107683528-107684224	697	GACATGATCTGTCTTGTTCATGCTT	TGAAAAAACACTTGCTCCTATCCC
ATM	chr11:107685736-107686312	613	GGGTGCTTGTGTGCATTGTATTAGC	ACCCTTATTGAGACAATGCCAACAT
ATM	chr11:107688058-107688691	650	CTGAATTGGATGGCATCTGCTCTA	TGGCATAAACTCTGAGACAGGTGG
ATM	chr11:107691503-107692135	633	TGGCTGTGTAAATATCCACCAACAT	CTGACTTTCCTGTGTCTCCCTGAA
ATM	chr11:107691658-107692264	665	GAGTTGGGAGTTACATATTGGTAATGATACA	TTCTGAATCCAGTTTAAATTTAGACCAA
ATM	chr11:107692911-107693471	597	CTGATGCTGGAGTGCATTAGCG	TCAAATTTCTTACCTGACGGAAGTGC
ATM	chr11:107695596-107696218	625	TTGTGAATCCCCCTTGTGCCTAGT	CAAAACTTTCTTGAAGGGTCAGGG
ATM	chr11:107696950-107697500	587	GCCACCTTCATGTTGAGTAGGATAAGG	TGATCCACCCACTTCAGCCTTC
ATM	chr11:107701047-107701669	655	AGAGCTCTGACCGCATAGCATTTT	TACCCTTGCCCAAGGCTTAAAGT
ATM	chr11:107701802-107702377	649	GAGACAGACAGACAGACAGATAGGCA	TCGACCACATGATGGACTGATAGAA
ATM	chr11:107703466-107704051	622	TTTCCACCCACCAAGGAAA	TGTGGGTGGCTGGGCTAATG
ATM	chr11:107704950-107705510	597	TCTTGAAGGCAGTAGAAGTTGCTGGA	CCAGGTATGGCGTGCACCTG
ATM	chr11:107705936-107706600	696	GGAGAGTCCCCTTTGTCTTTGAT	TTGCATCATTTACAGCTTGTGAGC
ATM	chr11:107707142-107707720	579	AGATACTGCAGTGGGTAGAGCGTG	TAGAGACAGGGTTTTGCTGTGTCG
ATM	chr11:107707571-107708204	649	CCATTCCCTCTAAGAAATGGAAATACA	ATCATTCCATTGTCTAGATTTGTGCAT
ATM	chr11:107707895-107708483	625	AATTTCTGACTAAACCAGAGGTAGCCA	CACTTTGCCAACTGCTTTGAGGA
ATM	chr11:107708462-107708787	362	CCTCAAAGCAGTTGGCAAAGTGAA	GCATCACAAAGTGCCTCAACACTTC
ATM	chr11:107708582-107709209	628	TGTTTTTAAGTCCCAGGGCAGTTT	GACGTCAACTTGCACTATTCAAGGA
ATM	chr11:107709569-107710197	683	GGTTCCTCAGGTGGAATCTGGTCT	GCATAAGCACACGGAAACTCTCCT
ATM	chr11:107710731-107711373	697	AGTTAAAGTTACGAGCGTGAGCCA	CTGTGTACTCAACTTGGATTGGGG
ATM	chr11:107711517-107712123	633	CAGGTGTTTGCAGTATGCCTTCCT	GGACTACAAGCACATGCCATCATC
ATM	chr11:107718932-107719475	580	TGATGGGCAGGCTCTCAAACA	TTTCACTCACACACTTTTATTCTGATG
ATM	chr11:107721341-107721894	590	CCCAATGCTGTGATGCCACC	CCTGCCAAACAACAAAGTGCTCA
ATM	chr11:107722913-107723608	699	TGGGTCTCAACTTTAGCCACAATAA	TTGTTTTGGTGGAATAGCCCTGAT
ATM	chr11:107729507-107730099	629	TGGATTTGAGGTGGATCTCACAGA	GGCACTGGAATACGATTCTAGCACTAA
ATM	chr11:107730405-107731005	601	GGCTGAAGGCATTTCTAAACCACT	GGAGTTCAAGACCAGTCTGACCAA
ATM	chr11:107740795-107741378	641	ACCCCTAACCATGGAGGAAGAATG	AGCAAATTCATTGTCCACCAACA
ATM	chr11:107741079-107741675	633	CAGCAGAGGCCGGAAGATGA	CCCAGCCCCGAATGACCATTAT
ATM	chr11:107741271-107741899	662	CCAGAGTTTCAACAAAGTAGCTGAACG	TCACCTCCCAGGTTCAAGAGATTTC
ATM	chr11:107741618-107742216	635	TGGTCTTAAGGAACATCTCTGCTTTCA	CAAGAGAATTCATGAAGTAGAAGGCAA
ATM	chr11:107742138-107742657	556	AAGCCCTTCTGTACTGTCCATGTATGT	TTGCCTTGGCCTGGGAAATC
ATM	chr11:107742240-107742894	620	CCCTATCCATTGGGCTTCTTCTTT	GGGAGCAAAGAACCCAGGGC
ATM	chr11:107742240-107742894	657	CCCTATCCATTGGGCTTCTTCTTT	GATGCTGTAGCTGTCTGGAACAA
ATM	chr11:107742800-107743394	631	GCAAGCCCTGGGTTCTTTGC	GGGACAGAGAAATGTTCCACTTCTACC
ATM	chr11:107743240-107743895	658	TGACCGTAAGGATTTCCCTTTCT	ACCCATGAAGATTTAGGGCTTTC
ATM	chr11:107743765-107744370	633	TGGTGTATCTTTTTCTTACAAGCTGCC	TGGGTCACTGACTTAGCATACAACAA
ATM	chr11:107744011-107744572	598	TGCATGGTATGCTATGAGGCTCC	TGAGCAACTGACTGGCAAACCC
ATM	chr11:107744451-107745113	677	GGAGAAATAAGTTGTCCAAGGCAAGA	TTCTCCTTAGAACGAGTCCCATGC
BRCA1	chr17:38449676-38450260	621	TTTGGCAGCAACAGGAAATACAAA	TCAAGAACCGGTTTCCAAAGACA
BRCA1	chr17:38450099-38450693	631	GCTTCCTTCTGGTGGGATCTG	GGGAGGAAATTCTGAGGCAGGT
BRCA1	chr17:38450672-38451219	584	ACCTGCCTCAGAAATTTCTCCC	TGCAGCCAGCCACAGGTACA
BRCA1	chr17:38451018-38451610	593	TGCCTGTAATTCCAGCTACTCAGG	TGGTGGTACGTGTCTGTAGTTCCA

BRCA1	chr17:38452863-38453470	654	GAACTTCTAGGCTCCCACCTTGAC	CCAAGACTCCCTCATCCTCAAAAT
BRCA1	chr17:38454531-38454932	438	TTGGCACAGGTATGTGGGCA	CATGGCATATCAGTGGCAAATTGA
BRCA1	chr17:38456336-38456841	542	CAGCAGCTCAACGCCATCTG	TGGACATTGGACTGCTTGTCCC
BRCA1	chr17:38462347-38462755	445	GAACCCGAGACGGGAATCCA	TGACGTGTCTGCTCCACTTCCA
BRCA1	chr17:38468728-38469145	454	GGCCTGCATAATTCTTGATGATCC	GGAATCCATGTGCAGCAGGC
BRCA1	chr17:38469233-38469773	577	CCCAGCATCACCAGCTTATCTGA	GCCTTGGCGTCTAGAAGATGGG
BRCA1	chr17:38472653-38473237	621	GCCTGGCCACACTCCAAAT	TGCTCGTGACAAGTTTGCCAGA
BRCA1	chr17:38472753-38473302	586	GACTATCATCCATGCTATGCTCAACA	ACTAGTATTCTGAGCTGTGTGCTAGA
BRCA1	chr17:38476099-38476698	636	TGCTGGTAAATTCACCCATGTGA	TCAGCTCGTGTTGGCAACATA
BRCA1	chr17:38476548-38476930	419	GCTTCTCCCTGCTCACACTTTCTTC	GCTACTTTGGATTTCACCAACACTG
BRCA1	chr17:38479623-38480265	643	CCCCATGTTATATGTCAACCCTGA	AAAGTCCTTCACACAGCTAGGACG
BRCA1	chr17:38479905-38480299	431	CGTCAAATCGTGTGGCCAG	CAGCTGGGAGATATGGTGCCTC
BRCA1	chr17:38481747-38482329	619	CCATCAGTTTCCAAGCTTGTTGAGG	GCATCTGTCTGTTGCATTGCTTG
BRCA1	chr17:38487763-38488291	565	TGCCTTGGGTCCCTCTGACTG	GGGCATTAATTGCATGAATGTGG
BRCA1	chr17:38496190-38496818	687	TTAGCAAATGGGTTTGAAGGTTT	TAAATTCCTTGCTTTGGGACACCT
BRCA1	chr17:38496693-38497337	645	CCGTTGCTACCGAGTGTCTGTCTA	ATGAGATGTGCACCCACAGTGATA
BRCA1	chr17:38497064-38497511	484	TCACTCAGACCAACTCCCTGGC	GGAGTCCTAGCCCTTTCACCCA
BRCA1	chr17:38497068-38497625	594	TCAGACCAACTCCCTGGCT	CTGATGACCTGTTAGATGATGGTGAA
BRCA1	chr17:38497484-38498049	602	TGTGTATGGGTGAAAGGGCTAGGA	TCACCTGAAAGAGAAATGGGAAATGA
BRCA1	chr17:38497841-38498430	626	GGCCCTCTGTTTCTACCTAGTTCTGC	TGTGCAACATTCTTGCCCACTC
BRCA1	chr17:38498167-38498726	596	ATTTGGAGTAATGAGTCCAGTTTCGTT	TCTCGTTACTGGAAGTTAGCACTCT
BRCA1	chr17:38498648-38499242	631	TCAAATGCTGCACACTGACTCACA	TGAGGAGGAAGTCTTCTACCAGGCA
BRCA1	chr17:38499078-38499482	441	GGTTTCTGCTGTGCCTGACTGG	TGATAAATCAGGGAATAACCAAACGG
BRCA1	chr17:38499285-38499872	624	CGAGTTCCATATTGCTTATACTGCTGC	GGGAGTCTGAATCAAATGCCAAAG
BRCA1	chr17:38499660-38500239	616	GGAGGCTTGCCTTCTTCCGA	CATGCCAGCTCATTACAGCATGA
BRCA1	chr17:38499977-38500495	555	TCTCTAGGATTCTCTGAGCATGGCA	TGGTTGATTTCACCTCCAAGG
BRCA1	chr17:38500257-38500851	631	GCTCCACATGCAAGTTTGAAACAGA	TGCCTGGCCTGCCCTTTACT
BRCA1	chr17:38501285-38501853	605	TGGGTTGTAAAGGTCCCAAATGGT	CTGCCTCCCAGGTTGAAGCC
BRCA1	chr17:38502623-38503015	429	CACCAAATCCCAAGTCGTGTGTT	CGAAGCCCATGCCTTTAACCA
BRCA1	chr17:38505141-38505506	402	TCTTCAAGGTGGGAACGCGTC	TCCATGGTGTCAAGTTTCTCTTCAGG
BRCA1	chr17:38509319-38509889	607	CAATGCTCAATAAAGAGATGTTGCCA	CATAGGGTTTCTCTTGTTTCTTTGA
BRCA1	chr17:38510241-38510764	560	AAGGTGTGAGACCAGTGGGAGTAATTT	TGCAATGCATTATATCTGCTGTGGAT
BRCA1	chr17:38511518-38512056	575	AAATTGGCCGGGCATGGTAG	TCAACCAGAAGAAAGGGCCTTCA
BRCA1	chr17:38511741-38512186	482	CAGCCCTACTTTACATAAGTCTGCAA	GCTCTTAAGGGCAGTTGTGAGATTA
BRCA1	chr17:38521024-38521673	678	GACAGAGCGAGACTTTGTCTCAAAA	TTGTGTTGAAAAGGAGAGGAGTGG
BRCA1	chr17:38529340-38529971	632	TTGGAGAAAGCTAAGGCTACCACC	TGACAGATGGGTATTCTTTGACGG
BRCA1	chr17:38530137-38530734	666	CTCTACTTCCCTCTTGCGCTTTCT	CTTCCCTCGCGACCTACAACT
BRCA1	chr17:38530564-38531237	674	TAGCGATTCTGACCTTCGTACAGC	ATTCCAAGGGAGACTTCAAGCAG
ERCC2	chr19:50546451-50547026	624	ACTAACGTCCAGTGAACGCGCT	GTCCTTCTCCGACTCCCTAGCTG
ERCC2	chr19:50547076-50547724	696	CTCACCCCAACTTCTCTCACCT	CCAGTTCCAGATTCTGTAGAATGA
ERCC2	chr19:50547530-50548205	677	CTGGGAAATGAACGGGAAACAG	AAAGTGCCGAGGGAATCGACTTT
ERCC2	chr19:50548034-50548716	688	GTGCCTAGGGACAGAGGGGAG	ACAGTCAGCCCTCCACCAAT
ERCC2	chr19:50549541-50550173	635	AGCAGCAGAGAAGCAAGGAACCTA	CCCTTCTGCACTCATTTTATTGG

ERCC2	chr19:50550498-50551109	665	CCAGTGCACAATACACTGTGACCA	TAACAGGGTTGCTGAGGGTTCATT
ERCC2	chr19:50552145-50552709	641	GGGAGATCAGGGAGGATACATTCC	AGGGTGTGAATGCTCTGTGGGT
ERCC2	chr19:50552434-50553046	634	CAGGATCTTGGGGTAGATGTCCAG	GTGGGCTCTCTACTTGGGATCCTT
ERCC2	chr19:50556357-50557008	677	GAATTTCTCTGGCCTCCTCCCTTA	GTCGTGCTAGCAGGTGTGACAAGT
ERCC2	chr19:50558600-50559220	645	GAGATTCTCCAATCCAGCCAGGT	CAGGATCAAAGAGACAGACGAGCA
ERCC2	chr19:50559079-50559771	696	CTCACCTGCAGCACTTCGTC	CATACTTCTGCCTGGCCTGTGTCT
ERCC2	chr19:50559588-50560214	639	CAATCTTGGGGTCCAGGAGGTAGT	CACAGCCTCACAGCCTCCTATGT
ERCC2	chr19:50559816-50560412	633	CAGGGAGATGCAGACAGGCA	CCCTGCATTAAGTTCCACGC
ERCC2	chr19:50563472-50564059	625	AACCAGGCTTGCCAGAGACTCTAA	ACTGCTCAAGAACTGTGCCAGAGA
ERCC2	chr19:50563547-50564095	585	GGAGGAAGTGTGCTTGCCTGG	GGCAGGCATATCCGCTGGAG
ERCC2	chr19:50563763-50564257	531	GAGCCAGTCCCAGAAACGGC	CCCAACATGCAGGGTCATGG
ERCC2	chr19:50564733-50565330	634	TGCAGGTAAATATTTGGCACAGTAGC	GCTCAACGTGGACGGGCTC
ERCC2	chr19:50565302-50565927	626	AGTAGACCAGGAGCCCCTCA	TGAGATCGAGTCTCTCGGCTCTTT
H2AFX	chr11:118469715-118470325	632	CCTCCCACCCCTATTATCAGGAAA	GTGCTTAGCCCAGGACTTTCAGAC
H2AFX	chr11:118469862-118470452	627	CGTGGAAGGGTTAGCTGCAGAA	GGAAGACTTGGCCTTCCGCTC
H2AFX	chr11:118470365-118470972	608	GTGCTGCTGCCAAGAAGAC	GAGGGCCTCACTCACCTTCAG
H2AFX	chr11:118470769-118471363	670	CTTGCCCCGCAGTCTGAAG	TCTGTTCTAGTGTGTTGAGCCGTCG
H2AFX	chr11:118470788-118471465	678	CGGCTCAGCTCTTTCCATGAG	TTGGAGAAAAGAGCCAATCAGGAG
LIG4	chr13:107657854-107658452	599	GGGTAGAATTGTTACAGCTGGACTTG	TCCACGGTTTGAATAAAATTTCCA
LIG4	chr13:107658427-107659021	631	CAAGTCCAGCTGTAACAATTCTACCC	GGGAAGATCATAGTCGTGTTGCAGA
LIG4	chr13:107658691-107659357	667	TTCTTTCTTGGCTTTGGGCTATTG	TTGCCCCGTGAATATGATTGCTATG
LIG4	chr13:107659241-107659863	673	CCATTTCTTCAGGAGTCTGCTCGT	AGATGACAAGGAGTGGCATGAGTG
LIG4	chr13:107659744-107660318	628	TCTTGTGGTTCATCATCACCACT	CCTCTATCCATCTACAAGCCAGACA
LIG4	chr13:107659887-107660486	636	ACGCAAGGTGCAGCCAGTTT	GGGCATGAGACTCTGAGAAAGAGG
LIG4	chr13:107660197-107660888	698	CCTTTACCCCAATATCCTCCAACA	TCTGCATTTAAACCAATGCTAGCTG
LIG4	chr13:107660463-107661042	616	CCTCTTTCTCAGAGTCTCATGCCC	GGATTTAAAGCTTGGTGTTAGTCAGCA
LIG4	chr13:107660834-107661402	605	CCTTCTCAATGTGCTCAATATCTGCAA	TCCTCAGCTAGAAAGAGAGAGAATGGC
LIG4	chr13:107661249-107661844	632	TCCAGCATCTCCATGAGTTCCA	AACTTCAAATTAGGGTTGGAGCAAA
LIG4	chr13:107664667-107665326	667	GAGCAGACAAAGACGCTAGAAGGG	GTGGGGAGTCAAGTAGGGGAAGTG
LIG4	chr13:107665526-107666176	668	GCCACACACACCCCAAACC	GAGGCTATCACTAGCCAGAGCACA
MDC1	chr6:30775839-30776419	631	CATGAGTGGCATCGAGCAATAACT	CCTGATTTTGCCTTTGCTCTGTCT
MDC1	chr6:30778056-30778701	687	GGGATAGATGGAGCAAATGTAGCA	AAATGCTAGGCAGCAGAGCTGATT
MDC1	chr6:30778580-30779183	669	AGGGTCGGTCACCACATATTCATC	AGCCCCCAAAGTAAGAGACAAAGG
MDC1	chr6:30779082-30779646	632	GCCATCAGCACCCATCTCTACAAT	GAATCCCTTACAGCCATTCTGAG
MDC1	chr6:30779588-30780153	639	TGAATTGGTGTCTCAAGAAGCTGG	GCCACTAGGTGCAGGACAAATAGG
MDC1	chr6:30780525-30781149	635	GAGACGTAGGCTCAGGGGTAACAG	CCCACATATCAGGCTACTAGGGGA
MDC1	chr6:30780824-30781496	673	GCAGGACAAATAGGTCCTCTGTCA	GGGCTGGAGGATCAATCTCTAAAA
MDC1	chr6:30780824-30781496	694	TCAGGGGCTATAGGGACAGTTGAT	GATCCTCTCTTCTCCGCATCAGT
MDC1	chr6:30781256-30781880	626	GTAGCCTGAGAGGTGGGTTTCAGAG	CCTCACTTGCTTCTGTTTCTCCCT
MDC1	chr6:30782861-30783502	677	CACACGTGGATGATGGTAAGGAAA	GATACACAGAGAGGGGAGCCAGAG
MDC1	chr6:30783362-30783980	655	ACCTGACTGGCTCCCAGAAGGTA	ACCAGGAGACCAACATCCAGAGAG
MDC1	chr6:30783519-30784152	639	TTGGGCACCTTCTCTTCTAACTCG	TCCCTCTCCCTCTCTCTCTTCC
MDC1	chr6:30786907-30787506	642	GATCACTTGAGGTCGGGAGTTTGT	TGTCTTATATTCTCCCCGACCAG

MDC1	chr6:30787433-30788050	686	CTGATTCTCCAGAAAGCACTGGGT	CAAACAGATGTGAAAGCAGTTGGG
MDC1	chr6:30787893-30788495	631	GCTGGAAGCTGGCTCTTTCTTACA	CAGCGATACAGATGACGAGGAAGA
MDC1	chr6:30788436-30789038	674	TCTTTCAGATGTGCCAAAGTCAGC	AGATGTGGAAGAAGGTCAGCAACC
MDC1	chr6:30789156-30789773	685	AGGGATACCCCAACTCAACTGTGA	GAGACCTCCTAAGGTTTTGAGCCC
MDC1	chr6:30789418-30790048	649	CACAGAGGAAGATGTGGTCCTTGA	TAATGCATATGGAGGCCTTGAGTG
MDC1	chr6:30790528-30791214	699	TCTCAAAGCACGGGAATTACAGGT	GCTGAGGTGAGAGAATTGCTTGAA
MDC1	chr6:30792710-30793286	631	AACTCCGTCTTTATGACAGGCCAA	AAGCGGTAGTGGGTTGTCCCTT
MRE11A	chr11:093791680-93792263	620	TGAGGCAGCCACTAACCAAGTG	CCCACTCTTCTTTCTCCTTTGC
MRE11A	chr11:93789924-93790518	595	TGATGGAATCCCTCTACAGGTCAA	TTCAGTTCACCGCTAAGGAAAGTG
MRE11A	chr11:93790206-93790525	356	TCCATAACAGGCTGAACCAAATGA	TGAGCACTGATGGAATCCCTCTACA
MRE11A	chr11:93790371-93790813	479	TGCGTCTAATGGCAGAAGCACC	CATTGAGAGGAAGACATCTGTAGGGAA
MRE11A	chr11:93790501-93791160	693	TGTAGAGGGATTCCATCAGTGCTC	ACGCCTGGCTGATTTTTGTATTTT
MRE11A	chr11:93790822-93791406	621	CCTGCTCTCCCAAAGCCTCC	GGAGGCAGTGTCTGGATGATGC
MRE11A	chr11:93791078-93791702	689	TCACAAAATGACCTGAATTAGCTGGA	ACACTTGGTTAGTGGCTGCCTCAT
MRE11A	chr11:93791531-93792212	699	TATTTACAGGACAATGCCTTCCA	TGCCTAGTTCTAGGAGGAAACGGG
MRE11A	chr11:93792063-93792643	630	GAGAAATCCTGGCATTGACATTCC	GCCAAAGTTGAGGGAAGAGCTTA
MRE11A	chr11:93792621-93793211	627	AAGCTCTTCCCTCAACTTTGGCT	AGATACATGCACACACAGCAGGATAAA
MRE11A	chr11:93802483-93803058	646	TGGAGGCTGAGAGTAGGATGTGTG	TGAGGAAATTGAAGCACAGAGAGG
MRE11A	chr11:93808340-93808994	665	AGTCTAGGCGACAGAATGAGGCAC	GAGCCTATGCAAGTCATTCACCAG
MRE11A	chr11:93809865-93810243	415	GCTCCTTCCAGCTTTAATGTTCCA	CAGTTGGGCATTGAGTTATGCG
MRE11A	chr11:93818381-93818954	574	CTACCACGTCCAGCCTATTTCTT	TTGGACTCCATATCCTAGCCATCA
MRE11A	chr11:93819823-93820439	647	CTAAGTGCATGTGGCCATTCAAAA	AACTCTTGGGTGCAAGTGATCCTC
MRE11A	chr11:93828956-93829542	623	GCAGCCATCCTAAGCCAACCC	TGCAGCAAGGTGCACAAGAGTG
MRE11A	chr11:93831998-93832625	694	TCCATGGGGAACAAAACACTTTAG	GAGGAGTATTCATGTGTATGCCTTATCC
MRE11A	chr11:93832241-93832603	399	TCGAGGGCATCAATATGACGTTT	CAGGCCTCTACATTTACGTGTCC
MRE11A	chr11:93833579-93833975	433	TTTCCCTGCTGTGCAGCAACT	CCATGTTGAGCAAGCTGGCAGT
MRE11A	chr11:93836707-93837325	685	CACGTTGTGCACATGTACCCTAGA	CAGGGGGAGATGTAATCATTCTGC
MRE11A	chr11:93840495-93840993	535	TTGCCTCCGATGGTGATTGC	GCTGAGGAAAGCCTTATTGAAACATGA
MRE11A	chr11:93842925-93843486	598	CACACGATAGTCTCCCATTCCTCA	TGACTCGGTGTTTCATTTCTCTCCA
MRE11A	chr11:93844148-93844803	673	TTGAATTTGCCTAATGAGCAGCAA	GCTTTCTCTTTTCGGGTTTCCACT
MRE11A	chr11:93848872-93849513	642	GCATGGTGGCTTATGCTTGTAAATC	AAGATTACAGGCACACACCACCAT
MRE11A	chr11:93851104-93851690	623	TCCTGCTCTTTCACTTGAGAATCA	GCAGATGCACTTTGTGCCTTGG
MRE11A	chr11:93852229-93852814	633	GGTGTTCACTCCTACTCCTGGCTT	CCACAAGCACTGTTTATTATAGTTGGGG
MRE11A	chr11:93858544-93859140	633	CCGAGTAGCTGGGTCAGTTCCAC	TGGCCTGAATCAGAGACTTGGTG
MRE11A	chr11:93863534-93864079	582	GCAGGCAAGGTAAGCACCTGA	TTTGGGCCTGGGTTACATGA
MRE11A	chr11:93865381-93865970	662	TGCAAGACTCCAATCTATAGCTGCAT	AAGAGCACGGGAAAGGAAAATAGG
MRE11A	chr11:93866249-93866869	626	AAAATAGCCAGGTTTGGGGAAGAG	GACAGGGAATAACAACCCACCTGA
RAD50	chr5:131920445-131921084	656	AGCACCTAGCCCTCTGCTTCG	GTAGCGACCTGTAACTGAAGGCG
RAD50	chr5:131922511-131923103	629	TCCTACAGCCTGGAGTTAATGTGAGAA	TGTCAACAACGGTTACTACTGGGTGC
RAD50	chr5:131939145-131939740	632	TCTCCTAATGATGCTGAATAAAGGAGG	GGAGGAGGCTGTGTGTGCGT
RAD50	chr5:131942768-131943237	506	TGATGAAGCCATTTCTAACGGGA	ATGCCCAATGGTTGCTGCTG
RAD50	chr5:131943218-131943758	577	CAGCAGCAACCATTGGGCAT	GCTTGATTTAGCCAGTCCACGATG
RAD50	chr5:131950876-131951537	670	AATGACTTTTGTGGCAGGTGTTGA	TGCTCATCAGTCCCTTGAAAAACC

RAD50	chr5:131951269-131951916	669	GAAAAATGGAAAAGGTTTGTGGTGG	ACCATACCTAGCTCCCTCCTGTCC
RAD50	chr5:131952046-131952625	580	TTGCTTCAATAAAGTTTTTCTGCC	ATGGCGAAAACCGTCTCTACTAA
RAD50	chr5:131952285-131952840	592	ACAGCTGCAAGCAGATCGCC	TGGGACCAATGTCAAATATGTGGTCTA
RAD50	chr5:131953044-131953607	632	TGATGTTACACAATGATAAAATTGCC	TCGGGTTGTAGAACCAAAGAGTCA
RAD50	chr5:131954414-131954989	612	TTGGTCAGGGACCACATCACA	TGGTCAGCATCTCCATTTGGG
RAD50	chr5:131954563-131955072	546	TCTCACATTTCTTTCCTGTTTGACCC	TCTATGACTTATGAGTGCAAGGTAGGC
RAD50	chr5:131955267-131955870	674	TCGACTTGGTACTCCACTCTTAAGGC	TTGCTGGTATCACTGCTCAGAAGA
RAD50	chr5:131958269-131958857	660	GTGAGTCAGTGTCTAGGGGGAGA	CCACAGGTGGTAGTTGTGTCTCTCA
RAD50	chr5:131958991-131959528	574	TGCTCTTTGGAAGCGAATATCGG	AAGTGATATAAGACAGGGCATAACCAGC
RAD50	chr5:131966678-131967137	496	GGAGAAACCTGGCCAACACCA	CAAATTCAGCCACCATGGAACA
RAD50	chr5:131967208-131967764	593	TCAGATACCCTCAGGGAGAACTGC	AAGAGCAAATATATGTGGACAGGAAGG
RAD50	chr5:131968184-131968541	394	CCTGCCCTGTAAGCTTTCCCTG	TGCTCCTCCAGTTGCTGACGA
RAD50	chr5:131968209-131968557	385	GTGGCCAGCAGGGAACATCA	GGATAATTCCACAGTCTGCTCCTCC
RAD50	chr5:131968219-131968837	664	GGGAACATCAAGCTGATTTGAGAA	AATGAGCATGTTTGCCTAGACAGC
RAD50	chr5:131971975-131972579	668	CATTTACTGGCTGTTGTGACCCTG	ATCGCAGACAAGTCCCTTTCTCAC
RAD50	chr5:131972368-131972937	606	TTCATAGCACACGTCGGACA	TTTCTTTGTGTTTCTCGCATTAC
RAD50	chr5:131972555-131973105	587	GGTGAGAAAAGGGACTTGTCTGCG	CCACCACGCTTGGCCTCTTT
RAD50	chr5:131979446-131979999	590	TCCTTCACACTGGCTTATTCTCCC	TGTGCAGCAGGCTAGCAGATGT
RAD50	chr5:131981443-131982091	668	GCTATTTAGCAACCTATGTGCGGC	AGGATGAGGCAGGAGAATCATTTG
RAD50	chr5:132000305-132000887	619	CAGGCCTTCCTGTGACCCGT	TCCAGGGAGGTAATGCTGGC
RAD50	chr5:132001420-132002040	647	GCCTGGAGGAACTCTTAACAGGG	GAGAATGCTTCAGGCCCTTCTTTT
RAD50	chr5:132004019-132004675	696	TCAGCGTTGTTCTGAGCATTTTGT	GAACCCCTCACAGTGACTCTCTCC
RAD50	chr5:132005586-132006177	628	GGAGAAGAGACTCCTGCCTGGCT	TGGAATGGGATGAAGAGCAGCA
RAD50	chr5:132005782-132006374	629	CGCTCACAGCAGCGTAACTTCC	CCACATGCAAGGAAGTAAATTCAGAGG
RAD50	chr5:132005974-132006573	636	TGCCATAGAAATGTAGGTCCTCAGAAA	GAAGGTGGTGGGTACTGACTTAGATGA
RAD50	chr5:132006247-132006835	625	TGCAAATGCATGCTTCTTCTCAA	GGGAGCAGGCCTTGACTCTG
RAD50	chr5:132006718-132007308	640	CCTCTGCGTCTATCCTGTGTAGCA	ACCACCCCCAGGATACTCTGTCTT
RAD50	chr5:132007037-132007701	665	TGCTGCAACAAGTACACTTTCAT	CAGGGGTACAAATAAAATTGGGGA
RAD50	chr5:132007405-132008002	634	TTTATCCCAAGAATGCAAGATTTCAGA	GCCCAGGCAGTCTGGCTCAT