

ids	Log2(fold change)
DM_Proline	-4.284582819 proline metabolism
Proline_DM_COOP	-4.284582819 proline metabolism
SOD2	-4.268787475 Folate metabolism
Folate_DM_COOP	-2.545283038 Folate metabolism
DM_Folate	-2.545283038 Folate metabolism
CA12_CA2_CA9_CA14_CA1_CA3_CA4_CA7_CA13	-2.369776277 nitrogen metabolism
Aspartate_DM_COOP	-2.05460882 aspartate metabolism
DM_Aspartate	-2.05460882 aspartate metabolism
carnitineAcylTransferasel	-1.670562162 lipids metabolism
ENO1_ENO3_ENO2	-1.505199688 glycolytic pathway
MTHFD1_3	-1.25347137 folate metabolic pathway
Palmitate_DM_COOP	-1.167201395 palmitate metabolism
DM_Palmitate	-1.167201395 palmitate metabolism
SQLF	-1.143418033
GCL	-1.129948759
mGSRnadph	-1.099258939
mGSRnadh	-1.099258939
DM_Urea	-1.061293465
palmitateActivation	-0.9670331
HMGCR	-0.917450812
TranspCystineSer	-0.912675278
ACO1_IREB2	-0.880865788
ACO2_ACO1_1	-0.880865788
betaOxidation	-0.878995563
Urea_DM_COOP	-0.83646439
Palmitate_UP_COOP	-0.778284167
ALDH4A1_2	-0.777546472
ALDH4A1_1	-0.777546472
FDFT1_2	-0.687774654
FDFT1_1	-0.687774654
TKTL1_TKTL2_TKT_2	-0.678250385
TKTL1_TKTL2_TKT_1	-0.678250385
Complex1ROS	-0.605831865
OAT	-0.590359872
carnitineAcylTransferasel1	-0.589582149
ID1_IDI2	-0.578715919
AKG_DM_COOP	-0.569817648
HMGCS1_HMGCS2	-0.554812071
DLSTP1_DLD_OGDH_PDHX_DLST_DHTKD1_OGDHL	-0.554765462
DHCR24_LEFTY1	-0.553829688
LSS	-0.524680714
GCK_HKDC1_HK1_ADPGK_HK2_HK3	-0.507108916
GPI	-0.483360682
GS	-0.475363661
MPC1_MPC2_MPC1L	-0.219084955
LDH	-0.182734938
DM_Glucose	0.074627175
Glucose_DM_COOP	0.074627175
DM_AKG	0.213720885
LHPP_PPA2_PRUNE_EIF4A2_NAV2_PPA1_1	0.42297536
TYMS	0.424278355
PRPS2_PRPS1_PRPS1L1	0.47260837
PYCR1_PYCR2_PYCR1_LEFTY1_2	0.479447542
PYCR1_PYCR2_PYCR1_LEFTY1_1	0.479447542
MDH2	0.492942548
Lactatel_DM_COOP	0.494256927
DM_Lactatel	0.494256927
ACLY	0.495021758
GART_1	0.514908059
GART_2	0.514908059
OGDH_GART_OGDHL	0.514908059
GLS	0.549620339
GLS2	0.549620339
ACACB_PRKAG2_PRKAB2_ACACA_PRAAA2	0.558136215
ME2_ME3_1	0.562417156
Asparagine_DM_COOP	0.585687666
DM_Aspargine	0.585687666
RPE_LOC729020	0.592214156
TranspCystineGlu	0.600260089
SLC25A5_SLC25A4_SLC25A6	0.621127462
ALDH3B1_ALDH3A1_ALDH3B2_ALDH1A3	0.621127462
Glutamine_DM_COOP	0.629720883
DM_Glutamine	0.629720883
TNRC6B_ADSL_1	0.635729181
TNRC6B_ADSL_2	0.635729181
SHMT1_2	0.647763394
TransportFolate	0.669747064
G6PPer	0.681511534
ATIC_1	0.716214326
ATIC_2	0.716214326
IDH3	0.751429959
CAD_3	0.758558062
CAD_1	0.758558062
CAD_2	0.758558062
ARID4B_GGPS1_FDPS_FDPSP7_1	0.767508061
ARID4B_GGPS1_FDPS_FDPSP7_2	0.767508061
Alanine_DM_COOP	0.775208763
DM_Alanine	0.775208763
Serine_DM_COOP	0.900339379
DM_Serine	0.900339379
RPIA_LOC101060545	0.911031623
Glycine_DM_COOP	0.915279126
DM_Glycine	0.915279126
ATPsynthase	0.929361346
AK	1.020522549
PFAS	1.027643105
CASB_CASA	1.150245473
IMPDH2	1.161815824
CMPI1_DTYMK	1.188041537
DHFR1_DHFR_4	1.290720546
DHFR1_DHFR_5	1.290720546
DHFR1_DHFR_6	1.290720546
DHFR1_DHFR_2	1.290720546
Ex_SC_H2O	1.324704252
MTHFD1_AL445665_1_AQP7P4_LOC286297_2	1.46153521
AK2_TAF9_AK1_AK7_AK3_AK5_AKD1_AK4_AK8_1	1.579405647
Arginine_DM_COOP	1.604353361
DM_Arginines	1.604353361
OGDH_ODC1_OGDHL	1.633632399
MTHFD1_2	1.661709798
MTHFD2_2	1.661709798 mitochondrial one-carbon metabolism (Fig. 1d), a metabolic system recently implicated in rapid cancer cell proliferation
MTHFD2_4	1.661709798 mitochondrial one-carbon metabolism (Fig. 1d), a metabolic system recently implicated in rapid cancer cell proliferation
ALDOC_ALDOB_ALDOA_2	1.705661546
ALDOC_ALDOB_ALDOA_1	1.705661546
VPS29_PSPH_PSPHP1	2.031170948 One carbon pool by folate
CTPS2_GATM_CTPS1	2.040658166 Pyrimidine metabolism
ASNS	2.544354243 asparagine metabolism, adaptation to nutrient deprivation and/or hypoxia.
PEPCK	2.853019955 metabolic pathway of gluconeogenesis
AGAT	2.879052713 galactose metabolism
PHGDH_UBAC2	4.191346901 Glycine, serine and threonine metabolism
PSAT1	4.226572589 Serine pathway has a key role in cancer metabolism, using glycolysis-derived glucose for serine production and tumor growth. unrestrained cell cycle progression