

# **The effects of artificially dosed adult rumen contents on abomasum transcriptome and associated microbial community structure in calves**

**Naren Gaowa<sup>1</sup>, Wenli Li<sup>2\*</sup>, Brianna Murphy<sup>2</sup>, Madison Cox<sup>3</sup>**

1 State Key Laboratory of Animal Nutrition, Beijing Engineering Technology, Research Center of Raw Milk Quality and Safety Control, College of Animal Science and Technology, China Agricultural University, No.2 Yuanmingyuan West Road, Haidian, Beijing 100193, China.

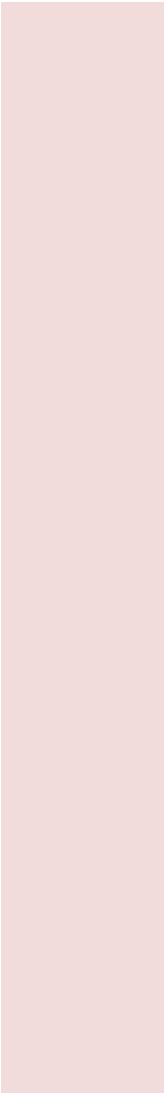
2 The Cell Wall Utilization and Biology Laboratory, USDA Agricultural Research Service, US Dairy Forage Research Center, Madison, WI 53706, USA

3 Department of Microbiology, University of Wisconsin-Madison, Madison, WI, 53706, USA

\*Correspondence: [wenli.li@ars.usda.gov](mailto:wenli.li@ars.usda.gov)

**Supplementary Table 2.** GO term annotation for the URGs and DRGs

| Category   | Term                                 | Count | %     | FDR    | Genes  |
|------------|--------------------------------------|-------|-------|--------|--|
| GOTERM_BP. | GO:0002376~immune system process     | 26    | 7.69  | 0.0000 | TRPM4, IFIH1, FFAR3, LY86, HERC6, PML, TLR2, RSAD2, NLRX1, TRIM25, PADI4, OAS2, SRC, LGALS9, ISG20, DDX58, IFIT3, KCNN4, IRF5, PYCARD, MST1R, MX1, DHX58, ZBP1, ADAR, SYK  |
| GOTERM_BP. | GO:0045087~innate immune response    | 24    | 7.10  | 0.0004 | IFIH1, ELF4, LY86, HERC6, TLR2, TRIM14, PML, RSAD2, NLRX1, TRIM25, PADI4, OAS2, SRC, ISG20, IFIT3, DDX58, IRF5, PYCARD, MST1R, MX1, DHX58, SYK, ADAR, ZBP1   |
| GOTERM_BP. | GO:0051607~defense response to virus | 15    | 4.44  | 0.0012 | IFIH1, PML, RSAD2, TRIM25, OAS2, ISG20, IFIT3, DDX58, IRF5, ISG15, PYCARD, MX1, DHX58, ADAR, ZBP1  |
| GOTERM_BP. | GO:0009615~response to virus         | 11    | 3.25  | 0.0020 | IFIT3, DDX58, IFIH1, RSAD2, MST1R, OAS2, MX1, SRC, DHX58, ISG20, ADAR  |
| GOTERM_CC. | GO:0016020~membrane                  | 167   | 49.41 | 0.0000 | CASR, ADCY1, TSPAN3, REP15, LYPD8, NELL2, TLR2, AQP5, SCTR, DAB1, UNC5B, CREB3L1, GNG3, MCOLN2, MX1, HTR1E, SYK, CLCA2, NCF2, VANGL1, GATM, EFNB1, CDHR2, SLC22A23, UNC5CL, SPIRE2, CHPT1, SGSM1, F5, LPAR5, HRASLS, CCR3, SLC37A1, PARP14, RIPK3, MST1R, IGSF9, FBXL2, SLC38A5, SLC38A4, SLC2A10, RTP4, LITAF, STK10, ITGB4, OAS2, EPHB1, SRC, TMEM63B, ACE, LGALS3BP, B3GNT7, CNR2, AGRN, TMEM79, BLNK, SLC28A3, ST6GAL1, PTPN3, KCNB2, SLC6A11, ACER2, ATP11A, EVL, ITGA3, DOCK8, ADGRG7, GUCY2C, HOMER2, ATP13A5, DDX58, GGT7, P2RX1, PARP9, ATP2A3, FREM2, SLC35G2, SYT13, SYTL2, MYH14, GRK5, MERTK, ABO, PDZD3, SYT17, SLC9A1, ADAR, SORL1, LRRC19, CDCP1, ANPEP, PMVK, MCF2L, CANT1, TMEM54, MCTP2, PXMP4, NPC1L1, SYNJ2, HHIP, RAMP1, IHH, TRPM4, GAPT, MPP1, RPH3AL, ARHGAP27, HEPACAM2, NECTIN4, ARRDC4, MMP15, SLC3A1, LPIN2, LDLRAD3, RAB11FIP4, MAST1, CHRM5, SEMA4G, DGAT2, CD82, SEMA4B, CARD19, GPA33, ERN2, EQTN, SEZ6, KCNH3, DEGS2, SORD, FFAR3, GPR63, PML, NLRX1, RSAD2, ABHD2, ABHD1, SLC19A1, GPRC5B, AMPH, PCSK2, DAPP1, DISP1, CD177, HS6ST1, DFNA5, |



CNNM4, GPR119, BAIAP2L2, SLC12A3,  
DHRS13, SWAP70, TMC5, DLGAP4, ASIC2,  
ITPR3, GJB1, RGS14, TMPRSS4, KCNN4,  
FCGR2B, TMEM163, SLC6A6, ABCC3, CHN2,  
SMPD3, GFRA2, ABCC6

|            |   |     |       |        |   |
|------------|---|-----|-------|--------|---|
| GOTERM_CC. | GO:0005737~cytoplasm                                | 145 | 42.90 | 0.0032 | CASR, ADCY1, NELL2, DQX1, TLR2, CALB1, ISG20, RCBTB1, WNT4, WDR73, ISG15, MX1, NQO1, PITX1, TWIST2, SYK, MDH1B, NCF2, DTX3L, EFNB1, PCTP, UNC5CL, MLXIPL, IFI44, PKIB, FBP2, SPIRE2, FRY, TNNT2, SGSM1, HNF4A, RASGRF1, TXNDC8, HRASLS, PARP14, RIPK3, IFIH1, SLC2A10, RTP4, LITAF, TDRD7, STK10, ITGB4, OAS2, EPHB1, SRC, ADAP1, RASAL1, MOV10, ACE, MEIS2, AGRN, DHX58, TMEM79, BLNK, AGBL3, BHMT2, PTPN3, SLC6A11, ARID3A, EVL, AK5, MISP, HOMER2, LGALS9, AK8, DDX58, POC1A, PARP9, SALL1, SYTL2, MYH14, GRK5, MERTK, PDZD3, SLC9A1, ADAR, MYO7B, PAX6, LRRC19, SULT2B1, IFI44L, ANPEP, PMVK, MCF2L, AFMID, PAK6, ACOT7, MCTP2, CERKL, TRIM6, SYNJ2, HHIP, FAM83H, FAM83G, FANCA, CABLES1, SH3PXD2B, CCDC88C, CAPSL, HERC6, RPH3AL, ARHGAP27, FBLIM1, HEPACAM2, PADI4, LPIN2, DAPK2, CTNNBIP1, MAST1, EYA2, TTLL10, EVPL, ADM, ZMIZ1, RIN2, HIPK4, TXNRD1, EQTN, SEZ6, PML, AMPH, ZFP36L1, ALDH1A1, DAPP1, MYOM3, PYCARD, XAF1, ZBP1, DFNA5, CAPN5, SWAP70, TRIM25, ITPR3, GJB1, RGS14, IFIT3, RPS6KA4, IRF5, FCGR2B, TDP1, CFAP206, NEUROD1, CHN2, SMPD3 |
| GOTERM_MF. | GO:0008137~NADH dehydrogenase (ubiquinone) activity | 19  | 2.95  | 0.0000 | NDUFA4, NDUFA5, ND1, NDUFA2, NDUFA8, ND4, NDUFB8, NDUFB9, ND3, NDUFC2, NDUFA13, NDUFA10, NDUFA12, NDUFS7, NDUFV2, NDUFS8, NDUFS3, NDUFS2, NDUFS1  |
| GOTERM_MF. | GO:0004129~cytochrome-c oxidase activity            | 14  | 2.18  | 0.0000 | NDUFA4, COX7A2, COX3, COX8B, COX2, COX1, COX7B, COX6B1, COX7C, COX4I1, COX6A1, COX7A2L, COX5A, COX5B  |
| GOTERM_MF. | GO:0016491~oxidoreductase activity                  | 54  | 8.40  | 0.0000 | ACOX2, LDHB, CYB5R1, PRDX5, PRDX2, PRDX3, UQCRCF51, PDHB, HIBADH, NDUFS7, HMOX1, NDUFS8, LOXL4, SMOX, PDHA1, HADH, NDUFS3, ATP8, NDUFS2, IMPDH2, NDUFS1, SUOX, ND1, ND4, AIFM1, ND3, GMPR, COQ6, PYCR2, NNT, DLD, MDH2, MDH1, CYP2U1, HSD17B10, ME3, ACADSB, HSD17B12, EGLN3, CYTB, AASS, MMACHC,   |

IDH2, SOD1, IDH3A, SOD2, SDHA, COX2,  
UOX, COX1, TDH, NDUFV2, RDH14, BCO2

|            |  |    |      |        |   |
|------------|--|----|------|--------|---|
| GOTERM_MF. | GO:0003954~NADH dehydrogenase activity                                     | 10 | 1.56 | 0.0000 | NDUFS7, ND1, NDUFA9, NDUFB8, NDUFS8, NDUFV2, NDUFA13, NDUFS3, NDUFS2, NDUFS1  |
| GOTERM_MF. | GO:0046933~proton-transporting ATP synthase activity, rotational mechanism | 10 | 1.56 | 0.0000 | ATP5E, ATP5B, ATP5F1, ATP5C1, ATP5L, ATP5O, ATP5A1, ATP5G1, ATP5H, ATP5G3   |
| GOTERM_MF. | GO:0008121~ubiquinol-cytochrome-c reductase activity                       | 7  | 1.09 | 0.0000 | UQCRC10, UQCRC11, UQCRC12, CYTB, UQCRCF1, UQCRCQ, UQCRCB  |
| GOTERM_MF. | GO:0003824~catalytic activity  | 39 | 6.07 | 0.0002 | UQCRC2, ETNPPL, ARSB, SLC27A1, LDHB, BCAT2, UQCRC1, HINT1, HINT2, ENPP4, ARSJ, PGAM1, AASS, ACAT1, PDHB, CKB, FAHD1, GOT2, TPI1, GOT1, OPLAH, SYN3, HDC, CKMT2, PIGC, IMPDH2, ECI2, LYZ2, LYZ1, SUCLG1, ACACB, GMPR, GLUL, CTH, PPM1K, TDH, OAT, MDH2, MDH1 |
| GOTERM_MF. | GO:0009055~electron carrier activity                                       | 12 | 1.87 | 0.0009 | ACOX2, SDHA, ACADSB, UQCRC11, COX7A2, COX1, CYC1, CYCS, CYTB, COX7A2L, NDUFA12, NDUFS1  |
| GOTERM_MF. | GO:0051287~NAD binding   | 12 | 1.87 | 0.0013 | LDHB, HSD17B10, ME3, NNT, DLD, IDH2, IDH3B, AHCYL2, NDUFS2, IDH3A, HIBADH, MDH1   |
| GOTERM_MF. | GO:0015078~hydrogen ion transmembrane transporter activity                 | 9  | 1.40 | 0.0070 | ATP5F1, ATP5L, ATP5G1, ATP5H, ATP5G3, ATP8, ATP6V0B, ATP6, ATP5J  |
| GOTERM_MF. | GO:0016651~oxidoreductase activity, acting on NAD(P)H                      | 6  | 0.93 | 0.0291 | NDUFA5, AIFM1, NDUFS8, NDUFS3, NDUFS2, NDUFS1   |

|            |  |     |       |        |   |
|------------|--|-----|-------|--------|---|
| GOTERM_BP. | GO:0055114~oxidation-reduction process | 86  | 13.37 | 0.0000 | UQCRC2, MRPS36, ACOX2, LDHB, CYB5R1, UQCRC1, CYC1, NDUFAB1, PRDX5, PRDX2, PRDX3, UQCRFS1, UQCRQ, HIBADH, PDHB, NDUFS7, NDUFS6, UQCR10, UQCR11, HMOX1, NDUFS8, SMOX, LOXL4, PDHA1, NDUFS3, HADH, NDUFS2, IMPDH2, NDUFS1, ND1, SUOX, NDUFB11, NDUFB10, ND4, AIFM1, ND3, CYCS, NDUFC2, NDUFC1, GMPR, NDUFA10, NDUFA12, COQ6, PYCR2, NNT, UQCRH, DLD, MDH2, MDH1, UQCRB, NDUFB3, CYP2U1, HSD17B10, NDUFB5, ACADSB, ME3, NDUFB6, TXN2, NDUFB8, NDUFB9, HSD17B12, EGLN3, CYTB, AASS, MMACHC, IDH2, NDUFA4, NDUFA5, NDUFA2, NDUFA3, NDUFA8, NDUFA9, NDUFA6, SOD1, NDUFA1, IDH3A, SOD2, NDUFV3, SDHA, COX2, UOX, COX1, TDH, NDUFV2, BCO2, RDH14   |
| GOTERM_BP. | GO:0006810~transport                   | 136 | 21.15 | 0.0000 | SLC22A16, SLC9A7, GABRB1, SLC7A8, NDUFAB1, AQP4, SLC7A6, GOT2, UQCR10, UQCR11, SLC2A4, SLC25A23, SLC9B2, SLC4A2, NALCN, ATP8, ATP6, KCND2, SLC25A30, SEC61B, CD36, SLC25A35, ATP5C1, RAB12, ATP6V1G3, DYNLRB1, TRAPPC3, SNX9, SCN1B, TXN2, ATP6V0B, OAZ1, TOMM5, MTCH1, APOBR, SLC30A4, SLC35F3, HCN1, HCN2, GABARAPL2, ATP5J2, TOMM40, MPC2, VDAC2, VDAC3, ABCB5, NDUFV3, SLC25A11, COX2, COX1, SLC25A10, TOMM40L, NDUFV2, FABP3, ATP7B, UQCRC2, KCNJ16, SLC27A1, ATP5E, UQCRC1, SLC16A10, LRRC8B, ATP5B, TIMM17A, CYC1, UQCRFS1, UQCRQ, NDUFS7, NDUFS6, SLC1A2, NDUFS8, SLC25A3, ATP5L, SLC22A3, ATP5O, NDUFS3, NDUFS2, ATP5H, NDUFS1, ATP5J, ND1, NDUFB11, NDUFB10, ND4, SLC25A4, ATP4A, SLC25A5, ATP4B, ND3, NDUFC2, GIF, NDUFC1, NDUFA10, ATP6V1D, NDUFA12, SLC26A7, UQCRH, CLIC5, CLIC6, SDCCAG3, SORT1, RANGRF, EIF5A2, UQCRB, MYO5A, NDUFB3, NDUFB5, RAB3C, NDUFB6, NDUFB8, NDUFB9, TIMM10, CYTB, ATP5G1, ATP5G3, SEC14L1, TMED6, KCNE2, SLC39A6, |

NDUFA4, NDUFA5, CPT1B, NDUFA2,  
NDUFA3, NDUFA8, NDUFA9, NDUFA6,  
ATP5F1, NDUFA1, SDHA, PHAX, SMDT1,  
SLC16A7, ATP6V1E1, MCFD2, ATP5A1

|            |  |    |      |        |   |
|------------|--|----|------|--------|---|
| GOTERM_BP. | GO:0015992~proton transport  | 23 | 3.58 | 0.0000 | ATP5E, ATP5J2, ATP4A, ATP4B, ATP5B, ATP5F1, CYTB, ATP5G1, ATP6V1D, ATP5G3, ATP6V0B, NNT, ATP6V1E1, ATP5C1, ATP5L, SLC9B2, ATP5O, ATP5A1, ATP6V1G3, ATP5H, ATP8, ATP5J, ATP6 |
| GOTERM_BP. | GO:0015986~ATP synthesis coupled proton transport                      | 13 | 2.02 | 0.0000 | ATP5E, ATP5B, ATP5F1, ATP5G1, ATP5G3, ATP5C1, ATP5L, ATP5O, ATP5A1, ATP5H, ATP8, ATP5J, ATP6  |
| GOTERM_BP. | GO:0006122~mitochondrial electron transport, ubiquinol to cytochrome c | 10 | 1.56 | 0.0000 | UQCRC2, UQCC3, UQCR10, UQCRC1, UQCRH, CYC1, CYCS, CYTB, UQCRQ, UQCRB  |
| GOTERM_BP. | GO:0006754~ATP biosynthetic process                                    | 12 | 1.87 | 0.0000 | ATP5E, UQCC3, ATP5J2, CHCHD10, ATP5B, GBAS, ATP5C1, ATP5L, ATP5O, ATP5A1, ATP8, ATP6  |
| GOTERM_BP. | GO:0006120~mitochondrial electron transport, NADH to ubiquinone        | 9  | 1.40 | 0.0000 | NDUFS6, ND4, NDUFB8, NDUFB9, DLD, NDUFV2, NDUFC2, COQ9, NDUFA10   |
| GOTERM_BP. | GO:0006099~tricarboxylic acid cycle                                    | 12 | 1.87 | 0.0000 | SDHA, DLST, SUCLG1, CS, IDH2, IDH3B, DLAT, PDHA1, PDHB, MDH2, IDH3A, MDH1   |

|            |   |    |      |        |  |
|------------|---|----|------|--------|--|
| GOTERM_BP. | GO:0046034~ATP metabolic process                                    | 12 | 1.87 | 0.0000 | ATP5J2, ATP5B, AK1, AK3, ATP5C1, ATP5L, ATP5O, ATP5A1, ATP5G1, ATP5H, NDUFS1, ATP5J  |
| GOTERM_BP. | GO:0006811~ion transport  | 46 | 7.15 | 0.0001 | KCNJ16, SLC22A16, ATP5E, SLC9A7, SCN1B, LRRC8B, GABRB1, ATP5B, ATP5G1, ATP5G3, ATP6V0B, SLC30A4, SLC9B2, ATP5L, SLC22A3, KCNE2, ATP5O, SLC4A2, SLC39A6, NALCN, ATP5H, ATP8, ATP6, ATP5J, HCN1, HCN2, ATP5J2, KCND2, ATP4A, ATP4B, ATP5F1, TOMM40, GIF, VDAC2, ATP6V1D, VDAC3, SMDT1, SLC26A7, ATP6V1E1, CLIC5, TOMM40L, CLIC6, ATP5C1, ATP5A1, ATP6V1G3, ATP7B |
| GOTERM_BP. | GO:0006103~2-oxoglutarate metabolic process                         | 8  | 1.24 | 0.0012 | GOT2, MRPS36, DLST, GOT1, DLD, IDH2, IDH3B, IDH3A  |
| GOTERM_BP. | GO:0006123~mitochondrial electron transport, cytochrome c to oxygen | 7  | 1.09 | 0.0013 | COX8B, CYCS, COX7C, COX4I1, COX6A1, COX5A, COX5B   |
| GOTERM_BP. | GO:0022904~respiratory electron transport chain                     | 7  | 1.09 | 0.0317 | SDHA, NDUFA5, NDUFS6, COX3, CYTB, PPARGC1A, SOD2   |
| GOTERM_BP. | GO:1902600~hydrogen ion transmembrane transport                     | 7  | 1.09 | 0.0317 | UQCR10, COX8B, COX7B, ATP5G1, ATP5G3, ATP6V0B, UQCRB   |



|            |                          |     |       |        |  |
|------------|--------------------------|-----|-------|--------|--|
| GOTERM_CC. | GO:0005739~mitochondrion | 217 | 33.75 | 0.0000 | HCCS, LDHB, TMEM143, HIBADH, GOT2, SLC9B2, PDHA1, ATP8, GNG5, TMEM14C, MRPL34, ATP6, MRPL35, APOO, MRPL53, BSG, MRPL51, SUCLG1, GLUL, NNT, CD36, DLD, MRPL49, ATP5C1, ATPIF1, MDH2, MDH1, HSD17B10, ACADSB, TXN2, CHCHD3, CHCHD2, ACAT1, IDH2, PEMT, COX6B1, MRPL55, PHYHIPL, PHB, JTB, MPC2, ACACB, DLAT, VDAC2, AFG3L2, VDAC3, CHCHD10, COX3, COX2, COX1, HEBP2, COX6A1, BCO2, ARSB, SLC27A1, ATP5E, TIMM17A, ATP5B, SLIRP, CKB, ASAH2, GBAS, SLC25A3, ATP5L, ATP5O, ADCY10, ATP5H, COX17, DNAJC19, ATP5J, NDUFB11, NDUFB10, SLC25A4, SLC25A5, AIFM1, NDUFA13, NDUFA10, NDUFA12, PFDN4, BCAT2, AASS, COX7A2L, MRPL11, MMACHC, CKMT2, MRPL16, REXO2, MARS, ECI2, CPT1B, COX7A2, IMMT, CS, SOD1, SOD2, CAPRIN2, SDHA, PRELID2, MRPL21, TFRC, UOX, MRPL27, ATP6V1E1, POLDIP2, BNIP3L, ATP5A1, MRPS36, NDUFAB1, ROMO1, COX5A, COX5B, PDHB, FAHD1, UQCR10, GHITM, UQCR11, CISD3, SLC25A23, TCAIM, HADH, STAP1, TMEM126A, SLC25A30, ISCU, PYCR2, MRPS18B, SLC25A35, ME3, HACD3, COX7B, COX7C, GADD45GIP1, TOMM5, MTCH1, BLOC1S1, HSPE1, ATP5J2, COX8B, AK3, IDH3B, TOMM40, IDH3A, NDUFV3, SLC25A11, USMG5, SLC25A10, TOMM40L, TDH, NDUFV2, MYH10, UQCRC2, ETNPPL, ACOX2, CYB5R1, UQCRC1, SGPP1, HINT2, CYC1, PRDX5, PRDX2, PRDX3, UQCRFS1, UQCRQ, NDUFS7, NDUFS6, NDUFS8, PXMP2, NDUFS3, NDUFS2, NDUFS1, ND1, SUOX, ND4, ND3, NOL7, CYCS, NDUFC2, COX4I1, COQ9, NDUFC1, COQ6, ISCA1, C1QBP, UQCRH, PPM1K, PEBP1, OAT, UQCRB, NDUFB3, NDUFB5, NDUFB6, NDUFB8, NDUFB9, FKBP4, TIMM10, CYTB, ATP5G1, PTPMT1, ATP5G3, SNN, OXCT1, HSPA9, NDUFA4, NDUFA5, DLST, NDUFA2, NDUFA3, NDUFA8, NDUFA9, NDUFA6, ATP5F1, NDUFA1, UQCC3, DBT, SMDT1, BOLA1, |
|------------|--------------------------|-----|-------|--------|--|



|            |  |     |       |        |   |
|------------|--|-----|-------|--------|---|
| GOTERM_CC. | GO:0005743~mitochondrial inner membrane              | 108 | 16.80 | 0.0000 | <p>HCCS, ROMO1, COX5A, COX5B, GOT2, FAHD1, UQCR10, UQCR11, GHITM, SLC25A23, HADH, TMEM14C, ATP6, APOO, SUCLG1, TMEM126A, SLC25A30, NNT, SLC25A35, ATP5C1, MDH2, HSD17B10, COX7B, COX7C, CHCHD3, ACAT1, MTCH1, COX6B1, IDH2, ATP5J2, LGALS3, COX8B, PHB, MPC2, AFG3L2, VDAC2, VDAC3, NDUFV3, SLC25A11, USMG5, COX3, COX2, COX1, SLC25A10, NDUFV2, COX6A1, UQCRC2, ATP5E, SLC27A1, UQCRC1, ATP5B, TIMM17A, CYC1, UQCRFS1, UQCRQ, NDUFS7, NDUFS6, SLC25A3, ATP5L, ATP5O, NDUFS3, ATP5H, NDUFS2, DNAJC19, NDUFS1, ATP5J, ND1, NDUFB11, NDUFB10, SLC25A4, AIFM1, SLC25A5, NDUFC2, COX4I1, NDUFA13, COQ9, NDUFC1, NDUFA12, COQ6, UQCRH, UQCRB, NDUFB3, NDUFB5, NDUFB6, NDUFB8, NDUFB9, TIMM10, CYTB, ATP5G1, COX7A2L, PTPMT1, CKMT2, NDUFA4, NDUFA5, NDUFA2, NDUFA3, COX7A2, NDUFA8, NDUFA9, IMMT, NDUFA6, ATP5F1, NDUFA1, SOD2, SDHA, UQCC3, SMDT1, ATP5A1</p> |
| GOTERM_CC. | GO:0070469~respiratory chain                         | 44  | 6.84  | 0.0000 | <p>UQCRC2, NDUFB3, NDUFB5, NDUFB6, UQCRC1, NDUFB8, NDUFB9, CYC1, NDUFAB1, CYTB, UQCRFS1, UQCRQ, NDUFS7, NDUFS6, UQCR10, UQCR11, NDUFS8, NDUFS3, NDUFS2, NDUFS1, NDUFA4, ND1, NDUFA5, NDUFA2, NDUFB11, NDUFA3, NDUFB10, ND4, NDUFA8, NDUFA9, NDUFA6, ND3, CYCS, NDUFC2, NDUFC1, NDUFA10, NDUFA1, NDUFA12, NDUFV3, COX2, UQCRH, COX1, NDUFV2, UQCRB</p>   |
| GOTERM_CC. | GO:0005747~mitochondrial respiratory chain complex I | 32  | 4.98  | 0.0000 | <p>NDUFB3, NDUFB5, NDUFB6, NDUFB8, NDUFB9, NDUFAB1, NDUFS7, NDUFS6, NDUFS8, NDUFS3, NDUFS2, NDUFS1, NDUFA4, NDUFA5, ND1, NDUFB11, NDUFA2, NDUFA3, NDUFB10, NDUFA8, ND4, NDUFA9, NDUFA6, ND3, NDUFC2, NDUFA13, NDUFC1, NDUFA10, NDUFA1,</p>  |

NDUFA12, NDUFV3, NDUFV2

|            |   |     |       |        |  |
|------------|---|-----|-------|--------|--|
| GOTERM_CC. | GO:0043209~myelin sheath  | 46  | 7.15  | 0.0000 | UQCRC2, LDHB, UQCRC1, ATP5B, PGAM1, RDX, PRDX2, CCT2, PRDX3, COX5A, UQCRCFS1, COX5B, CKB, GOT2, SLC25A3, ATP5O, MSN, PDHA1, PLCB1, NDUFS3, ATP5H, NDUFS1, HSPA9, DLST, SLC25A4, IMMT, SLC25A5, PHB, CYCS, ATP5F1, DLAT, NDUFA10, VDAC2, SOD1, IDH3A, SOD2, SDHA, GLUL, DLD, NDUFV2, ATP5C1, COX6A1, PEBP1, ATP5A1, MDH2, MDH1  |
| GOTERM_CC. | GO:0005753~mitochondrial proton-transporting ATP synthase complex | 15  | 2.33  | 0.0000 | ATP5E, ATP5J2, ATP5B, ATP5F1, ATP5G1, USMG5, ATP5C1, ATP5L, ATP5O, ATP5F1, ATP5A1, ATP5H, ATP8, ATP5J, ATP6  |
| GOTERM_CC. | GO:0016020~membrane   | 323 | 50.23 | 0.0000 | HCCS, LDHB, SLC9A7, CADM4, SGMS2, PGAM1, AQP4, TMEM143, SIDT2, KLHDC7A, GOT2, HTR1B, TMEM145, DIRAS2, GAB2, ILK, VMA21, SLC9B2, MUC15, ATP8, GNG5, TMEM14C, CDH24, ATP6, APOO, C5AR2, BSG, MDGA1, HTR4, LIFR, PLAUR, RND2, CD36, NNT, UNC13D, CCR5, SSTR1, ATP5C1, RAB12, ATP6V1G3, MDH2, SUCO, SCN1B, HSD17B12, ENPP4, CHCHD3, TMCC3, ATP6V0B, CDC42EP1, DMD, PEMT, PABPC1, GCNT1, LAMTOR1, LGALS3, LAMTOR2, PHB, PMEL, JTB, MPC2, ACACB, VDAC2, AFG3L2, VDAC3, KDR, EPHA5, CLGN, EPHA6, COX3, COX2, COX1, COX6A1, GRK1, NXPE2, KCNJ16, SLC27A1, ATP5E, SLC16A10, TIMM17A, ATP5B, TMEM161B, RTN1, INSRR, ASAH2, VEPH1, POMGNT1, MAP1LC3A, SLMAP, SERPINA5, SLC25A3, SLC22A3, ATP5L, ATP5O, ADCY10, ATP5H, DPEP1, USH2A, ATP5J, ZDHHC2, NDUFB11, NDUFB10, GPR176, PIK3C2G, SLC25A4, ATP4A, AIFM1, SLC25A5, ATP4B, NDUFA12, ZDHHC14, IL20RA, SLC26A7, CLIC5, CLIC6, PTGDR, SORT1, VOPP1, STBD1, EIF5A2, MYO5A, RAB3C, RPL36, COX7A2L, KIT, FNDC4, PCNX2, CKMT2, KCNE2, C1GALT1, |

DTNA, MARS, ECI2, CPT1B, A4GALT, COX7A2, IMMT, NPR3, APPL1, FZD7, SDHA, TFRC, SLC16A7, CDH16, CDH18, BNIP3L, MBOAT1, MYCBPAP, MBOAT2, MBOAT4, ATP5A1, PXYLP1, PGK1, PHLDB2, SLC22A16, GABRB1, SLC7A8, ROMO1, COX5A, SLC7A6, ST3GAL1, UQCR10, DYSF, UQCR11, GHITM, SLC2A4, TIAM2, ST3GAL4, ANK3, SLC25A23, ELOVL3, ST3GAL6, SLC4A2, PDGFD, NALCN, PRKACB, RNF149, RNF34, MATK, CUTA, TMEM203, KCND2, SMIM13, TMEM126A, SLC25A30, ABHD17B, SEC61B, SLC25A35, DYNLRB1, FILIP1L, SNX9, GAL3ST3, ARHGDIG, HACD3, COX7B, NKAIN2, COX7C, PAQR3, IKBIP, GPR22, TOMM5, APOBR, BLOC1S1, MTCH1, TMEM30C, SLC30A4, SLC35F3, HSPE1, SDF2, HCN1, HCN2, ATP5J2, CCPG1, COX8B, TMEM92, TOMM40, SNAPIN, WIPI1, ABCB5, NDUFV3, SLC25A11, USMG5, ATF4, CRBN, GPR34, PPIB, SLC25A10, PLCG2, TOMM40L, NDUFV2, SPCS1, KCTD16, ATP7B, UQCRC2, CYB5R1, UQCRC1, SGPP1, LRRC8B, PRKAG1, CYC1, UQCRFS1, UQCRCQ, NDUFS6, PRMT1, SLC1A2, PLEKHB1, TMEM171, HMOX1, NDUFS8, PXMP2, PIGC, LOXL4, MSN, PLCB1, NDUFS3, NDUFS2, IMPDH2, NDUFS1, ND1, BTNL9, PTGER3, ND4, ND3, TMEM255B, NDUFC2, COX4I1, NDUFC1, KRTCAP2, ATP6V1D, LDLRAD4, COQ6, LYPD6B, LARP4, C1QBP, UQCRH, CHST9, EMC6, NKIRAS1, UQCRB, FKBP2, NDUFB3, CYP2U1, NDUFB5, NDUFB6, FKBP5, NDUFB8, NDUFB9, TIMM10, CYTB, TMEM35B, RDX, PTPMT1, ATP5G1, ATP5G3, TMEM258, TMED6, RGMA, SNN, COL17A1, RASGRP1, SYN3, RASGRP2, MYZAP, RNF128, PALM3, SLC39A6, TMEM45A, NDUFA4, DLST, NDUFA5, NDUFA2, NDUFA3, NDUFA8, FLT3, NDUFA6, ATP5F1, IGSF9B, NDUFA1, TMEM55A, UQCC3, TMEM47, SMDT1, BMPR1B, RDH14

|            |   |     |       |        |  |
|------------|---|-----|-------|--------|--|
| GOTERM_CC. | GO:0070062~extracellular exosome  | 152 | 23.64 | 0.0000 | SRP14, GNA14, LDHB, CADM4, FAM20A, RUSC2, FAM20C, PGAM1, SLC7A8, CCT2, COX5A, SIDT2, PDHB, ST3GAL1, GOT2, UQCR10, DYSF, GHITM, GOT1, SLC2A4, TIAM2, ST3GAL4, ST3GAL6, ROBO4, IGLL1, RNF149, PDGFD, PRKACB, GNG5, ATP6, CUTA, BSG, PDXK, TNIK, SUCLG1, LIFR, PDXP, PLAUR, GLUL, ATP5C1, MDH2, MDH1, SNX9, BPIFB1, ACADSB, ENPP4, CHCHD3, PIN4, ACAT1, TPI1, PSMB6, FGA, BLOC1S1, CACYBP, IDH2, ENTPD6, EIF3I, HSPE1, PABPC1, GPR155, ATP5J2, ACY1, LAMTOR1, LGALS3, LAMTOR2, AK1, PHB, TOMM40, PTPN13, VDAC2, SERPINI1, VDAC3, EMILIN1, USMG5, DNAJB9, PPIB, COX2, HEBP2, PLCG2, FABP3, MYH10, UQCRC2, ARSB, CYB5R1, OPCML, PRKAG1, HINT1, ATP5B, ESD, RASSF9, PRDX5, PRDX2, PRDX3, YBX1, CKB, SERPINA5, ACOT11, SLC25A3, ITIH4, ATP5L, ATP5O, LOXL4, MSN, PLCB1, ATP5H, IMPDH2, DPEP1, ZCCHC11, NDUFB10, SLC25A5, NDUFA13, COX4I1, ATP6V1D, CTH, CLIC5, DDT, CLIC6, UBE2M, PEBP1, CTSF, FKBP2, MYO5A, NDUFB3, FKBP5, FKBP4, NDUFB9, RDX, RGMA, ANXA9, MARS, HSPA9, NDUFA4, DLST, GSTA3, LYZ2, A4GALT, COX7A2, LYZ1, PM20D2, CS, ATP5F1, NPR3, KLK1, APPL1, SOD1, SOD2, TFRC, CDH16, ATP6V1E1, ATP5A1, PGK1, PRSS23 |
| GOTERM_CC. | GO:0005750~mitochondrial respiratory chain complex III                                  | 9   | 1.40  | 0.0000 | UQCRC2, UQCC3, UQCR10, UQCRC1, UQCRH, CYC1, UQCRFS1, UQCRQ, UQCRB  |
| GOTERM_CC. | GO:0045263~proton-transporting ATP synthase complex, coupling factor F(o)               | 9   | 1.40  | 0.0000 | ATP5J2, ATP5F1, ATP5L, ATP5G1, ATP5H, ATP5G3, ATP8, ATP6, ATP5J  |
| GOTERM_CC. | GO:0000276~mitochondrial proton-transporting ATP synthase complex, coupling factor F(o) | 9   | 1.40  | 0.0000 | ATP5J2, ATP5F1, ATP5L, ATP5O, ATP5G1, ATP5H, ATP5G3, ATP8, ATP5J   |
| GOTERM_CC. | GO:0005751~mitochondrial respiratory chain complex IV                                   | 9   | 1.40  | 0.0000 | NDUFA4, COX8B, COX2, COX1, COX7C, COX4I1, COX6A1, COX5A, COX5B   |

|            |  |    |      |        |  |
|------------|--|----|------|--------|--|
| GOTERM_CC. | GO:0005759~mitochondrial matrix              | 23 | 3.58 | 0.0002 | ME3, ACADSB, NDUFA9, SUCLG1, CS, AK3, NDUFA10, ACAT1, PDHB, GOT2, ISCA1, ISCU, C1QBP, PPM1K, OXCT1, BLOC1S1, REXO2, DLD, HSPE1, PDHA1, HADH, OAT, MDH2 |
| GOTERM_CC. | GO:0005758~mitochondrial intermembrane space | 14 | 2.18 | 0.0007 | SUOX, PRELID2, CHCHD10, NDUFA8, AIFM1, BLOC1S1, REXO2, CYCS, COX6B1, AK3, CHCHD2, SOD1, COX17, NDUFS1  |
| GOTERM_CC. | GO:0031966~mitochondrial membrane            | 14 | 2.18 | 0.0223 | NDUFA2, NDUFB6, NDUFA9, ATP5B, NDUFA6, ND3, COX4I1, NDUFA13, UQCRRS1, NDUFA1, SLC25A10, PEMT, SLC9B2, NDUFS3   |