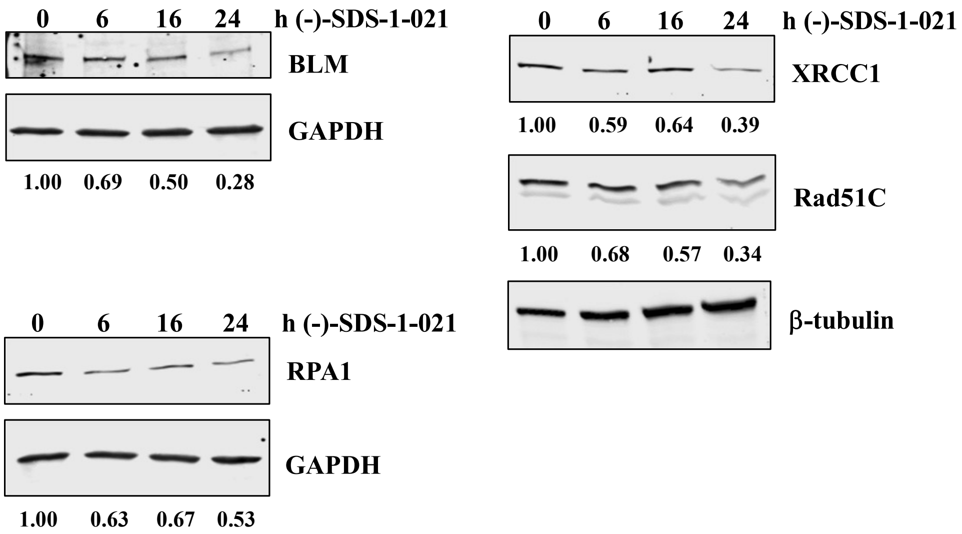
A

Symbol	Name	Log, Fold Change	Adj. p-value
ACTB	actin beta	-0.636370937	5.7814E-06
ACTL6A	actin like 6A	-0.471717992	2.90671E-06
BLM	BLM RecQ like helicase	-0.476665305	7.74594E-06
BRD8	bromodomain containing 8	-0.738430419	4.48569E-11
CDC7	cell division cycle 7	-0.700233022	1.88184E-07
ERCC6	ERCC excision repair 6, chromatin remodeling factor	-0.530745659	0.001416183
FANCM	FA complementation group M	-0.573460014	0.000140507
GINS2	GINS complex subunit 2	-0.900240107	3.06055E-23
GINS4	GINS complex subunit 4	-0.48599873	2.52933E-06
H2AX	H2A.X variant histone	-1.091249193	1.90066E-08
HDGFL2	HDGF like 2	-0.99982922	3.61184E-14
INIP	INTS3 and NABP interacting protein	-0.43829688	1.26451E-05
MBTD1	mbt domain containing 1	-1.000407161	2.0939E-14
MCM2	minichromosome maintenance complex component 2	-0.23799234	0.020411553
MCM3	minichromosome maintenance complex component 3	-0.430770709	2.25252E-06
MCM5	minichromosome maintenance complex component 5	-0.545834473	1.50411E-07
MCM6	minichromosome maintenance complex component 6	-0.670505317	4.79145E-12
MMS19	MMS19 homolog, cytosolic iron-sulfur assembly component	-0.206042809	0.046273294
MORF4L1	mortality factor 4 like 1	-0.907771869	3.06377E-14
MORF4L2	mortality factor 4 like 2	-0.419326161	9.30427E-05
MRGBP	MRG domain binding protein	-0.706933304	6.10919E-10
NABP2	nucleic acid binding protein 2	-0.590730714	5.01043E-09
NSMCE1	NSE1 homolog, SMC5-SMC6 complex component	-0.491856523	3.95488E-05
NSMCE4A	NSE4 homolog A, SMC5-SMC6 complex component	-0.51618941	2.47823E-06
NUCKS1	nuclear casein kinase and cyclin dependent kinase substrate 1	-0.76368152	3.43711E-10
PARP1	poly(ADP-ribose) polymerase 1	-0.945084921	1.06948E-24
PPP4C	protein phosphatase 4 catalytic subunit	-0.507038628	1.43288E-05
RAD51C	RAD51 paralog C	-0.665361468	7.31802E-07
RAD54B	RAD54 homolog B	-0.748776117	2.42903E-05
RADX	RPA1 related single stranded DNA binding protein, X-linked	-1.080026498	0.000335607
RECQL4	RecQ like helicase 4	-0.391144034	0.02659027
RMI2	RecQ mediated genome instability 2	-1.259521743	4.56323E-11
RPA1	replication protein A1	-1.080490817	8.60383E-33
RPA2	replication protein A2	-0.264740006	0.006070761
RUVBL2	RuvB like AAA ATPase 2	-0.304921681	0.013341315
SAMHD1	SAM and HD domain containing deoxynucleoside triphosphate triphosphohydrolase 1	-1.784767697	1.39798E-44
SHLD1	shieldin complex subunit 1	-0.723218188	0.010762896
SHLD2	shieldin complex subunit 2	-0.286024455	0.027059805
SMC5	structural maintenance of chromosomes 5	-0.905439951	2.80877E-22
SPIDR	scaffold protein involved in DNA repair	-0.589954307	6.13696E-07
SWI5	SWI5 homologous recombination repair protein	-0.558223224	2.03893E-06
TONSL	tonsoku like, DNA repair protein	-0.451827542	0.004066081
UBQLN4	ubiquilin 4	-0.293885848	0.002180197
XRCC1	X-ray repair cross complementing 1	-0.686336177	3.49661E-08
XRCC2	X-ray repair cross complementing 2	-0.349168994	0.000961042
XRCC3	X-ray repair cross complementing 3	-0.377619127	0.016287229
YEATS4	YEATS domain containing 4	-0.593143495	2.17734E-07
ZSWIM7	zinc finger SWIM-type containing 7	-0.61092711	0.000116039

B



Supplementary Figure S2. A. (-)-SDS-1-021 downregulated genes (adj. p-value < 0.05) annotated with the GO term “double-strand break repair by homologous recombination” (GO:0000724). **B.** Validation of (-)-SDS-1-021 downregulation of HR genes by western blot. U251 cells were treated with vehicle or 10 nM (-)-SDS-1-021 for the indicated times and immunoblotted for selected HR genes. GAPDH and β-tubulin were used as loading controls. Normalized ratios of HR proteins to loading control are shown below the blots.