

Supplemental Tables

Table S1 The full name, function of the 16 CPRMs

Gene	Full Name	Function
ATP7A	ATPase Copper Transporting Alpha	This gene encodes a transmembrane protein that functions in copper transport across membranes, which has been found to be involved in the resistance of colorectal cancer to oxaliplatin.
ATP7B	ATPase Copper Transporting Beta	This protein is a monomer, and functions as a copper-transporting ATPase which exports copper out of the cells, such as the efflux of hepatic copper into the bile. Researches have shown this protein plays a role in the development of resistance to oxaliplatin in colorectal cancer.
CDKN2A	Cyclin Dependent Kinase Inhibitor 2A	This gene encodes a 156 amino acid, 16kD cell-cycle inhibitor protein, which normally blocks abnormal cell growth and proliferation by binding to complexes of cyclin-dependent kinases (CDK) 4 and 6, and cyclin D. This binding inhibits the kinase activity of the enzyme, which arrests the cell cycle in the G1 phase.
DBT	Dihydrolipoamide Branched Chain Transacylase E2	This gene encodes the transacylase (E2) subunit of branched-chain alpha-keto acid dehydrogenase complex (BCKD) which is an inner-mitochondrial enzyme complex involved in the breakdown of the branched-chain amino acids isoleucine, leucine, and valine.
DLAT	Dihydrolipoamide S-acetyltransferase	This gene encodes component E2 of the multi-enzyme pyruvate dehydrogenase complex (PDC), which accepts acetyl groups formed by the oxidative decarboxylation of pyruvate and transfers them to coenzyme A. It is involved in mediating carbon entry to the TCA cycle.
DLD	Dihydrolipoamide Dehydrogenase	The encoded protein has been identified as a moonlighting protein based on its ability to perform mechanistically distinct functions. In homodimeric form, the encoded protein functions as a dehydrogenase and is found in several multi-enzyme complexes that regulate energy metabolism. However, as a monomer, this protein can function as a protease.
DLST	Dihydrolipoamide S-succinyltransferase	This gene encodes a mitochondrial protein which is one of the three components (the E2 component) of the 2-oxoglutarate dehydrogenase complex that catalyzes the overall conversion of 2-oxoglutarate to succinyl-CoA and CO(2), which is required for lysine succinylation of histones.
FDX1	Ferredoxin 1	Transfers electrons from NADPH through ferredoxin reductase to mitochondrial cytochrome P450, involved in steroid, vitamin D, and bile acid metabolism.
GCSH	Glycine Cleavage System Protein H	The protein encoded by this gene is the H protein, a component of glycine cleavage system, which transfers the methylamine group of glycine from the P protein to the T protein
GLS	Glutaminase	This gene encodes the K-type mitochondrial glutaminase. The encoded protein is an phosphate-activated amidohydrolase that catalyzes the hydrolysis of glutamine to glutamate and ammonia, which is an essential step in the metabolism of glutamine in colorectal cancer cells.

LIAS	Lipoic Acid Synthetase	Catalyzes the final step in the de novo pathway for the biosynthesis of lipoic acid, a potent antioxidant.
LIPT1	Lipoyltransferase 1	Transfers the lipoyl moiety to apoproteins which is the second step of the process of transferring lipoic acid to proteins.
MTF1	Metal Regulatory Transcription Factor 1	This gene encodes a transcription factor that induces expression of metallothioneins and other genes involved in metal homeostasis in response to heavy metals such as cadmium, zinc, copper, and silver.
PDHA1	Pyruvate Dehydrogenase E1 Subunit Alpha 1	This gene encodes the E1 alpha 1 subunit containing the E1 active site, and plays a key role in the function of the PDH complex which provides the primary link between glycolysis and the tricarboxylic acid (TCA) cycle.
PDHB	Pyruvate Dehydrogenase E1 Subunit Beta	This gene encodes beta subunit of the E1 enzyme. The protein is a component of the pyruvate dehydrogenase (PDH) complex, which provides the primary link between glycolysis and the tricarboxylic acid (TCA) cycle.
SLC31A1	Solute Carrier Family 31 Member 1	The gene product is a copper transporter located in the cell membrane, with high binding affinity. Overexpression of this gene may result in elevated intracellular accumulation of oxaliplatin in the dorsal root ganglia, which increases the susceptibility of colorectal cancer patients to oxaliplatin-induced peripheral neurotoxicity.

Table S2 The clinical characteristics of the individuals in our transcriptome cohort

Patients	Age	Gender	Vessel embolus	Nerve invasion	Cancerous node	EGFR	pTNM	TNM Stage	CuproScore	Group
1	69	male	(-)	(-)	(-)	(±)	T3N0M0	II	0.692437	Low
2	58	male	(-)	(-)	(-)	(+)	T3N2aM1	IV	2.00655	High
3	68	male	(-)	(-)	(-)	(-)	T3N0M0	II	0.972819	High
4	57	male	(-)	(-)	(-)	(+)	T3N0M0	II	1.493446	High
5	56	female	(-)	(+)	(+)	(+)	T3N0M0	II	-1.45930	Low
6	38	male	(-)	(-)	(-)	(+)	T3N0M0	II	0.921751	Low
7	56	male	(-)	(-)	(-)	(+)	T3N0M0	II	-11.7853	Low
8	50	male	(-)	(-)	(-)	(+)	T3N0M0	II	0.490920	Low
9	66	male	(-)	(-)	(-)	(+)	T3N0M0	II	2.078367	High
10	56	male	(-)	(-)	(-)	(+)	T3N1M0	III	1.654392	High
11	47	female	(+)	(-)	(-)	(+)	T2N2bM0	III	0.109704	Low
12	72	female	(-)	(-)	(-)	(±)	T3N1M0	III	2.824237	High
13	70	female	(+)	(+)	(-)	(+)	T3N1M0	III	-2.24821	Low
14	67	male	(-)	(-)	(-)	(+)	T2N2M0	III	-0.26896	Low
15	71	male	(+)	(-)	(+)	(+)	T4N2aM1	IV	4.256269	High

Table S3 Real-time PCR primer sequences of 16 CPRMs

Name	Description	Primer Sequences (5' to 3')
ATP7B(F)	Forward Primer	GGCCGTCATCACTTATCAGCC
ATP7B(R)	Reverse Primer	GGGAGCCACTTTGCTCTTGA
SLC31A1(F)	Forward Primer	GGGGATGAGCTATATGGACTCC
SLC31A1(R)	Reverse Primer	TCACCAAACCGGAAAACAGTAG
DLST(F)	Forward Primer	GAACTGCCCTCTAGGGAGAC
DLST(R)	Reverse Primer	AACCTTCCTGCTGTTAGGGTA
GCSH(F)	Forward Primer	GGAAGCGTTGGGAGATGTTGT
GCSH(R)	Reverse Primer	TCTGAAGGGTTACTCAGTGTCA
DBT(F)	Forward Primer	CAGTTCGCCGTCTGGCAAT
DBT(R)	Reverse Primer	CCTGTGAATACCGGAGGTTTTG
ATP7A(F)	Forward Primer	TGACCCTAAACTACAGACTCCAA
ATP7A(R)	Reverse Primer	CGCCGTAACAGTCAGAAACAA
FDX1(F)	Forward Primer	GCCTCTTTGGAGTCTCTCGC
FDX1(R)	Reverse Primer	CCCAACCGTGATCTGTCTGT
LIAS(F)	Forward Primer	CAGCCCAGTCAGACCGTTAAG
LIAS(R)	Reverse Primer	TTTCTGGCGTTTTAGGTTTCCT
LIPT1(F)	Forward Primer	CCTCTGTTGTAATTGGTAGGCAT
LIPT1(R)	Reverse Primer	CTGGGGTTGGACAGCATTACAG
DLD(F)	Forward Primer	CTCATGGCCTACAGGGACTTT
DLD(R)	Reverse Primer	GCATGTTCCACCAAGTGTTCAT
DLAT(F)	Forward Primer	CGGAACTCCACGAGTGACC
DLAT(R)	Reverse Primer	CCCCGCCATACCCTGTAGT
PDHA1(F)	Forward Primer	TGGTAGCATCCCGTAATTTTGC
PDHA1(R)	Reverse Primer	ATTCGGCGTACAGTCTGCATC
PDHB(F)	Forward Primer	AAGAGGCGCTTTCCTACTGGAC
PDHB(R)	Reverse Primer	ACTAACCTTGTATGCCCCATCA
MTF1(F)	Forward Primer	CACAGTCCAGACAACAACATCA
MTF1(R)	Reverse Primer	GCACCAGTCCGTTTTTATCCAC
GLS(F)	Forward Primer	TCTACAGGATTGCGAACGTCT
GLS(R)	Reverse Primer	CTTTGTCTAGCATGACACCATCT
CDKN2A(F)	Forward Primer	GATCCAGGTGGGTAGAAGGTC
CDKN2A(R)	Reverse Primer	CCCCTGCAAACCTTCGTCCT