

Supplement table 1. Differentially expressed of 19 cuproptosis-related genes between esophageal cancer and healthy control tissues

Gene	ConMean	TreatMean	LogFC	P value	FDR
NFE2L2	5.461	5.701	0.062	0.059	0.059
NLRP3	0.624	0.464	-0.429	1.38×10^{-7}	1.74×10^{-7}
ATP7B	1.021	1.854	0.861	6.94×10^{-6}	8.24×10^{-6}
ATP7A	1.418	2.342	0.724	3.17×10^{-43}	1.21×10^{-42}
SLC31A1	2.214	4.217	0.930	5.09×10^{-49}	7.27×10^{-48}
FDX1	2.234	3.427	0.617	1.00×10^{-44}	4.76×10^{-44}
LIAS	2.361	2.073	-0.188	1.38×10^{-11}	2.01×10^{-11}
LIPT1	2.002	1.698	-0.238	8.56×10^{-14}	1.35×10^{-13}
LIPT2	0.862	1.884	1.127	1.58×10^{-32}	4.29×10^{-32}
DLD	4.785	4.412	-0.117	1.50×10^{-8}	2.04×10^{-8}
DLAT	3.103	3.857	0.314	2.31×10^{-26}	4.39×10^{-26}
PDHA1	6.011	4.422	-0.443	1.80×10^{-47}	1.14×10^{-46}
PDHB	4.969	3.236	-0.619	7.66×10^{-49}	7.27×10^{-48}
MTF1	1.777	2.619	0.560	1.84×10^{-30}	4.37×10^{-30}
GLS	3.860	4.119	0.094	0.012	0.014
CDKN2A	1.546	2.481	0.6824	0.013	0.014
DBT	1.748	2.235	0.354	1.27×10^{-16}	2.20×10^{-16}
GCSH	3.283	2.407	-0.448	1.31×10^{-32}	4.14×10^{-32}
DLST	5.143	4.647	-0.146	5.30×10^{-28}	1.12×10^{-27}

ConMean, the average expression value of the control group; TreatMean, the mean expression value of esophageal cancer group; FDR, false discovery rate; FC, fold change.