Table 3. List of hypomethylated and upregulated genes and their reported associations with colorectal cancer (CRC) or other cancer types.

Gene	role	Linked to CRC or other cancers	Reference
Slc39a14	This gene encodes a member of the SLC39A family of divalent metal transporters that mediates the cellular uptake of manganese, zinc, iron, and cadmium.	The SLC39A14-exon4B transcript variant is a CRC biomarker with high sensitivity and organ-confined specificity.	DOI: 10.1002/ijc.27399
Map3k6	*MAP3K6* (Mitogen-Activated Protein Kinase Kinase Kinase 6) is a gene that encodes a kinase enzyme involved in signaling pathways that regulate various cellular processes, including cell growth, survival, and response to stress.	Germline mutations in *MAP3K6* are linked to familial gastric cancer	doi: 10.1371/journal.pgen.1004669
Slc4a4	*SLC4A4* (Solute Carrier Family 4 Member 4) encodes a sodium bicarbonate cotransporter, which plays an important role in regulating pH balance within cells and across tissues, particularly in the kidneys and other epithelial tissues.	*SLC4A4* may serve as a novel biomarker for predicting prognosis in patients with colon adenocarcinoma.	doi: 10.12659/MSM.925016
Arntl	Arntl is a core component of the circadian clock machinery and plays a key role in regulating various physiological processes, including metabolic and immune functions.	*BMAL1* (Arntl) is linked to bevacizumab resistance in colorectal cancer through the regulation of vascular endothelial growth factor A (VEGFA)	DOI: 10.1016/j.ebiom.2019.07.004
Myo6	*MYO6* (Myosin VI) is a motor protein that moves along actin filaments and plays critical roles in cellular processes such as endocytosis, secretion, and cell migration	*Overexpression of myosin VI promotes the progression of gastric cancer cells.*	https://doi.org/10.1016/j.gene.2016.08.015
Matk	*MATK (Megakaryocyte-Associated Tyrosine Kinase), also known as CHK, is a member of the C-terminal Src kinase (CSK) family.*	*CSK-homologous kinase is a potential tumor suppressor gene in colorectal cancer, often epigenetically silenced through promoter methylation.*	https://doi.org/10.1038/s41388-021-01755-z

Pcyt1a	*PCYT1A (Phosphate Cytidylyltransferase 1, Choline, Alpha) is a gene encoding an enzyme involved in the synthesis of phosphatidylcholine, a major phospholipid in cell membranes.*	*PCYT1A suppresses proliferation and migration via inhibiting mTORC1 pathway in lung adenocarcinoma*	doi: 10.1016/j.bbrc.2020.05.164.
Cacna2d2	*CACNA2D2 (Calcium Voltage-Gated Channel Auxiliary Subunit Alpha2delta 2) is a gene that encodes a subunit of voltage-gated calcium channels, which play a crucial role in calcium influx regulation.*	*CACNA2D2 is a tumor suppressor gene in several types of cancer including CRC.*	doi: 10.18632/oncotarget.15815
Bcas1	*BCAS1 is a candidate oncogene, amplified in various human cancers, including breast and prostate cancer, leading to more aggressive tumors.*	*BCAS1 inhibits β-Arrestin 2, thereby promoting the proliferation and migration of glioblastoma cells.*	**https://doi.org/10.3390/cancers14163890**
Dll1	*DLL1 (Delta-Like Ligand 1) is a ligand in the Notch signaling pathway, which is crucial for cell communication and regulates cell differentiation, proliferation, and apoptosis.*	*The Notch ligand DLL1 exhibits carcinogenic properties in human breast cancer cells.*	doi: 10.1371/journal.pone.0217002
Rxra	*RXRA is a nuclear receptor regulates gene expression by binding to retinoic acid and other ligands. This gene controls processes related to cell growth, differentiation, apoptosis, and metabolism.*	*RXRA influences the development of metachronous colorectal neoplasia and may be particularly important in the formation of proximal lesions.*	DOI: 10.1158/0008-5472.CAN-09-3264
Ada	*Ada is an adenosine deaminase, which is essential for breaking down adenosine and deoxyadenosine in purine metabolism.*	*Polymorphic sites in ADA may impact cell-mediated anti-tumor immune responses by regulating adenosine levels and affecting additional protein functions beyond its enzymatic activity.*	https://doi.org/10.3109/07357907.2010.483501
Hnf4a	*HNF4A is a nuclear transcription factor involved in regulating genes associated with metabolism, cell differentiation, and epithelial integrity.*	*In colorectal cancer, the transcription factor HNF4 has been associated with metastasis at both the RNA and protein levels.*	https://doi.org/10.1038/s41598-018-36168-8
Dpep1	*DPEP1 (Dipeptidase 1) is an enzyme primarily involved in the metabolism of dipeptides, particularly in the kidney, where it plays a role in breaking down certain peptides.*	*Dpep1enhances the proliferation of colon cancer cells through regulation of the DPEP1/MYC feedback loop.*	doi: 10.1016/j.bbrc.2020.08.063.

Hkdc1	*HKDC1 (Hexokinase Domain Containing 1) is a member of the hexokinase family, enzymes that play an essential role in glycolysis by catalyzing the phosphorylation of glucose to glucose-6-phosphate.*	*Upregulation of HKDC1 promotes glycolysis and disease progression in gastric cancer, while also conferring chemoresistance.*	doi: 10.1111/cas.15692
Lrig3	*LRIG3 is part of the LRIG family, known for regulating receptor tyrosine kinase signaling pathways, including the EGF receptor pathway.*	*LRIG3 may play a role in regulating EGF receptor signaling and act as a tumor suppressor gene in glioma pathogenesis.*	doi: 10.3389/fonc.2019.00447
Ace	*ACE is a key enzyme in the renin-angiotensin system, primarily responsible for regulating blood pressure and fluid balance.* *ACE also influences cancer biology by promoting cell proliferation, angiogenesis, and tumor growth.*	*Polymorphism in the angiotensin I-converting enzyme gene is associated with tumor size and patient survival in colorectal cancer.*	doi: 10.1593/neo.07418
Fbp2	*FBP2 (Fructose-1,6-Bisphosphatase 2) is an enzyme involved in gluconeogenesis, the metabolic pathway that generates glucose from non-carbohydrate sources*	*Fbp2 inhibits sarcoma progression by restricting mitochondrial biogenesis.*	DOI: 10.1016/j.cmet.2019.10.012
Pitx1	*PITX1 (Paired Like Homeodomain 1) is a transcription factor that plays an important role in regulating gene expression during development, particularly in limb and organ formation.*	*PITX1 plays a dual role in colon cancer, acting as both a tumor suppressor and an oncogene.*	doi: 10.3389/fonc.2023.1253238
Iqgap2	*Q motif-containing GTPase-activating protein 2 (IQGAP2) is a multidomain scaffolding protein that plays a significant role in various cellular processes, including cytoskeleton regulation, cell adhesion, and signal transduction.*	*Iqgap2 mRNA serves as an independent prognostic marker and is associated with immunosuppression in diffuse large B-cell lymphoma (DLBCL).*	https://doi.org/10.1186/s12885-021-08086-y
Sema5a	*SEMA5A (Semaphorin 5A) is a member of the semaphorin family of proteins, which are involved in various aspects of cellular signaling, particularly in the nervous system.*	*A combined expression signature of ULBP2 and SEMA5A serves as a prognostic and predictive biomarker for colon cancer.*	doi: 10.7150/jca.17872

SLC38A4	SLC38A4 (Solute Carrier Family 38 Member 4) is a member of the solute carrier (SLC) family of transport proteins, which are critical for the transport of various solutes across cell membranes.	*SLC38A4 can be used as a prognostic biomarker for colorectal cancer.*	DOI: 10.1016/j.heliyon.2024.e34464
Cdx1	CDX1 (Caudal Type Homeobox 1) is a critical transcription factor for maintaining the identity and function of intestinal epithelial cells.	*Cdx1 overexpression could increase malignancy in early stages of tumourigenesis.*	https://doi.org/10.1038/onc.2008.78
Aldh1	ALDH1 (Aldehyde Dehydrogenase 1) is an enzyme that plays a crucial role in the metabolism of aldehydes, particularly in the conversion of aldehydes to their corresponding carboxylic acids.	*Aldh1 could be a potential diagnostic and therapeutic target for colon cancer stem cells (CSCs).*	https://doi.org/10.3389/fonc.2022.1026278
Pfkfb4	Pfkfb4 (6-Phosphofructo-2-kinase/fructose-2,6-bisphosphatase 4) is an enzyme that plays a significant role in regulating glucose metabolism and energy homeostasis.	*High PFKFB4 expression was associated with both improved overall survival (OS) and post-progression survival (PPS) in Colon adenocarcinoma patients.*	https://doi.org/10.1038/s41598-023-43619-4
Mgat4a	MGAT4A (Mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase A) is an enzyme involved in glycoprotein biosynthesis.	*Aberrant expression of MGAT4A mRNA has been observed in various cancer cells and is known to enhance their invasiveness by modulating the functions of glycoproteins, including integrin β1.*	https://doi.org/10.1038/s42003-022-03661-w
Aldh9a1	ALDH9A1 (Aldehyde Dehydrogenase 9 Family Member A1) is an enzyme that plays a crucial role in the metabolism of aldehydes, particularly in the detoxification of harmful substances and the regulation of cellular processes.	*The abundance of ALDH9A1, is elevated in renal cell carcinoma (RCC).*	https://doi.org/10.1074/mcp.M800252-MCP200
Chmp4c	*Chmp4c* (Charged Multivesicular Body Protein 4C) is a member of the CHMP family of proteins, which are involved in the endosomal sorting complex required for transport (ESCRT) machinery.	*Chmp4c plays a role in the viability and motility of cervical cancer (CC) cells by regulating epithelial-mesenchymal transition, potentially aiding in the discovery of novel biomarkers for CC therapy.*	doi: 10.1002/2211-5463.12880

EPB41L1	*EPB41L1 (Erythrocyte Membrane Protein Band 4.1 Like 1) is a member of the band 4.1 family of proteins, which are known for their roles in maintaining the integrity and stability of the cytoskeleton in various cell types.*	*EPB41L1 is significantly upregulated in colorectal adenocarcinoma tissues, and its high expression level is associated with a poor prognosis for the patients.*	DOI: https://doi.org/10.21203/rs.3.rs-358130/v1
SNX7	*SNX7 (Sorting Nexin 7) is a member of the sorting nexin family of proteins, which are involved in intracellular trafficking and membrane dynamics.*	*SNX7 is emerging as a promising novel biomarker for the diagnosis, prognosis, and prediction of treatment responses to chemotherapy and immunotherapy in patients with hepatocellular carcinoma (HCC).*	doi: 10.1186/s12885-023-11405-0
Coro2a	CORO2A (Coronin 2A) is a protein that plays a role in the regulation of the actin cytoskeleton and is involved in various cellular processes.	*CORO2A has the potential to serve as a prognostic predictor for patients with triple-negative breast cancer (TNBC).*	doi: 10.3389/fonc.2020.00916
Dab1	DAB1 (Disabled 1) is a protein that plays a critical role in various cellular signaling pathways, particularly in neuronal development and migration.	*Genetic depletion of DAB1 inhibits cancer invasion and metastasis in mice with activated NOTCH signaling.*	DOI: 10.1158/2159-8290.CD-14-0595
Rbp7	RBP7 (RNA Binding Protein 7) is a protein involved in various cellular processes, particularly in RNA metabolism and gene regulation.	*RBP7 is a robust prognostic biomarker in colon cancer and functionally contributes to the malignant characteristics of colon cancer cells.*	doi: 10.7150/jca.35180
Ugdh	UGDH (UDP-glucuronic acid decarboxylase) is an enzyme involved in the metabolism of carbohydrates and the detoxification of various compounds in the body.	*UGDH is an enzyme that could be utilized as a potential prognostic marker in oncology and as a therapeutic target in cancer biology.*	doi: 10.18632/oncotarget.28514
Tpk1	TPK1 (Thiamine Phosphate Kinase 1) is an enzyme involved in thiamine metabolism and plays a crucial role in the synthesis of thiamine diphosphate.	TPK1 expression is a significant factor influencing the susceptibility of cancer cells to ionizing radiation.	https://doi.org/10.18632
Gfpt1	GFPT1 (Glutamine-Fructose-6-Phosphate Transaminase 1) is an enzyme that plays a key role in amino acid and carbohydrate metabolism.	*The enhanced levels of Gfpt1 promotes the growth of colorectal cancer.*	doi: 10.3390/ijms25094883.

Nadsyn1	NADSYN1 (NAD synthetase 1) is an enzyme that catalyzes the final step in the biosynthesis of nicotinamide adenine dinucleotide (NAD+)	The DNA copy number of Nadsyn1 was found to be elevated in several cancer types, including prostate, ovarian, and pancreatic cancers.	doi: 10.1038/s41586-019-1150-2
Lrrc1	The LRRC1 gene has the potential to function as an immune-associated prognostic biomarker for hepatocellular carcinoma (HCC).	The LRRC1 gene has the potential to function as an immune-associated prognostic biomarker for HCC.	doi: 10.1097/MD.0000000000034365
Car12	CAR12 (Carbonic Anhydrase 12) is an enzyme that catalyzes the reversible hydration of carbon dioxide to bicarbonate and a proton, playing a crucial role in maintaining acid-base balance and facilitating various physiological processes.	Car12 is upregulated in human as well as murine breast cancer tissue.	https://doi.org/10.1186/s13058-023-01644-1
Mst1r	MST1R (Macrophage Stimulating 1 Receptor) or RON, is a receptor tyrosine kinase involved in various cellular processes.	RON plays a role in carcinogenesis through its immune modulation of the tumor microenvironment, activation of various oncogenic pathways, and protective functions under cellular stress.	doi: 10.3390/cancers14082037
Tspan8	Tetraspanin 8 (TSPAN8) is a member of the tetraspanin family, characterized by four transmembrane domains and involvement in various cellular processes.	TSPAN8 enhances the stemness of cancer cells through the activation of sonic Hedgehog signaling.	https://doi.org/10.1038/s41467-019-10739-3
Celf5	CELF (CUGBP Elav-like family) proteins are RBPs (RNA-binding proteins) with pleiotropic capabilities in RNA processing.	Members of the CELF family have been linked to widespread changes in cancer proliferation and invasion, resulting in their identification as potential tumor suppressors or even oncogenes.	doi: 10.3390/ijms222011056
Dpp4	Dipeptidyl peptidase-4 (DPP-4), also known as CD26, is a multifunctional enzyme involved in various physiological processes.	DPP-4 inhibitors enhance the incidence of newly developed metastasis in primary thyroid cancer among diabetic patients.	doi: 10.1002/ijc.31870.

Slc12a8	SLC12A8 (Solute Carrier Family 12 Member 8) is a protein-coding gene that encodes a cation-chloride cotransporter.	The upregulation of SLC12A8 promoted resistance to apoptosis, EMT, and reduced reactive oxygen species (ROS) production.	doi: 10.21037/tcr-24-87
Aldh1b1	Aldehyde dehydrogenase 1B1 (ALDH1B1) is an enzyme that plays a crucial role in the metabolism of aldehydes, particularly in the detoxification of alcohol-derived acetaldehyde.	ALDH1B1 is significantly upregulated in colorectal adenocarcinoma, and silencing ALDH1B1 inhibits the growth of human colon cancer spheroids and xenografts.	https://doi.org/10.1371/journal.pone.0121648
Krt20	Keratin 20 (KRT20) is a type I intermediate filament protein predominantly expressed in the gastrointestinal epithelium, including the colon.	Colorectal cancer cells typically exhibit high levels of keratin 20 (K20) expression	DOI: 10.14670/HH-27.347
Chst4	Carbohydrate sulfotransferase 4 (CHST4) is an enzyme that catalyzes the transfer of sulfate groups to specific carbohydrate structures	CHST4 functions as a tumor suppressor in hepatocellular carcinoma associated with hepatitis B virus (HCC-HBV).	doi: 10.3389/fonc.2020.554331
Sec24a	SEC24A (SEC24 Homolog A) is a protein that plays a crucial role in the transport of proteins from the endoplasmic reticulum (ER) to the Golgi apparatus.	SEC24A is involved in enhancing the invasion and metastasis of human gastric cancer (GC) cells.	PMCID: PMC6962814 PMID: 31949794
Arhgap26	ARHGAP26 (Rho GTPase-activating protein 26) is an enzyme that regulates the activity of Rho GTPases	The recurrent RhoGAP gene fusion CLDN18-ARHGAP26 enhances RHOA activation and stimulates focal adhesion kinase and YAP-TEAD signaling in diffuse gastric cancer.	https://doi.org/ 10.1136/gutjnl-2023-329686
Aff3	AFF3 (AF4/FMR2 family member 3) is a gene encoding a nuclear transcriptional activator involved in RNA elongation and gene expression regulation.	AFF3 may be a promising potential marker for the diagnosis and prognosis of GC patients.	doi: 10.1002/jcla.24437
Rgs22	Regulator of G-protein signaling 22 (RGS22) is a protein that modulates G-protein signaling pathways	RGS22 is overexpressed in low-metastatic epithelial cancers and plays a role in cell migration and invasion processes in esophageal cancer cell lines.	DOI: 10.1007/s10585-011-9390-z

Kctd12	KCTD12 (Potassium Channel Tetramerization Domain Containing 12) is a protein-coding gene involved in various cellular processes, including the regulation of GABA-B receptor signaling and potential roles in cancer progression.	KCTD12 is a novel regulator of colorectal cancer (CRC) cell stemness and may act as a promising prognostic marker and therapeutic target for CRC patients.	https://doi.org/10.1038/srep20460
Fyb2	FYB2, also known as FYN binding protein 2, is an adaptor protein involved in T-cell receptor (TCR)-mediated activation of signaling pathways.	FYB2 may serve as a novel prognostic biomarker in liver hepatocellular carcinoma (LIHC)	https://doi.org/10.3390/livers2040027
Ighg3	IGHG3 contributes to the structure of IgG3 antibodies, which are crucial for immune defense against pathogens.	Ighg3 is overexpressed in non-small cell lung carcinoma.	doi: 10.3892/ijo.26.1.247.
Frat1	FRAT1 (FRAT Regulator of WNT Signaling Pathway 1) is a protein-coding gene that plays a pivotal role in the Wnt signaling pathway, which is essential for regulating cell proliferation, differentiation, and survival.	Knocking out the FRAT1 gene reduces the expression of β-catenin, cyclin D1, and c-myc in liver cancer cells, inhibiting tumor cell proliferation by modulating the Wnt/β-catenin signaling pathway.	doi: 10.3892/or.2016.5130.
Rnasel	RNase L is activated by 2-5A molecules, which are synthesized in response to viral infections.	RNase L is a crucial element in interferon (IFN)-mediated antiviral signaling and has demonstrated antitumor effects in cancer.	https://doi.org/10.1038/s41419-019-1902-9
Syne2	SYNE2 (Spectrin Repeat Containing Nuclear Envelope Protein 2), also known as Nesprin-2, is a protein that plays a crucial role in maintaining the structural integrity of the nucleus by anchoring it to the actin cytoskeleton.	SYNE2 plays a significant role in the regulation of p21 and is associated with the clinical outcomes of HBV-related hepatocellular carcinoma (HCC) in a TP53-independent manner.	https://doi.org/10.1038/srep31237
Kalrn	Kalirin (KALRN) is a gene encoding a protein that functions as a Rho guanine nucleotide exchange factor (RhoGEF), playing a pivotal role in regulating the actin cytoskeleton and influencing neuronal development and synaptic plasticity	The KALRN mutation serves as a valuable biomarker for predicting patients' responses to immunotherapy in cancer.	doi: 10.1136/jitc-2019-000293

Nptx2	Neuronal Pentraxin 2 (NPTX2) is a protein involved in synaptic function and plasticity within the central nervous system.	NPTX2 enhances the growth of colorectal cancer and liver metastasis through the activation of the canonical Wnt/β-catenin pathway via FZD6.	https://doi.org/10.1038/s41419-019-1467-7
Itpk1	Inositol-tetrakisphosphate 1-kinase (ITPK1) is an enzyme that plays a crucial role in inositol phosphate signaling pathways, which are essential for various cellular processes, including cell proliferation, differentiation, and apoptosis.	ITPK1 enhances the sensitivity of tumor cells to IgA-dependent neutrophil-mediated killing in vivo.	doi: 10.4049/jimmunol.2300372.
Sh3rf2	SH3RF2 (SH3 Domain Containing Ring Finger 2) is a protein-coding gene that encodes an E3 ubiquitin-protein ligase involved in various cellular processes, including apoptosis regulation and protein stability.	SH3RF2 acts as an oncogene by regulating the stability of the PAK4 protein.	doi: 10.1093/carcin/bgt338.
Naaladl1	NAALADL1 (N-acetylated alpha-linked acidic dipeptidase-like 1) is a protein-coding gene that encodes an aminopeptidase enzyme involved in peptide catabolism.	NAALADL1 gene expression is low in typical prostate cancer cell lines but is elevated in the human medullary thyroid carcinoma TT cell line.	doi: 10.1073/pnas.2025710119
Clrn3	CLRN3 (Clarin 3) is a protein-coding gene located on chromosome 10, known for its involvement in lysosomal function and cellular processes.	CLRN3 significantly reduced the malignant biological behavior of colorectal cancer (CRC) cells	**https://doi.org/10.3390/biom14080891**
Pls1	Plastin 1, also known as I-plastin or fimbrin, is an actin-bundling protein encoded by the PLS1 gene.	Plastin 1 promotes the metastasis of colorectal cancer by activating the IQGAP1/Rac1/ERK pathway.	doi: 10.1111/cas.14438
Fcgbp	FCGBP (Fc gamma binding protein) is a protein involved in mucosal immunity and has been implicated in various cancers.	FCGBP is a prognostic biomarker that is associated with immune infiltration in glioma.	https://doi.org/10.3389/fonc.2021.769033
Liph	Lipase H (LIPH) is a membrane-bound enzyme that catalyzes the production of 2-acyl lysophosphatidic acid (LPA), a	LIPH (lipase H) is significantly overexpressed in breast cancer tissues and is associated with poorer prognoses in breast cancer.	doi: 10.2147/IJGM.S332233

	bioactive lipid mediator involved in various physiological processes.		
GPR133 (ADGRD1)	GPR133, also known as ADGRD1, is an adhesion G protein-coupled receptor (aGPCR) involved in various cellular processes, including tumor progression.	GPR133 is a key mediator of the hypoxic response in glioblastoma (GBM) and plays significant protumorigenic roles.	https://doi.org/10.1038/oncsis.2016.63
Dcst1	DCST1 (DC-STAMP Domain Containing 1) is a protein-coding gene that encodes a protein involved in various cellular processes, including immune response and cell signaling.	DCST1-AS1 enhances TGF-β-induced epithelial-mesenchymal transition and increases chemoresistance in triple-negative breast cancer cells through the action of ANXA1.	doi: 10.3389/fonc.2020.00280
Gucy2c	Guanylate cyclase 2C (GUCY2C) functions as a receptor for endogenous peptides such as guanylin and uroguanylin, as well as for heat-stable enterotoxins produced by certain pathogens.	GUCY2C is a promising target for immunotherapy and serves as a diagnostic marker for both primary and metastatic disease.	doi: 10.1080/14728222.2021.1937124
Fcmr	The FCMR gene encodes the Fc mu receptor, a protein that binds to the Fc region of immunoglobulin M (IgM) antibodies.	Therapeutically targeting Fcmr during oncogenesis reduced tumor growth, whether used alone or in combination with anti-PD-1.	https://doi.org/10.1038/s41467-019-10619-w
Tnfrsf14	TNFRSF14, also known as Herpesvirus Entry Mediator (HVEM), is a member of the tumor necrosis factor (TNF) receptor superfamily.	TNFRSF14 (HVEM) is a promising new immune checkpoint for cancer immunotherapy in humanized mice.	https://doi.org/10.1101/711119
Dao	Diamine oxidase (DAO), also known as amine oxidase, copper-containing 1 (AOC1), is an enzyme responsible for the oxidative deamination of biogenic amines, including histamine, putrescine, and spermidine.	Plasma diamine oxidase activity serves as a biomarker for assessing gastrointestinal tract toxicities in gastric cancer patients undergoing chemotherapy.	https://doi.org/10.1159/000336799
Sytl3	Synaptotagmin-like 3 (SYTL3) acts as a peripheral membrane protein that interacts with RAB27A and is involved in the process of vesicular trafficking, facilitating the transport and release of cellular vesicles.	SYTL3 functions as a regulator of cortical neuronal migration in the developing brains of both humans and mice.	https://doi.org/10.1016/j.celrep.2021.108802

Ak7	Adenylate kinase 7 (AK7) catalyzes the reversible phosphorylation of adenine nucleotides, playing a crucial role in maintaining cellular energy homeostasis.	Adenylate kinase 7 serves as a prognostic indicator for overall survival in ovarian cancer.	doi: 10.1097/MD.0000000000024134
Bach2	BACH2 (BTB Domain And CNC Homolog 2) is a transcription factor that plays a pivotal role in regulating immune responses and has been implicated in various cancers.	The transcription factor BACH2 facilitates tumor immunosuppression.	DOI: 10.1172/JCI82884
Abcc8	ABCC8, known as ATP-binding cassette sub-family C member 8, encodes the sulfonylurea receptor 1 (SUR1) protein, a subunit of the ATP-sensitive potassium (K-ATP) channel.	ABCC8 mRNA expression may serve as an independent prognostic indicator for glioma patients and could predict their sensitivity to temozolomide treatment.	doi: 10.1038/s41598-020-69676-7
Anpep	ANPEP, also known as alanylal aminopeptidase, is a membrane-bound enzyme plays a crucial role in peptide digestion and metabolism.	ANPEP is a macrophage-related gene that may play a significant role in tumor metabolism.	https://doi.org/10.1158/1538-7755.DISP21-PO-153
Rap1gap2	Rap1GAP2 (Rap1 GTPase-activating protein 2) functions as a GTPase-activating protein (GAP) for Rap1, a small GTPase involved in regulating cell adhesion, migration, and proliferation.	Rap1GAP may play a role in tumor progression in colorectal cancer (CRC) and could serve as a potential target for prognostic prediction in CRC patients.	https://doi.org/10.3892/ol.2018.8305
Dgki	Diacylglycerol kinase iota (DGKI) is part of the type IV diacylglycerol kinase subfamily which plays a crucial role in regulating intracellular levels of diacylglycerol (DAG) and phosphatidic acid (PA)	DGKI overexpression may serve as a potential molecular marker for poor prognosis in gastric cancer (GC), with the MAPK signaling pathway identified as a key pathway associated with DGKI regulation in this context.	https://doi.org/10.3389/fmed.2020.00320
Nos1ap	Nitric oxide synthase 1 adaptor protein (NOS1AP), functions as an adaptor protein that interacts with neuronal nitric oxide synthase (nNOS), playing a crucial role in neuronal signaling and synaptic function.	A protein complex consisting of SCRIB, NOS1AP, and VANGL1 regulates cell polarity and migration and is linked to the progression of breast cancer.	DOI: 10.1038/onc.2011.528
Trpm4	Transient Receptor Potential Melastatin 4 (TRPM4) is a calcium-activated, non-selective cation channel that allows the influx of monovalent cations, such as	TRPM4 is significantly expressed in human colorectal tumor buds and plays a role in the proliferation, cell cycle	**https://doi.org/10.1002/1878-0261.12566**

	sodium and potassium, while being impermeable to calcium.	regulation, and invasion of colorectal cancer cells.	
Slc43a2	SLC43A2, is a protein that functions as a transporter for large neutral amino acids, including methionine. It plays a crucial role in cellular amino acid uptake, influencing various metabolic processes.	SLC43A2 has been identified as an oncogene that regulates methionine metabolism and tumor proliferation across various cancer types.	doi: 10.1038/s41586-020-2682-1.
Atp6v0a2	ATP6V0A2, is a component of the vacuolar-type H+-ATPase (V-ATPase) complex, which is responsible for acidifying intracellular compartments such as endosomes, lysosomes, and the Golgi apparatus.	The ATP6V0A2 subunit is overexpressed in ovarian cancer and is linked to cell membrane dynamics that drive metastasis.	https://doi.org/10.1038/s41419-021-04495-w
A4gnt	Alpha-1,4-N-acetylglucosaminyltransferase (A4GNT) is an enzyme responsible for adding N-acetylglucosamine (GlcNAc) to glycoproteins, a modification that influences protein function and stability.	A4gnt knockout mice, the absence of αGlcNAc in gland mucin leads to the development of gastric adenocarcinoma.	doi: 10.1111/cas.12305
Crybg2	Crystallin beta-gamma domain-containing protein 2 is predicted to possess carbohydrate binding activity.	*The association of Crybg2 with colon cancer has not yet been elucidated*.	https://www.ncbi.nlm.nih.gov/gene/55057
Slc5a4b	Predicted to facilitate low-affinity D-glucose symporter activity, function upstream of or within proton transmembrane transport.	*The association of Slc5a4b with colon cancer has not yet been elucidated*.	https://www.ncbi.nlm.nih.gov/gene/6527
Slc4a8	t *Slc4a8* ransports sodium and bicarbonate ions across cell membranes	*The association of Slc4a8 with colon cancer has not yet been elucidated*.	https://doi.org/10.1016/j.mam.2012.07.009
Myo7b	Myo7b, or myosin VIIB, is a protein found in the brush border microvilli of epithelial cells in the colon and kidneys	*The association of Myo7b with colon cancer has not yet been elucidated*.	doi: 10.1016/j.cub.2016.08.014

Epb41l4b	PB41L4B (erythrocyte membrane protein band 4.1 like 4B) is a gene that encodes a protein involved in regulating the circumferential actomyosin belt in epithelial cells.	*Epb41l4b* is downregulated in CRC.	doi: 10.1042/BSR20200141
Espn	Espin (encoded by the ESPN gene) is a multifunctional actin-bundling protein crucial for the organization and function of actin filament-rich structures, such as microvilli in mechanosensory and chemosensory cells.	High expression levels of ESPN are independently linked to a poor prognosis in patients with esophageal squamous cell carcinoma (ESCC), while the downregulation of ESPN inhibits the growth of ESCC cells.	https://doi.org/10.1186/s12935-018-0713-x
Shroom3	SHROOM3, a gene linked to chronic kidney disease, influences the structure of podocytes.	*The association of Shroom3 with colon cancer has not yet been elucidated.*	https://doi.org/10.1038/s41598-020-77952-9
Atp2b2	ATP2B2, also known as plasma membrane calcium-transporting ATPase 2 (PMCA2), is a gene encoding a protein responsible for regulating calcium ion concentrations within cells.	*The association of Atp2b2 with colon cancer has not yet been elucidated.*	doi: 10.1007/s00439-018-1965-1
2200002D01Rik	The gene 2200002D01Rik is a protein-coding gene in mice, also known as RIKEN cDNA 2200002D01 gene.	*The association of 2200002D01Rik with colon cancer has not yet been elucidated.*	https://www.ncbi.nlm.nih.gov/gene/72275
Dnajc13	DNAJC13 is an endosome-related protein and believed to regulate endosomal membrane trafficking.	*The association of Dnajc13 with colon cancer has not yet been elucidated.*	https://doi.org/10.1093/hmg/ddy003
Leap2	Liver-expressed antimicrobial peptide 2 (LEAP2) is a cysteine-rich, cationic antimicrobial peptide predominantly expressed in the liver.	*The association of Leap2 with colon cancer has not yet been elucidated.*	https://doi.org/10.1016/j.fsi.2023.109225
Fsd1l	FSD1L (Fibronectin Type III and SPRY Domain Containing 1 Like) is a protein-coding gene associated with hydrocephalus, a condition characterized by the accumulation of cerebrospinal fluid in the brain.	*The association of Fsd1l with colon cancer has not yet been elucidated.*	https://www.genecards.org/cgi-bin/carddisp.pl?gene=FSD1L

Itgad	The ITGAD gene encodes the integrin alpha D protein, a component of the beta-2 integrin family of membrane glycoproteins.	*The association of Itgad with colon cancer has not yet been elucidated*.	https://www.genecards.org/cgi-bin/carddisp.pl?gene=ITGAD
Gm36640	Gm36640 is a predicted gene located on mouse chromosome 6, spanning positions 135,256,550 to 135,290,997 on the positive strand. It is classified as a long non-coding RNA (lncRNA) gene.	*The association of Gm36640 with colon cancer has not yet been elucidated*.	https://www.informatics.jax.org/marker/MGI%3A5595799