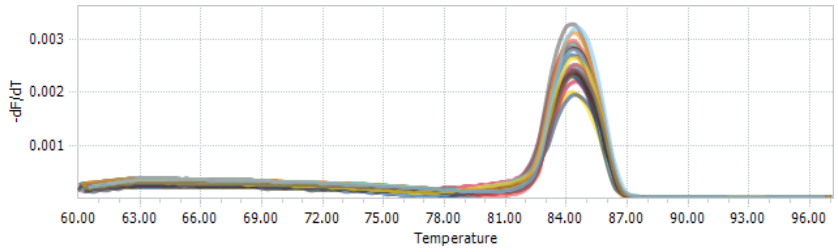
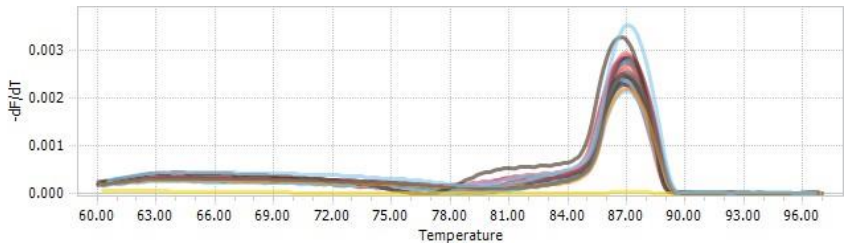
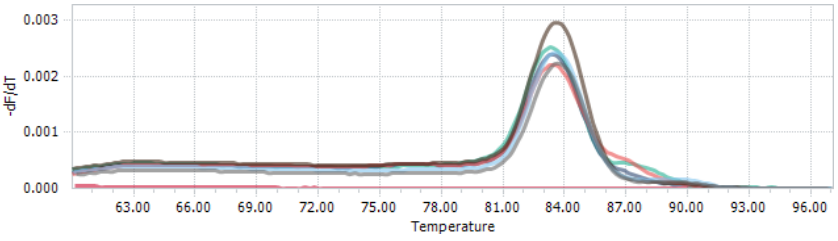
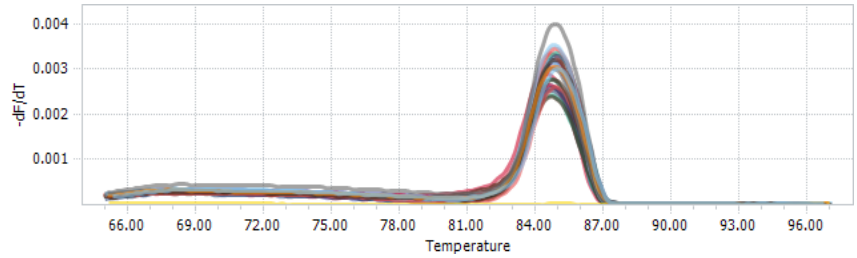
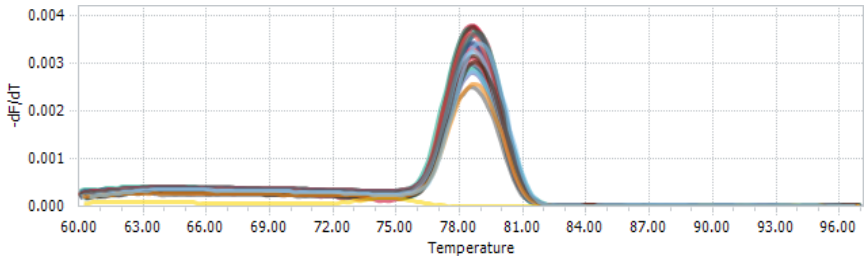
# Endoplasmic Reticulum Stress and Impairment of Ribosome Biogenesis Mediate the Apoptosis Induced by *Ocimum* x *africanum* Essential Oil ina Human Gastric Cancer Cell Line

**Supplementary files**

**Figure S1**

| | |
|---|---|
| *TP53* |   |
| *BAX* |   |
| *BCL2* |   |
| *BCL-xL* |   |

| | |
|---|---|
| *CASP8* | 0.004<br>0.003<br>0.002<br>0.001<br>0.000<br>-dF/dT<br>60.00<br>63.00<br>66.00<br>69.00<br>72.00<br>75.00<br>78.00<br>81.00<br>84.00<br>87.00<br>90.00<br>93.00<br>96.00<br>Temperature |

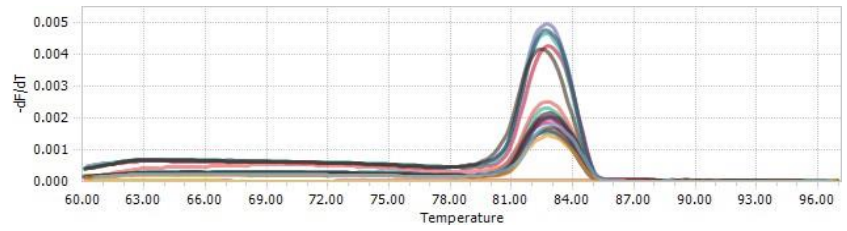
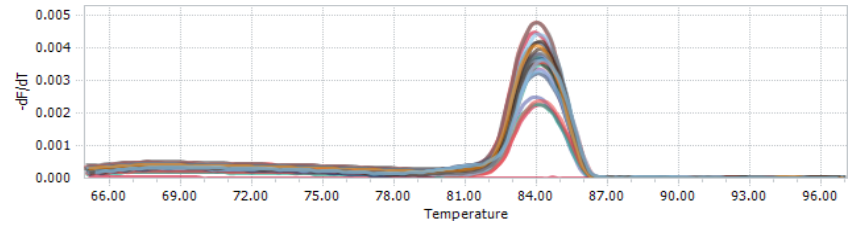
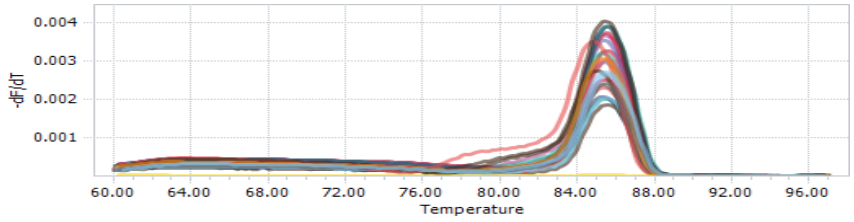
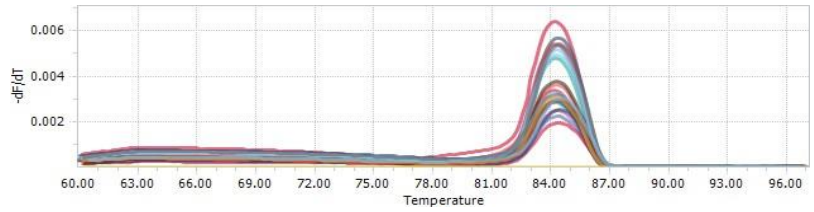
| | |
|---|---|
| *CASP12* |  |
| *CASP9* |  |
| *CASP3* |  |
| *GAPDH* |  |

**Figure S1. Melting curve analysis of apoptosis-related genes in this study.**

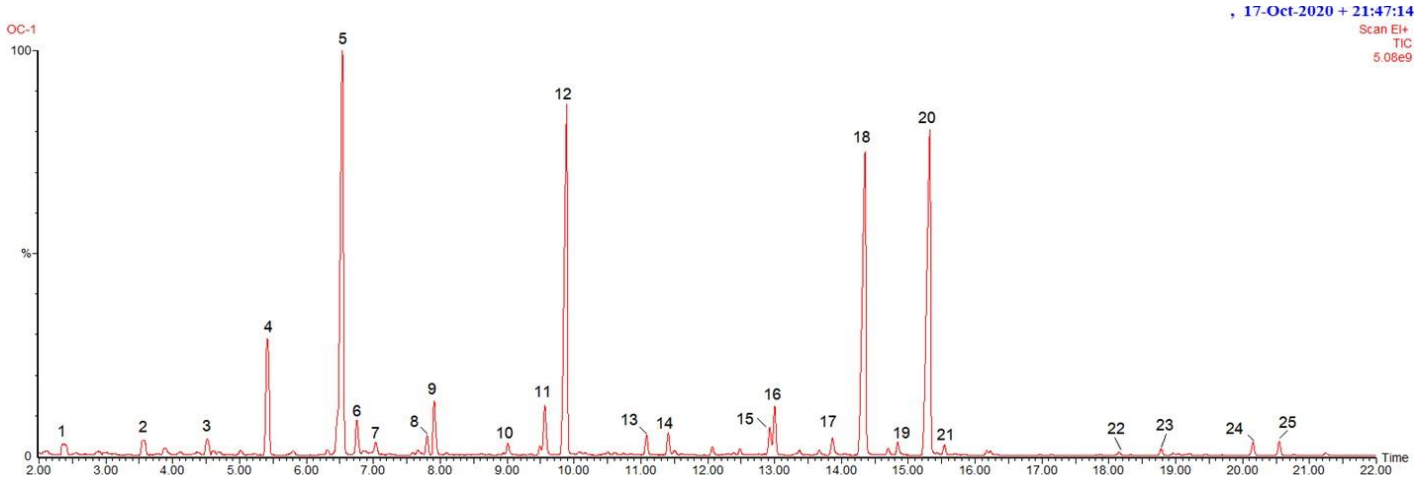
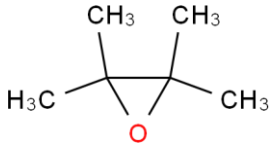
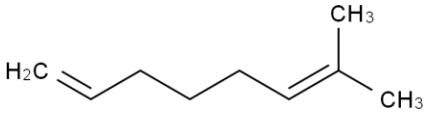
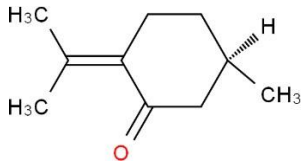
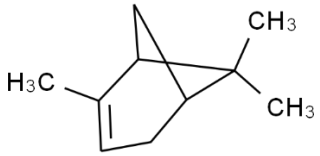
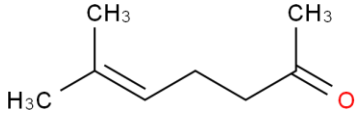
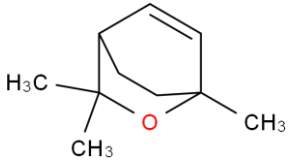
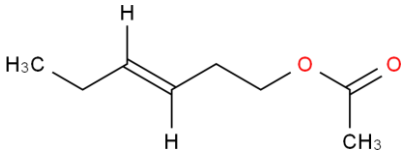
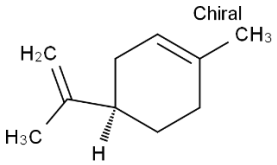
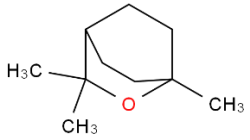
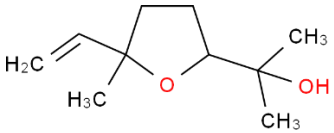
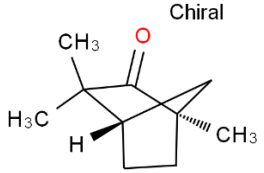
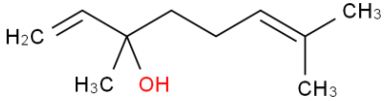
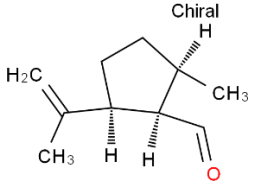


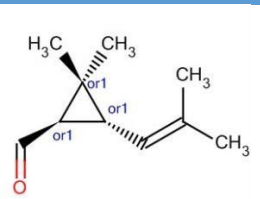
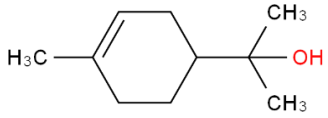
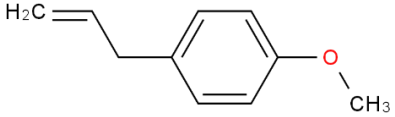
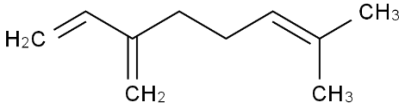
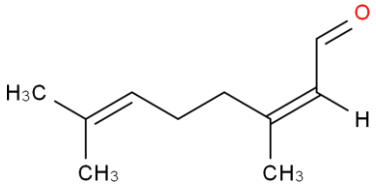
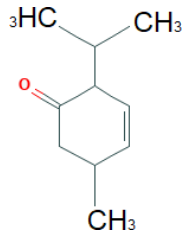

**Figure S2.** The chromatogram of OAEO by GC-MS analysis.

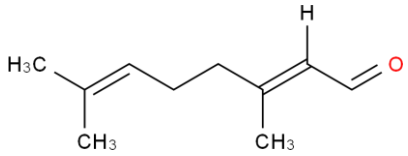
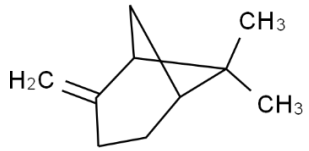
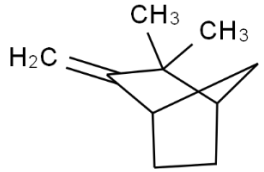
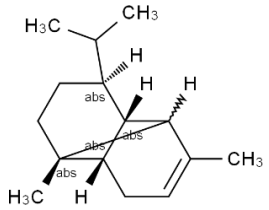
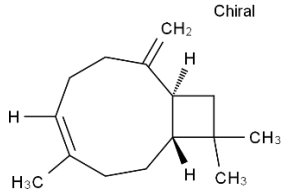
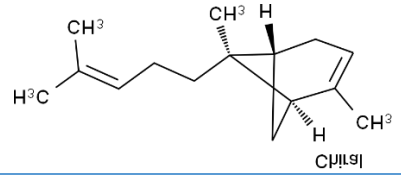
**Table S1**

**Chemical constituents of the essential oil from *O.* x *africanum*, analyzed by GC-MS**

| No. | Quality | Retention time | Compound name | CAS NO. | Chemical structure | Area average | % |
|---|---|---|---|---|---|---|---|
| 1 | 94.95 | 2.37 | tetramethyl Oxirane | 5076-20-0 |  | 10986343 | 0.81 |
| 2 | 84.45 | 3.56 | 7-methyl-1,6-octadiene | 42152-47-6 |  | 13448578 | 0.99 |
| 3 | 86.50 | 4.51 | Pulegone | 89-82-7 |  | 11474182.5 | 0.84 |
| 4 | 98.95 | 5.42 | α-pinene | 80-56-8 |  | 81397820 | 5.99 |
| 5 | 98.65 | 6.53 | 5-hepten-2-one, 6-methyl- | 110-93-0 |  | 285837548 | 21.02 |
| 6 | 86.75 | 6.75 | 2,3-dehydro-1,8-cineole | 92760-25-3 |  | 19813475 | 1.46 |

| No. | Quality | Retention time | Compound name | CAS NO. | Chemical structure | Area average | % |
|---|---|---|---|---|---|---|---|
| 7 | 97.35 | 7.05 | 3-hexen-1-ol, acetate, (e)- | 3681-82-1 |  | 7459219 | 0.55 |
| 8 | 98.75 | 7.81 | D-limonene | 5989-27-5 |  | 10275373 | 0.76 |
| 9 | 98.90 | 7.91 | Eucalyptol | 470-82-6 |  | 31025552 | 2.28 |
| 10 | 96.10 | 9.01 | Trans-linalool oxide (furanoid) | 34995-77-2 |  | 7279653 | 0.54 |
| 11 | 98.75 | 9.56 | L-fenchone | 7787-20-4 |  | 29133935.5 | 2.14 |
| 12 | 93.20 | 9.89 | Linalool | 78-70-6 |  | 240195266.5 | 17.66 |
| 13 | 74.95 | 11.08 | Photocitral A | 55253-28-6 |  | 10928007.5 | 0.80 |

| No. | Quality | Retention time | Compound name | CAS NO. | Chemical structure | Area average | % |
|---|---|---|---|---|---|---|---|
| 14 | 86.55 | 11.41 | Trans-chrysanthemal | 20104-05-6 |  | 12090359 | 0.89 |
| 15 | 98.35 | 12.92 | α-terpineol | 98-55-5 |  | 15687055 | 1.15 |
| 16 | 98.45 | 13.00 | Estragole | 140-67-0 |  | 26457225.5 | 1.95 |
| 17 | 89.40 | 13.87 | β-myrcene | 123-35-3 |  | 11841534 | 0.87 |
| 18 | 89.65 | 14.35 | Neral | 106-26-3 |  | 240318174.5 | 17.67 |
| 19 | 96.20 | 14.84 | 3-cyclohexen-1-one, 2-isopropyl-5-methyl | 900155-47-0 |  | 6861887 | 0.50 |

| No. | Quality | Retention time | Compound name | CAS NO. | Chemical structure | Area average | % |
|---|---|---|---|---|---|---|---|
| **20** | 97.15 | 15.32 | Citral | 5392-40-5 |  | 261080006.5 | 19.20 |
| **21** | 87.80 | 15.53 | β-pinene | 127-91-3 |  | 5207827 | 0.38 |
| **22** | 87.20 | 18.15 | Camphene | 79-92-5 |  | 1903792 | 0.14 |
| **23** | 94.10 | 18.77 | Copaene | 3856-25-5 |  | 3931733 | 0.29 |
| **24** | 97.65 | 20.16 | Caryophyllene | 87-44-5 |  | 7625188 | 0.56 |
| **25** | 97.05 | 20.55 | Trans-α-bergamotene | 13474-59-4 |  | 7732154 | 0.57 |

**Gene Ontology (GO) enrichment analysis by STIRNG software**

Parameters were set as shown below.

- Network Type: full STRING network
- Required score: medium confidence (0.400)
- FDR stringency: medium (5 percent)
- Organism: Homo sapiens

Gene Ontology (GO) enrichment analysis, Kyoto Encyclopedia of Genes and Genomes (KEGG)enrichment, Uniprot analyses were performed to predict the key pathways.

**Table S2.** List of up-regulated proteins

| **prot_acc** | **prot_desc** | **SUM_Q** |
|---|---|---|
| GRP78_HUMAN | 78 kDa glucose-regulated protein | 26.6000 |
| CH60_HUMAN | 60 kDa heat shock protein, mitochondrial | 15.6000 |
| HSP71_HUMAN | Heat shock 70 kDa protein 1A/1B | 10.8000 |
| FLNB_HUMAN | Filamin-B | 10.0000 |
| HSP76_HUMAN | Heat shock 70 kDa protein 6 | 8.8000 |
| EZRI_HUMAN | Ezrin | 7.6000 |
| HS71L_HUMAN | Heat shock 70 kDa protein 1-like | 5.1000 |
| FAS_HUMAN | Fatty acid synthase | 4.5000 |
| CLH1_HUMAN | Clathrin heavy chain 1 | 4.5000 |
| TXND5_HUMAN | Thioredoxin domain-containing protein 5 | 4.4286 |
| K1C18_HUMAN | Keratin, type I cytoskeletal 18 | 4.2143 |
| HSP7C_HUMAN | Heat shock cognate 71 kDa protein | 4.1818 |

| | | |
|---|---|---|
| SH3L3_HUMAN | SH3 domain-binding glutamic acid-rich-like protein 3 | 4.1212 |
| K2C8_HUMAN | Keratin, type II cytoskeletal 8 | 4.0820 |
| UBA1_HUMAN | Ubiquitin-like modifier-activating enzyme 1 | 4.0000 |
| HSP72_HUMAN | Heat shock-related 70 kDa protein 2 | 3.8667 |
| K22E_HUMAN | Keratin, type II cytoskeletal 2 epidermal | 3.7561 |
| ATPB_HUMAN | ATP synthase subunit beta, mitochondrial | 3.3333 |
| ACTN3_HUMAN | Alpha-actinin-3 | 3.3333 |
| K2C7_HUMAN | Keratin, type II cytoskeletal 7 | 3.3333 |
| K2C79_HUMAN | Keratin, type II cytoskeletal 79 | 3.0000 |
| K2C73_HUMAN | Keratin, type II cytoskeletal 73 | 3.0000 |
| K2C6B_HUMAN | Keratin, type II cytoskeletal 6B | 2.6471 |
| ACTB_HUMAN | Actin, cytoplasmic 1 | 2.6414 |
| K2C5_HUMAN | Keratin, type II cytoskeletal 5 | 2.6364 |
| ENPL_HUMAN | Endoplasmin | 2.4737 |
| CRIP1_HUMAN | Cysteine-rich protein 1 | 2.4146 |
| ENOA_HUMAN | Alpha-enolase | 2.2222 |
| K2C75_HUMAN | Keratin, type II cytoskeletal 75 | 2.1818 |
| CAP1_HUMAN | Adenylyl cyclase-associated protein 1 | 2.1667 |
| GTR1_HUMAN | Solute carrier family 2, facilitated glucose transporter member 1 | 2.1667 |
| RBM3_HUMAN | Putative RNA-binding protein 3 | 2.1500 |

| | | |
|---|---|---|
| OLA1_HUMAN | Obg-like ATPase 1 | 2.1429 |
| NQO1_HUMAN | NAD(P)H dehydrogenase [quinone] 1 | 2.0909 |
| AN32A_HUMAN | Acidic leucine-rich nuclear phosphoprotein 32 family member A | 2.0833 |
| AN32B_HUMAN | Acidic leucine-rich nuclear phosphoprotein 32 family member B | 2.0833 |
| EF1G_HUMAN | Elongation factor 1-gamma | 2.0000 |
| GANAB_HUMAN | Neutral alpha-glucosidase AB | 2.0000 |
| K22O_HUMAN | Keratin, type II cytoskeletal 2 oral | 2.0000 |
| KRT84_HUMAN | Keratin, type II cuticular Hb4 | 2.0000 |
| K2C71_HUMAN | Keratin, type II cytoskeletal 71 | 2.0000 |
| K2C3_HUMAN | Keratin, type II cytoskeletal 3 | 2.0000 |
| K2C72_HUMAN | Keratin, type II cytoskeletal 72 | 2.0000 |

**Table S3.** List of down-regulated proteins

| **prot_acc** | **prot_desc** | **SUM_Q** |
|---|---|---|
| RS5_HUMAN | 40S ribosomal protein S5 | 6.5333 |
| TAGL2_HUMAN | Transgelin-2 | 5.9703 |
| RL31_HUMAN | 60S ribosomal protein L31 | 5.5417 |
| PRDX2_HUMAN | Peroxiredoxin-2 | 5.1333 |
| TPIS_HUMAN | Triosephosphate isomerase | 3.9000 |
| RS19_HUMAN | 40S ribosomal protein S19 | 3.6667 |
| RS4X_HUMAN | 40S ribosomal protein S4, X isoform | 3.4545 |

| | | |
|---|---|---|
| IF6_HUMAN | Eukaryotic translation initiation factor 6 | 3.3077 |
| PPIB_HUMAN | Peptidyl-prolyl cis-trans isomerase B | 3.1667 |
| 1433Z_HUMAN | 14-3-3 protein zeta/delta | 3.1228 |
| S10A6_HUMAN | Protein S100-A6 | 2.8101 |
| H2A1B_HUMAN | Histone H2A type 1-B/E | 2.5725 |
| RS17_HUMAN | 40S ribosomal protein S17 | 2.5000 |
| PAL4B_HUMAN | Peptidylprolyl cis-trans isomerase A-like 4B | 2.3659 |
| LEG3_HUMAN | Galectin-3 | 2.2963 |
| FKB1A_HUMAN | Peptidyl-prolyl cis-trans isomerase FKBP1A | 2.2759 |
| PRDX6_HUMAN | Peroxiredoxin-6 | 2.2308 |
| RS20_HUMAN | 40S ribosomal protein S20 | 2.2308 |
| DEST_HUMAN | Destrin | 2.2222 |
| RL27_HUMAN | 60S ribosomal protein L27 | 2.1818 |
| RS16_HUMAN | 40S ribosomal protein S16 | 2.1429 |
| H90B3_HUMAN | Putative heat shock protein HSP 90-beta-3 | 2.1000 |
| RL7A_HUMAN | 60S ribosomal protein L7a | 2.0909 |
| RL18_HUMAN | 60S ribosomal protein L18 | 2.0625 |
| CAPZB_HUMAN | F-actin-capping protein subunit beta | 2.0000 |