Data Article

Microarray dataset supporting a role for ATF4 in isoginkgetin-induced gene expression in HCT116 cells.

Erin van Zyl¹, Victoria Tolls¹, Bruce C McKay¹,²,*

¹ Department of Biology, Carleton University
² Institute of Biochemistry, Carleton University

A R T I C L E   I N F O

Article history:
Received 21 December 2021
Revised 18 February 2022
Accepted 28 March 2022
Available online 1 April 2022

Dataset link: Microarray analysis of isoginkgetin-treated HCT116 and HCT116p53-/- cells (Original data)

Keywords:
ATF4
Isoginkgetin
Microarray
Spliceosome inhibition

A B S T R A C T

Isoginkgetin (IGG) is a compound originally derived from the leaves of Ginkgo biloba trees. It was subsequently identified through a chemical screen to be an inhibitor of both the major and minor spliceosome, with an IC50 value of 30 μM [1]. Little is currently known about the overall effects of spliceosome inhibition on human cells. Here, we treated HCT116 and a p53 null subline of colon cancer cells with 30 μM IGG for 8 hours. Total RNA was isolated, and Affymetrix oligonucleotide microarray analysis was completed using samples from two biologically independent experiments. A relatively small number of transcripts were differentially expressed in these cell lines. There was considerable overlap in the upregulated but not the downregulated transcripts. PANTHER Reactome analysis of these shared upregulated transcripts identified enriched pathways involving the ATF4 transcription factor important in the integrated stress response [2].

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DOI of original article: 10.1016/j.bbamcr.2021.119123
* Corresponding author.
E-mail address: brucemckay@cunet.carleton.ca (B.C. McKay).
Social media: @erinanzyl (E. van Zyl), @McKay_Lab (B.C. McKay)

https://doi.org/10.1016/j.dib.2022.108126
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Specifications Table

| Subject                          | Genetics: General |
|---------------------------------|-------------------|
| Specific subject area           | Genome wide changes in gene expression following isoginkgetin treatment |
| Type of data                    | Table             |
| How data were acquired          | RNA isolation, Affymetrix microarrays, PANTHER gene ontology reactome analysis |
| Data format                     | Raw (linked)      |
| Parameters for data collection  | HCT116 and a subline deleted of the p53 tumour suppressor were treated with 30 μM IGG, an equivalent volume of DMSO as a vehicle control, or left untreated for 8 hours. |
| Description of data collection  | Total RNA was isolated using Qiagen RNeasy mini kits, labelled, hybridized to Affymetrix Human Transcriptome 2.0 oligonucleotide microarrays at the Affymetrix Microarray Facility, Stemcore Laboratory, Ottawa Hospital Research Institute (Ottawa, ON, Canada) |
| Data source location            | Institution: Carleton University |
|                                 | City/Town/Region: Ottawa |
|                                 | Country: Ontario |
| Data accessibility              | Repository name: Gene Expression Omnibus (GEO) |
|                                 | Data identification number: GSE180623 |
|                                 | Direct URL to data: https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE180623 |
|                                 | Probe-level files: GSM5466186-GSM466197 |
|                                 | Gene-Level files: GSM5468322- GSM5466340 |
| Related research article        | van Zyl E, Tolls V, Blackmore A, McKay BC. Isoginkgetin leads to decreased protein synthesis and activates an ATF4-dependent transcriptional response. Biochim Biophys Acta Mol Cell Res. 2021;1868(12):119123. |

Value of the Data

- This microarray data provides information on the transcriptional response of HCT116 and HCT116 p53 null cells following treatment with the pre-mRNA splicing inhibitor, IGG. The data set includes both gene level and individual probe level signal intensities.
- The gene level analysis can be used to gain understanding of the changes in gene expression in the presence and absence of p53 in response to IGG.
- The probe (exon) level analysis can be used to generate additional information on pre-mRNA splicing and alternative splicing.
- The data provided here and linked through the Gene Expression Omnibus (GEO) repository could be used by investigators interested in 1. cellular responses to spliceosome inhibition, 2. the effect of IGG on pre-mRNA splicing and 3. the effects of IGG on non-coding RNAs.

1. Data Description

The dataset includes gene level and probe level analysis of the cellular responses to the splicing inhibitor IGG in HCT116 colon cancer cells and an isogenic subline deleted of p53 (HCT116 p53 -/-) [3]. IGG significantly increased the expression of 53 mRNAs and decreased the abundance of 26 in the parental HCT116 cell line (Tables 1 and 2). In the p53 knockout subline, IGG significantly increased the expression of 82 and decreased the expression of 53 mRNAs (Tables 3 and 4). Only 22 of the increased and 3 of the decreased mRNAs were common to both cell lines and therefore they were regulated in a p53-independent manner (Fig. 1A and B). Panther Reactome Analysis of these shared transcripts identified only 3 over-represented pathways among these shared transcripts. Two of the 3 p53-independent responses “Response of EIF2AK1 (HRI) to heme deficiency” and “ATF4 activates genes in response to endoplasmic reticulum stress” involve the ATF4 transcription factor [2].
| Transcript Cluster ID | Gene Symbol | Gene ID   | Fold Change |
|-----------------------|-------------|-----------|-------------|
| TC15000300.HG.1       | CHAC1       | 79094     | 6.19        |
| TC16000473.HG.1       | MT1F        | 4494      | 3.87        |
| TC17001820.HG.1       | SLC16A6     | 9120      | 3.29        |
| TC10000449.HG.1       | DDIT4       | 54541     | 3.23        |
| TC08001369.HG.1       | SLC10A5     | 347051    | 2.46        |
| TC04001570.HG.1       | SLC7A11     | 23657     | 2.4         |
| TC16000471.HG.1       | MT1CP-201   | 441771    | 2.31        |
| TC16000476.HG.1       | MT1X        | 4501      | 2.31        |
| TC14002222.HG.1       | IGDH3-22    | 28497     | 2.25        |
| TC19000356.HG.1       | GDF15       | 9518      | 2.19        |
| TC12001625.HG.1       | DDIT4       | 54541     | 3.23        |
| TC06001089.HG.1       | ULBP1       | 80329     | 2.05        |
| TC17001723.HG.1       | SRSF1       | 6426      | 1.95        |
| TC11003457.HG.1       | ARL2        | 402       | 1.94        |
| TC09002706.HG.1       | BAAT        | 570       | 1.87        |
| TC16002074.HG.1       | MT1A        | 4499      | 1.98        |
| TC19000032.HG.1       | ATP5D       | 66043     | 1.95        |
| TC01000377.HG.1       | SESN2       | 83667     | 1.82        |
| TC15000461.HG.1       | ANXA2       | 302       | 1.81        |
| TC07001898.HG.1       | CREB3L2     | 64764     | 1.78        |
| TC01003796.HG.1       | SLC30A1     | 7779      | 1.73        |
| TC19000732.HG.1       | GFY         | 100507003 | 1.71        |
| TC16000057.HG.1       | NPW         | 283869    | 1.71        |
| TC05002075.HG.1       | STC2        | 8614      | 2.00        |
| TC19001871.HG.1       | TMEM238     | 388564    | 1.69        |
| TC0X002235.hg.1       | RTL8A       | 26071     | 1.66        |
| TC14002240.HG.1       | IGDH3-3     | 28501     | 1.65        |
| TC16000474.HG.1       | MT1H        | 4496      | 1.65        |
| TC07001630.HG.1       | ASNS        | 440       | 1.64        |
| TC16000480.HG.1       | HERPUD1     | 9709      | 1.63        |
| TC16002035.HG.1       | MT1A        | 4489      | 1.63        |
| TC22000627.HG.1       | XBP1        | 7494      | 1.63        |
| TC11002483.HG.1       | IFITM2      | 10581     | 1.61        |
| TC16002034.HG.1       | MT2A        | 4502      | 1.61        |
| TC01003194.HG.1       | H2AC21      | 317772    | 1.6         |
| TC17001617.HG.1       | ARL17A      | 51326     | 1.6         |
| TC19000156.HG.1       | OR7D2       | 162998    | 1.6         |
| TC10002938.HG.1       | ADIRF       | 10974     | 1.59        |
| TC08000227.HG.1       | DUSP4       | 1846      | 1.57        |
| TC01006390.HG.1       | HNRNP1      | 3192      | 1.57        |
| TC09000260.HG.1       | FAM27E3     | 100131997 | 1.56        |
| TC06004075.HG.1       | LYG5B       | 58496     | 1.56        |
| TC20000009.HG.1       | TRIB3       | 57761     | 1.56        |
| TC22000467.HG.1       | IKGC        | 3514      | 1.55        |
| TC04002952.HG.1       | AREG        | 374       | 1.54        |
| TC6. QBL_HAP6000133.HG.1 | IER3 | 8870      | 1.54        |
| TC15002759.HG.1       | CKMT1B      | 1159      | 1.53        |
| TC26000265.HG.1       | HIST1H2BM   | 8342      | 1.53        |
| TC05001898.HG.1       | PLAC8L1     | 153770    | 1.53        |
| TC00002223.HG.1       | IGDH2-21    | 28502     | 1.52        |
| TC01005437.HG.1       | SLC6A9      | 6536      | 1.52        |
| TC01001090.HG.1       | TXNIP       | 10628     | 1.51        |

1 Transcript Cluster ID assigned from Affymetrix Transcriptome Analysis Console (TAC) 4.0
2 Gene symbols and IDs were obtained from NCBI gene (https://www.ncbi.nlm.nih.gov/gene/)
3 Fold change relative to DMSO vehicle control.
Table 2
List of downregulated transcripts in HCT116 cells following IGG treatment.

| Transcript Cluster ID       | Gene Symbol | NCBI Gene ID | Fold Change |
|-----------------------------|-------------|--------------|-------------|
| TC17000934.HG.1             | CCDC137     | 339230       | -1.51       |
| TC03000672.HG.1             | EEFSEC      | 60678        | -1.51       |
| TC12000747.HG.1             | ELK3        | 2004         | -1.51       |
| TC17000996.HG.1             | METTL16     | 79066        | -1.51       |
| TC22000709.HG.1             | TXN2        | 25828        | -1.51       |
| TC17000838.HG.1             | CDR2L       | 30850        | -1.52       |
| TC17002052.HG.1             | MAP2K4      | 6416         | -1.52       |
| TC03002349.HG.1             | PRKCD       | 5580         | -1.52       |
| TC20001762.HG.1             | RBM12       | 10137        | -1.52       |
| TC19001036.HG.1             | SGTA        | 6449         | -1.52       |
| TC17000162.HG.1             | COX10       | 1352         | -1.53       |
| TC20001531.HG.1             | BCL2L1      | 598          | -1.54       |
| TC11002866.HG.1             | DLAT        | 1737         | -1.54       |
| TC15001257.HG.1             | EHD4        | 30844        | -1.56       |
| TC06000796.HG.1             | PM20D2      | 135293       | -1.56       |
| TC07003019.HG.1             | ABHD11      | 83451        | -1.56       |
| TC6_MANN_HAP4000139.HG.1    | C6orf47     | 57827        | -1.58       |
| TC02001139.HG.1             | SLC39A10    | 57181        | -1.61       |
| TC03000321.HG.1             | TSR2        | 90121        | -1.62       |
| TC08001507.HG.1             | SLC25A32    | 81034        | -1.63       |
| TC16001353.HG.1             | CHMP1A      | 5119         | -1.68       |
| TC22001208.HG.1             | DGR2        | 9993         | -1.73       |
| TC16000149.HG.1             | PMM2        | 5373         | -1.73       |
| TC12000189.HG.1             | EMF1        | 2012         | -1.77       |
| TC05000701.HG.1             | EGR1        | 1958         | -1.78       |
| TC12000334.HG.1             | TEAD4       | 7004         | -1.92       |

1 Transcript Cluster ID assigned from Affymetrix Transcriptome Analysis Console (TAC) 4.0
2 Gene symbols and IDs were obtained from NCBI gene [https://www.ncbi.nlm.nih.gov/gene/](https://www.ncbi.nlm.nih.gov/gene/)
3 Fold change relative to DMSO vehicle control.

Table 3
List of upregulated transcripts in the HCT116 p53 +/- subline following IGG treatment.

| Transcript Cluster ID       | Gene Symbol | NCBI Gene ID | Fold Change |
|-----------------------------|-------------|--------------|-------------|
| TC12001420.HG.1             | RNY5        | 6090         | 10.21       |
| TC15000300.HG.1             | CHAC1       | 79094        | 8.44        |
| TC19000356.HG.1             | GDF15       | 9518         | 5.28        |
| TC17001820.HG.1             | SLC16A6     | 9120         | 4.77        |
| TC10000449.HG.1             | DDIT4       | 54541        | 4.66        |
| TC04001570.HG.1             | SLC7A11     | 23657        | 4.33        |
| TC02002445.HG.1             | NRA42       | 4929         | 3.9         |
| TC01003796.HG.1             | SLC30A1     | 7779         | 3.78        |
| TC08002271.HG.1             | DUSP4       | 1846         | 3.75        |
| TC05002075.HG.1             | STC2        | 8614         | 3.18        |
| TC01000377.HG.1             | SESN2       | 83667        | 2.85        |
| TC16000476.HG.1             | MT1X        | 4501         | 2.62        |
| TC16000640.HG.1             | CMIP        | 80790        | 2.6         |
| TC06001089.HG.1             | ULBP1       | 80329        | 2.59        |
| TC16000473.HG.1             | MT1F        | 4494         | 2.56        |
| TC01006089.HG.1             | SLC30A1     | 7779         | 2.53        |
| TC01005688.HG.1             | PSMA5       | 5686         | 2.42        |
| TC07001898.HG.1             | CREB3L2     | 64764        | 2.42        |
| TC07001630.HG.1             | ASNS        | 440          | 2.37        |
| TC08001059.HG.1             | DUSP4       | 1846         | 2.33        |
| TC15002652.HG.1             | ST20        | 400410       | 2.23        |
| TC02002818.HG.1             | SGC2        | 7857         | 2.21        |
| TC16000480.HG.1             | HERPUD1     | 8709         | 2.18        |
| TC04002953.HG.1             | AREG        | 374          | 2.03        |
| TC04002952.HG.1             | AREG        | 374          | 2.02        |
| TC09002484.HG.1             | FBXO10      | 26267        | 1.98        |
| TC06002799.HG.1             | VEGFA       | 7422         | 1.96        |

(continued on next page)
| Transcript Cluster ID | Gene Symbol | NCBI Gene ID | Fold Change |
|-----------------------|-------------|--------------|-------------|
| TC09000358.HG.1 | PSAT1 | 29968 | 1.95 |
| TC08000710.HG.1 | LNCOC1 | 100288181 | 1.93 |
| TC11001536.HG.1 | CSTF3 | 1479 | 1.92 |
| TC06002024.HG.1 | TUBE1 | 51775 | 1.91 |
| TC02001273.HG.1 | PK55 | 150967 | 1.9 |
| TC08002558.HG.1 | LNCOC1 | 100288181 | 1.88 |
| TC03001929.HG.1 | SLC33A1 | 9197 | 1.88 |
| TC04001058.HG.1 | FGFBP1 | 9982 | 1.87 |
| TC22000317.HG.1 | ATF4 | 468 | 1.87 |
| TC22000627.HG.1 | XBP1 | 7494 | 1.87 |
| TC05002974.HG.1 | RPL37 | 6167 | 1.83 |
| TC16000501.HG.1 | CCDC113 | 29070 | 1.82 |
| TC11003010.HG.1 | CARS | 27267 | 1.8 |
| TC08001317.HG.1 | NKA | 79576 | 1.79 |
| TC11001124.HG.1 | GRAMD1B | 57476 | 1.75 |
| TC12001625.HG.1 | DINT3 | 1649 | 1.74 |
| TC16001234.HG.1 | AARS | 234734 | 1.73 |
| TC10001569.HG.1 | AVP11 | 60370 | 1.72 |
| TC16000190.HG.1 | C16orf45 | 89927 | 1.68 |
| TC03000888.HG.1 | PSAT1P4 | 100287630 | 1.68 |
| TC01004662.HG.1 | SPAG17 | 200162 | 1.67 |
| TC11000856.HG.1 | PCF11 | 51585 | 1.67 |
| TC12003284.HG.1 | RHOF | 54509 | 1.65 |
| TC09000508.HG.1 | NR4A3 | 8013 | 1.64 |
| TC01004603.HG.1 | SARS | 6301 | 1.64 |
| TC06002667.HG.1 | ZSCAN12P1 | 221584 | 1.64 |
| TC09000160.HG.1 | FAM27E3 | 100131997 | 1.63 |
| TC04000460.HG.1 | GPAT3 | 84803 | 1.62 |
| TC02002074.HG.1 | EIF2AK3 | 9451 | 1.61 |
| TC01003555.HG.1 | PTP4A1P7 | 100421681 | 1.61 |
| TC03001683.HG.1 | TMEM39A | 55254 | 1.61 |
| TC07001559.HG.1 | SEMA3C | 10512 | 1.6 |
| TC17002686.HG.1 | SP2-AS1 | 100506325 | 1.6 |
| TC12001976.HG.1 | TMEM116 | 89894 | 1.6 |
| TC17001617.HG.1 | ARL17A | 51326 | 1.6 |
| TC13000319.HG.1 | GAS6-AS1 | 650669 | 1.59 |
| TC04001496.HG.1 | SEC24D | 9871 | 1.59 |
| TC17000396.HG.1 | SLFN5 | 162394 | 1.58 |
| TC02002067.HG.1 | KRCC1 | 1632B2 | 1.57 |
| TC06000056.HG.1 | RREB1 | 6239 | 1.56 |
| TC02001948.HG.1 | GGTT1 | 2673 | 1.56 |
| TC170001631.HG.1 | SP2-AS1 | 100506325 | 1.56 |
| TC20000599.HG.1 | GPCPD1 | 56261 | 1.56 |
| TC12001282.HG.1 | EPS8 | 156607 | 1.56 |
| TC09000066.HG.1 | LURAP1L | 286343 | 1.55 |
| TC21000284.HG.1 | HSPA13 | 33097 | 1.54 |
| TC09000962.HG.1 | IFNE | 338376 | 1.54 |
| TC17002458.HG.1 | DERL2 | 51009 | 1.53 |
| TC16000472.HG.1 | MT1B | 4490 | 1.52 |
| TC11001289.HG.1 | CARS | 27267 | 1.52 |
| TC16000469.HG.1 | MT1JP | 4498 | 1.52 |
| TC11002361.HG.1 | HYOU1 | 10525 | 1.52 |
| TC09001325.HG.1 | NFI3 | 4783 | 1.52 |
| TC22000477.HG.1 | MIR3198-1 | 100423025 | 1.52 |
| TC150002609.HG.1 | AP352 | 10239 | 1.52 |
| TC01002060.HG.1 | SREBP2-AS1 | 112637020 | 1.51 |
| TC04002517.HG.1 | UCDH | 7358 | 1.51 |
| TC20001122.HG.1 | CSRP2BP | 100303755 | 1.51 |
| TC01003623.HG.1 | EDEM3 | 80267 | 1.51 |
| TC09001589.HG.1 | HSPA5 | 3309 | 1.51 |
| TC16000474.HG.1 | MT1H | 4496 | 1.5 |

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1. Transcript Cluster ID assigned from Affymetrix Transcriptome Analysis Console (TAC) 4.0
2. Official gene symbol from NCBI gene webpage
3. Gene ID identifiers from NCBI gene webpage
4. Relative fold changes compared to DMSO vehicle control, analyzed using Affymetrix Transcriptome Analysis Console (TAC) 4.0

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Table 4
List of downregulated transcripts in the HCT116 p53 -/- subline following IGG treatment.

| Transcript Cluster ID1 | Gene Symbol2 | NCBI Gene ID3 | Fold Change4 |
|------------------------|--------------|---------------|--------------|
| TC10000577.HG.1        | LINC00857    | 6659          | 1.51         |
| TC16001601.HG.1        | CMTM3        | 84056         | 1.51         |
| TC07002499.HG.1        | SERPIN1      | 89795         | 1.51         |
| TC14001209.HG.1        | SGPP1        | 6558          | 1.51         |
| TC11003273.HG.1        | PCF11-AS1    | 7025          | 1.52         |
| TC17000692.HG.1        | STXB4        | 730755        | 1.52         |
| TC12001637.HG.1        | CTDSF2       | 84159         | 1.52         |
| TC14000353.HG.1        | DACT1        | 51339         | 1.54         |
| TC02000192.HG.1        | CLIP4        | 79745         | 1.54         |
| TC13000431.HG.1        | GAS6-AS2     | 100506394     | 1.55         |
| TC17002807.HG.1        | TIMP2        | 7077          | 1.55         |
| TC04000883.HG.1        | MIR1305      | 100302270     | 1.55         |
| TC18000205.HG.1        | MALT1        | 10892         | 1.56         |
| TC0X001397.hg.1        | MOSPD1       | 56180         | 1.57         |
| TC05002969.HG.1        | DAB2         | 1601          | 1.58         |
| TC07002368.HG.1        | ZNF107       | 51427         | 1.59         |
| TC09002524.HG.1        | ANKRD20A3    | 441425        | 1.60         |
| TC03002235.HG.1        | NR2C2        | 7182          | 1.61         |
| TC09000999.HG.1        | DDX58        | 23586         | 1.61         |
| TC17001532.HG.1        | PTRF         | 284119        | 1.61         |
| TC01000353.HG.1        | SFN          | 2810          | 1.61         |
| TC03002676.HG.1        | ACTL6A       | 86            | 1.62         |
| TC17002855.HG.1        | AXIN2        | 8313          | 1.63         |
| TC05003395.HG.1        | TRIM52       | 84851         | 1.63         |
| TC03003038.HG.1        | ZBTB20       | 26137         | 1.63         |
| TC10000377.HG.1        | ARID5B       | 84159         | 1.63         |
| TC04001830.HG.1        | TRIML2       | 205860        | 1.64         |
| TC03002740.HG.1        | FAM43A       | 131583        | 1.64         |
| TC03001512.HG.1        | ID2B         | 84099         | 1.64         |
| TC04002781.HG.1        | SH3D19       | 152503        | 1.65         |
| TC04001615.HG.1        | ZNF827       | 152485        | 1.67         |
| TC07001980.HG.1        | CTAGE4       | 100128553     | 1.67         |
| TC05000795.HG.1        | SH3RF2       | 153769        | 1.67         |
| TC17001803.HG.1        | SMURF2       | 64750         | 1.69         |
| TC04002771.HG.1        | ZNF827       | 152485        | 1.70         |
| TC17001722.HG.1        | VEZF1        | 7716          | 1.70         |
| TC10002813.HG.1        | CALHM2       | 51063         | 1.70         |
| TC14002241.HG.1        | IGHD2-2      | 28505         | 1.70         |
| TC19002012.HG.1        | UCA1         | 652995        | 1.74         |
| TC12002734.HG.1        | SLC2A3       | 6515          | 1.74         |
| TC03001959.HG.1        | SPTSSB       | 165679        | 1.75         |
| TC11000715.HG.1        | MYEOV        | 26579         | 1.85         |
| TC12000189.HG.1        | EMP1         | 2012          | 1.86         |
| TC05000218.HG.1        | ITCG2        | 3673          | 1.88         |
| TC07001605.HG.1        | SAMD9        | 54809         | 1.90         |
| TC02001139.HG.1        | SLC39A10     | 57181         | 1.92         |
| TC15002251.HG.1        | SMAD3        | 4088          | 1.94         |
| TC12000747.HG.1        | ELK3         | 2004          | 1.95         |
| TC05002612.HG.1        | SLC12A2      | 6558          | 1.99         |
| TC12000656.HG.1        | NAV3         | 89795         | 2.00         |
| TC13001403.HG.1        | KATNAL1      | 84056         | 2.02         |
| TC06000135.HG.1        | SOX4         | 6659          | 2.11         |
| TC10002092.HG.1        | ARID5B       | 84159         | 2.25         |
| TC17001485.HG.1        | KRTAP2-3     | 730755        | 2.48         |
| TC05002512.HG.1        | NR2F1        | 7025          | 2.52         |

1 Transcript Cluster ID assigned from Affymetrix Transcriptome Analysis Console (TAC) 4.0
2 Official gene symbol from NCBI gene webpage
3 Gene ID identifiers from NCBI gene webpage
4 Relative fold changes compared to DMSO vehicle control, analyzed using Affymetrix Transcriptome Analysis Console (TAC) 4.0
Table 5
Summary of Panther Reactome analysis of transcripts induced by IGG in both cell lines.

| Reactome pathway                                      | Enrichment | P value  |
|-------------------------------------------------------|------------|----------|
| Metallothioneins bind metals                          | >100       | 7.88E-04 |
| >-Response to metal ions                              | >100       | 1.47E-03 |
| Response to EIF2AK1 (HRI) to heme deficiency          | >100       | 1.76E-03 |
| ATF4 activates genes in response to ER stress         | >100       | 8.69E-03 |
| >-PERK regulates gene expression                      | 87.76      | 1.40E-02 |
| >-Unfolded protein response                           | 41.15      | 6.00E-03 |

1 Panther Reactome Pathways that were enriched. ‘>’ indicates that the Reactome Pathway above is nested.
2 Fold enrichment above expected.
3 The probability of observing this enrichment in a random list of genes of this size determined by Fisher exact test with Bonferroni correction for multiple testing.

Fig. 1. Venn diagrams representing IGG upregulated and downregulated transcripts in HCT116 and its p53 null subline. IGG increased (A) and decreased (B) the expression of mRNAs in HCT116 expressing and deleted of p53 (p53 +/- and p53 -/ -). Images were created from data in Tables 1-4 at https://bioinformatics.psb.ugent.be/webtools/Venn/.

2. Experimental Design, Materials and Methods

2.1. Cell culture and drug treatment

HCT116 and HCT116 p53 +/- colon cancer cells were seeded in 6cm dishes at 250,000 cells/dish 24 hours prior to drug treatment. Cells were treated with 30 μM IGG, an equivalent volume of DMSO as a vehicle control, or left untreated for 8 hours. Two biologically independent experiments were performed.

2.2. RNA isolation and microarrays

After 8 hours of treatment, media was removed, and cells were washed with PBS. Total RNA was isolated using the Qiagen RNAeasy Mini RNA isolation kit according to manufacturer's in-
structions. RNA purity and concentration was determined using the DeNovix DS-11 spectrophotometer. RNA was sent for Agilent Bioanalyzer quality assessment and RNA was then processed for analysis of the Human Transcriptome 2.0 Array at the Stemcore facility at the Ottawa Hospital research institute (OHRI), Ottawa, ON Canada.

2.3. Data analysis

Analysis was performed at the probe- and gene-level using the Transcriptome Analysis Console (TAC) 4.0 Software from Affymetrix. Microarray data was analysed using the Affymetrix Transcriptome Analysis Console (TAC) 4.0 software with default settings. A gene was considered expressed in a particular condition if it was detected in 50% of more of the samples and the sample had a DABG p-value of less than 0.05. A one-way between-subject unpaired ANOVA was used to determine statistical significance and was subject to false discovery rate (FDR) multi-test correction (Benjamini–Hochberg Step-Up FDR) for both analyses. A threshold of a 1.5-fold change was also applied and unknown transcripts were removed to identify upregulated (Tables 1 and 3) and downregulated (Tables 2 and 4) transcripts. Panther reactome analysis of RNAs induced in both cell lines (Fig. 1A) was performed online (http://geneontology.org/).

CRediT Author Statement

Erin van Zyl: Formal analysis, Investigation, Writing – original draft, Writing – review & editing; Victoria Tolls: Methodology, Investigation, Formal analysis; Bruce McKay: Conceptualization, Methodology, Formal analysis, Resources, Writing – review & editing, Supervision, Funding acquisition.

Declaration of Competing Interest

The authors have no competing interests to declare.

Data Availability

Microarray analysis of isoginkgetin-treated HCT116 and HCT116p53−/− cells (Original data) (NCBI GEO).

Acknowledgments

This work was funded through grants from the Natural Sciences and Engineering Research Council of Canada (RGPIN-2014-03645 and RGPIN-2019-06146) to B.C.M. E.V.Z. is supported with a Vanier Canada Graduate Scholarship through the Natural Sciences and Engineering Research Council of Canada.

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