

Correlation of platinum cytotoxicity to drug-DNA adduct levels in a breast cancer cell line panel

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Table S1. Table of nucleotide and amino acid mutations present in the DNA repair genes of all six breast cancer cell lines used in this study.

Cell line	Gene	cDNA	AA	Classification	FATHMM prediction	FATHMM score
MDA-MB-468	ATR	c.2633+5A>G	p.?	Unknown	NEUTRAL	0.11506
MDA-MB-468	BLM	c.1661A>T	p.D554V	Substitution - Missense	PATHOGENIC	0.99367
MDA-MB-468	BRCA2	c.2895G>C	p.M965I	Substitution - Missense	NEUTRAL	0.10067
MDA-MB-468	CANX	c.1764G>A	p.K588K	Substitution - coding silent	PATHOGENIC	0.8761
MDA-MB-468	ERBB2	c.454delG	p.V153fs*2	Deletion - Frameshift		
MDA-MB-468	FANCA	c.2605C>T	p.Q869*	Substitution - Nonsense	PATHOGENIC	0.99497
MDA-MB-468	MUS81	c.495G>A	p.Q165Q	Substitution - coding silent	PATHOGENIC	0.81424
MDA-MB-468	PTEN	c.253+1G>T	p.?	Unknown	PATHOGENIC	0.90626
MDA-MB-468	REV1	c.1715C>T	p.A572V	Substitution - Missense	PATHOGENIC	0.95603
MDA-MB-468	TP53	c.818G>A	p.R273H	Substitution - Missense	PATHOGENIC	0.99523
MDA-MB-468	XRCC5	c.1606C>T	p.L536F	Substitution - Missense	PATHOGENIC	0.75834
BT-549	AHCY	c.1141G>A	p.V381I	Substitution - Missense		0.65714
BT-549	DOT1L	c.4339_4359del21	p.G1452_A1458delGGAASSA	Deletion - In frame		
BT-549	FANCL	c.406A>G	p.I136V	Substitution - Missense		0.54314
BT-549	FGFR1	c.153G>A	p.L51L	Substitution - coding silent	PATHOGENIC	0.7364
BT-549	MUTYH	c.1271G>T	p.W424L	Substitution - Missense	PATHOGENIC	0.95199
BT-549	POLQ	c.7793A>G	p.H2598R	Substitution - Missense	PATHOGENIC	0.97237
BT-549	PTEN	c.821delG	p.V275fs*1	Deletion - Frameshift		
BT-549	TP53	c.747G>C	p.R249S	Substitution - Missense	NEUTRAL	0.2434
MDA-MB-231	AR	c.1983A>G	p.T661T	Substitution - coding silent	NEUTRAL	0.10652
MDA-MB-231	ATM	c.3014A>T	p.N1005I	Substitution - Missense	NEUTRAL	0.08843
MDA-MB-231	MPG	c.520+7A>G	p.?	Unknown	NEUTRAL	0.00868
MDA-MB-231	MSH3	c.2659G>A	p.G887R	Substitution - Missense	PATHOGENIC	0.98796
MDA-MB-231	MSH4	c.2444A>G	p.Q815R	Substitution - Missense	PATHOGENIC	0.9816
MDA-MB-231	PNKP	c.1126+7G>A	p.?	Unknown	NEUTRAL	0.0229
MDA-MB-231	RECQL	c.1667_1667+3delAGTA	p.?	Unknown		
MDA-MB-231	TP53	c.839G>A	p.R280K	Substitution - Missense	PATHOGENIC	0.99573
MCF7	ERCC6	c.3297T>A	p.S1099R	Substitution - Missense	NEUTRAL	0.16277
MCF7	ERCC8	c.741A>G	p.K247K	Substitution - coding silent	PATHOGENIC	0.83829
MCF7	HLTF	c.859G>T	p.V287F	Substitution - Missense	PATHOGENIC	0.96516
MCF7	NBN	c.127C>T	p.R43*	Substitution - Nonsense	PATHOGENIC	0.705
MCF7	PIK3CA	c.1633G>A	p.E545K	Substitution - Missense	PATHOGENIC	0.97342
MCF7	XRCC4	c.590A>G	p.K197R	Substitution - Missense	PATHOGENIC	0.95478
Hs-578-T	EXO1	c.1514+4T>C	p.?	Unknown	NEUTRAL	0.09544
Hs-578-T	POLD3	c.1030T>C	p.Y344H	Substitution - Missense	PATHOGENIC	0.70197
Hs-578-T	POLE	c.6012C>T	p.I2004I	Substitution - coding silent	NEUTRAL	0.04781
Hs-578-T	POLQ	c.7126C>T	p.R2376*	Substitution - Nonsense	PATHOGENIC	0.95276
Hs-578-T	TP53	c.469G>T	p.V157F	Substitution - Missense	NEUTRAL	0.24495
T47D	EHMT1	c.136G>T	p.A46S	Substitution - Missense	NEUTRAL	0.08978
T47D	PRDX2	c.520G>A	p.A174T	Substitution - Missense	PATHOGENIC	0.95722
T47D	PIK3CA	c.3140A>G	p.H1047R	Substitution - Missense	PATHOGENIC	0.96139
T47D	TP53	c.580C>T	p.L194F	Substitution - Missense	PATHOGENIC	0.99165