**Supplementary File to**

**Fatty acid metabolism is related to the immune microenvironment changes of papillary thyroid cancer and SCD is a new tumor biomarker**

**Abbreviation**

**PTC, Papillary thyroid carcinoma; FAM, fatty acid metabolism; DEGs, Differentially expressed genes; FASN, fatty acid synthase; ACC, acetyl-CoA carboxylase; TCGA, The Cancer Genome Atlas; GEO, Gene Expression Omnibus; DMEM, Dulbecco's Modified Eagle Medium; DMEM/F12, Dulbecco's Modified Eagle Medium/Nutrient Mixture F-12; qPCR, quantitative Polymerase Chain Reaction; OD, optical density; cDNA, complementary DNA; PBS, Phosphate Buffered Saline; FAs, fatty acids; ACACB, Acetyl-CoA Carboxylase Beta; ADH1B, Alcohol Dehydrogenase 1B; FAO, fatty acid oxidation; HCC, hepatocellular carcinoma; LUAD, lung adenocarcinoma; LUSC, lung squamous cell carcinoma; HT, Hashimoto's thyroiditis; GC, gastric cancer.**

**Table S1. Primer sequence in this study.**

**Table S2. 309 FAM-related genes were originated from MSigDB database.**

**Table S3. 24 DEGs of 309 FAM-related genes.**

**Table S1.** **Primer sequence in this study.**

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| --- | --- |
| **Primer name** | **Primer sequence** |
| β-actin (F)β-actin (R)ACACB (F)ACACB (R)ADH1B (F)ADH1B (R)SCD (F)SCD (R) | CATGTACGTTGCTATCCAGGCCTCCTTAATGTCACGCACGATCAAGCCGATCACCAAGAGTAAACCCTGAGTTATCAGAGGCTGGAGGGGGCTGTTTATGGTGGGGTACGGATACTTTTCCCAGAGTTCTAGCTCCTATACCACCACCATCGTCTCCAACTTATCTCCTCC |

**Table S2. 309 FAM-related genes were originated from MSigDB database.**

|  |  |
| --- | --- |
| **Symbol** | **Description** |
| AADATABCC1ABCD1ACAA1ACAA2ACACAACACBACAD10ACAD11ACADLACADMACADSACADSBACADVLACAT1ACAT2ACBD4ACBD5ACBD6ACBD7ACLYACO2ACOT1ACOT11ACOT12ACOT13ACOT2ACOT4ACOT6ACOT7ACOT8ACOT8ACOT9ACOX1ACOX2ACOX3ACOXLACSBG1ACSBG2ACSF2ACSF3ACSL1ACSL3ACSL4ACSL5ACSL6ACSM3ACSM6ACSS1ADH1AADH1BADH1CADH4ADH5ADH6ADH7ADIPOR2ADSLAKR1C3ALADALDH1A1ALDH1B1ALDH2ALDH3A1ALDH3A2ALDH9A1ALDOAALOX12ALOX12BALOX15ALOX15BALOX5ALOX5APALOXE3AMACRAOC3APEX1AQP7AUHAWAT1BCKDHBBLVRABMPR1BBPHLCA2CA4CA6CBR1CBR1CBR3CBR4CD1DCD36CELCIDEACPOXCPT1ACPT1BCPT1CCPT2CROTCRYZCYP1A1CYP1A2CYP1B1CYP2C19CYP2C8CYP2C9CYP2J2CYP2U1CYP4A11CYP4A22CYP4B1CYP4F11CYP4F2CYP4F22CYP4F3CYP4F8CYP8B1D2HGDHDBIDECR1DECR2DHCR24DLDDLSTDPEP1DPEP2DPEP3ECH1ECHS1ECI1ECI2EHHADHELOVL1ELOVL2ELOVL3ELOVL4ELOVL5ELOVL6ELOVL7ENO2ENO3EPHX1EPHX2ERP29ETFDHFAAHFAAH2FABP1FABP2FADS1FADS2FASNFHFMO1G0S2GABARAPL1GAD2GAPDHSGCDHGGT1GGT5GLULGPD1GPD2GPX1GPX2GPX4GRHPRGSTZ1H2AZ1HACD1HACD2HACD3HACD4HACL1HADHHADHAHADHBHAO2HCCSHIBCHHMGCLHMGCS1HMGCS2HPGDHPGDSHSD17B10HSD17B11HSD17B12HSD17B3HSD17B4HSD17B7HSD17B8HSDL2HSP90AA1HSPH1HTD2IDH1IDH3BIDH3GIDI1IL4I1INMTKMT5ALDHALGALS1LTA4HLTC4SMAOAMAPKAPK2MCATMCEEMDH1MDH2ME1MECRMETAP1MGLLMID1IP1MIFMIX23MLYCDMMAAMMUTMORC2NBNNCAPH2NDUFAB1NSDHLNTHL1NUDT19NUDT7ODC1OLAHOSTCPCBD1PCCAPCCBPCTPPDHA1PDHBPECRPHYHPLA2G4APON1PON2PON3PPARAPPARDPPT1PPT2PRDX6PRKAA2PRKAB2PRKAG2PRXL2BPSME1PTGDSPTGESPTGES2PTGES3PTGISPTGR1PTGR2PTGS1PTGS2PTPRGPTSRAP1GDS1RDH11RDH16REEP6RETSATRXRAS100A10SCDSCD5SCP2SDHASDHCSDHDSERINC1SLC22A5SLC22A5SLC25A17SLC25A20SLC27A2SLC27A3SMSSUCLA2SUCLG1SUCLG2TBXAS1TDO2TECRTECRLTHEM4THEM5THRSPTP53INP2UBE2L6UGDHURODUROSVNN1XISTYWHAH | Aminoadipate AminotransferaseATP Binding Cassette Subfamily C Member 1 (ABCC1 Blood Group)ATP Binding Cassette Subfamily D Member 1Acetyl-CoA Acyltransferase 1Acetyl-CoA Acyltransferase 2Acetyl-CoA Carboxylase AlphaAcetyl-CoA Carboxylase BetaAcyl-CoA Dehydrogenase Family Member 10Acyl-CoA Dehydrogenase Family Member 11Acyl-CoA Dehydrogenase Long ChainAcyl-CoA Dehydrogenase Medium ChainAcyl-CoA Dehydrogenase Short ChainAcyl-CoA Dehydrogenase Short/Branched ChainAcyl-CoA Dehydrogenase Very Long ChainAcetyl-CoA Acetyltransferase 1Acetyl-CoA Acetyltransferase 2Acyl-CoA Binding Domain Containing 4Acyl-CoA Binding Domain Containing 5Acyl-CoA Binding Domain Containing 6Acyl-CoA Binding Domain Containing 7ATP Citrate LyaseAconitase 2Acyl-CoA Thioesterase 1Acyl-CoA Thioesterase 11Acyl-CoA Thioesterase 12Acyl-CoA Thioesterase 13Acyl-CoA Thioesterase 2Acyl-CoA Thioesterase 4Acyl-CoA Thioesterase 6Acyl-CoA Thioesterase 7Acyl-CoA Thioesterase 8Acyl-CoA Thioesterase 8Acyl-CoA Thioesterase 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Transfer ProteinPyruvate Dehydrogenase E1 Subunit Alpha 1Pyruvate Dehydrogenase E1 Subunit BetaPeroxisomal Trans-2-Enoyl-CoA ReductasePhytanoyl-CoA 2-HydroxylasePhospholipase A2 Group IVAParaoxonase 1Paraoxonase 2Paraoxonase 3Peroxisome Proliferator Activated Receptor AlphaPeroxisome Proliferator Activated Receptor DeltaPalmitoyl-Protein Thioesterase 1Palmitoyl-Protein Thioesterase 2Peroxiredoxin 6Protein Kinase AMP-Activated Catalytic Subunit Alpha 2Protein Kinase AMP-Activated Non-Catalytic Subunit Beta 2Protein Kinase AMP-Activated Non-Catalytic Subunit Gamma 2Peroxiredoxin Like 2BProteasome Activator Subunit 1Prostaglandin D2 SynthaseProstaglandin E SynthaseProstaglandin E Synthase 2Prostaglandin E Synthase 3Prostaglandin I2 SynthaseProstaglandin Reductase 1Prostaglandin Reductase 2Prostaglandin-Endoperoxide Synthase 1Prostaglandin-Endoperoxide Synthase 2Protein Tyrosine Phosphatase Receptor Type G6-Pyruvoyltetrahydropterin SynthaseRap1 GTPase-GDP Dissociation Stimulator 1Retinol Dehydrogenase 11Retinol Dehydrogenase 16Receptor Accessory Protein 6Retinol SaturaseRetinoid X Receptor AlphaS100 Calcium Binding Protein A10Stearoyl-CoA DesaturaseStearoyl-CoA Desaturase 5Sterol Carrier Protein 2Succinate Dehydrogenase Complex Flavoprotein Subunit ASuccinate Dehydrogenase Complex Subunit CSuccinate Dehydrogenase Complex Subunit DSerine Incorporator 1Solute Carrier Family 22 Member 5Solute Carrier Family 22 Member 5Solute Carrier Family 25 Member 17Solute Carrier Family 25 Member 20Solute Carrier Family 27 Member 2Solute Carrier Family 27 Member3Spermine SynthaseSuccinate-CoA Ligase ADP-Forming Subunit BetaSuccinate-CoA Ligase GDP/ADP-Forming Subunit AlphaSuccinate-CoA Ligase GDP-Forming Subunit BetaThromboxane A Synthase 1Tryptophan 2,3-DioxygenaseTrans-2,3-Enoyl-CoA ReductaseTrans-2,3-Enoyl-CoA Reductase LikeThioesterase Superfamily Member 4Thioesterase Superfamily Member 5Thyroid Hormone ResponsiveTumor Protein P53 Inducible Nuclear Protein 2Ubiquitin Conjugating Enzyme E2 L6UDP-Glucose 6-DehydrogenaseUroporphyrinogen DecarboxylaseUroporphyrinogen III SynthaseVanin 1X Inactive Specific TranscriptTyrosine 3-Monooxygenase/Tryptophan 5-Monooxygenase Activation Protein Eta |

**Table S3. 24 DEGs of 309 FAM-related genes.**

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| **Symbol** | **Description** |
| ACACBACBD7ACOT7ADH1BALDH1A1ALOX15BALOX5CA2CA4CPT1CCYP1B1CYP4B1ELOVL4FMO1G0S2HACD1HPGDSLGALS1OLAHS100A10SCDTDO2THRSPTP53INP2 | Acetyl-CoA Carboxylase BetaAcyl-CoA Binding Domain Containing 7Acyl-CoA Thioesterase 7Alcohol Dehydrogenase 1B (Class I), Beta PolypeptideAldehyde Dehydrogenase 1 Family Member A1Arachidonate 15-Lipoxygenase Type BArachidonate 5-LipoxygenaseCarbonic Anhydrase 2Carbonic Anhydrase 4Carnitine Palmitoyltransferase 1CCytochrome P450 Family 1 Subfamily B Member 1Cytochrome P450 Family 4 Subfamily B Member 1ELOVL Fatty Acid Elongase 4Flavin Containing Dimethylaniline Monoxygenase 1G0/G1 Switch 23-Hydroxyacyl-CoA Dehydratase 1Hematopoietic Prostaglandin D SynthaseGalectin 1Oleoyl-ACP HydrolaseS100 Calcium Binding Protein A10Stearoyl-CoA DesaturaseTryptophan 2,3-DioxygenaseThyroid Hormone ResponsiveTumor Protein P53 Inducible Nuclear Protein 2 |