

(a)

Gene/node	Degree	Chr	Gene info
MRPL24	7	1	mitochondrial ribosomal protein L24
UQCRCFS1	3	19	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1
MRPL15	3	8	mitochondrial ribosomal protein L15
DNAJA3	2	16	DnaJ (Hsp40) homolog, subfamily A, member 3
DLD	1	7	dihydrolipoamide dehydrogenase
ETFA	1	15	electron-transfer-flavoprotein, alpha polypeptide
ISCA1	1	9	iron-sulfur cluster assembly 1 homolog (<i>S. cerevisiae</i>)
MRPL44	1	2	mitochondrial ribosomal protein L44
MRPS23	1	17	mitochondrial ribosomal protein S23
MRPS5	1	2	mitochondrial ribosomal protein S5
VDAC3	1	8	voltage-dependent anion channel 3
MRPS35	1	12	mitochondrial ribosomal protein S35
ST6GALNAC6	1	9	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 6

(b)

Gene set	OR (95% C.I.)	q-val
MIPS_55S_RIBOSOME_MITOCHONDRIAL	190 (51-690)	1.8e-07
MOOTHA_HUMAN_MITODB_6_2002	53 (15-210)	2.6e-06
MOOTHA_MITOCHONDRIA	51 (15-200)	2.6e-06
MIPS_28S_RIBOSOMAL_SUBUNIT_MITOCHONDRIAL	150 (24-670)	0.0064
MITOCHONDRIAL_PART	50 (11-180)	0.0065
MITOCHONDRION	29 (7.3-100)	0.0065
MIPS_39S_RIBOSOMAL_SUBUNIT_MITOCHONDRIAL	120 (20-530)	0.0065
MITOCHONDRIAL_MATRIX	98 (16-410)	0.0091
MITOCHONDRIAL_LUMEN	98 (16-410)	0.0091
STEIN_ESRRA_TARGETS_UP	24 (6.1-83)	0.011
CHIANG_LIVER_CANCER_SUBCLASS_UNANNOTATED_DN	34 (7.5-120)	0.015
MOOTHA_PGC	21 (5.2-72)	0.018
STEIN_ESRRA_TARGETS	17 (4.2-58)	0.043

(a) Gene/node details, and (b) significantly enriched gene sets, for the mitochondrial module found as significant in the LUAD data set. Q -values in (b) indicate significance of enrichment in the corresponding gene set by the genes in this module, calculated according to a one-sided Fisher's exact test. Further details about these gene sets can be found from the website of the Broad Institute Molecular Signatures Database (<http://www.broadinstitute.org>).