



RESEARCH ARTICLE

A systems biology-based study to assess the effects of TNF- α \pm apigenin in triple-negative breast cancer cell line

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Abstract

Triple-negative breast cancer (TNBC) is a type of breast cancer that lacks estrogen, progesterone, and HER2 receptors. Various treatment methods are available for breast cancer, but therapies with minimal toxic side effects are particularly important. This study computationally investigates the impact of apigenin, a compound used in traditional Chinese medicine, on the TNBC cell line. The GSE120550 dataset was retrieved from the NCBI-GEO database. BRB-ArrayTools were used for pre- and post-processing to identify significantly differentially expressed genes. Additionally, the DAVID web server was utilized to analyze three main components: "biological process," "cellular component," and "molecular function," along with the KEGG signaling pathway. Finally, a Venn diagram was employed to thoroughly investigate the number of shared genes among 15 groups derived from 6 compared sample sets. The primary analysis of 6 pairs of samples revealed significant differentially expressed genes (DEGs), which were prioritized using the TOPPgene web server. These identified genes, playing key roles in inhibiting the progression of BC, are involved in various signaling pathways. Protein-protein interaction network analysis highlighted the biomarkers associated with the inhibitory effects of apigenin across the 15 sets derived from the 6 sample pairs. The findings of this study confirm the inhibitory effects of apigenin, with no toxic side effects, on patients with TNBC. This natural compound holds promise for future therapeutics and novel drug designs.

Keywords

apigenin; TNF- α ; systems biology; pharmacology; triple-negative breast cancer; anti-cancer agent

Introduction

Triple-negative breast cancer (TNBC) arises from the absence of 3 key receptors: Estrogen Receptor (ER), Progesterone Receptor (PR), and human epidermal growth factor receptor 2 (HER2). It accounts for approximately 10-15% of invasive breast cancer cases, with a high risk of relapse even after treatment (1, 2). Diagnosis TNBC can be challenging due to its histologically similarity to basal-like BC, which is associated with BRCA1 dysfunction in the relevant signaling pathways (3). Common treatments approaches for TNBC include surgery followed by chemotherapy and radiation therapy, or the reverse for more manageable cases (4). As a focus of global cancer research, therapeutic agents are needed to target receptors and signalling

pathways. Tumor necrosis factor-alpha (TNF- α) is a critical target, playing a dual role (a "double-edged sword") in both promoting and inhibiting cancer growth (5). Although no clinical trials have reported effective TNF- α inhibition due to its high toxicity (5), its role in inflammation and cancer progression can be significant in the host cells of cancerous tissues (5, 6). Traditional Chinese medicine, such as Triptolide and Tubeimu, has been used since ancient times as a source for developing anti-metastatic agents to treat TNBC (7, 8).

TNF- α is a crucial pro-inflammatory cytokine that plays a significant role in the tumor microenvironment, particularly in TNBC. Its importance stems from its influence on tumor progression. TNBC lacks estrogen and progesterone receptors and has low HER2 expression, making it one of the most difficult subtypes of breast cancer to treat due to its aggressive nature and high propensity for metastasize (9, 10). The MDA-MB-231 cell line is commonly used in TNBC research due to its high invasiveness and resistance to conventional therapies(9).

TNF- α promotes cell migration, increases invasion, and facilitates metastasis in MDA-MB-231 cells by upregulating signaling pathways such as NF- κ B and MAPK (11). Increasing evidence suggests that TNF- α plays a crucial role in cancer progression and may also have therapeutic potential. Studies on MDA-MB-231 cells have shown that TNF- α significantly alters IL-1 α expression (12). Additionally, TNF- α secretes chemokines that worsen the tumor microenvironment, further promoting tumor cell migration and invasion (13, 14).

Apigenin, phytonutrient found in fruits and vegetable, has demonstrated promising anti-cancer properties. It inhibits the proliferation of cancer cells, including MDA-MB-231 cell lines (15, 16). Apigenin suppresses pro-tumor factors such as TNF- α , IL-1 α , and IL-6, thereby reducing their tumor-promoting effects (14, 16). For instance, apigenin was found to inhibit the release of CCL2, which is induced by TNF- α , thereby preventing tumor migration and metastasis (14). Additionally, apigenin induces apoptosis and cell cycle arrest in MDA-MB-231 cells, highlighting its potential as a therapeutic agent against TNBC, particularly in its early stages (15, 16).

In the future, understanding the interaction between TNF- α and apigenin in TNBC cell lines, such as MDA-MB-231, could help address the complex therapeutic landscape of TNBC treatment. Apigenin not only inhibits inflammatory pathways but also induces cell death, counteracting the tumor-promoting effects of TNF- α . Due to this dual action, a growing body of research suggests that apigenin can enhance the efficacy of chemotherapy in TNBC, particularly when combined with other treatments targeting the TNF- α signaling pathway (12, 17).

Among natural compounds with low toxicity, apigenin derived from the *Apium* genus, is one of the most extensively studied molecules for its anti-cancer properties due to its flavonoid structure (18, 19). Numerous studies have also explored apigenin's antioxidant, anti-allergic,

antimicrobial, and anti-inflammatory activities, along with its derivatives (20-22). Apigenin's remarkable role lies in its ability to induce cell cycle arrest and apoptosis by targeting various signaling pathways, including Wnt/ β -catenin, PI3K/Akt/mTOR and STAT3 (23-25).

Recent attention has focused on the effects of apigenin treatment, particularly in combination with TNF- α , on gene expression in TNBC cells, including the MDA-MB-231 cell lines. TNF- α , a pro-inflammatory cytokine in the tumor microenvironment, often promotes cancer progression through signalling pathways such as MAPK and NF- κ B (26, 27). Apigenin, a flavonoid known for its anti-inflammatory and anti-cancer properties, regulates process such as apoptosis, inflammation, and cell survival (28).

TNF- α stimulates the production of inflammatory cytokines such as IL-6 and IL-1 β in MDA-MB-231 cells, leading to increased proliferation and survival (26). These cytokines activate downstream signalling pathways that promote tumor growth and metastasis through various mechanisms. Research has shown that apigenin can effectively counteract these effects by inhibiting the production of IL-6 and TNF- α , both of which contribute to TNF- α -induced inflammation (26). This anti-inflammatory action may significantly reduce the expression of pro-tumorigenic genes in TNBC cells, potentially decreasing the aggressiveness of the tumors.

Apigenin has been shown to induce apoptosis in MDA-MB-231 cells by modulating various apoptotic pathways involved in cell death. Studies indicate that apigenin upregulates pro-apoptotic genes and downregulates anti-apoptotic genes, leading to a significant increase in cell death when TNF- α is present (28). For instance, apigenin induces the expression of BAX, a pro-apoptotic gene, while suppressing BCL-2, an anti-apoptotic gene. This shift in gene expression favors apoptosis, impacting cell survival. To survive, cancer cells must alter their gene expression to overcome the apoptotic signals induced by TNF- α .

Apigenin modulates the NF- κ B signaling pathway in a manner that is highly relevant for analysing its effects on TNF- α induced gene expression. TNF- α enhances NF- κ B activity, which promotes the transcription of genes involved in inflammation, survival and proliferation when activated (29). Apigenin inhibits the phosphorylation of I κ B α , a key regulator in the NF- κ B pathway, preventing NF- κ B from translocating to the nucleus and thereby inhibiting gene transcription (29). This reduction in NF- κ B activity can lead to the downregulation of various NF- κ B target genes, including those involved in cell invasion and migration, such as matrix metalloproteinase-9 (MMP-9) (30).

Apigenin has also demonstrated the potential to modulate chemokine expression, an important areas of application. Research indicates that TNF- α promotes the production of chemokines, such as CXCL1, which are associated with tumor cell migration and dissemination throughout the body (27). When MDA-MB-231 cells are

treated with apigenin, their metastatic capabilities may be reduced by downregulating these chemokines (27). Given that TNBC is particularly prone to metastasis, which adversely affects prognosis, this effect of apigenin is significant.

The current study focuses on a systems biology approach to analyse significant differentially expressed genes in the TNBC cell line, considering the role of TNF- α as a tumor-promoting agent, both with and without apigenin treatment. Additionally, the study will investigate biological processes, molecular functions, and cellular components to identify the signalling pathways involved, which could inform future novel drug design and discovery.

Materials and Methods

Fig. 1 provides a detailed flowchart of the procedure, serving as a comprehensive diagram for biomarker analyses (31, 32).

Microarray Database

The GSE120550 dataset, from platform GPL17692 [HuGene-2_1-st] Affymetrix Human Gene 2.1 ST Array [transcript (gene) version], was obtained from the publicly available NCBI-GEO database of the National Center (i.e., <https://www.ncbi.nlm.nih.gov/gds/>). The dataset includes 12 samples of MDA-MB-231 cells treated with TNF- α [40 ng/ml] \pm apigenin [40 μ M] for (n TNF- α = 3: GSM3402894, GSM3402895 and GSM3402896; n apigenin = 3: GSM3402897, GSM3402898 and GSM3402899; n TNF- α +apigenin = 3: GSM3402900, GSM3402901 and GSM3402902) and untreated control (n=3; GSM3402891, GSM3402892 and GSM3402893).

Identification of significant genes between four types of samples and gene prioritization

Dr. Richard Simon and his team developed BRB-ArrayTools (v4.6.0) (<https://brb.nci.nih.gov/BRB-ArrayTools/>) to identify significant differentially expressed genes (DEGs) in treated and untreated MDA-MB-231 cell lines.

The pre-treatment procedure included quantile normalization and gene annotation using the R package, "pd.hugene.2.1.st" (33). Next, the "gcrma" R package

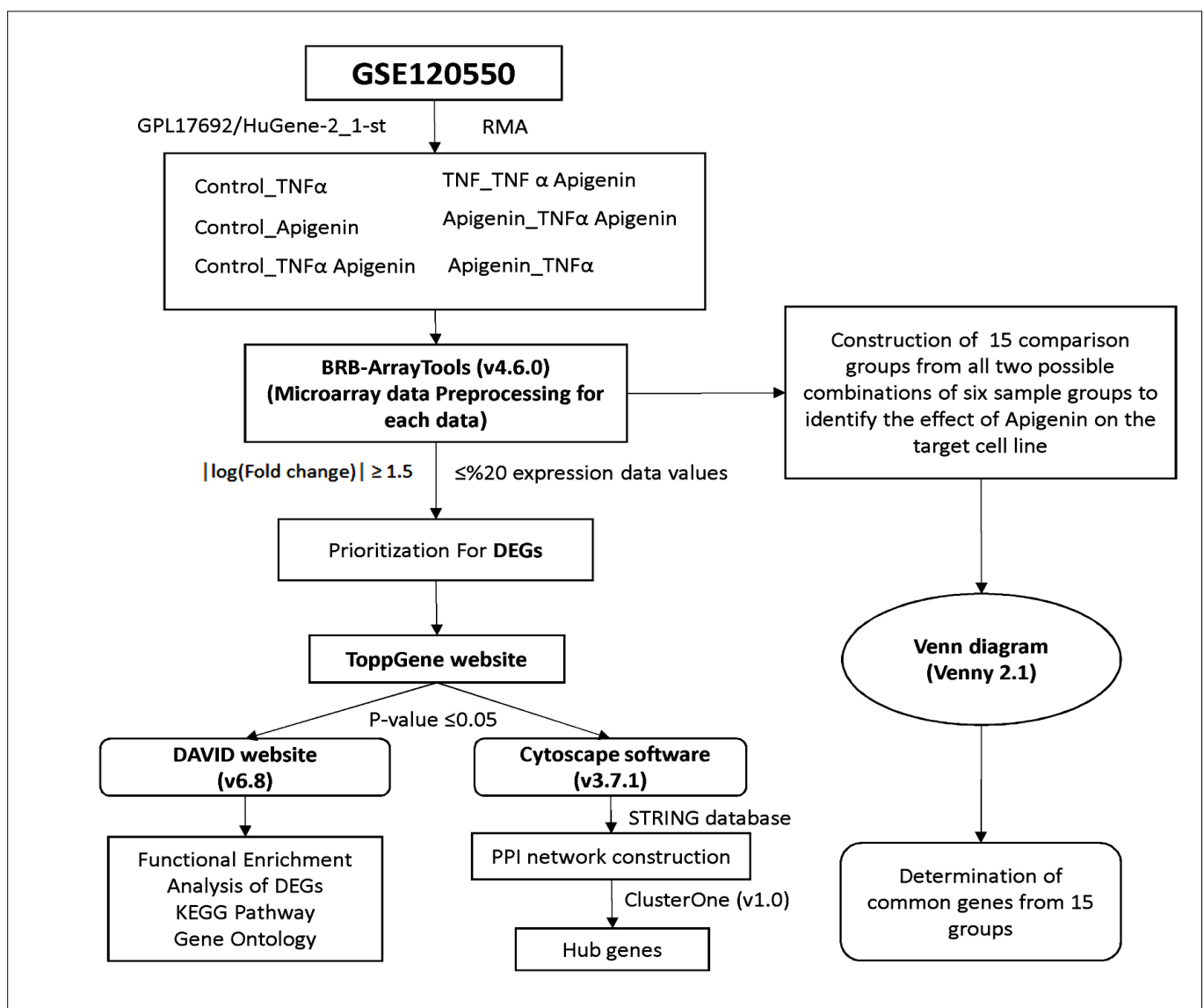


Fig. 1. An step by step flowchart to identify the conclusion on effect of TNF- α \pm Apigenin on TNBC cell line cancer. (BRB-ArrayTools (v4.6.0) (i.e., <https://brb.nci.nih.gov/BRB-ArrayTools/>), ToppGene website (i.e., <https://toppgene.cchmc.org>), DAVID website (v6.8) (<https://david.ncifcrf.gov/>), Cytoscape software (v3.7.1) (<https://cytoscape.org/>), Venn diagram (Venny 2.1) (<https://bioinfogp.cnb.csic.es/tools/venny/>).

was used to assess probe intensities from the raw microarray data. Differentially expressed genes were then classified between the 2 sample groups using univariate permutation tests and fold change threshold values of 10,000 and 1.5.

To prioritize the identified DEGs, two websites were utilized: GeneCards (17) and ToPPGene (<https://toppgene.cchmc.org>). The keyword "breast cancer" was used to search GeneCards to extract gene symbol evidence for the training group. The ToPPGene websites then ranked the significant DEGs (test group) from the BRB-ArrayTools output based on a p-value less than or equal to 0.05, using the training genes evidence obtained from GeneCards.

GEO and KEGG enrichment analyses

DAVID v. 6.8 (Database for Annotation, Visualization, and Integrated Discovery) was used to identify various Gene Ontology (GO) terms and enriched functional gene groups, including biological processes, cellular components, and molecular functions, as well as to perform KEGG (Kyoto Encyclopedia of Genes and Genomes) signalling pathway analysis (34, 35).

Construction of protein-protein interaction, gene-disease, and gene-drug networks

To create the protein-protein interaction (PPI) network, the STRING database was used with a confidence score cutoff value of 0.4, and the network was visualized with Cytoscape v.3.7.1 using ClusterOne v.1.0 (36, 37). Associations between target genes within statistically significant modules (p-value of ≤ 0.05) were examined to identify potential biomarkers with the highest connectivity degree.

Venn diagram

Venny2.1.0 (38) was used to map the genes from any two of the six constructed groups (i.e., 15 sets) to illustrate the number and rate of shared genes between them.

Results

Statistical analyses revealed several upregulated and downregulated differentially expressed genes (DEGs) (Table 1). However, there were no significant DEGs identified when comparing the apigenin and TNF- α + apigenin treatments in the MDA-MB-231 cancer cell line. Additionally, the ToPPGene web server ranked DEGs for further pro-

Table 1. List of top 10 significant DEGs determined by BRB-ArrayTools.

	Gene symbol	FC	P-value		Gene symbol	FC	P-value
	Upregulated				Upregulated		
	VIPR1	2.47	1.48E-05		LOC284344	10.37	< 1e-07
	CDK15	2.26	0.0003859		MIR100	10.14	3.00E-07
	OLFML2A	2.16	3.81E-05		ARC	6.32	2.29E-05
	PLPP4	1.99	0.0002055		ARRDC4	6.08	5.08E-05
	ITGB4	1.98	7.30E-05		MIR3143	5.91	8.00E-07
	RHOD	1.96	0.0004039		IDI2-AS1	5.37	2.10E-06
	HTRA1	1.89	0.0008368		RASD1	5.27	2.70E-06
	IGFBP4	1.85	0.0003397		EGR1	5.13	1.30E-05
	CPA4	1.85	0.0003467		SLC30A1	5.05	6.00E-07
(A) Control_ TNF-α	BMP4	1.73	8.99E-05	(B) Control_Apigenin	LOC284344	10.37	< 1e-07
	Downregulated				Downregulated		
	IER3	0.67	0.0004881		NUB1	0.67	0.00061
	OPTN	0.66	0.0006317		SASS6	0.66	0.000471
	IER3	0.65	0.0005174		EHD4	0.66	0.000579
	SERPINB8	0.64	0.0007988		ACTR3	0.66	0.00071
	PKIA	0.63	0.0005714		FYN	0.66	0.00088
	ARHGAP42	0.62	0.0003596		DUSP6	0.66	0.000924
	4-Mar	0.62	0.0004407		STC1	0.66	0.000927
	ACO1	0.62	0.0009106		CCDC77	0.66	0.00094
	ETS1	0.61	0.0001548		ITSN2	0.66	0.00095
	DOCK9	0.61	0.0003044		HPS3	0.66	0.000958
	Upregulated				Upregulated		
(C) Control_ TNF-α Apigenin	CYP1B1	6.31	0.000123	(D) TNF-α _TNF-α Apigenin	IL1A	9.19	5.00E-07
	CAVIN2	6.28	9.50E-05		CEMIP	5.94	1.20E-06
	PDE7B	5.73	0.000153		CYP1B1	5.79	1.90E-06
	PLK1	5.2	0.00013		IL24	5.76	2.30E-06

	ADAMTS15	4.84	0.000671		IKBKE	5.01	2.00E-07
	SPTLC3	4.81	2.29E-05		PLK1	4.78	2.00E-07
	IGFBP1	4.78	6.43E-05		CAVIN2	4.67	6.10E-06
	KIF20A	4.51	0.000148		MIR4435-2HG	4.32	5.21E-05
	KLHL4	3.8	0.000504		SHISA2	4.16	1.50E-06
	CYP1B1	6.31	0.000123		KIF20A	3.73	7.20E-06
	Downregulated				Downregulated		
(C) Cotrol_TNF-α Apigenin	MICB	0.66	0.000141	(D) TNF-α_TNF-α Apigenin	NCOA4	0.67	0.000627
	ARPC5L	0.66	0.00037		NEB	0.67	0.000638
	PLK3	0.66	0.000828		GLYR1	0.66	0.000331
	RNPS1	0.65	0.00021		MAK16	0.66	0.000449
	SUPT16H	0.65	0.000498		INF2	0.66	0.000583
	BAIAP2	0.65	0.000541		LUZP1	0.65	0.000226
	SMIM15	0.65	0.00071		IPO7	0.65	0.000294
	TSR1	0.64	8.90E-06		SPECC1	0.65	0.000377
	ZNF850	0.64	0.000151		ARL5B	0.65	0.000383
	SLC35F2	0.64	0.000343		COPS2	0.65	0.000538
	Gene symbol	FC	P value		Gene symbol	FC	P value
	Upregulated				Upregulated		
	SNORA2B	2.02	0.000758		MIR100	12.25	0.000356
	-	-	-		LOC284344	9.15	7.86E-05
	-	-	-		MIR3143	6.86	0.000159
	-	-	-		RASD1	6.36	0.000535
	-	-	-		SLC30A1	5.33	2.71E-05
	-	-	-		ARC	5.07	0.00056
	-	-	-		IDI2-AS1	4.83	0.000546
	-	-	-		GADD45B	4.74	6.00E-07
	-	-	-		HIF1A-AS2	4.49	0.000364
	-	-	-		VN1R108P	4.32	0.000624
	Downregulated				Downregulated		
(E) Apigenin_TNF-α Apigenin	ATP2B1	0.67	0.000708	(F) Apigenin_TNF-α	CCL28	0.66	0.000283
	FAM98A	0.67	0.000943		BCKDK	0.65	0.000119
	CFLAR	0.65	0.000264		PIK3CA	0.65	0.00021
	DDX58	0.65	0.000686		NCEH1	0.65	0.000212
	CDV3	0.64	0.000374		PDE6D	0.65	0.000341
	POMK	0.64	0.00039		CKAP5	0.65	0.000823
	PAGE5	0.64	0.000707		MCM8	0.64	6.59E-05
	R3HCC1L	0.63	0.000169		VAMP7	0.64	0.000237
	SLC25A22	0.63	0.000303		ACTR3	0.64	0.000633
	HIVEP1	0.62	0.000574		MYO1B	0.64	0.000757

tein-protein interaction analysis (Table 2). The PPI network analysis identified hub genes affected by various treatments, including apigenin and TNF- α (Table 3).

The GO analysis, encompassing biological processes, cellular components, molecular functions, and KEGG pathway mapping, was performed using DAVID v6.8, the Database for Annotation, Visualization, and Integrated

Discovery. The results revealed significant terms for groups 2 and 6 (Control vs. Apigenin, Apigenin vs. TNF- α +Apigenin, and Control vs. TNF- α +Apigenin):

- Biological Processes (BP): GO:0043981~histone H4-K5 acetylation, GO:0043982~histone H4-K8 acetylation, GO:0043984~histone H4-K16 acetylation; GO:0043547~positive regulation of the GTPase ac-

Table 2. The list of 10 top DEGs ranked by ToPPGene web server (i.e., <https://toppgene.cchmc.org>)

	Rank	Gene symbol	Overall p Value
(A) Control_TNF-α	1	OPTN	0.003685
	2	IRAK2	0.007693
	3	PANX1	0.012981
	4	TNIP1	0.017472
	5	GPRC5B	0.024466
	6	SERPINB8	0.025938
	7	MFAP2	0.027366
	8	ACO1	0.028311
	9	ROBO4	0.035488
	10	NUAK2	0.042567
(B) Control_Apigenin	1	ANKRD1	0.005784
	2	DYNC2H1	0.005877
	3	MUL1	0.00624
	4	RASA3	0.006318
	5	IL1RAPL1	0.006765
	6	TAF2	0.006776
	7	NDC1	0.007182
	8	LAMTOR3	0.00807
	9	NFIA	0.008719
	10	IL31RA	0.008975
(C) Control_TNF-α Apigenin	1	ANKRD1	0.005366
	2	MUL1	0.005921
	3	TAF13	0.009175
	4	TAF9B	0.010446
	5	TFDP2	0.010772
	6	PANX1	0.011572
	7	SEC24B	0.014874
	8	WIPI1	0.014885
	9	TNIP1	0.015007
	10	PPP1R15B	0.015423
(D) TNF-α_TNF-α Apigenin	1	TAF7	0.0051
	2	RASA3	0.006503
	3	ANKRD1	0.006634
	4	MUL1	0.00727
	5	NDC1	0.007911
	6	CREB3L2	0.009494
	7	MBD5	0.010524
	8	NUP42	0.010755
	9	IL31RA	0.010787
	10	CRISPLD2	0.012033

	Rank	Gene symbol	Overall p Value
(E) Apigenin_TNF-α Apigenin	1	IRAK2	0.005829
	2	POMK	0.013584
	3	NAV2	0.013962
	4	TNIP1	0.014482
	5	DOCK10	0.023973
	6	MLLT6	0.07229
	7	REXO4	0.074127
	8	ARHGAP42	0.082052
	9	PARP12	0.092027
	10	IRAK2	0.203029
(F) Apigenin_TNF-α	1	CDK5RAP2	0.003076
	2	ANKRD1	0.005095
	3	RASA3	0.006446
	4	IL1RAPL1	0.006578
	5	IRAK2	0.007118
	6	NUP42	0.009236
	7	RAB3GAP1	0.009582
	8	ABR	0.010544
	9	GYS1	0.011166
	10	ARAP1	0.012808

tivity, GO:0007264~small GTPase mediated signal transduction, GO:0031023~microtubule organizing center organization; and GO:0016236 ~ macroautophagy, O:0006368~transcription elongation from RNA polymerase II promoter, GO:0000290~deadenylation-dependent decapping of nuclear-transcribed mRNA).

- Cellular component (CC): GO:0005654 ~ nucleoplasm, GO:0005829~cytosol, GO:0000123~histone; acetyltransferase complex; GO:0005829~cytosol, GO:0005794~Golgi apparatus, GO:0030659 ~ cytoplasmic vesicle membrane; and GO:0005669 ~ transcription factor TFIID complex, GO:0005654 ~ nucleoplasm, GO:0005829~cytosol).
- Molecular Function (MF): GO:0008270~zinc ion binding, GO:0061630~ubiquitin protein ligase activity, GO:0005085~guanyl-nucleotide exchange factor activity; GO:0005096~GTPase activator activity, GO:0005515~protein binding, GO:0005085~guanyl-nucleotide exchange factor activity; and GO:0044822~poly(A) RNA binding, GO:0005515 ~ protein binding, GO:0008270~zinc ion binding).
- KEGG pathways: hsa00562~Inositol phosphate metabolism, hsa03013~RNA transport, hsa04070~Phosphatidylinositol signalling system; hsa00500~Starch and sucrose metabolism; and hsa03022 ~ Basal transcription factors, hsa03040~Spliceosome, hsa05168~Herpes simplex infection.

Table 3. Potential significant hub genes identified using ClusterOne v1.0 Cytoscape plugin

Groups	Item	Gene Symbol	Connectivity Degree	Up/Downregulated
(B)	1	DDX46	5	Downregulated
	2	RNPS1	5	Upregulated
	3	TFIP11	5	Upregulated
	4	UBA3	5	Downregulated
	5	SPC25	4	Downregulated
	6	ATP8A1	3	Downregulated
	7	LAMTOR3	3	Upregulated
	8	SLCO4C1	3	Downregulated
	9	XPOT	3	Downregulated
(C)	1	CHERP	4	Downregulated
	2	SYF2	4	Downregulated
	3	TAF3	3	Downregulated
	4	SPC25	3	Upregulated
	5	DIEXF (UTP25)	2	Downregulated
	6	FKBP15	2	Downregulated
	7	MAK16	2	Downregulated
(D)	1	DDX46	3	Upregulated
	2	SF3A2	3	Downregulated
	3	SYF2	3	Downregulated
	4	TFIP11	3	Downregulated
	5	MGAM	3	Downregulated
	6	CENPI	2	Upregulated
	7	CENPN	2	Downregulated
	8	MIS12	2	Downregulated
	9	ACO1	2	Upregulated
	10	UBE2J1	3	Upregulated

Additionally significant terms for BP included GO: 0060325~face morphogenesis, GO: 0010976 ~ positive regulation of neuron projection development, GO: 0016567~protein ubiquitination; GO: 0002755~MyD88-dependent toll-like receptor signalling pathway.

For groups 4, 5, and 1, the following GO terms were identified:

- Biological Process (BP): GO: 0006954~inflammatory response; and GO: 0002755~MyD88-dependent toll-like receptor signaling pathway, GO: 0043124 ~ negative regulation of I-kappaB kinase/NF-kappaB signaling, GO: 0050729~positive regulation of inflammatory response.
- Cellular Component (CC): GO: 0005654 ~ nucleoplasm, GO: 0005829~cytosol, GO: 0005856 ~ cytoskeleton; and GO: 0005829~cytosol.
- Molecular Functions (MF): GO: 0008270~zinc ion binding, GO: 0008134~transcription factor binding,

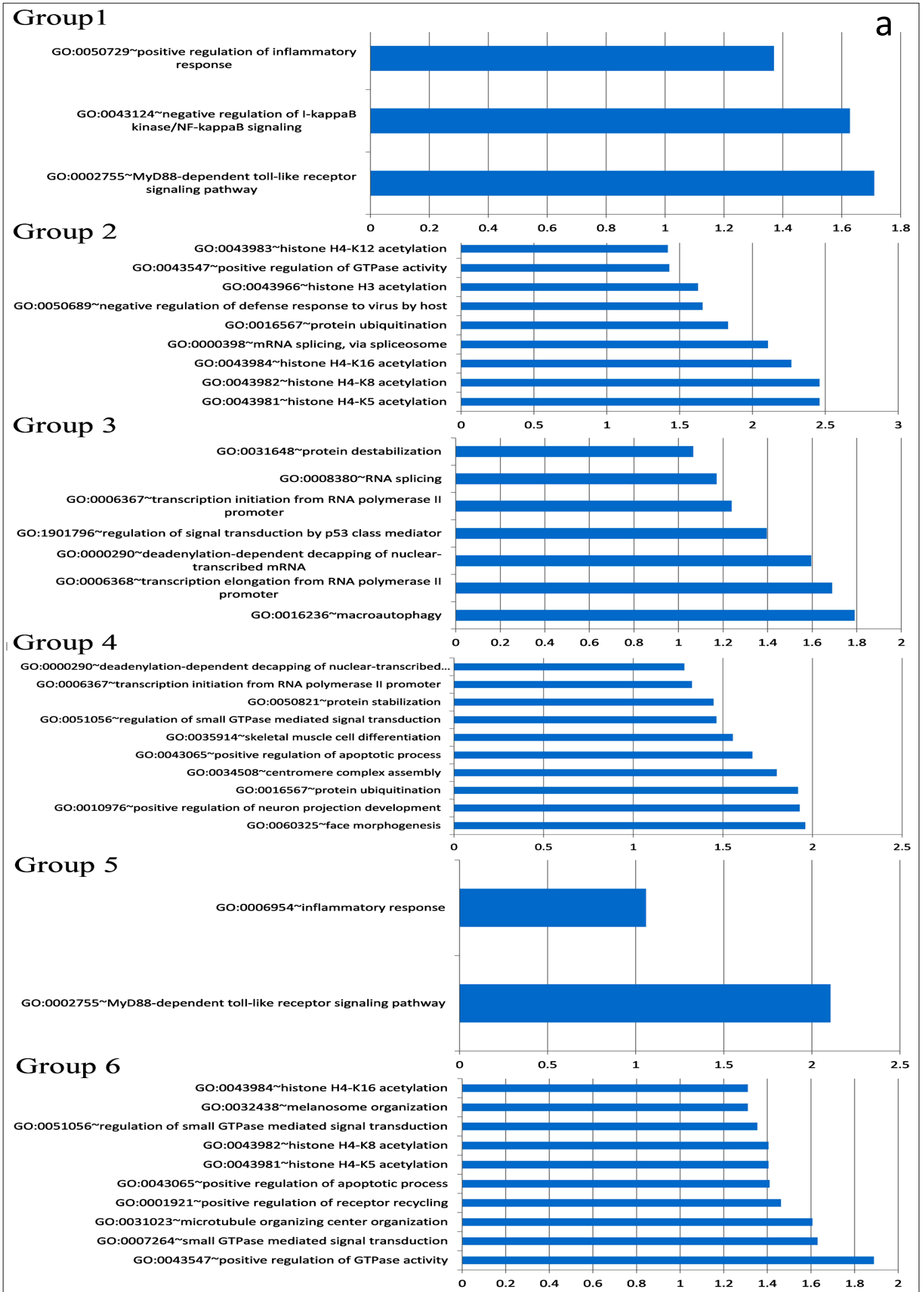
GO: 0005085~guanyl-nucleotide exchange factor activity; GO: 0005524~ATP binding.

No KEGG pathways were identified for these groups. Fig. 2 presents the results of these analyses.

This study investigates the effect of apigenin and TNF- α on MDA-MB-231 cancer cells, as well as the interaction between these 2 molecules. To achieve this, the study analyzed six treated and untreated groups across fifteen combinations. This detailed investigation aims to clarify the role of apigenin in inhibiting breast adenocarcinoma and invasive breast cancer.

In group 1, although the number of shared genes is limited, the inhibitory effect of apigenin is evident in this comparison. In group 2, apigenin shares only one out of twenty-nine genes, indicating that it could not counteract the effects of TNF- α .

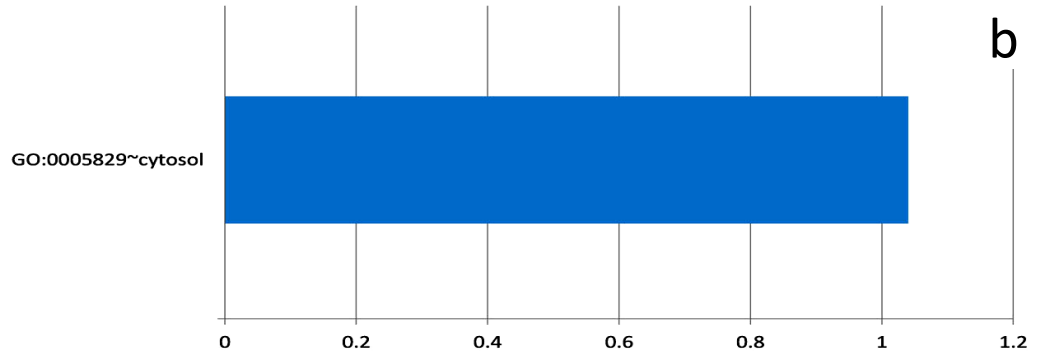
In group 3, the number of genes with altered expression levels suggests that apigenin inhibits the development of TNF- α . This means that apigenin's impact is more similar to its effects on normal cancer cells rather than on TNF- α -aggravated ones. In group 4, apigenin does



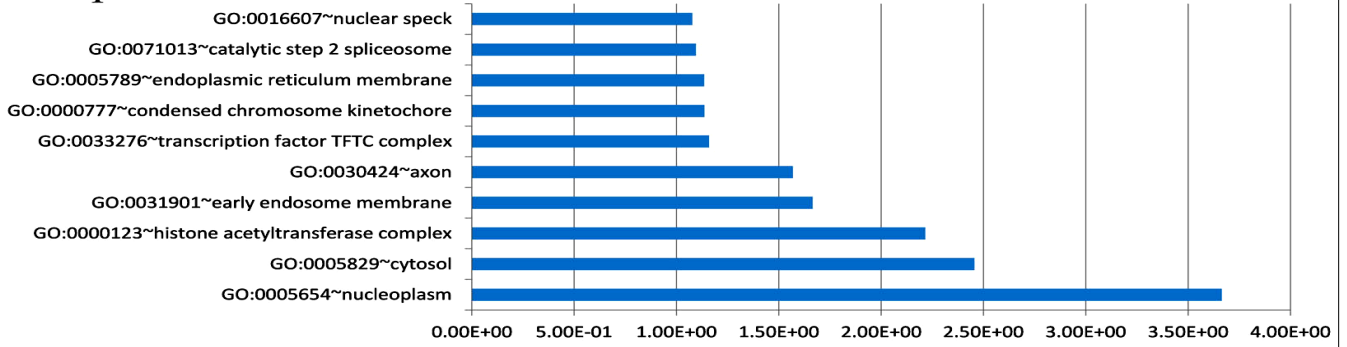
not alter gene expression, implying that it has minimal effect on TNF- α -aggravated cancer cells.

In group 5, despite several shared genes, only 1 gene shows a different expression, suggesting the anti-ci-

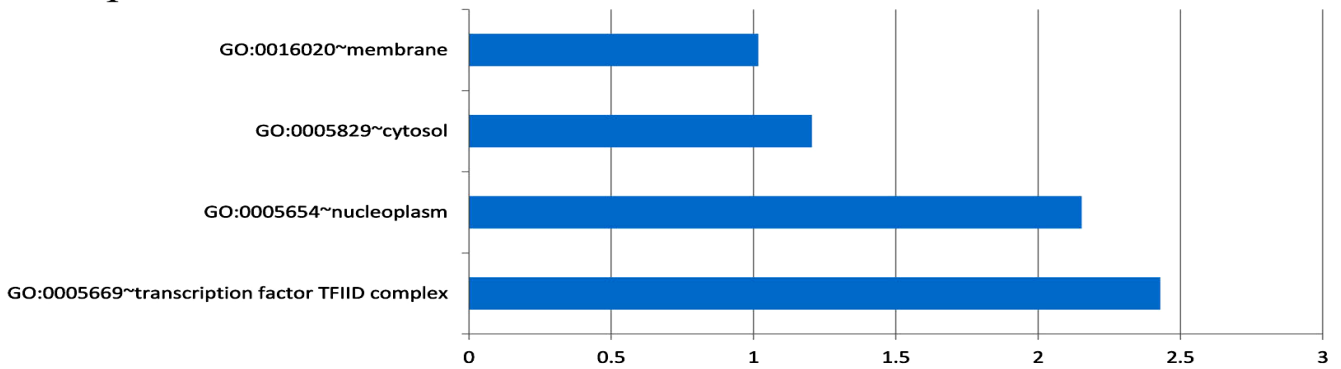
Group 1



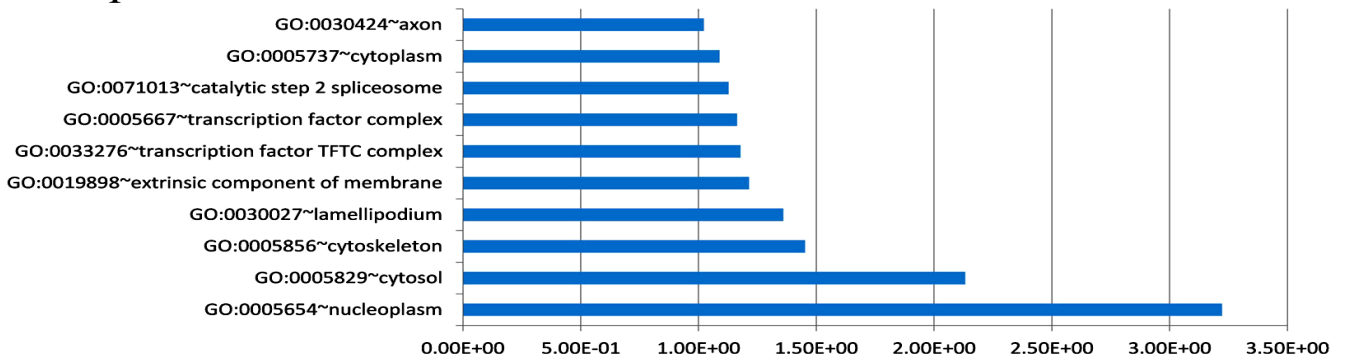
Group 2



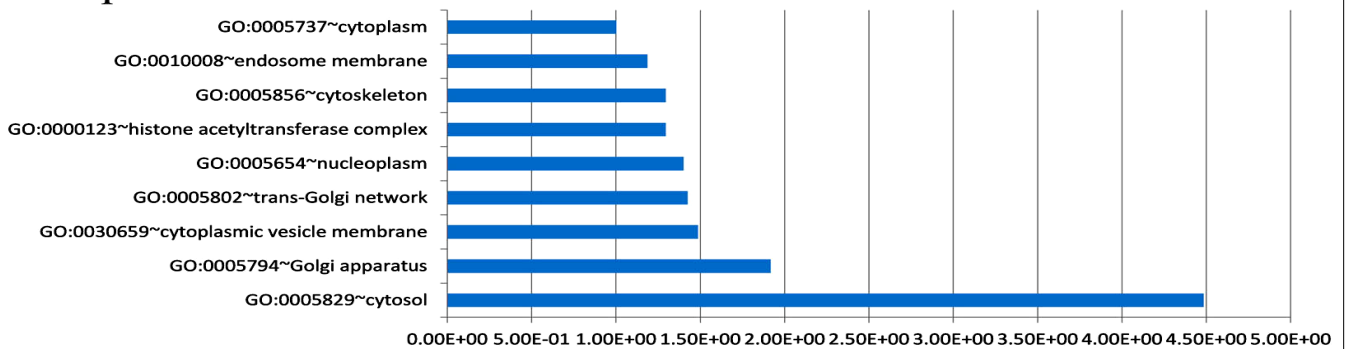
Group 3



Group 4

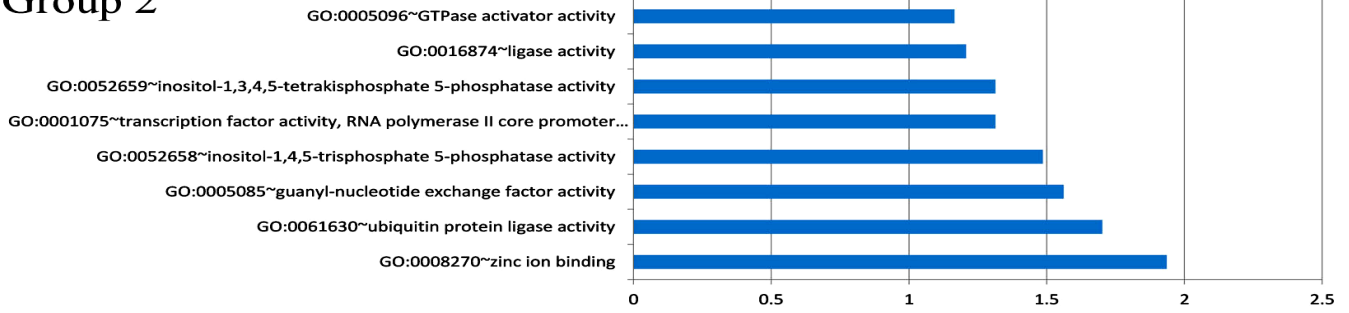


Group 6

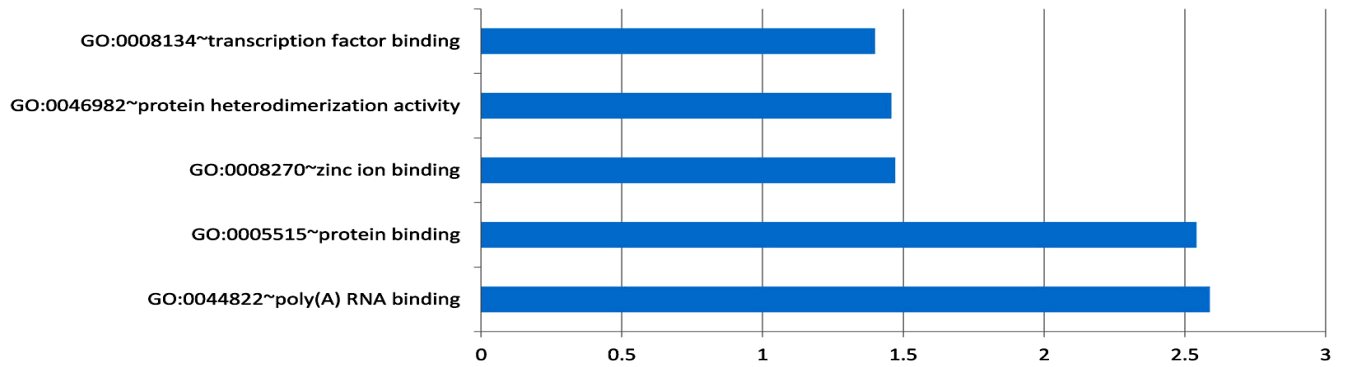


pated impact of apigenin. In group 6, the increasing number of shared genes with altered expression levels demon-

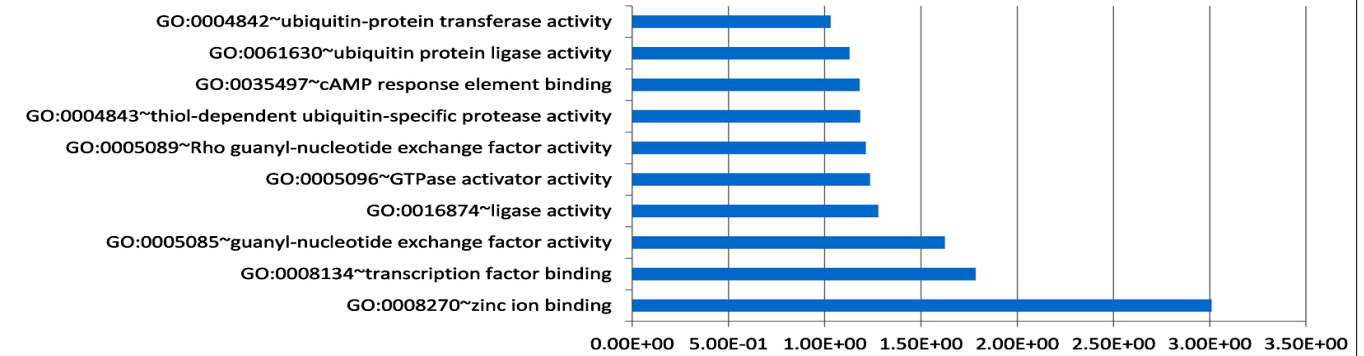
Group 2



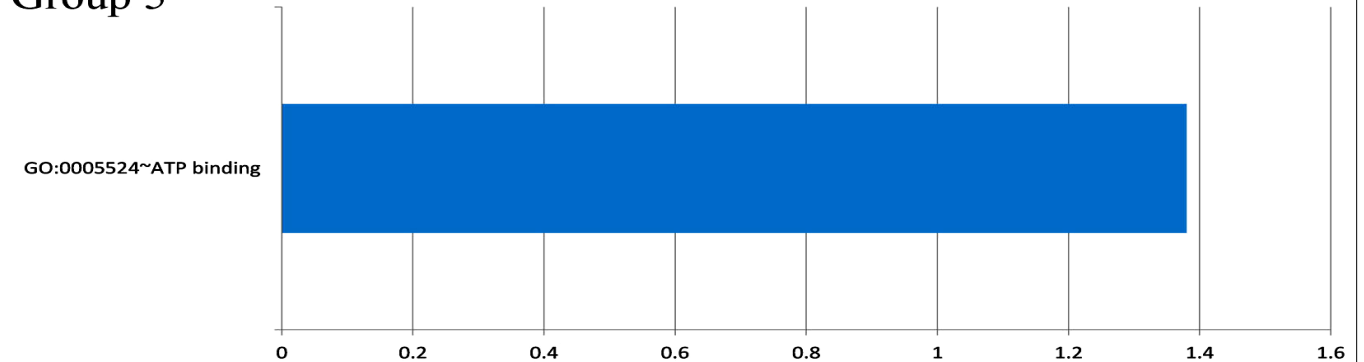
Group 3



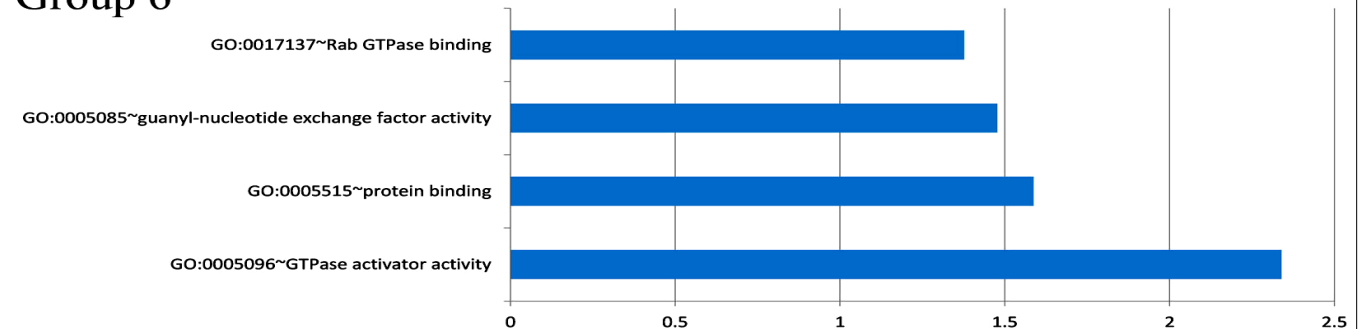
Group 4



Group 5



Group 6



strates apigenin's positive effect on normal cancer cells.

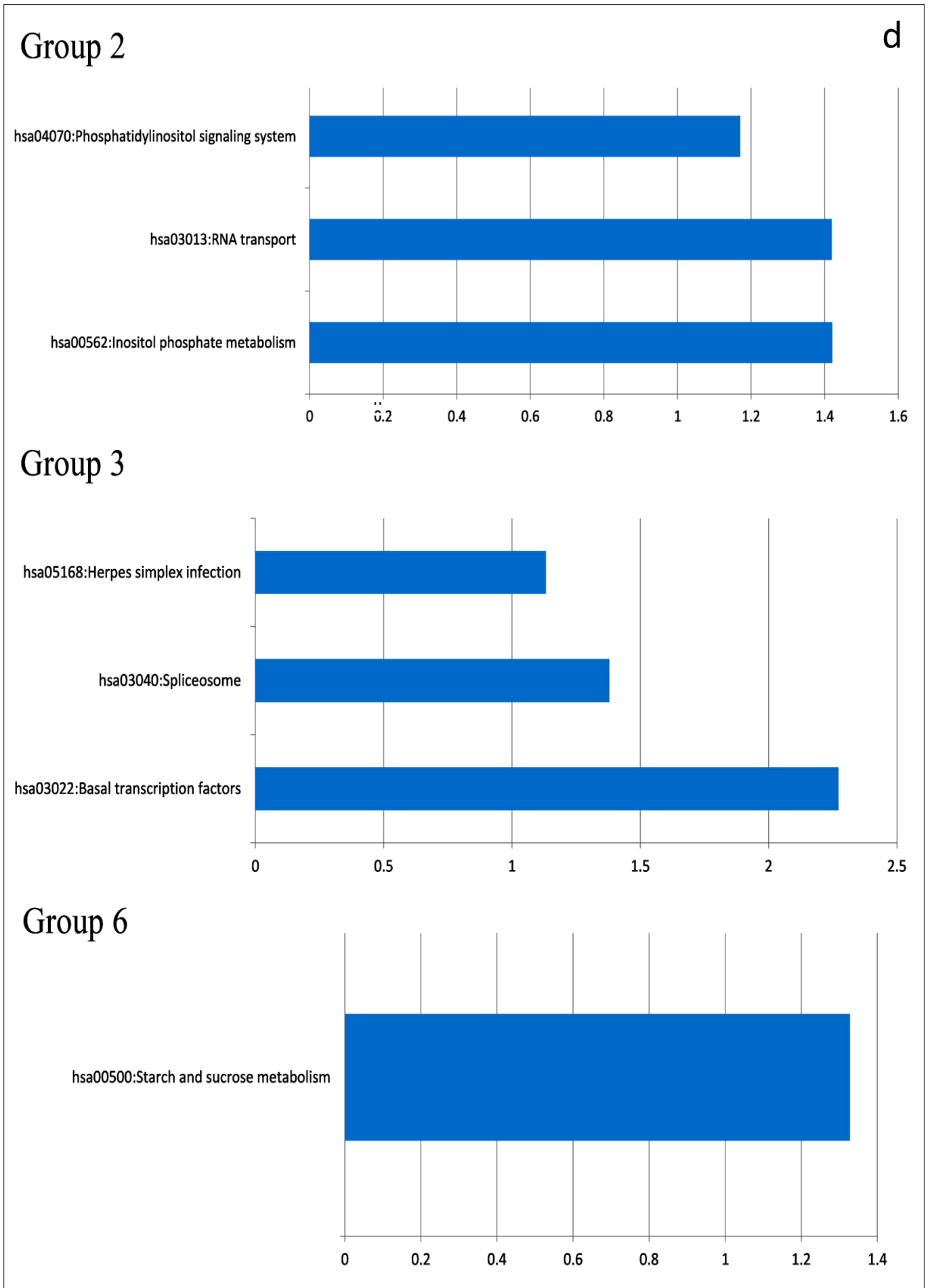


Fig. 2. DAVID's webservice results demonstrated for six groups on (a) biological processes (BP), (b) cellular components (CC), (c) molecular functions (MF), and (d) the KEGG signaling pathway analysis.

In group 7, numerous shared genes and changes in expression reveal both the inhibitory and cancer-inhibiting effects of apigenin on non-exacerbated cells. In group 8, the dominance of TNF- α over apigenin is observed, indicating that apigenin has a minimal impact on aggravated cancer cells. In group 9, despite the presence of shared genes, apigenin did not alter gene expression levels. In groups 10 and 11, apigenin's low impact on TNF- α -aggravated cancer cells is observed. In groups 12 and 13, apigenin's effect remains the same as in intensified cancer cells. In group 14, the expression changes in all shared genes demonstrate apigenin's positive impact on cancer cells not aggravated by TNF- α . In group 15, apigenin did not affect TNF- α -induced cancer cells.

Table 4 and Fig. 3 summarizes these findings, with the Venn diagrams providing further detail.

In summary, the aim of this article, as illustrated by the results in Table 4 and Fig. 3, is to compare the effects of TNF- α and apigenin on breast cancer and evaluate the potential of apigenin as a therapeutic drug. The table was prepared by analysing 15 comparative groups and conducting various analyses. Table 4 highlights which combination has a dominant effect in each group and its impact on gene expression. Additionally, the goal is to assess the influence of apigenin at both high and low concentrations of TNF- α on cancer cells and to determine its effectiveness in regulating the expression of genes affected by TNF- α .

Discussion

The potential anti-cancer effects of apigenin, a flavonoids found in many fruits and vegetables, have been extensively studied, particularly in breast cancer cells such as MDA-MB-231. This cell line is commonly used as a model for TNBC research. Apigenin inhibits the cell proliferation, migration, and invasion of MDA-MB-231 through various mechanisms. One of the key ways apigenin combat cancer is by inducing apoptosis in these cells. This cell death is mediated by caspases, and apigenin has been shown to trigger apoptosis by increasing the expression of p21WAF1/CIP1 and enhancing histone H3 acetylation, among other mechanisms (16, 39). Additionally, apigenin induces oxidative stress and DNA damage, both of which are critical factors in initiating apoptosis in cancer cells (16, 40).

MDA-MB-231 cells are known for their ability to migrate and invade surrounding tissues, which is crucial for cancer progression and metastasis. Apigenin not only promotes apoptosis but also blocks the migration and invasion of these cells. Studies have shown that apigenin suppresses the expression of matrix metalloproteinases (MMP-2 and MMP-9), enzymes critical for breaking down the extracellular matrix, a key process in tumor invasion (41). By downregulating these proteins, apigenin effectively reduces the invasive potential of MDA-MB-231 cells.

Moreover, apigenin inhibits tumor growth by exhibiting strong anti-inflammatory properties. Studies have shown that apigenin reduces the expression of pro-inflammatory cytokines, such as IL-6 and TNF- α , in MDA-MB-231 cells (12, 14). In addition to decreasing inflammation, which can contribute to tumor growth, apigenin disrupts signalling pathways involved in cancer cell proliferation and survival. By suppressing IL-6 signalling, apigenin may reduce the activation of STAT3, a key factor in the progression of aggressive breast cancers (14).

TNF- α , an inflammatory cytokine, plays a crucial role in the progression of various cancers, including breast

Table 4. Summary of effects for Apigenin treatment using fifteen groups' comparison

Group	Description	Gene ratio of DEGs in common	Effect	
			Apigenin	TNF α
1	Control-Apigenin vs. Control-TNF α	8/16	■	
2	Control-TNF α -Apigenin vs. Control-TNF α	1/29		■
3	TNF α -Apigenin vs. Control-TNF α	52/55	■	
4	TNF α -TNF α -Apigenin vs. Control-TNF α	0/33		■
5	Apigenin-TNF α -Apigenin vs. Control-TNF α	1/50		■
6	Control-TNF α -Apigenin vs. Control-Apigenin	258/258	■	
7	TNF α -Apigenin vs. Control-Apigenin	430/430	■	
8	TNF α -TNF α -Apigenin vs. Control-Apigenin	1/7		■
9	Apigenin- TNF α -Apigenin vs. Control-Apigenin	0/209		■
10	TNF α -Apigenin vs. Control-TNF α -Apigenin	4/221		■
11	TNF α -TNF α -Apigenin vs. Control-TNF α -Apigenin	1/12		■
12	Apigenin-TNF α -Apigenin vs. Control-TNF α -Apigenin	84/91	■	
13	TNF α -TNF α -Apigenin vs. TNF α -Apigenin	18/19	■	
14	Apigenin-TNF α -Apigenin vs. TNF α -Apigenin	245/245	■	
15	Apigenin-TNF α -Apigenin vs. TNF α -TNF α -Apigenin	0/24		■



Fig. 3. The presentation of fifteen Venn Diagrams for identification of the dissimilar and shared genes in TNBC cell line dataset which are ordered per sets listed in Table 4, respectively (left to right).

cancer. The MDA-MB-231 cell line, known for its triple-negative breast cancer phenotype, is ideal for studying TNF- α 's effects on cancer cells. TNF- α promotes tumor growth and invasion in these cells by activating signalling pathways and upregulating adhesion molecules. One of the key mechanisms by which TNF- α influences MDA-MB-231 cells is through the NF- κ B signalling pathway, which drives the expression of genes associated with inflammation and cancer progression. Upon exposure to TNF- α , MDA-MB-231 cells show increased levels of adhesion molecules like VCAM-1 and ICAM-1, which enhance adhesion to endothelial cells and promote metastasis (42, 43). Addi-

tionally, TNF- α stimulates the release of matrix metalloproteinases (MMPs), particularly MMP-9, which degrade extracellular matrix components, facilitating tumor cell invasion (44, 45).

TNF- α induces epithelial-mesenchymal transition (EMT) in MDA-MB-231 cells, leading to the loss of epithelial markers and the retention of mesenchymal characteristics, a critical step in cancer progression (46). Additionally, cancer cells expressing vimentin, a protein linked to increased motility, exhibit greater responsiveness to TNF- α treatment, further supporting its role in promoting EMT (47). TNF- α significantly influences MDA-MB-231 cells and

the tumor microenvironment by fostering an inflammatory setting that accelerates tumor growth and enhances treatment resistance. TNF- α facilitates tumor progression and metastasis by increasing the secretion of pro-inflammatory cytokines, such as IL-6 (48, 49). The interaction of TNF- α with other inflammatory mediators complicates the breast cancer microenvironment, making it a key factor in promoting inflammation and enhancing cancer cell invasiveness. For instance, studies on MDA-MB-231 cells show that TNF- α activates the P2Y2 receptor, which in turn stimulates inflammasomes that contribute to tumor progression and radiation resistance (30). Furthermore, TNF- α has been found to induce the production of granulocyte-macrophage colony-stimulating factor (GM-CSF) in MDA-MB-231 cells, indicating its involvement in shaping a pro-tumorigenic environment while limiting cancer cell proliferation (50).

Several studies indicate that breast cancer is the most common malignancy in both developing and developed countries (51, 52). Researchers have extensively explored the inhibitory effects of flavonoid-containing plants, such as Quercetin, Cuminum and Tangeretin, using various *in vitro* and *in situ* methodologies (53-56). Six studies have specifically highlighted the anti-cancer properties of apigenin in the MDA-MB-231 cell line through experimental approaches (12, 16, 39, 57-59). Since early diagnosis of breast cancer is critical in effectively inhibiting the disease, investigating the effects of apigenin is particularly important. This study was designed to explore the inhibitory impact of apigenin on the TNBC cell line. A comprehensive systems biology approach was employed to examine various biological processes, molecular functions, cellular components and signaling pathways affected by the presence or absence of TNF- α with or without apigenin. An extensive assessment of 15 treatment variations demonstrated the anti-cancer effect of apigenin during the early and potentially intermediate stages of breast cancer, as confirmed by literature (12). However, apigenin's inhibitory effect may also extend to the expression of certain genes during advanced stages of breast cancer, as suggested by *in vivo* studies (58). The significant influence of TNF- α on the MDA-MB-231 cell line, which served as a control group for comparisons, was evident (shown in Table 4 and Fig. 3). Moreover, recent studies have emphasized the importance of early breast cancer diagnosis through a comprehensive systems biology-based approach, identifying key biomarkers at each stage of the disease (31).

Furthermore, the biomarkers identified in this study provided valuable insights into predicting the stage of breast cancer, as highlighted in another computational-based study (32). A notable advantage of the current research is its comprehensive analysis of the entire genome, unlike other studies that focused on the expression of some specific genes, as seen in the six previously mentioned studies. Our results indicated that Histone H4 acetylation plays a central role in development or inhibition of breast cancer by influencing the expression of p53 or p21 proteins. This finding aligns with previous studies that observed overexpression of Histone H4 (60, 61). Additionally,

the positive regulation of GTPase pathways is of particular interest for breast cancer treatment, as supported by earlier research (62, 63). Among the various signalling pathways examined, the inositol phosphate metabolism pathway emerged as a significant factor associated with breast cancer and was the first major pathway identified through KEGG signaling in the study (64). The Phosphatidylinositol signaling system (i.e., PI3K signaling pathway) is well-recognized in the research community for its critical role in breast cancer, and computational approaches have demonstrated the potential positive effects of apigenin for breast cancer patients (65-67). Furthermore, since basal transcription factors are crucial in tumor growth and breast cancer development, targeting this pathway with apigenin is a significant aspect of its therapeutic potential (68).

Moreover, both experimental and computation research have demonstrated that apigenin has an inhibitory effect on Herpes simplex infection (69, 70). Additionally, the activation of nuclear factor-kappaB (NF- κ B) has been observed in patients with breast cancer. The computational analysis in this study highlighted the significant inhibitory role of apigenin in this pro inflammatory transcription factor (71, 72). In conclusion, the results of this extensive investigation into inhibiting TNBC development and progression suggests that apigenin, a naturally occurring flavonoid, holds promise for future novel drug design and discovery.

Conclusion

In the current study, the dataset for triple-negative breast cancer (TNBC) using the MDA-MB-231 cell line was analyzed to evaluate the inhibitory effects of apigenin on cancerous samples. Six sample pairs from the dataset were pre- and post-processed to identify significant DEGs. These DEG's were then ranked and prioritized for further analysis of their enrichment in BP, CC, MF and KEGG signaling pathways. Essential and statistically significant hub genes among the 6 groups were determined. Additionally, 15 combinations from the possible paired sets of these 6 groups were examined to confirm the inhibitory effect of apigenin on breast cancer. Overall, apigenin demonstrated effective inhibition of cancer cell growth, which could aid in the development of novel therapies.

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Authors' contributions

EA carried out the gathering and analyzing of studies and drafted the manuscript. SA participated in the design of the study and performed the statistical analysis. BS and SD conceived of the study and participated in its design and coordination as well as the analyses of data. All authors

read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interests to declare.

Ethical issues: None

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