Figure S1. Continued.

A

Download GenBank Graphics

Homo sapiens tumor protein p53 (TP53), RefSeqGene (LRG_321) on chromosome 17

Sequence ID: NG_017013.2 Length: 32772 Number of Matches: 1

Range 1: 15957 to 15987 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
58.4 bits(31)	1e-08	31/31(100%)	0/31(0%)	Plus/Plus

```
Query  1      ATGGAGGAGCCGCAGTCAGATCCTAGCGTCG  31
              ||||||||||||||||||||||||||||||||
Sbjct  15957  ATGGAGGAGCCGCAGTCAGATCCTAGCGTCG  15987
```

Fwd primer (FP53B)

Download GenBank Graphics

Homo sapiens tumor protein p53 (TP53), RefSeqGene (LRG_321) on chromosome 17

Sequence ID: NG_017013.2 Length: 32772 Number of Matches: 1

Range 1: 17593 to 17612 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
40.1 bits(20)	0.002	20/20(100%)	0/20(0%)	Plus/Plus

```
Query  1      TCAGCATCTTATCCGAGTGG  20
              ||||||||||||||||||||
Sbjct  17593  TCAGCATCTTATCCGAGTGG  17612
```

Fwd primer (p53-F1)

Download GenBank Graphics

Homo sapiens tumor protein p53 (TP53), RefSeqGene (LRG_321) on chromosome 17

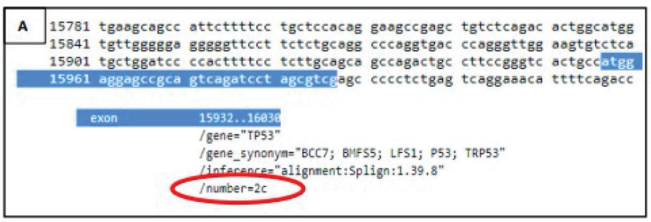
Sequence ID: NG_017013.2 Length: 32772 Number of Matches: 1

Range 1: 22907 to 22942 GenBank Graphics ▼ Next Match ▲ Previous Match

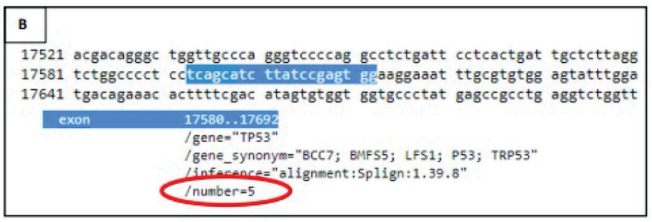
Score	Expect	Identities	Gaps	Strand
67.6 bits(36)	4e-11	36/36(100%)	0/36(0%)	Plus/Minus

```
Query  1      TCAGTCTGAGTCAGGCCCTTCTGTCTTGAACATGAG  36
              ||||||||||||||||||||||||||||||||||||
Sbjct  22942  TCAGTCTGAGTCAGGCCCTTCTGTCTTGAACATGAG  22907
```

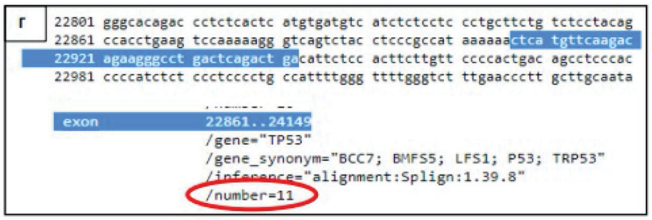
Rev primer (BP53B)



Fwd primer (FP53B) in exon 2

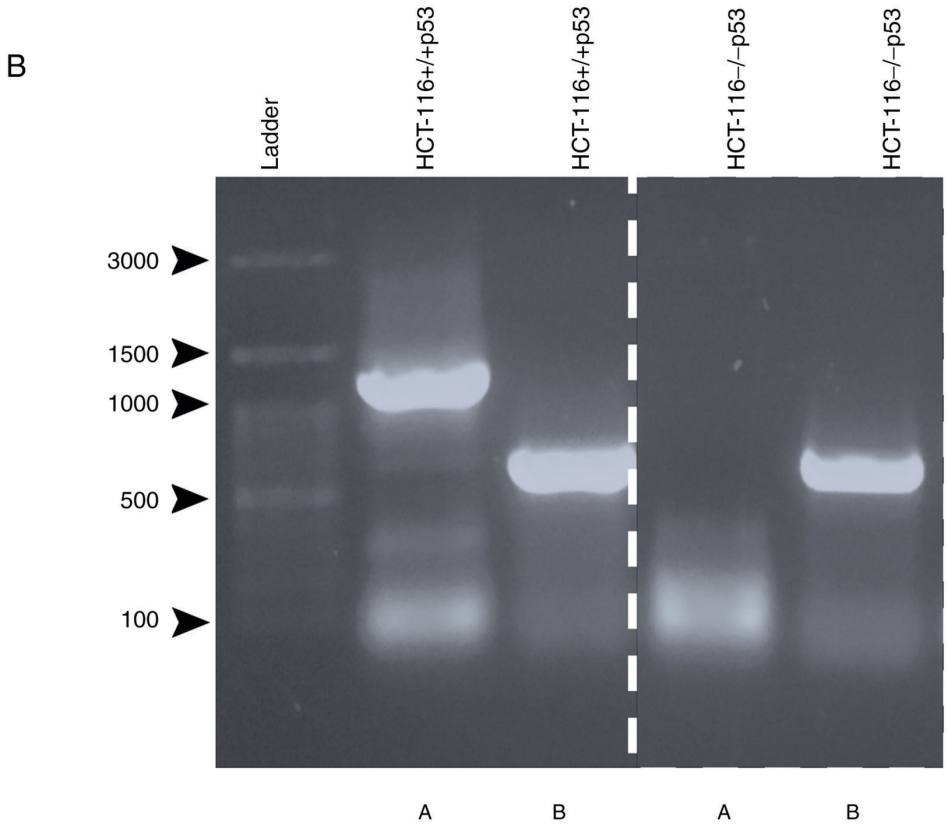


Fwd primer (p53-F1) in exon 5



Rev primer (BP53B) in exon 11

Figure S1. Continued.



>NM_000546.6 Homo sapiens tumor protein p53 (TP53), transcript variant 1, mRNA

```
product length = 1182
Forward primer  1    ATGGAGGAGCCGCAGTCAGATCCTAGCGTCG  31
Template        143  ..............................  173

Reverse primer  1     TCAGTCTGAGTCAGGCCCTTCTGTCTTGAACATGAG  36
Template        1324  ....................................  1289
```

>NM_000546.6 Homo sapiens tumor protein p53 (TP53), transcript variant 1, mRNA

```
product length = 610
Forward primer  1    TCAGCATCTTATCCGAGTGG  20
Template        715  ....................  734

Reverse primer  1     TCAGTCTGAGTCAGGCCCTTCTGTCTTGAACATGAG  36
Template        1324  ....................................  1289
```

Figure S1. Evaluation of native and truncated transcripts of *TP53* in HCT-116 (+/+p53) and HCT-116 (-/-p53) cDNA. (A) BLAST analysis of the utilized oligos. (B) DNA agarose electrophoresis analysis of the products resulting from amplification of *TP53* gene sequences with the following primer pairs: a) FP53B/BP53B primers, for amplification of a 1,182 bp sequence and b) p53-F1/BP53B primers, for amplification of a 610 bp sequence. (C) Detection of p53 in total cytoplasmic extract samples of HCT-116 (+/+p53) and HCT-116 (-/-p53) cells by western blotting with an anti-p53 antibody. The polyclonal antibody for the detection of p53 protein was produced against the full-length protein, thus its use enables the detection of both full-length protein (53 kDa) and the various isoforms of p53 protein expressed by the cell, as the specific case of truncated p53 protein (47 kDa) caused by the absence of exon 2. The amount of protein loaded from each sample is equivalent to 40 μg, while an anti-β-actin antibody (43 kDa) was used as a positive control. A Nippon Genetics protein control molecular weight marker was also used.

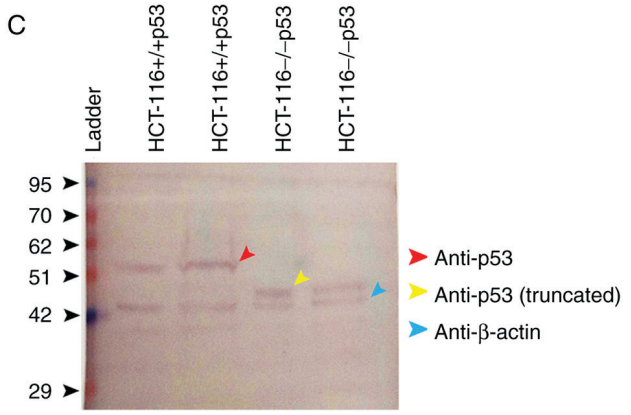


Figure S2. Growth kinetics of the (A) HCT-116 (+/+p53) and (B) HCT-116 (-/-p53) cells. Cells were seeded in a concentration of $1.5x10^5$ cells/ml and incubated for up to 96 h. Measurements were carried out at the 24, 48, 72 and 96 h timepoints. Standard deviations for all measurements were calculated from 3 biological replicates.

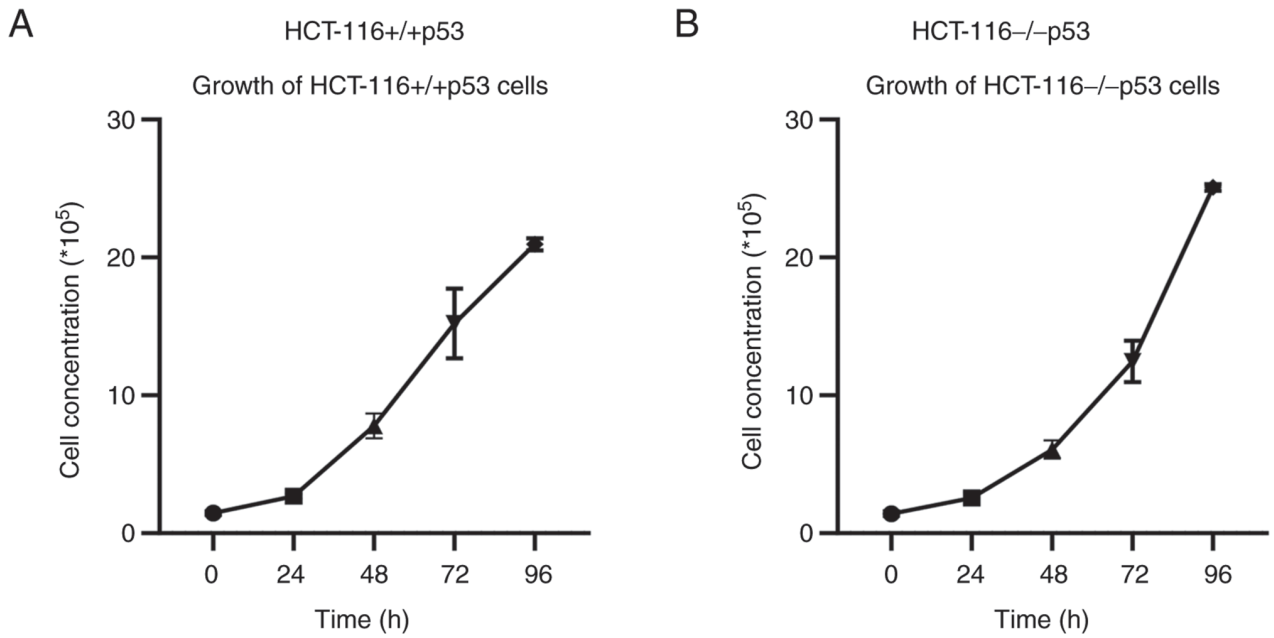


Figure S3. Continued.

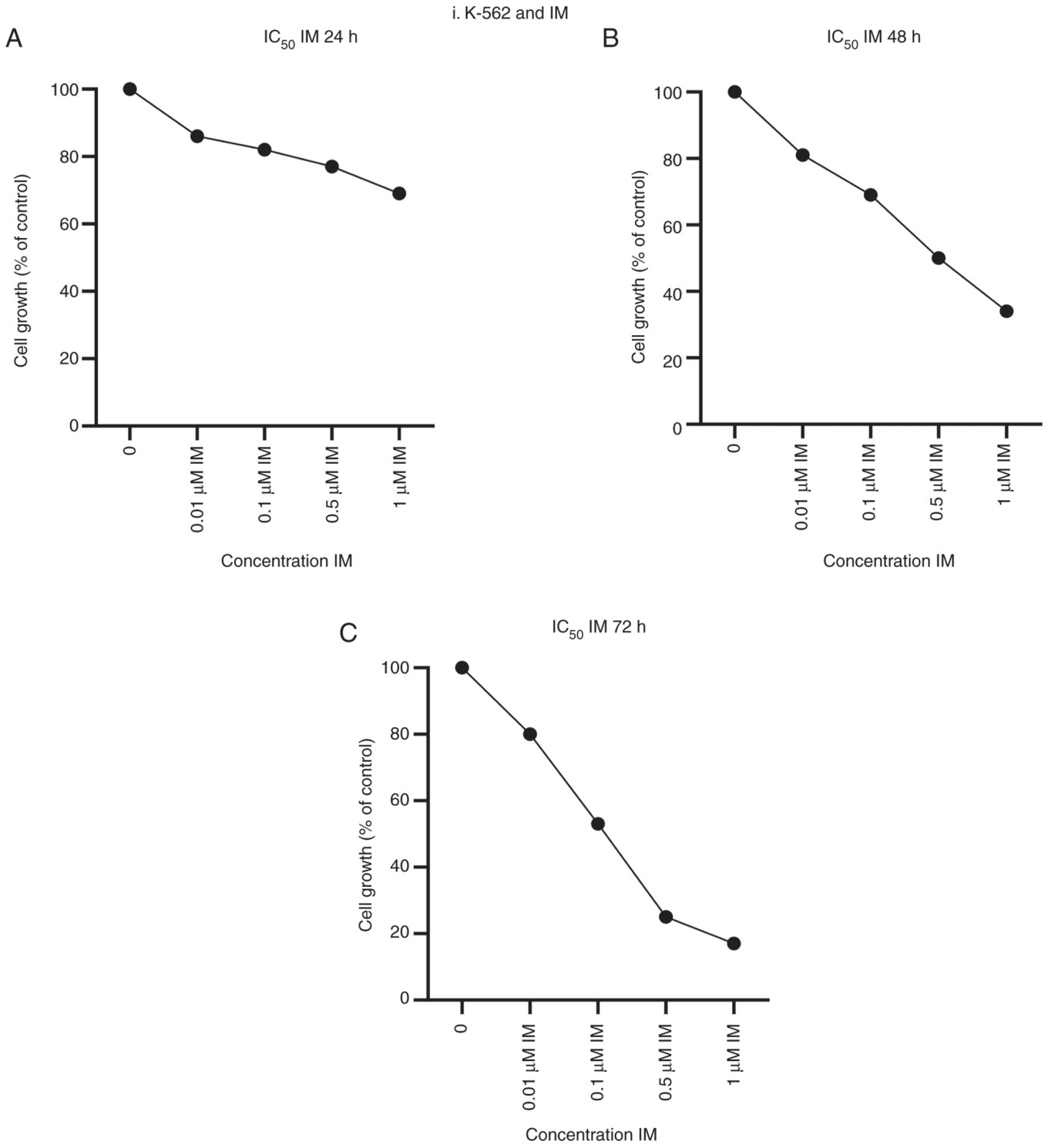


Figure S3. Continued.

ii. K-562 and DCA

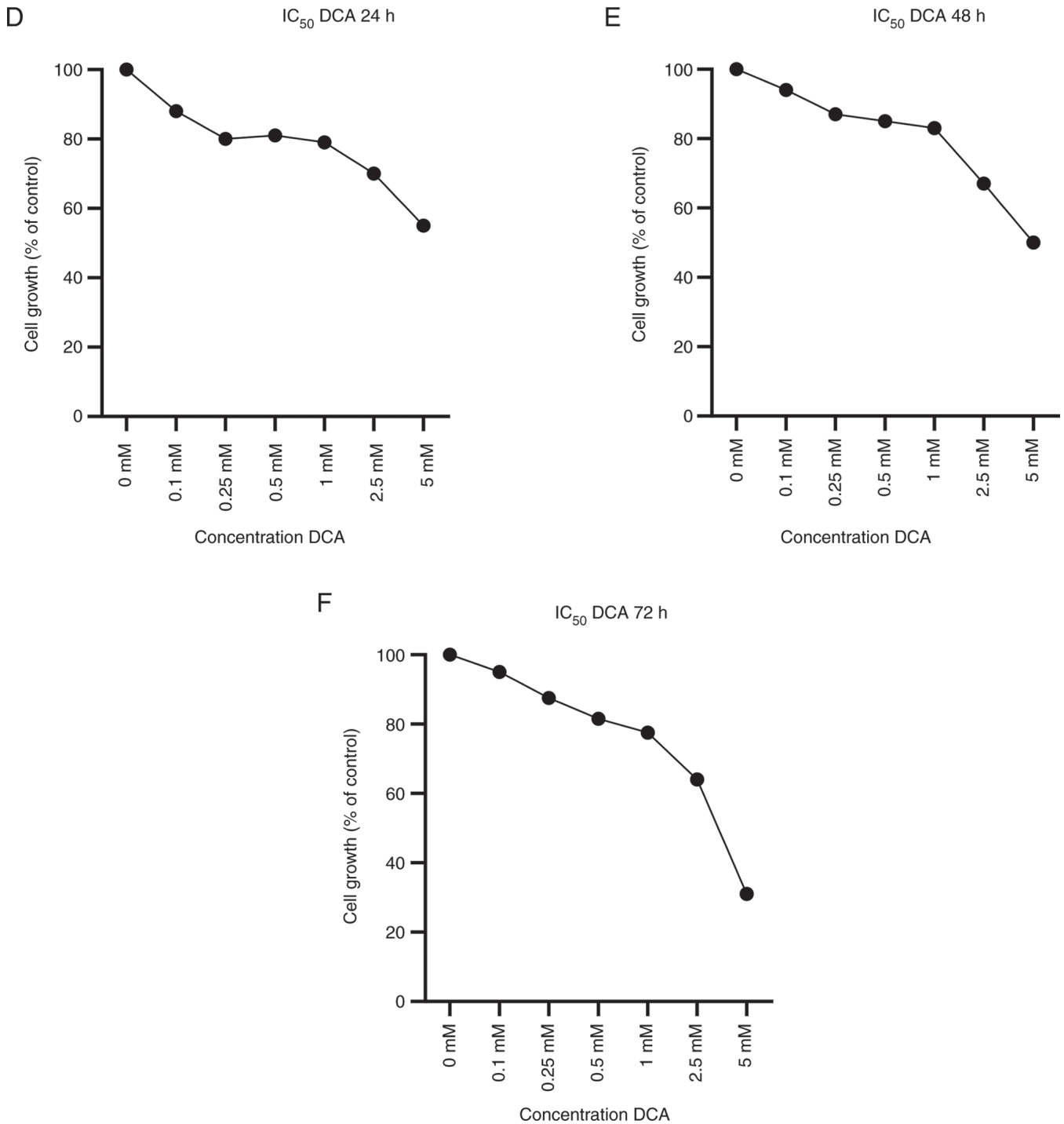


Figure S3. Continued.

iii. K-562R and IM

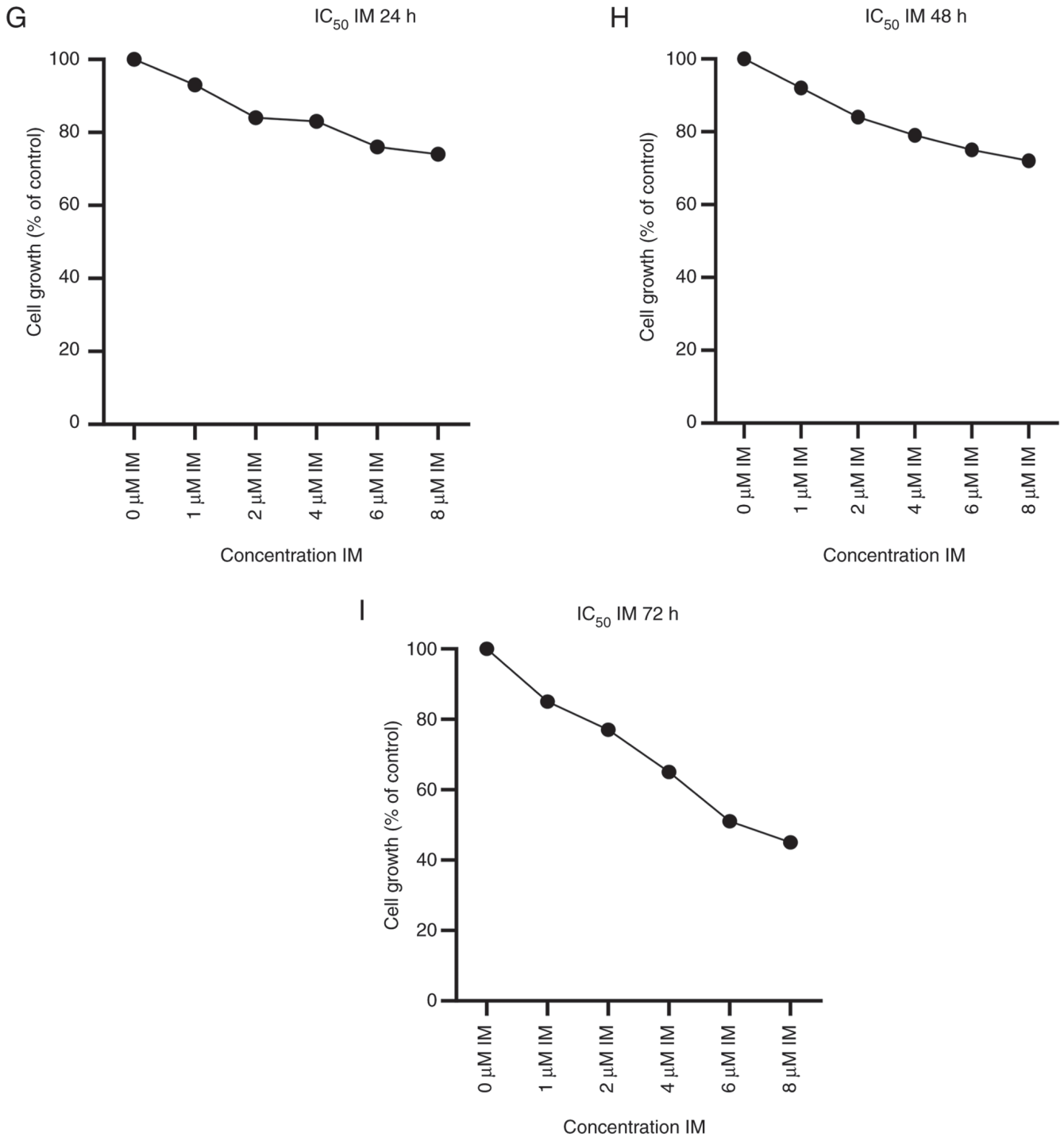


Figure S3. Dose-dependent effects of IM and DCA on the cell growth of K-562 and K-562R cells for up to 72 h. i) (A-C) Dose-dependent effect of IM on the cell growth of K-562 (0, 0.01, 0.1, 0.5 and 1 μM) for 24, 48 and 72 h. The cells were seeded at 1x10^5 cells/ml. ii) (D-F) Dose-dependent effect of DCA on the cell growth of K-562 (0, 0.1, 0.25, 0.5, 1, 2.5 and 5 mM) for 24, 48 and 72 h. The cells were seeded at 1x10^5 cells/ml. iii) (G-I) Dose-dependent effect of IM on the cell growth of K-562R (0, 1, 2, 4, 6 and 8 μM) for 24, 48 and 72 h. The cells were seeded at 2x10^5 cells/ml. iv) (J-L) Dose-dependent effect of DCA on the cell growth of K-562R (0, 2, 4, 6 and 8 mM) for 24, 48 and 72 h. The cells were seeded at 2x10^5 cells/ml. IM, imatinib; DCA, dichloroacetate.

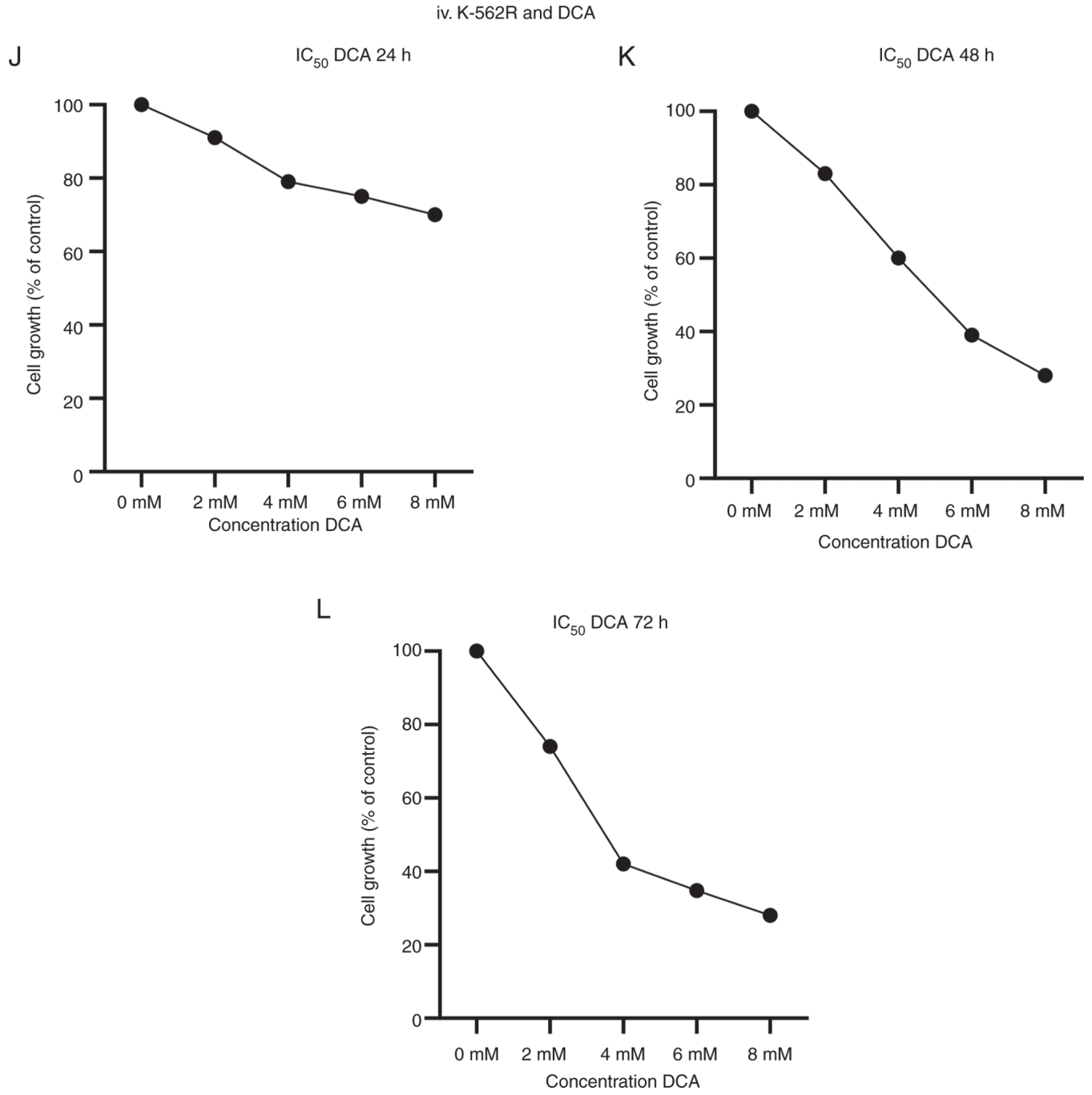


Figure S4.Continued.

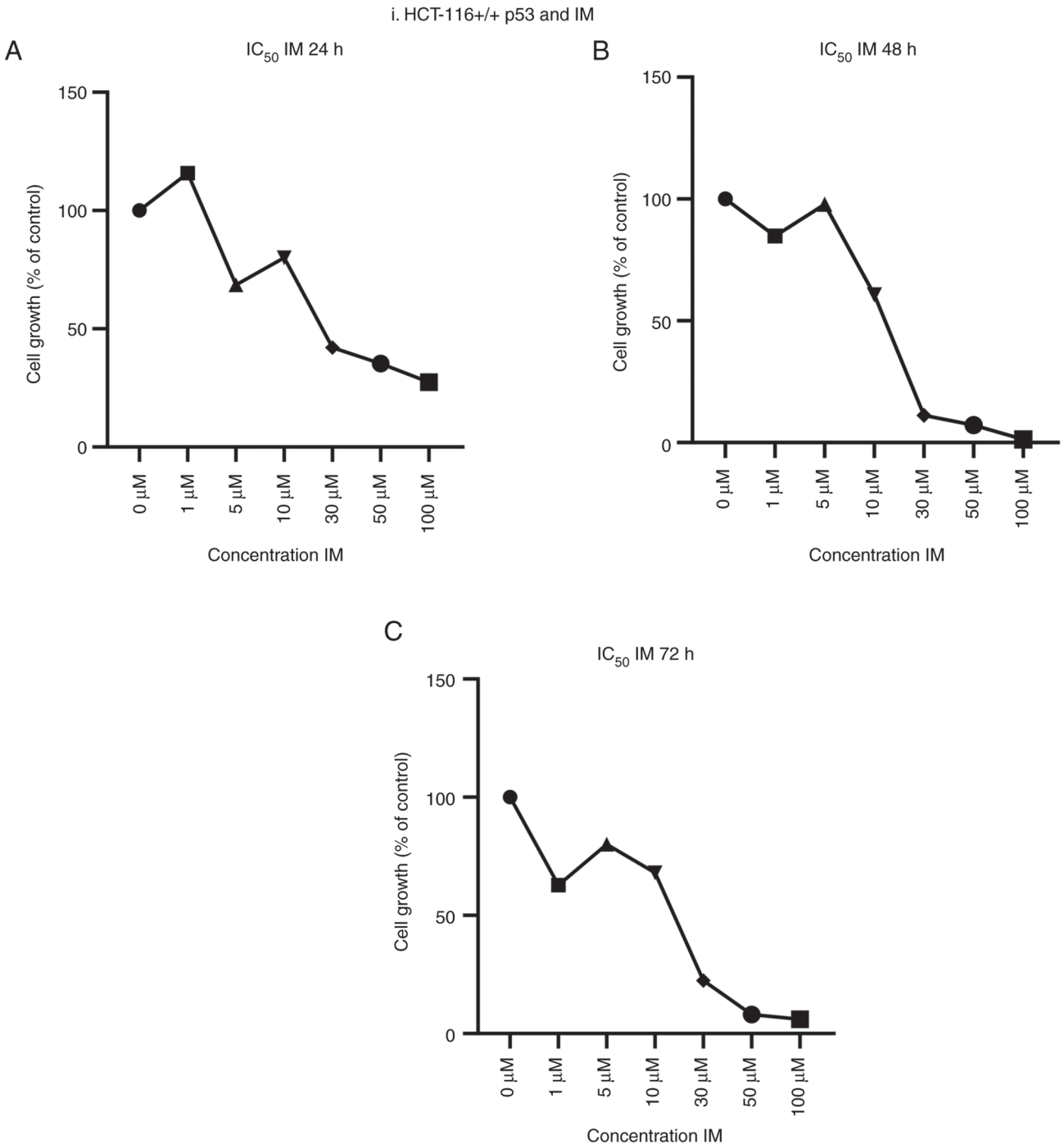


Figure S4. Continued.

ii. HCT-116+/+ p53 and DCA

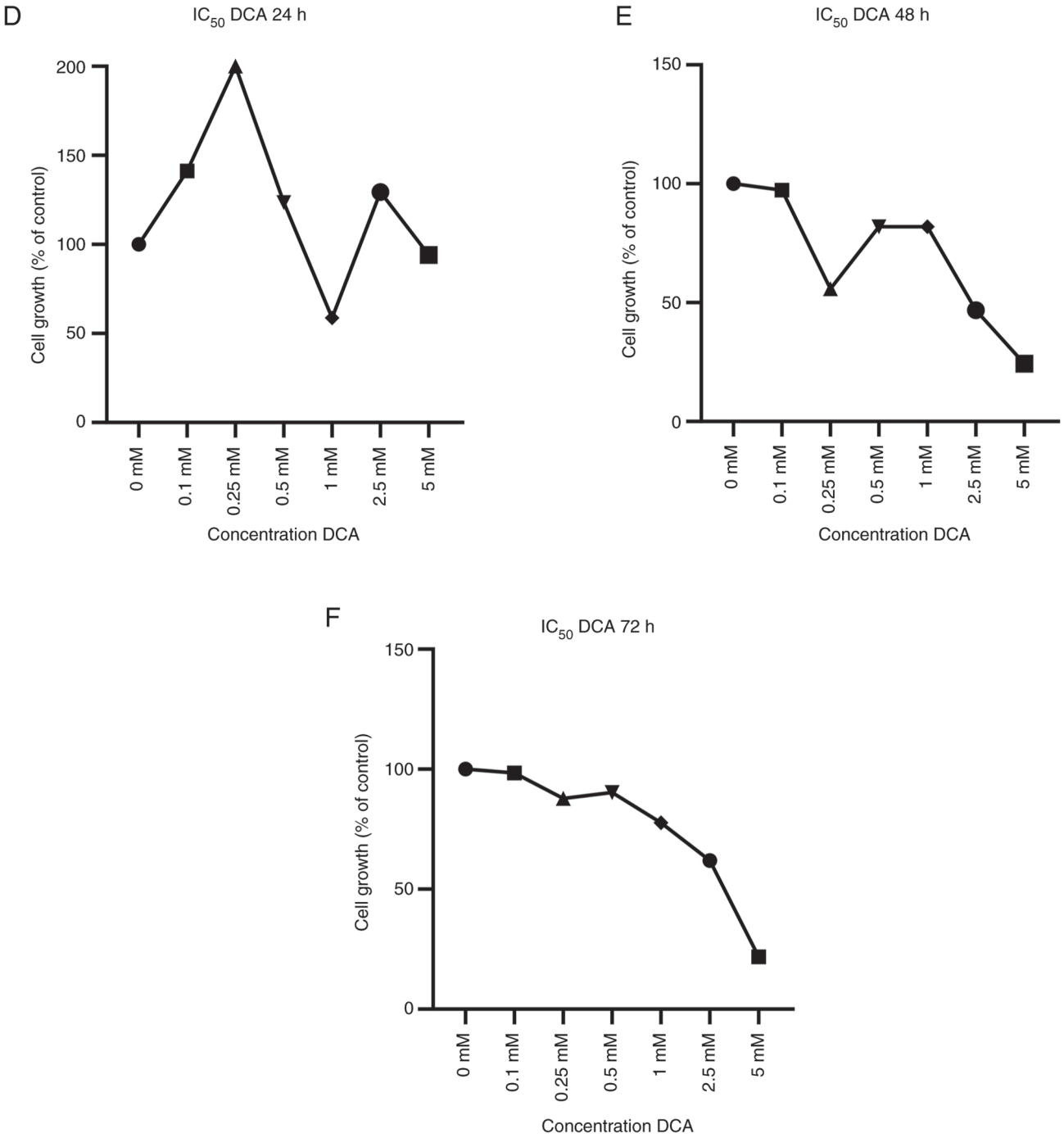


Figure S4.Continued.

iii. HCT-116-/- p53 and IM

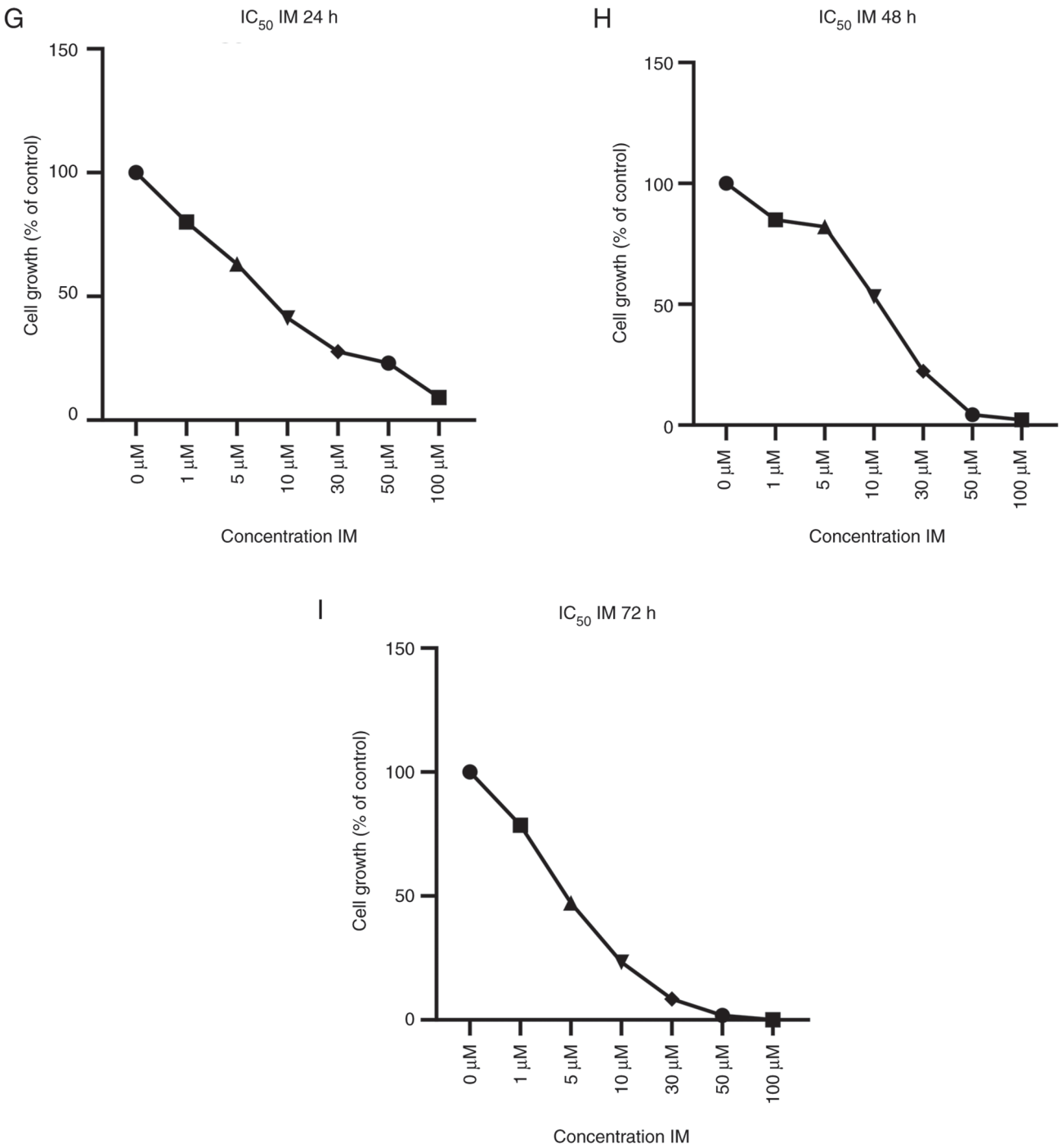


Figure S4. Dose-dependent effects of IM and DCA on the cell growth of HCT-116 (+/+p53) and HCT-116 (-/-p53) cells for up to 72 h. i) (A-C) Dose-dependent effect of IM on the cell proliferation of HCT-116 (+/+p53) cells (0, 1, 5, 10, 30, 50 and 100 μM) for 24, 48 and 72 h. Cells were seeded in an initial cell concentration of $0.25x10^5$ cells/ml. ii) (D-F) Dose-dependent effect of DCA on the cell proliferation of HCT-116 (+/+p53) cells (0, 0.1, 0.25, 0.5, 1, 2.5 and 5 mM) for 24, 48 and 72 h. Cells were seeded in an initial cell concentration of $0.25x10^5$ cells/ml. iii) (G-I) Dose-dependent effect of IM on the cell proliferation of HCT-116 (-/-p53) cells (0, 1, 5, 10, 30, 50 and 100 μM) for 24, 48 and 72 h. Cells were seeded in an initial cell concentration of $0.25x10^5$ cells/ml. iv) (J-L) Dose-dependent effect of DCA on the cell proliferation of HCT-116 (-/-p53) cells (0, 0.1, 0.25, 0.5, 1, 2.5 and 5 mM) for 24, 48 and 72 h. Cells were seeded in an initial cell concentration of $0.25x10^5$ cells/ml. IM, imatinib; DCA, dichloroacetate.

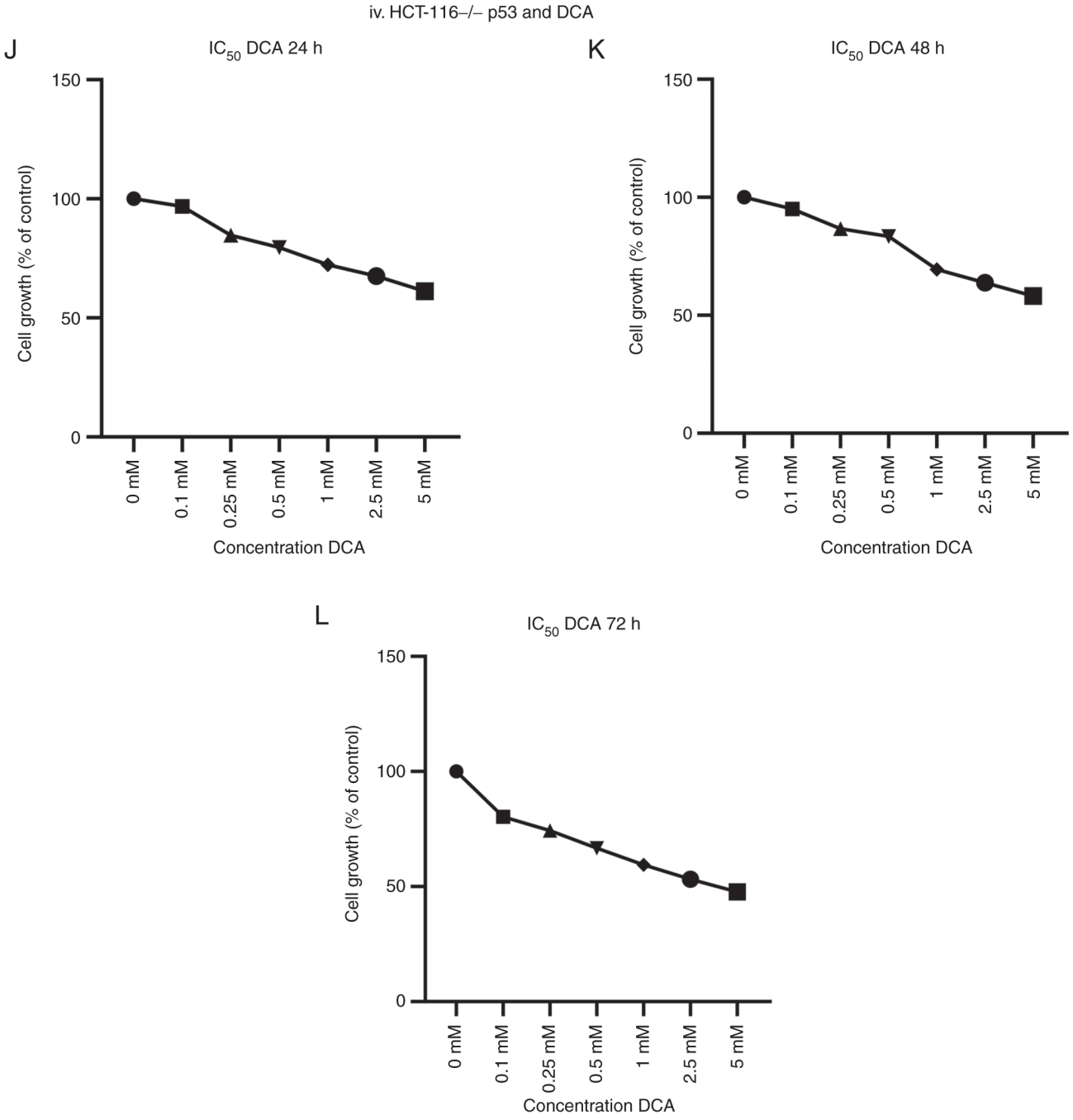


Figure S5. Network biology models reveal intricate connections of the 10 proteins screened by western blotting associated with oxidative phosphorylation, glycolysis, hypoxia and oxidative stress. (A) Multipartite Enrichr knowledge graph depicting the 10 selected proteins with biostatistical significant biological pathways deriving from 5 distinct databases. The nodes are color-coded based on the enclosed legend. (B) STRING protein-protein interaction network revealing connections among the 10 proteins under investigation.

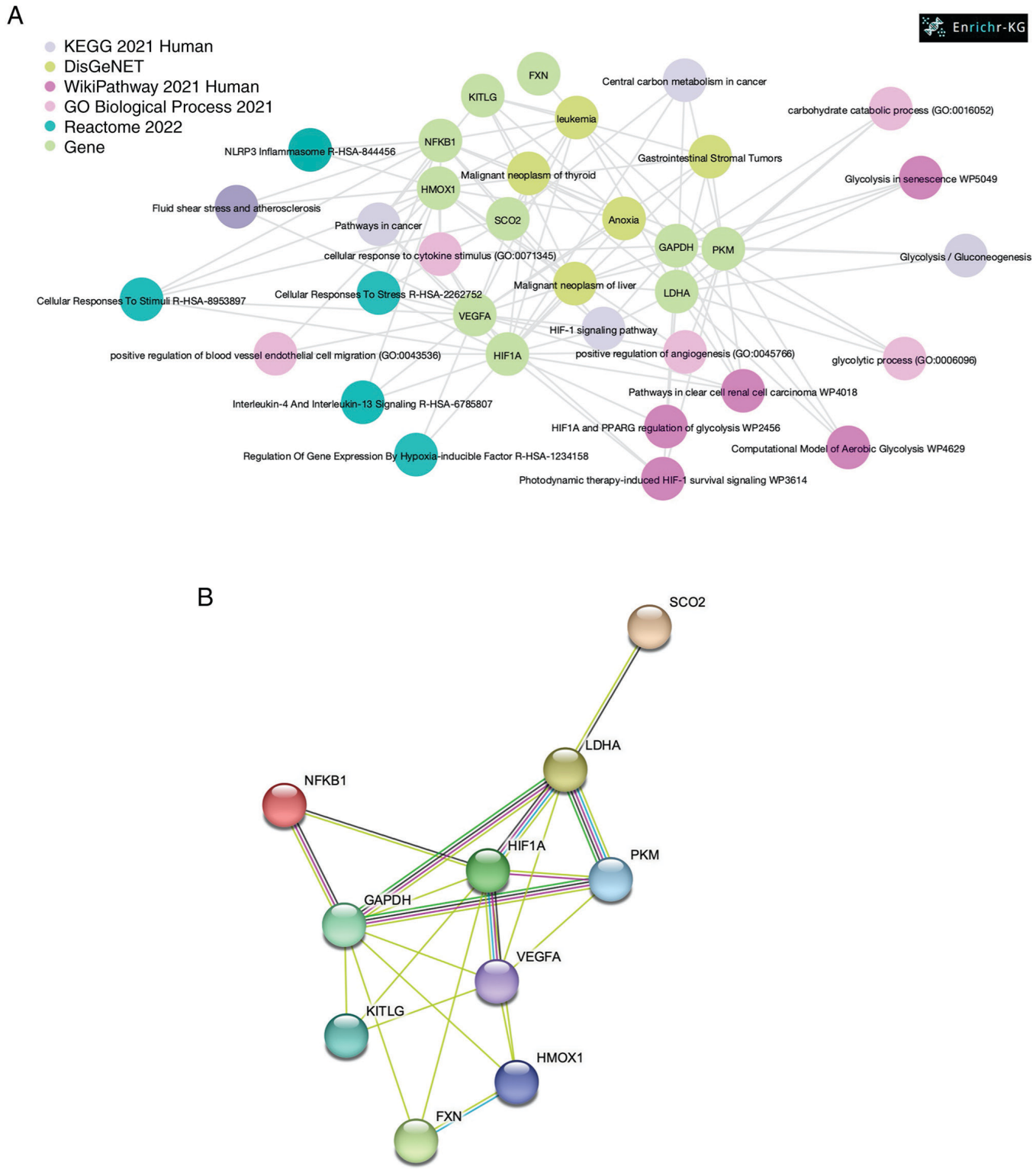


Figure S6. Flow cytometric analysis images showing the accumulation of 2',7'-dichlorofluorescein diacetate-stained reactive oxygen species in populations of (A) K-562 and (B) K-562R cells. IM, imatinib; DCA, dichloroacetate.