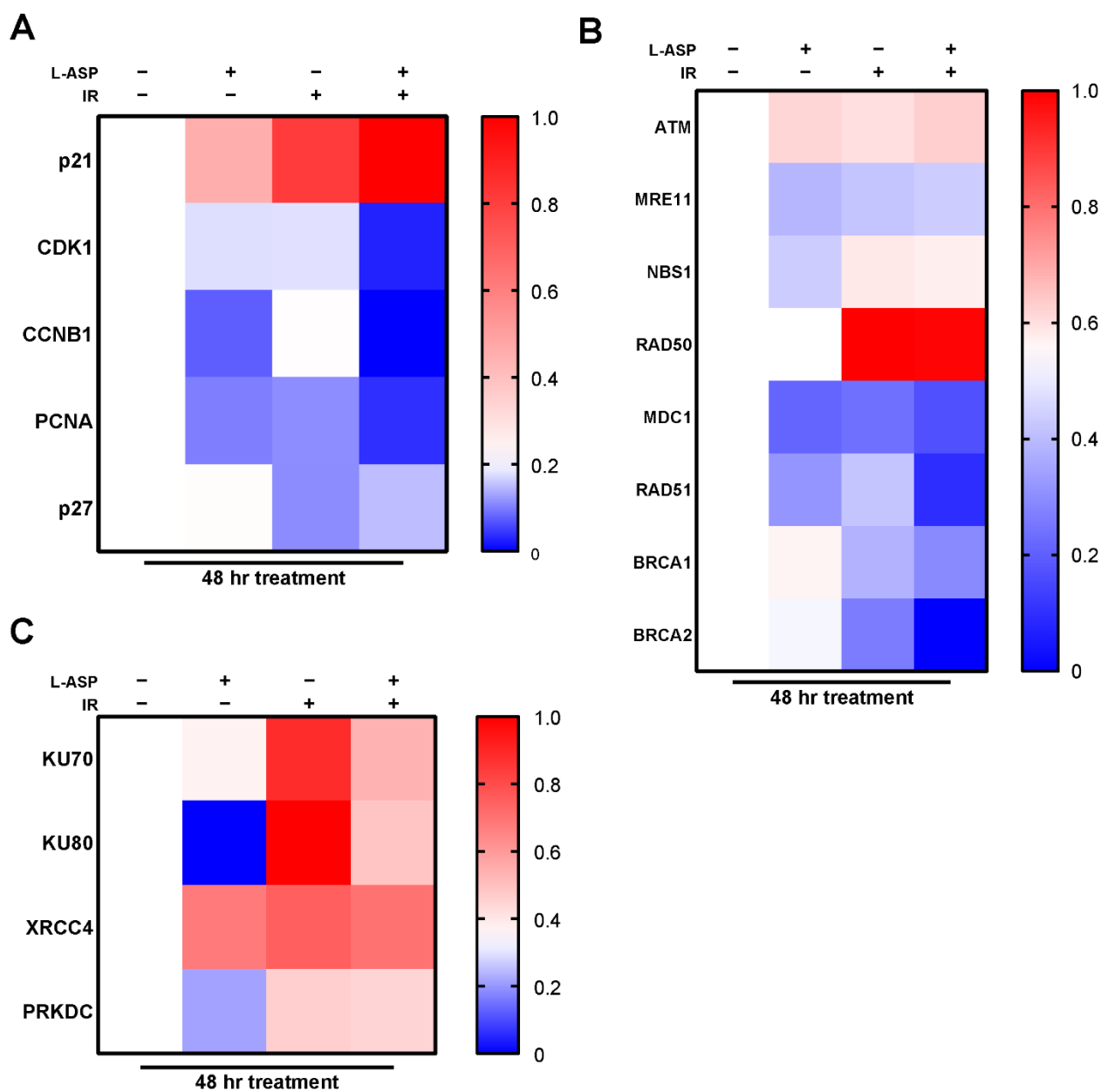
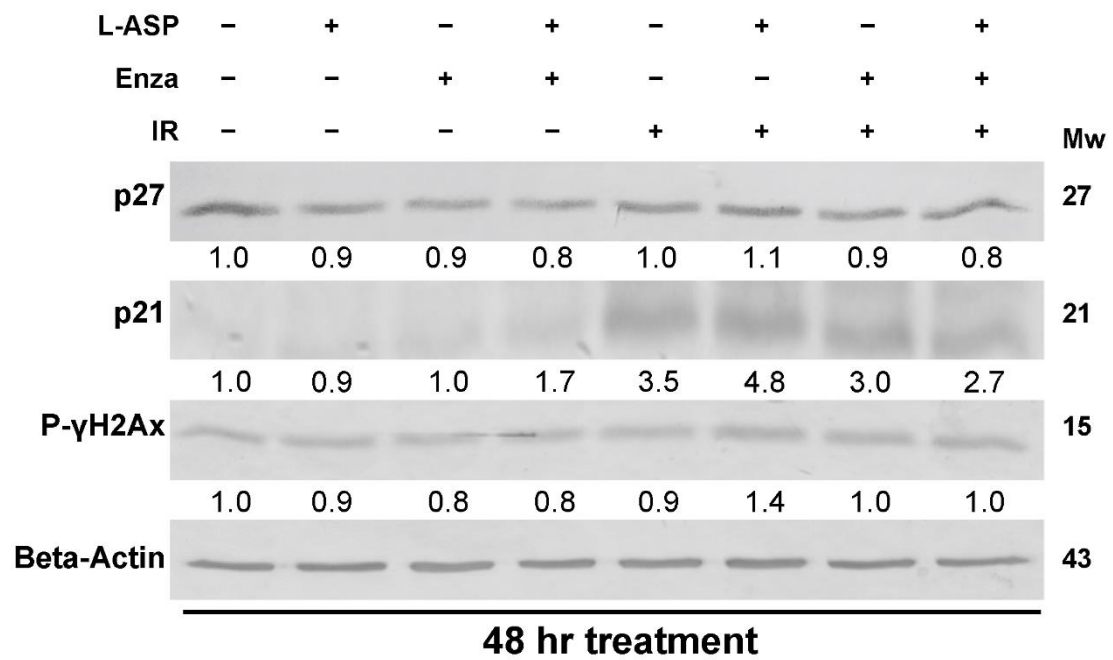


**Figure S1.** (A) Fold change of GLS1, GLS2, PPAT and CAD in benign and prostate cancer patients in the gse29079 data set, obtained from R2-Genomics analysis (n = 95). (B) ARCaP<sub>M</sub> and PC3 cells were counted after culturing in media containing indicated concentrations of glutamine (L-Gln) and L-ASP for 48 hrs. (C) Apoptotic status of PC3 and ARCaP<sub>M</sub> were determined by FACS analysis of cell surface Annexin V after treatment with indicated concentrations of L-Gln. (D) Cell cycle analysis was performed on PC3 and ARCaP<sub>M</sub> cells following incubation under control conditions or treatment with L-ASP.



**Figure S2.** 22RV1 cells were incubated with L-ASP (2 IU/ml) and administered 4 Gy of radiation. Cells were harvested 48 hrs. after irradiation (IRR). (A) mRNA expression of cell cycle checkpoint markers were determined by RT-PCR. (B) mRNA expression of factors involved with homologous recombination of DNA repair were determined by RT-PCR. (C) mRNA expression of factors involved with non-homologous end joining were determined by RT-PCR. mRNA expression was normalized to  $\beta$ -actin and untreated samples.



**Figure S3.** 22RV1 cells were incubated with L-ASP (2 IU/ml), enzalutamide (10  $\mu$ M) or both. Cells were harvested 48 hrs. after exposure to 4 Gy of radiation. Western blots of 22RV1 cell lysates were probed for p27, p21, and P- $\gamma$ -H2Ax. Representative blots are shown with mean relative quantitation indicated normalized to  $\beta$ -actin expression. Molecular weights (kDa) are indicated.

**Table S1.** List of primer sequences used for RT-PCR.

Gene	Direction	Sequence
ACTB	Forward	5'-CTTCGCGGGCGACGAT-3'
ACTB	Reverse	5'-CCACATAGGAATCCTTCTGACC-3'
p21	Forward	5'-AGTCAGTTCCTTGTGGAGCC-3'
p21	Reverse	5'-GCATGGGTCTGACGGACAT-3'
CDK1	Forward	5'-TGGGAAGTTGGTAGCTCTGAA-3'
CDK1	Reverse	5'-CCAGGGTGCTTGCCATGTA-3'
CCNB1	Forward	5'-GACCTGTGTCAGGCTTCTCTG-3'
CCNB1	Reverse	5'-GGTATTTTGGTCTGACTGCTTGC-3'
PCNA	Forward	5'-CCTGCTGGGATATTAGCTCCA-3'
PCNA	Reverse	5'-CAGCGGTAGGTGTCGAAGC-3'
p27	Forward	5'-AGTCAGTTCCTTGTGGAGCC-3'
p27	Reverse	5'-GCATGGGTCTGACGGACAT=3'
CDK4	Forward	5'-ATGGCTACCTCTCGATATGAGC-3'
CDK4	Reverse	5'-CATTGGGACTCTCACACTCT-3'
CDK6	Forward	5'-CCAGATGGCTCTAACCTCAGT-3'
CDK6	Reverse	5'-AACTTCCACGAAAAAGAGGCTT-3'
CCND1	Forward	5'-GCTGCGAAGTGGAAACCATC-3'
CCND1	Reverse	5'-CCTCCTTCTGCACACATTGAA-3'
SOD2	Forward	5'-CTGGACAAACCTCAGCCCTAAC-3'
SOD2	Reverse	5'-AACCTGAGCCTTGACACCAAC-3'
CAT	Forward	5'-GTGCGGAGATTCAACACTGCCA-3'
CAT	Reverse	5'-CGGCAATGTTCTCACACAGACG-3'
NRF2	Forward	5'-CACATCCAGTCAGAAACAGTGG-3'
NRF2	Reverse	5'-GGAATGTCTGCGCCAAAAGCTG-3'
ATM	Forward	5'-TGTTCCAGGACACGAAGGGAGA-3'
ATM	Reverse	5'-CAGGGTTCTCAGCACTATGGGA-3'
NBS1	Forward	5'-TCTGTCAGGACGGCAGGAAAGA-3'
NBS1	Forward	5'-CACCTCCAAAGACAACCTGCGGA-3'
MRE11	Reverse	5'-CAGCAACCAACAAAGGAAGAGGC-3'
MRE11	Forward	5'-GAGTTCCTGCTACGGGTAGAAG-3'
RAD50	Reverse	5'-GGAAGAGCAGTTGTCCAGTTACG-3'
RAD50	Forward	5'-GAGTAAACTGCTGTGGCTCCAG-3'
RAD51	Reverse	5'-TCTCTGGCAGTGATGTCTTGGGA-3'
RAD51	Forward	5'-TAAAGGGCGGTGGCACTGTCTA-3'
MDC1	Reverse	5'-GGAATGTCTGCGCCAAAAGCTG-3'
MDC1	Forward	5'-GCTTCAGGTAAGTAGGAGGCA-3'
SIRT1	Reverse	5'-TAGCCTTGTGAGATAAGGAAGGA-3'
SIRT1	Forward	5'-ACAGCTTCACAGTCAACTTTGT-3'
CHOP	Reverse	5'-GGAAACAGAGTGGTCATTCCC-3'
CHOP	Forward	5'-CTGCTTGAGCCGTTTATTCTC-3'
ku70	Reverse	5'-GGTTTCAAGCCGTTGGTACTGC-3'
ku70	Forward	5'-CTCCAGACACTTGATGAGCAGAG-3'
ku80	Reverse	5'-GTTCTAAAGGTCTTTCAGCAAGA-3'
ku80	Forward	5'-AAAAGCCACGCCGACTTGAGGA-3'
PRKDC	Reverse	5'-GCGCCATATCTGTCATCTGCTG-3'
PRKDC	Forward	5'-TTATAGCGGCGCTTCAGGTGCA-3'
XRCC4	Reverse	5'-ATGGCTCCTCAGGAGAATCAGC-3'
XRCC4	Forward	5'-GAGGTCTTCTGGGCTGCTGTTT-3'
BRCA1	Reverse	5'-CTGAAGACTGCTCAGGGCTATC-3'
BRCA1	Forward	5'-AGGGTAGCTGTTAGAAGGCTGG-3'
BRCA2	Reverse	5'-GGCTTCAAAAAGCACTCCAGATG-3'
BRCA2	Forward	5'-GGATTCTGTATCTTGTGACGTTCC-3'
GLUL	Reverse	5'-TAAGGACCCCTAACAAAGCTGGT-3'
GLUL	Forward	5'-CCGTTTACAGGTGTGCCTCAA-3'
AR	Reverse	5'-AGTCATCGGTGACAGACCCCTT-3'
AR	Forward	5'-GTGCAGCGTTATCTCCAACAG-3'

# RAW FIGURES

