

**Table S4 Gene Ontology (GO) analysis of the genetic interactions identified with Pol  $\delta$  (*cdc2-2*) mutation**

Gene Ontology analysis was performed using Gorilla (Eden et al. 2009), last update May 2015.

The GO term and their description are listed. The p-value, the False Discovery Rate (FDR) q-value and the enrichment (defined as follows: N is the total number of genes, B is the total number of genes associated with a specific GO term, n is the number of genes in the top of the user's input list or in the target set when appropriate, b is the number of genes in the intersection. Enrichment =  $(b/n) / (B/N)$ ) are shown for each GO term and hits with p-values of less than 0.01 were included. Results are listed beginning with GO categories with the highest enrichment.

GO term	Description	P-value	FDR q-value	Enrichment (N, B, n, b)	Genes
GO:0000709	meiotic joint molecule formation	2.13E-04	2.14E-02	77.84 (4320,3,37,2)	<i>RAD51 RAD52</i>
GO:0044819	mitotic G1/S transition checkpoint	2.13E-04	2.09E-02	77.84 (4320,3,37,2)	<i>RAD9 BRE1</i>
GO:0097551	mitochondrial double-strand break repair	2.13E-04	2.04E-02	77.84 (4320,3,37,2)	<i>RAD50 XRS2</i>
GO:0097552	mitochondrial double-strand break repair via homologous recombination	2.13E-04	2.00E-02	77.84 (4320,3,37,2)	<i>RAD50 XRS2</i>
GO:0031571	mitotic G1 DNA damage checkpoint	2.13E-04	1.95E-02	77.84 (4320,3,37,2)	<i>RAD9 BRE1</i>
GO:0030491	heteroduplex formation	1.57E-07	2.94E-05	66.72 (4320,7,37,4)	<i>RAD51 RAD55 RAD57 RAD54</i>
GO:0000707	meiotic DNA recombinase assembly	4.24E-04	3.51E-02	58.38 (4320,4,37,2)	<i>RAD55 RAD57</i>
GO:1902807	negative regulation of cell cycle G1/S phase transition	4.24E-04	3.45E-02	58.38 (4320,4,37,2)	<i>RAD9 BRE1</i>
GO:2000134	negative regulation of G1/S transition of mitotic cell cycle	4.24E-04	3.38E-02	58.38 (4320,4,37,2)	<i>RAD9 BRE1</i>
GO:0044783	G1 DNA damage checkpoint	4.24E-04	3.32E-02	58.38 (4320,4,37,2)	<i>RAD9 BRE1</i>
GO:0032071	regulation of endodeoxyribonuclease activity	7.02E-04	5.05E-02	46.70 (4320,5,37,2)	<i>RAD54 RAD50</i>
GO:0006277	DNA amplification	7.02E-04	4.97E-02	46.70 (4320,5,37,2)	<i>RAD52 POL32</i>
GO:0000730	DNA recombinase assembly	3.15E-05	3.57E-03	43.78 (4320,8,37,3)	<i>RAD52 RAD55 RAD57</i>
GO:0031573	intra-S DNA damage checkpoint	3.15E-05	3.48E-03	43.78 (4320,8,37,3)	<i>RAD9 DDC1 BRE1</i>
GO:0000722	telomere maintenance via recombination	1.95E-09	1.68E-06	43.78 (4320,16,37,6)	<i>RAD51 RAD52 RAD57 RAD54 BRE1 RAD50</i>
GO:0000077	DNA damage checkpoint	6.47E-09	3.10E-06	36.87 (4320,19,37,6)	<i>BMH1 RAD9 RAD24 DDC1 BRE1 RAD17</i>

GO:0044773	mitotic DNA damage checkpoint	6.66E-05	7.18E-03	35.03 (4320,10,37,3)	<i>RAD9 DDC1 BRE1</i>
GO:0042138	meiotic DNA double-strand break formation	6.66E-05	7.01E-03	35.03 (4320,10,37,3)	<i>BRE1 RAD50 XRS2</i>
GO:0006312	mitotic recombination	3.11E-08	9.58E-06	29.19 (4320,24,37,6)	<i>RAD51 RAD52 RAD57 RAD54 BRE1 RAD50</i>
GO:0006284	base-excision repair	1.56E-04	1.60E-02	26.94 (4320,13,37,3)	<i>POL32 RAD50 XRS2</i>
GO:0031570	DNA integrity checkpoint	1.06E-07	2.30E-05	24.16 (4320,29,37,6)	<i>BMH1 RAD9 RAD24 DDC1 BRE1 RAD17</i>
GO:0044774	mitotic DNA integrity checkpoint	3.00E-04	2.64E-02	21.89 (4320,16,37,3)	<i>RAD9 DDC1 BRE1</i>
GO:0000726	non-recombinational repair	3.62E-04	3.12E-02	20.60 (4320,17,37,3)	<i>RAD52 RAD50 XRS2</i>
GO:0000727	double-strand break repair via break-induced replication	5.10E-04	3.93E-02	18.44 (4320,19,37,3)	<i>RAD52 POL32 RAD50</i>
GO:0000723	telomere maintenance	6.35E-09	3.91E-06	18.31 (4320,51,37,8)	<i>RAD51 RAD52 TEN1 RAD57 RAD54 BRE1 RAD50 XRS2</i>
GO:0060249	anatomical structure homeostasis	6.35E-09	3.42E-06	18.31 (4320,51,37,8)	<i>RAD51 RAD52 TEN1 RAD57 RAD54 BRE1 RAD50 XRS2</i>
GO:0000725	recombinational repair	6.68E-08	1.52E-05	18.16 (4320,45,37,7)	<i>RAD52 POL32 DDC1 RAD54 BRE1 RAD50 XRS2</i>
GO:0032200	telomere organization	7.46E-09	3.22E-06	17.96 (4320,52,37,8)	<i>RAD51 RAD52 TEN1 RAD57 RAD54 BRE1 RAD50 XRS2</i>
GO:0000724	double-strand break repair via homologous recombination	9.39E-06	1.23E-03	16.68 (4320,35,37,5)	<i>RAD52 POL32 RAD54 BRE1 RAD50</i>
GO:0006271	DNA strand elongation involved in DNA replication	6.92E-04	5.06E-02	16.68 (4320,21,37,3)	<i>POL32 RFC5 PRI1</i>
GO:0006302	double-strand break repair	1.01E-06	1.61E-04	12.38 (4320,66,37,7)	<i>RAD52 POL32 RAD54 BRE1 RAD50 RAD17 XRS2</i>
GO:0006310	DNA recombination	9.25E-11	1.99E-07	11.98 (4320,117,37,12)	<i>RAD51 RAD52 RAD24 POL32 NMD2 RAD57 DDC1 RAD54 BRE1 RAD50 RAD17 XRS2</i>
GO:0000075	cell cycle checkpoint	1.12E-05	1.42E-03	11.30 (4320,62,37,6)	<i>BMH1 RAD9 RAD24 DDC1 BRE1 RAD17</i>
GO:0007093	mitotic cell cycle checkpoint	5.75E-04	4.35E-02	10.15 (4320,46,37,4)	<i>BMH1 RAD9 DDC1 BRE1</i>
GO:0045930	negative regulation of mitotic cell cycle	9.89E-04	6.88E-02	8.81 (4320,53,37,4)	<i>BMH1 RAD9 DDC1 BRE1 BRE1</i>
GO:0006260	DNA replication	3.90E-04	3.29E-02	7.78 (4320,75,37,5)	<i>LGE1 POL32 TEN1 RFC5 PRI1</i>
GO:0006281	DNA repair	3.38E-09	2.43E-06	7.70 (4320,197,37,13)	<i>RAD51 RAD52 RAD55 RAD24 POL32 RAD50 RAD17 RAD9 RAD57 RAD54 DDC1 BRE1 XRS2</i>
GO:0006974	cellular response to DNA damage stimulus	1.64E-10	2.36E-07	7.61 (4320,230,37,15)	<i>RAD51 BMH1 RAD52 RAD55 RAD24 POL32 RMI1 RAD50 RAD17 RAD9 RAD57 RAD54 DDC1</i>

						<i>BRE1 XRS2</i>
GO:0006259	DNA metabolic process	6.89E-13	2.97E-09	7.09	(4320,313,37,19)	<i>RAD51 RAD52 RAD55 RAD24 LGE1 POL32 RMI1 TEN1 RFC5 RAD50 RAD17 RAD9 RAD57 NMD2 RAD54 DDC1 BRE1 XRS2 PRI1</i>
GO:1903046	meiotic cell cycle process	4.93E-08	1.42E-05	6.97	(4320,201,37,12)	<i>RAD51 RAD52 BMH1 LGE1 RAD24 RAD55 RAD57 DDC1 BRE1 RAD50 RAD17 XRS2</i>
GO:0051052	regulation of DNA metabolic process	6.59E-04	4.90E-02	6.95	(4320,84,37,5)	<i>RAD9 TEN1 RAD54 BRE1 RAD50</i>
GO:0051276	chromosome organization	1.53E-06	2.35E-04	6.52	(4320,179,37,10)	<i>RAD51 RAD52 RMI1 TEN1 RAD57 RAD54 BRE1 RAD50 RFC5 XRS2</i>
GO:0042592	homeostatic process	2.79E-05	3.25E-03	5.36	(4320,196,37,9)	<i>RAD51 RAD52 TEN1 RAD57 PMR1 RAD54 BRE1 RAD50 XRS2</i>
GO:0033554	cellular response to stress	1.11E-07	2.28E-05	4.39	(4320,426,37,16)	<i>RAD51 RAD52 BMH1 NCB2 RAD55 RAD24 POL32 RMI1 RAD50 RAD17 RAD9 RAD57 RAD54 DDC1 BRE1 XRS2</i>
GO:0051716	cellular response to stimulus	4.40E-07	7.60E-05	3.97	(4320,470,37,16)	<i>RAD51 RAD52 BMH1 NCB2 RAD55 RAD24 POL32 RMI1 RAD50 RAD17 RAD9 RAD57 RAD54 DDC1 BRE1 XRS2</i>
GO:0022402	cell cycle process	1.67E-06	2.40E-04	3.87	(4320,452,37,15)	<i>RAD51 RAD52 BMH1 RAD55 LGE1 RAD24 RMI1 RAD50 RFC5 RAD17 RAD9 RAD57 DDC1 BRE1 XRS2</i>
GO:0006950	response to stress	9.26E-07	1.54E-04	3.77	(4320,496,37,16)	<i>RAD51 RAD52 BMH1 NCB2 RAD55 RAD24 POL32 RMI1 RAD50 RAD17 RAD9 RAD57 RAD54 DDC1 BRE1 XRS2</i>
GO:0065008	regulation of biological quality	2.60E-04	2.34E-02	3.63	(4320,322,37,10)	<i>RAD51 RAD52 LGE1 TEN1 RAD57 PMR1 RAD54 BRE1 RAD50 XRS2</i>
GO:0050896	response to stimulus	1.48E-05	1.77E-03	3.06	(4320,610,37,16)	<i>RAD51 RAD52 BMH1 NCB2 RAD55 RAD24 POL32 RMI1 RAD50 RAD17 RAD9 RAD57 RAD54 DDC1 BRE1 XRS2</i>
GO:0090304	nucleic acid metabolic process	5.65E-10	6.09E-07	2.99	(4320,1054,37,27)	<i>RAD55 LGE1 RAD24 LEA1 RAD50 RAD9 CFD1 NMD2 HTZ1 RAD54 PRI1 RAD51 RAD52 SAD1 CAF40 NCB2 POL32 RMI1 TEN1 RFC5 RAD17 INO2 RAD57 DDC1 BRE1 SMI1 XRS2</i>
GO:0006139	nucleobase-containing compound metabolic process	1.57E-08	6.16E-06	2.60	(4320,1211,37,27)	<i>RAD55 LGE1 RAD24 LEA1 RAD50 RAD9 CFD1 NMD2 HTZ1 RAD54 PRI1 RAD51 RAD52 SAD1 CAF40 NCB2 POL32 RMI1 TEN1 RFC5 RAD17 INO2 RAD57 DDC1 BRE1 SMI1 XRS2</i>
GO:0006725	cellular aromatic compound metabolic process	5.08E-08	1.37E-05	2.48	(4320,1273,37,27)	<i>RAD55 LGE1 RAD24 LEA1 RAD50 RAD9 CFD1 NMD2 HTZ1 RAD54 PRI1 RAD51 RAD52 SAD1 CAF40 NCB2 POL32 RMI1 TEN1 RFC5 RAD17 INO2 RAD57 DDC1 BRE1 SMI1 XRS2</i>
GO:0046483	heterocycle metabolic process	5.56E-08	1.41E-05	2.47	(4320,1278,37,27)	<i>RAD55 LGE1 RAD24 LEA1 RAD50 RAD9 CFD1 NMD2 HTZ1 RAD54 PRI1 RAD51 RAD52 SAD1</i>

					CAF40 NCB2 POL32 RMI1 TEN1 RFC5 RAD17 INO2 RAD57 DDC1 BRE1 SMI1 XRS2
GO:0034641	cellular nitrogen compound metabolic process	2.22E-08	7.98E-06	2.45 (4320,1332,37,28)	RAD55 LGE1 RAD24 LEA1 RAD50 RAD9 CFD1 NMD2 HTZ1 RAD54 PRI1 RAD51 RAD52 SAD1 CAF40 NCB2 POL32 RMI1 TEN1 RFC5 RAD17 INO2 RAD57 DDC1 BRE1 SPE1 SMI1 XRS2
GO:1901360	organic cyclic compound metabolic process	1.24E-07	2.43E-05	2.38 (4320,1323,37,27)	RAD55 LGE1 RAD24 LEA1 RAD50 RAD9 CFD1 NMD2 HTZ1 RAD54 PRI1 RAD51 RAD52 SAD1 CAF40 NCB2 POL32 RMI1 TEN1 RFC5 RAD17 INO2 RAD57 DDC1 BRE1 SMI1 XRS2
GO:0006807	nitrogen compound metabolic process	2.85E-08	9.46E-06	2.33 (4320,1455,37,29)	BMH1 RAD55 LGE1 RAD24 LEA1 RAD50 RAD9 CFD1 NMD2 HTZ1 RAD54 PRI1 RAD51 RAD52 SAD1 CAF40 NCB2 POL32 RMI1 TEN1 RFC5 RAD17 INO2 RAD57 DDC1 BRE1 SPE1 SMI1 XRS2
GO:0044260	cellular macromolecule metabolic process	6.48E-08	1.55E-05	2.08 (4320,1744,37,31)	BMH1 GPI15 RAD55 LGE1 RAD24 LEA1 RAD50 PRE8 RAD9 CFD1 HTZ1 NMD2 RAD54 PRI1 RAD51 RAD52 SAD1 CAF40 NCB2 POL32 RMI1 TEN1 SHR3 RFC5 RAD17 INO2 RAD57 DDC1 BRE1 SMI1 XRS2
GO:0043170	macromolecule metabolic process	2.20E-07	3.96E-05	1.98 (4320,1824,37,31)	BMH1 GPI15 RAD55 LGE1 RAD24 LEA1 RAD50 PRE8 RAD9 CFD1 HTZ1 NMD2 RAD54 PRI1 RAD51 RAD52 SAD1 CAF40 NCB2 POL32 RMI1 TEN1 SHR3 RFC5 RAD17 INO2 RAD57 DDC1 BRE1 SMI1 XRS2
GO:0044238	primary metabolic process	3.68E-06	5.13E-04	1.67 (4320,2314,37,33)	BMH1 GPI15 RAD55 LGE1 RAD24 LEA1 RAD50 PRE8 RAD9 CFD1 INP52 HTZ1 NMD2 RAD54 PRI1 RAD51 RAD52 SAD1 CAF40 NCB2 POL32 RMI1 TEN1 SHR3 RFC5 RAD17 INO2 RAD57 DDC1 BRE1 SPE1 SMI1 XRS2
GO:0044237	cellular metabolic process	1.64E-06	2.44E-04	1.65 (4320,2409,37,34)	BMH1 GPI15 RAD55 LGE1 RAD24 LEA1 RAD50 PRE8 RAD9 CFD1 INP52 HTZ1 NMD2 RAD54 PRI1 RAD51 RAD52 SAD1 CAF40 NCB2 POL32 RMI1 TEN1 SHR3 RFC5 RAD17 INO2 IPP1 RAD57 DDC1 BRE1 SPE1 SMI1 XRS2
GO:0071704	organic substance metabolic process	1.27E-05	1.57E-03	1.59 (4320,2416,37,33)	BMH1 GPI15 RAD55 LGE1 RAD24 LEA1 RAD50 PRE8 RAD9 CFD1 INP52 HTZ1 NMD2 RAD54 PRI1 RAD51 RAD52 SAD1 CAF40 NCB2 POL32 RMI1 TEN1 SHR3 RFC5 RAD17 INO2 RAD57 DDC1 BRE1 SPE1 SMI1 XRS2
GO:0008152	metabolic process	7.66E-06	1.03E-03	1.51 (4320,2709,37,35)	BMH1 GPI15 RAD55 LGE1 RAD24 LEA1 RAD50 PRE8 RAD9 CFD1 INP52 HTZ1 PMR1 NMD2 RAD54 PRI1 RAD51 RAD52 SAD1 CAF40 NCB2 POL32 RMI1 TEN1 SHR3 RFC5 RAD17 INO2

**Cellular components**

GO term	Description	P-value	FDR q-value	Enrichment (N, B, n, b)	Genes
GO:0030870	Mre11 complex	7.14E-05	2.05E-02	116.76 (4320,2,37,2)	RAD50 XRS2
GO:0030896	checkpoint clamp complex	7.14E-05	1.53E-02	116.76 (4320,2,37,2)	DDC1 RAD17
GO:0033061	DNA recombinase mediator complex	7.14E-05	1.23E-02	116.76 (4320,2,37,2)	RAD55 RAD57
GO:0033062	Rhp55-Rhp57 complex	7.14E-05	1.02E-02	116.76 (4320,2,37,2)	RAD55 RAD57
GO:0031389	Rad17 RFC-like complex	7.02E-04	6.71E-02	46.70 (4320,5,37,2)	RAD24 RFC5
GO:0044427	chromosomal part	1.89E-05	8.12E-03	4.41 (4320,291,37,11)	RAD9 RAD24 POL32 RMI1 TEN1 HTZ1 DDC1 BRE1 RFC5 RAD17 PRI1
GO:0044454	nuclear chromosome part	3.65E-04	3.92E-02	4.34 (4320,215,37,8)	RMI1 POL32 TEN1 HTZ1 DDC1 BRE1 RAD17 PRI1
GO:0044428	nuclear part	1.37E-04	1.69E-02	2.45 (4320,811,37,17)	RAD51 SAD1 RAD52 NCB2 RAD55 POL32 RMI1 TEN1 LEA1 RAD50 RAD17 RAD57 HTZ1 DDC1 BRE1 PRI1 XRS2
GO:0005634	nucleus	7.84E-06	6.74E-03	1.98 (4320,1591,37,27)	BMH1 LGE1 RAD55 RAD24 LEA1 RAD50 PRE8 RAD9 HTZ1 RAD54 RAD51 RAD52 SAD1 CAF40 NCB2 RMI1 POL32 TEN1 RFC5 RAD17 INO2 IPP1 RAD57 DDC1 BRE1 SMI1 XRS2