Table S2. Pathways enriched by synthetic lethal partners of DDR genes

Pathway id	Pathway	DAISY	MDSLP-CR	MDSLP-shF	CGI
KEGG:00310	Lysine degradation	0.046			
KEGG:00970	Aminoacyl-tRNA biosynthesis		0.001		
KEGG:01522	Endocrine resistance	0.014			
KEGG:03010	Ribosome		0.000		
KEGG:03013	RNA transport	0.001			
	mRNA surveillance pathway	0.000			
	Basal transcription factors	0.038			
KEGG:03040	· · · · · · · · · · · · · · · · · · ·	0.000		0.000	0.001
	MAPK signaling pathway				0.045
	FoxO signaling pathway	0.020			
KEGG:04110	•	0.000		0.012	
	Oocyte meiosis	0.005			
	Protein processing in endoplasmic reticulum				0.002
KEGG:04144	•				0.000
	Longevity regulating pathway - multiple species	0.000			0.000
	Cellular senescence	0.000			0.000
	Antigen processing and presentation		0.000		0.000
	Thermogenesis	0.000	0.003		
	Progesterone-mediated oocyte maturation	0.000			
	Estrogen signaling pathway				0.001
	Non-alcoholic fatty liver disease		0.009		
KEGG:05020	Prion disease				0.030
KEGG:05134	Legionellosis				0.000
KEGG:05145	Toxoplasmosis				0.000
KEGG:05161	Hepatitis B	0.000			
KEGG:05162	Measles				0.001
KEGG:05166	Human T-cell leukemia virus 1 infection	0.000		0.002	
KEGG:05167	Kaposi sarcoma-associated herpesvirus infection	0.024			
KEGG:05169	Epstein-Barr virus infection	0.002			
KEGG:05170	Human immunodeficiency virus 1 infection	0.013			
KEGG:05203	Viral carcinogenesis	0.018			
KEGG:05211	Renal cell carcinoma	0.005			
KEGG:05215	Prostate cancer	0.000			
KEGG:05220	Chronic myeloid leukemia	0.004			
	Small cell lung cancer	0.035			
	Non-small cell lung cancer	0.040			
	Lipid and atherosclerosis				0.008
	E2F-enabled inhibition of pre-replication complex f	0.048			
	E2F mediated regulation of DNA replication	0.002			
-	Transcription of E2F targets under negative contro				
	Transcription of E2F targets under negative control				
	Amplification of signal from the kinetochores	0.000			
	Amplification of signal from unattached kinetocho				
-			0.000		
REAU:R-HSA	The citric acid (TCA) cycle and respiratory electror	панъроп	0.000		

REAC:R-HSA G0 and Early G1		0.000		I	
REAC:R-HSAPolo-like kinase mediated eve	onte	0.000			
t		0.000			
· · · · · · · · · · · · · · · · · · ·					
REAC:R-HSA/Cell Cycle	Respiratory electron transport, ATP synthesis by chemiosmotic Cell Cycle 0.000				0.002
REAC:R-HSAAPC/C-mediated degradation	of call avels proteins	0.000			0.002
REAC:R-HSAActivation of ATR in response	· ·	0.012			
REAC:R-HSAUnwinding of DNA	to replication stress	0.001			
REAC:R-HSARHO GTPase Effectors		0.001			
		0.003			
REAC:R-HSA Generic Transcription Pathwa	•				
REAC:R-HSA Separation of Sister Chromat REAC:R-HSA Resolution of Sister Chromati		0.000			
		0.000			
REAC:R-HSA Mitotic Metaphase and Anaph	iase	0.000			
REAC:R-HSASUMOylation		0.002			
REAC:R-HSA SUMO E3 ligases SUMOylate	<u> </u>	0.003			
REAC:R-HSA PKMTs methylate histone lys	nes	0.050			0.000
REAC:R-HSA HDMs demethylate histones		0.000			0.000
REAC:R-HSA Chromatin modifying enzyme		0.000			0.003
REAC:R-HSA Regulation of HSF1-mediated heat shock response				0.000	
REAC:R-HSA HSP90 chaperone cycle for s		tors (SHR			0.001
REAC:R-HSA Cellular response to heat stre	SS				0.000
REAC:R-HSA Attenuation phase					0.000
REAC:R-HSA HSF1-dependent transactivat		0.000	0.004		0.000
REAC:R-HSA Transcriptional Regulation by	TP53	0.000	0.001		
REAC:R-HSA tRNA Aminoacylation	1.0		0.008		
REAC:R-HSA Mitochondrial tRNA aminoacy	viation	0.000	0.000		
REAC:R-HSA Mitotic G2-G2/M phases		0.000			
REAC:R-HSA Regulation of mitotic cell cycle		0.012			
REAC:R-HSA Mitotic G1 phase and G1/S tr	ansition	0.000			
REAC:R-HSA Chromatin organization		0.000			0.003
REAC:R-HSA Mitochondrial translation initia	ition		0.000		
REAC:R-HSA Mitochondrial translation			0.000		
REAC:R-HSA Mitochondrial translation elon	_		0.000		
REAC:R-HSA Mitochondrial translation term			0.000		
REAC:R-HSA TP53 Regulates Metabolic Go	enes		0.000		
REAC:R-HSA Regulation of TP53 Activity		0.000			
REAC:R-HSARHO GTPases Activate Form		0.000			
REAC:R-HSA HDR through Single Strand A	,			0.045	
REAC:R-HSA Respiratory electron transpor			0.000		
REAC:R-HSA TP53 Regulates Transcription	·	0.000			
REAC:R-HSA Regulation of TP53 Activity th	rough Acetylation	0.029			
REAC:R-HSA PTEN Regulation		0.006			
REAC:R-HSA CDC6 association with the Ol	·	0.000			
REAC:R-HSA Assembly of the pre-replicative	e complex	0.000			
REAC:R-HSA Mitotic Prometaphase		0.000			

REAC:R-HSAMitotic Anaphase	0.000			
REAC:R-HSA Mitotic Telophase/Cytokinesis	0.002			
REAC:R-HSAM Phase	0.000			
REAC:R-HSA Orc1 removal from chromatin	0.001			
REAC:R-HSA Activation of the pre-replicative complex	0.000			
REAC:R-HSA DNA Replication Pre-Initiation	0.000			
REAC:R-HSA Switching of origins to a post-replicative state	0.000			
REAC:R-HSA DNA strand elongation	0.000			
REAC:R-HSA Cyclin E associated events during G1/S transition	0.021			
REAC:R-HSA G1/S-Specific Transcription	0.000			
REAC:R-HSA G1/S Transition	0.000			
REAC:R-HSA Synthesis of DNA	0.000			
REAC:R-HSAS Phase	0.000			
REAC:R-HSA G2/M Transition	0.000			
REAC:R-HSA Cell Cycle, Mitotic	0.000			
REAC:R-HSA DNA Replication	0.000			
REAC:R-HSA G2/M Checkpoints				0.014
REAC:R-HSA Mitotic Spindle Checkpoint	0.000			
REAC:R-HSA Cell Cycle Checkpoints	0.000		0.034	0.037
REAC:R-HSA Cyclin A:Cdk2-associated events at S phase entry	0.029			
REAC:R-HSA mRNA Splicing - Major Pathway	0.000		0.000	
REAC:R-HSA mRNA Splicing - Minor Pathway			0.001	
REAC:R-HSA mRNA Splicing	0.000		0.000	
REAC:R-HSA mRNA 3'-end processing	0.000			
REAC:R-HSA Transport of Mature Transcript to Cytoplasm	0.000			
REAC:R-HSA Processing of Capped Intron-Containing Pre-mRN	0.000		0.000	
REAC:R-HSA Translation		0.000		
REAC:R-HSA RNA Polymerase II Transcription Termination	0.000			
REAC:R-HSA RNA Polymerase II Transcription	0.000			
REAC:R-HSA Chromosome Maintenance	0.007			
REAC:R-HSA Gene expression (Transcription	0.000			
REAC:R-HSA ESR-mediated signaling	0.037			
REAC:R-HSA Metabolism of RNA	0.000		0.000	
REAC:R-HSA EML4 and NUDC in mitotic spindle formation	0.000			
REAC:R-HSA Aberrant regulation of mitotic G1/S transition in car	0.020			
REAC:R-HSA Defective binding of RB1 mutants to E2F1,(E2F2,	0.020			
REAC:R-HSA Diseases of mitotic cell cycle	0.039			
REAC:R-HSA Aberrant regulation of mitotic cell cycle due to RB1	0.024			