Supplemental Table 1: Primer sequences for ChIP and RT-qPCR studies.

Chromatin Immunoprecipitation (ChIP) Primers		
Gene	**Forward Primer Sequence (5'-3')**	**Reverse Primer Sequence (5'-3')**
Trp53inp1	GATTGGTCGGCCTGCGG	TTGTTGTGCAGCTCTGGGAA
p21	ACCTAGTGTCGGGCATCTC	TCAGGTCTCCACCACCCTG
Gabarap	TCCGCTCTGGTGTAGTCCTT	GGCTCAGGCTTATGTGAACCA
Adrm1	TTTCTGCGAGTCGTGGAGGC	TGTTGCTGTGTCATAGGGGAGC
Prkaa2	ATTCTCCTTCCATCTCGGTCGC	CCGAGGCGTCCCGAGAAAAG
Jmy	GGAAAAAGGGGGCAGGGCT	GAGGGACGTAAACACGGGCA
Gtf2h1	AATGGTTGTGAGCCACCATGTG	GCCGACTGCTCTTCCAAACATC
Crebrf	CCCACCGGCAGTAAAAACTACG	TATGTCCTTCCTGACGGGTTCC
Sall1	CCCCCATTACTCAGCCGAAGTT	GAGGTTCCCGAAGTCCTGCAC
Col4a1	CTCCGAGACTGAGCACCTCG	AGAGACGGCGGGGAAATGC
RT-qPCR Primers		
Gene	**Forward Primer Sequence (5'-3')**	**Reverse Primer Sequence (5'-3')**
Gapdh	GGTTGTCTCCTGCGACTTCA	CCCTAGGCCCCTCCTGTTAT
Trp53inp1	GGCCAACTGAAGACAGGGTT	CCTCTGCTGAGAAACCAGGG
p21	CTAGGGGAATTGGAGTCAGGC	ACCAGGATTGGACATGGTGC
Gabarap	GAAAAAGCCCCCAAAGCTCG	CACTGGTGGGTGGAATGACA
Adrm1	CGGCTGACGGAACTCAATC	CTGAAGTCGTCATCCTGGCG
Prkaa2	ACGAACTAGCTGTGGATCGC	ATCATCGAAAGGGAGGGTGC
Jmy	AGGATGAAGCCTACAGCAGC	TCTCGCATGTCTCGGAATGG
Gtf2h1	GAAGCAGGATGGAGCACTGT	CCTTCACTGCATCCCGTTCT
Crebrf	TCAGCCTCAGAACCGCAAAT	CCAAGCCCAGATCCTGTGAG
Sall1	AACCCGGAAGAGGGAGTACA	TCGGGGTCGGATTGGAAATG
Col4a1	TCATTAGCAGGTGTGCGGTT	GTTAGGGCACTGCGGAATCT
Mdm2	TCCTATTGGTCCAGGAGGCG	CGGAGAGAACGCCGGAAG
Fas	ATAGGAGCGAAGCGGTTTGT	CCCACAGGCAGTCTAGAGCT
Aen	TCCGAACTCGGGTCTCTCTT	GCTGGTACAACTCCATGGCT
Plk3	AGAAGGCTGGTTCCCACGCTG	AGCGAACGATATGGCGGTGCTG
Ddit4l	GTGAAATCCGGCAGCGCCTAGG	TGCCCGTTGCAACCATGGTCAA
Sesn1	ATCCCTCGGCCACTAGGACACG	GTGCGTCTTCACTGCCCACCTG
Dram1	ACTTGGTGTCCTTGGCGCTTGG	TCATGGACCACAGGCACGGCTA
Dyrk3	CGGAGGTTGGGGGATGGTGTCT	AGTGCTGAGTGTGGCCTCTCGT
Noxa	GCCCAGATTGGGGACCTTAG	TCTTCCTGAGTTGAGCTGCG

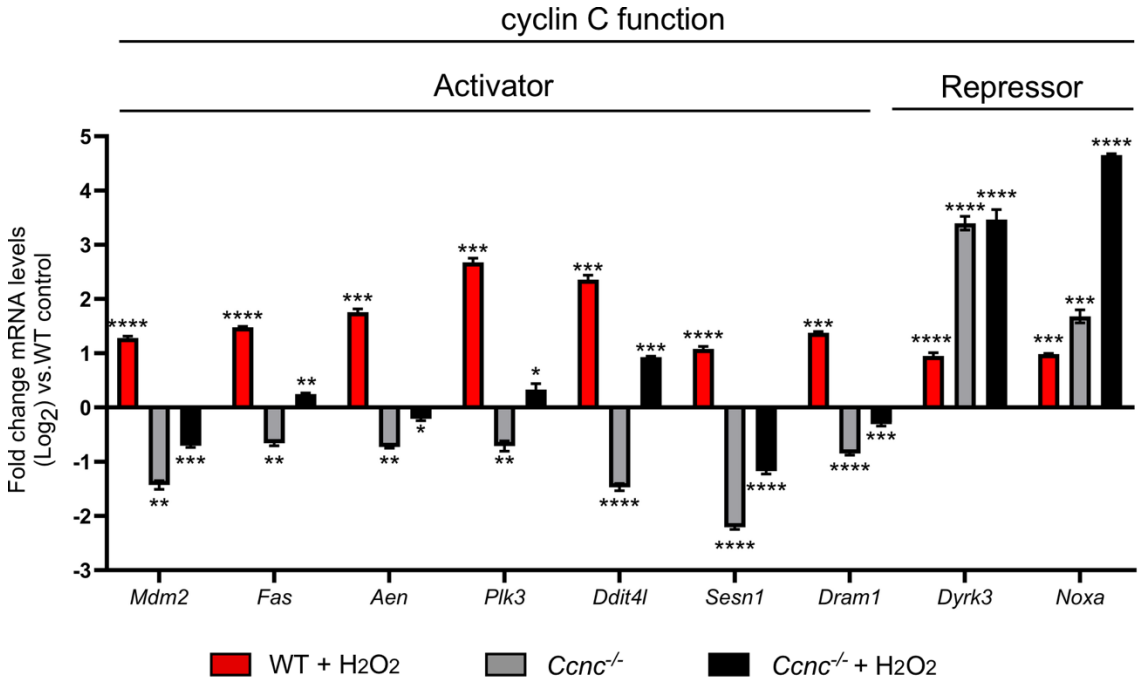

Figure S1: Cyclin C activator and repressor roles for H_2O_2-induced genes requiring p53. H_2O_2-induced genes identified by RNA-seq analysis were sorted into a cohort with the GO term "p53 regulated". RT-qPCR analysis was performed on nine randomly selected genes in WT and *Ccnc*$^{-/-}$ MEF cultures before and after H_2O_2 treatment. Values shown are based on untreated WT control. Statistical significance is indicated by the following: * p-value < 0.05, ** p-value < 0.01, *** p-value < 0.001, **** p-value < 0.0001.

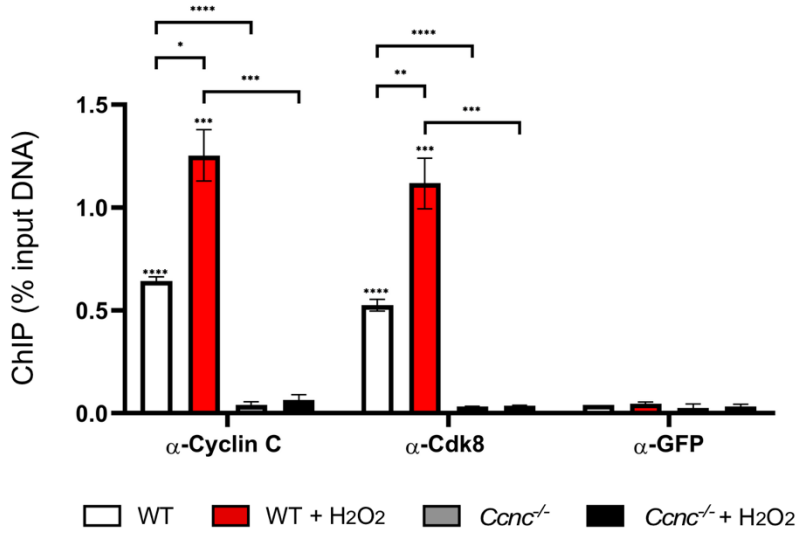

Figure S2: Cdk8 and cyclin C antibody specificity for ChIP experiments. ChIP analysis of *Trp53Inp1* in the cell cultures, conditions and antibodies as indicated. Data obtained from RT-qPCR analysis from DNA purified from ChIP was calculated as percent input DNA. Statistical significance is indicated by the following: * p-value < 0.05, ** p-value < 0.01, *** p-value < 0.001, **** p-value < 0.0001

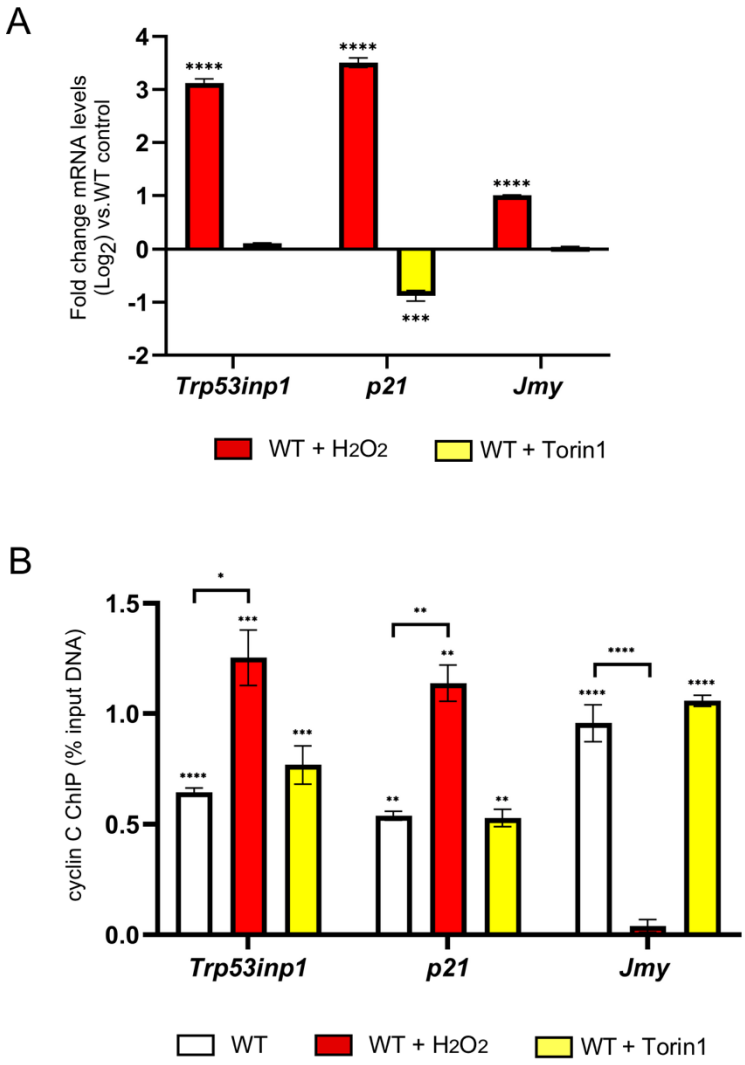

Figure S3: Genes within the p53-mediated response network are not induced during Torin1 stress. RT-qPCR (A) and ChIP (B) data analysis on the genes indicated. Data obtained for mRNA levels and cyclin C-dependent ChIP were compared to an untreated WT control and a non-specific antibody (GFP), resepctively. Statistical significance is indicated by the following: * p-value < 0.05, ** p-value < 0.01, *** p-value < 0.001, **** p-value < 0.0001.