

**Supplemental Table 3A. STRING-DB network analysis for biological process enrichment of Cluster 1 transcripts**

Pathway	Count	FDR	Targets
response to endoplasmic reticulum stress	15	8.67E-17	AARS,ASNS,DERL2,DNAJB11,DNAJB9,HERPUD1,HSP90B1,HSPA5,HYOU1,PDIA4,PDIA6,SDF2L1,SELK,SYVN1,TRIB3
response to topologically incorrect protein	14	1.30E-16	AARS,ASNS,DDIT3,DERL2,DNAJB11,DNAJB9,HERPUD1,HSP90B1,HSPA5,HYOU1,MANF,PDIA6,SDF2L1,SYVN1
cellular response to topologically incorrect protein	13	1.30E-16	AARS,ASNS,DDIT3,DERL2,DNAJB11,DNAJB9,HERPUD1,HSP90B1,HSPA5,HYOU1,PDIA6,SDF2L1,SYVN1
response to unfolded protein	13	1.89E-15	AARS,ASNS,DDIT3,DERL2,DNAJB11,DNAJB9,HERPUD1,HSP90B1,HSPA5,HYOU1,MANF,PDIA6,SYVN1
endoplasmic reticulum unfolded protein response	12	1.89E-15	AARS,ASNS,DDIT3,DERL2,DNAJB11,DNAJB9,HERPUD1,HSP90B1,HSPA5,HYOU1,PDIA6,SYVN1
cellular response to unfolded protein	12	2.24E-15	AARS,ASNS,DDIT3,DERL2,DNAJB11,DNAJB9,HERPUD1,HSP90B1,HSPA5,HYOU1,PDIA6,SYVN1
ERAD pathway	8	4.37E-10	DERL2,DNAJB9,HERPUD1,HSP90B1,HSPA5,SDF2L1,SEL1L,SYVN1
ER-associated ubiquitin-dependent protein catabolic process	7	2.20E-08	DERL2,DNAJB9,HSP90B1,HSPA5,SDF2L1,SEL1L,SYVN1
retrograde protein transport, ER to cytosol	5	8.76E-08	DERL2,HERPUD1,HSP90B1,SEL1L,SYVN1
IRE1-mediated unfolded protein response	6	1.39E-06	DNAJB11,DNAJB9,HSPA5,HYOU1,PDIA6,SYVN1
cellular response to stress	16	4.51E-06	AARS,ASNS,DDIT3,DERL2,DNAJB11,DNAJB9,HERPUD1,HSP90B1,HSPA5,HYOU1,PDIA4,PDIA6,SDF2L1,SELK,SYVN1,TRIB3
PERK-mediated unfolded protein response	4	5.44E-06	ASNS,DDIT3,HERPUD1,HSPA5
ubiquitin-dependent protein catabolic process	9	5.66E-05	DDIT3,DERL2,DNAJB9,HERPUD1,HSP90B1,HSPA5,SDF2L1,SEL1L,SYVN1
proteasome-mediated ubiquitin-dependent protein catabolic process	8	5.66E-05	DDIT3,DERL2,DNAJB9,HSP90B1,HSPA5,SDF2L1,SEL1L,SYVN1
response to stress	20	8.97E-05	AARS,ANG,ASNS,DDIT3,DERL2,DNAJB11,DNAJB9,HERPUD1,HSP90B1,HSPA5,HYOU1,MANF,PDIA4,PDIA6,SDF2L1,SELK,SLC7A5,SLFN11,SYVN1,TRIB3
regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway	4	0.00012	DDIT3,HERPUD1,HYOU1,SYVN1
cellular protein catabolic process	9	0.000122	DDIT3,DERL2,DNAJB9,HERPUD1,HSP90B1,HSPA5,SDF2L1,SEL1L,SYVN1
negative regulation of response to endoplasmic reticulum stress	4	0.000171	DERL2,HERPUD1,HYOU1,SYVN1
ATF6-mediated unfolded protein response	3	0.000294	DDIT3,HSP90B1,HSPA5
response to organic substance	16	0.000654	AARS,ANG,DDIT3,DERL2,DNAJB11,DNAJB9,HERPUD1,HSP90B1,HSPA5,HYOU1,MANF,PDIA6,SDF2L1,SEL1L,SYVN1,TRIB3
protein folding	6	0.000973	AARS,DNAJB11,HSP90B1,HSPA5,PDIA4,PDIA6
negative regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway	3	0.00174	HERPUD1,HYOU1,SYVN1
cell redox homeostasis	4	0.00267	DDIT3,ERO1LB,PDIA4,PDIA6
cellular response to organic substance	13	0.00349	AARS,DDIT3,DERL2,DNAJB11,DNAJB9,HERPUD1,HSP90B1,HSPA5,HYOU1,PDIA6,SDF2L1,SYVN1,TRIB3
proteolysis	10	0.00555	DDIT3,DERL2,DNAJB9,ERO1LB,HERPUD1,HSP90B1,HSPA5,SDF2L1,SEL1L,SYVN1
ER-nucleus signaling pathway	3	0.0113	ASNS,HERPUD1,HSP90B1
intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress	3	0.012	DDIT3,SELK,TRIB3
protein folding in endoplasmic reticulum	2	0.0367	HSP90B1,HSPA5

**Supplemental Table 3B. STRING-DB network analysis for biological process enrichment of Cluster 2 transcripts**

Pathway	Count	FDR	Targets
response to endoplasmic reticulum stress	14	1.39E-09	ASNS,ATF4,ATP2A2,DNAJC10,EIF2AK3,FAM129A,FKBP14,GFPT1,PDIA5,SEC31A,SYVN1,UBA5,WFS1,WIP11
endoplasmic reticulum unfolded protein response	10	1.58E-07	ASNS,ATF4,EIF2AK3,FKBP14,GFPT1,PDIA5,SEC31A,SYVN1,WFS1,WIP11
cellular response to unfolded protein	10	1.58E-07	ASNS,ATF4,EIF2AK3,FKBP14,GFPT1,PDIA5,SEC31A,SYVN1,WFS1,WIP11
protein N-linked glycosylation via asparagine	10	2.87E-07	GFPT1,MLEC,OSTC,PGM3,RPN1,SEC24D,SEC31A,ST6GALNAC4,SYVN1,UAP1
IRE1-mediated unfolded protein response	7	6.85E-06	FKBP14,GFPT1,PDIA5,SEC31A,SYVN1,WFS1,WIP11
cellular response to stress	22	0.000222	ASNS,ATF4,ATP2A2,CISD2,DDIT4,DNAJC10,EIF2AK3,FAM129A,FKBP14,GFPT1,LARP1B,MSH2,PDIA5,RAD9A,SEC31A,SLC1A4,SYVN1,TMEM39A,UBA5,UBE2T,WFS1,WIP11
nucleotide-sugar biosynthetic process	4	0.000491	GFPT1,PGM3,UAP1,UGDH
single-organism carbohydrate metabolic process	13	0.000538	ATF4,GFPT1,GOT1,MLEC,OSTC,PGM3,RPN1,SEC24D,SEC31A,ST6GALNAC4,SYVN1,UAP1,UGDH
UDP-N-acetylglucosamine biosynthetic process	3	0.000599	GFPT1,PGM3,UAP1
glycoprotein biosynthetic process	10	0.00125	GFPT1,MLEC,OSTC,PGM3,RPN1,SEC24D,SEC31A,ST6GALNAC4,SYVN1,UAP1
protein folding	8	0.00147	DNAJC10,FKBP11,FKBP14,MLEC,PDIA5,PPIL1,TUBB3,WFS1
carbohydrate metabolic process	14	0.00158	ATF4,GFPT1,GOT1,MLEC,OSTC,PGM3,RPN1,SEC24D,SEC31A,SLC3A2,ST6GALNAC4,SYVN1,UAP1,UGDH
signal peptide processing	3	0.00257	SEC11C,SPCS2,SPCS3
carbohydrate derivative biosynthetic process	12	0.00318	GFPT1,MLEC,OSTC,PGM3,PIGA,RPN1,SEC24D,SEC31A,ST6GALNAC4,SYVN1,UAP1,UGDH
peptidyl-amino acid modification	14	0.00354	EIF2AK3,FKBP11,FKBP14,GFPT1,MLEC,OSTC,PGM3,PPIL1,RPN1,SEC24D,SEC31A,ST6GALNAC4,SYVN1,UAP1
ER-nucleus signaling pathway	4	0.00416	ASNS,ATF4,ATP2A2,WFS1
amide biosynthetic process	10	0.00416	ASNS,C12orf65,CARS,EIF2AK3,MTHFD2,RPN1,SEC11C,SPCS2,SPCS3,TARS
post-translational protein modification	9	0.00416	GFPT1,MLEC,PGM3,PIGA,RPN1,SEC24D,SEC31A,ST6GALNAC4,UAP1
cellular protein metabolic process	29	0.00583	APP,ASNS,ATF4,C12orf65,CARS,DNAJC10,FKBP11,FKBP14,GFPT1,MLEC,MTMR4,OSTC,PDIA5,PGM3,PIGA,PPIL1,RPN1,SEC24D,SEC31A,ST6GALNAC4,SYVN1,TARS,TRIM5,TUBB3,UAP1,UBA5,UBE2T,WFS1,WIP11
PERK-mediated unfolded protein response	3	0.00685	ASNS,ATF4,EIF2AK3
single-organism metabolic process	32	0.0155	ALDH1L2,ANG,APP,ASNS,ATF4,CARS,CISD2,DNAJC10,EIF2AK3,GFPT1,GPT2,MLEC,MSH2,MTFR1,MTHFD2,MTMR4,OSTC,PDIA5,PGM3,PIGA,RAD9A,RPN1,SEC24D,SEC31A,ST6GALNAC4,SYVN1,TARS,UAP1,UBE2T,UGDH,WFS1,WIP11
glutamine transport	2	0.0217	SLC1A4,SLC1A5
endoplasmic reticulum calcium ion homeostasis	3	0.0228	APP,ATP2A2,WFS1
translation	8	0.0274	C12orf65,CARS,EIF2AK3,RPN1,SEC11C,SPCS2,SPCS3,TARS
response to stress	27	0.0464	ANG,ASNS,ATF4,ATP2A2,CISD2,DDIT4,DNAJC10,EIF2AK3,FAM129A,FKBP14,GFPT1,HABP4,LARP1B,MSH2,PDIA5,RAD9A,SEC31A,SLC1A4,SLC3A2,SP140,SYVN1,TMEM39A,TRIM5,UBA5,UBE2T,WFS1,WIP11

**Supplemental Table 3C. STRING-DB network analysis for biological process enrichment of Cluster 6 transcripts**

Pathway	Count	FDR	Targets
response to lipopolysaccharide	10	6.73E-06	ANKRD1,CYP27B1,IRAK2,NFKBIA,PDE4B,PEL1,PTGES,SERPINE1,TRIB1,ZC3H12A
positive regulation of B cell proliferation	5	7.14E-05	ADA,CD38,GPR183,PEL1,TNFRSF4
response to other organism	12	7.14E-05	ANKRD1,BATF,CYP27B1,IER3,IRAK2,NFKBIA,PDE4B,PEL1,PTGES,SERPINE1,TRIB1,ZC3H12A
regulation of cell activation	10	8.10E-05	ADA,C1QTNF1,CD38,EBI3,GPR183,HSPH1,MERTK,PEL1,TNFRSF4,ZC3H12A
response to bacterium	10	0.000127	ANKRD1,CYP27B1,IRAK2,NFKBIA,PDE4B,PEL1,PTGES,SERPINE1,TRIB1,ZC3H12A
regulation of leukocyte activation	9	0.000275	ADA,CD38,EBI3,GPR183,HSPH1,MERTK,PEL1,TNFRSF4,ZC3H12A
positive regulation of lymphocyte proliferation	6	0.000275	ADA,CD38,EBI3,GPR183,PEL1,TNFRSF4
response to external stimulus	17	0.000287	ADA,ANKRD1,BATF,CCL23,CCL4L2,CYP27B1,FPR1,FPR3,IER3,IRAK2,NFKBIA,PDE4B,PEL1,PTGES,SERPINE1,TRIB1,ZC3H12A
cellular response to lipopolysaccharide	6	0.000484	ANKRD1,IRAK2,NFKBIA,PDE4B,SERPINE1,ZC3H12A
positive regulation of lymphocyte activation	7	0.000594	ADA,CD38,EBI3,GPR183,HSPH1,PEL1,TNFRSF4
negative regulation of sequence-specific DNA binding transcription factor activity	6	0.000643	IRAK2,NFKBIA,PEL1,TNFRSF4,TRIB1,ZC3H12A
regulation of lymphocyte activation	8	0.000655	ADA,CD38,EBI3,GPR183,HSPH1,MERTK,PEL1,TNFRSF4
response to lipid	11	0.000753	ANKRD1,CD38,CYP27B1,IRAK2,NFKBIA,PDE4B,PEL1,PTGES,SERPINE1,TRIB1,ZC3H12A
regulation of cytokine production	9	0.0013	ALOX15B,EBI3,NFKBIA,PDE4B,PEL1,SERPINE1,TNFRSF4,TNFRSF9,ZC3H12A
regulation of cell proliferation	14	0.00138	ADA,ALOX15B,CCL23,CD38,CYP27B1,EBI3,GPR183,NFKBIA,PEL1,PTGES,SLAMF1,TNFRSF4,TNFRSF9,TRIB1
regulation of localization	17	0.0019	ADA,ALOX15B,ANKRD1,C1QTNF1,CD38,CLIC2,HSPH1,IER3,MERTK,NFKBIA,PDE4B,SERPINE1,SLAMF1,TNFRSF4,TNFRSF9,TRIB1,ZC3H12A
cellular response to zinc ion	3	0.00324	MT1G,MT1H,MT1M
negative regulation of biological process	23	0.00336	ALOX15B,ANKRD1,C1QTNF1,CCL23,CLIC2,CYP27B1,DNAJA4,GPR132,HSPH1,IRAK2,LIMA1,MERTK,MT1G,MT1H,MT1M,NFKBIA,PDE4B,PEL1,PTGES,SERPINE1,TNFRSF4,TRIB1,ZC3H12A
negative regulation of multicellular organismal process	11	0.00336	ADA,C1QTNF1,CD38,FKBP4,NFKBIA,PDE4B,SERPINE1,TNFRSF4,TNFRSF9,TRIB1,ZC3H12A
defense response	13	0.00353	BATF,CCL23,CCL4L2,CD163,CHST2,CYP27B1,IRAK2,NFKBIA,PEL1,PTGES,RNF19B,SERPINE1,TNFRSF4
positive regulation of immune system process	10	0.00477	ADA,CD38,EBI3,GPR183,HSPH1,IRAK2,PDE4B,SERPINE1,TNFRSF4,TRIB1
multi-organism process	16	0.00503	ANKRD1,BATF,CD38,CYP27B1,FKBP4,IER3,IRAK2,MERTK,NFKBIA,PDE4B,PEL1,PTGES,SERPINE1,SLAMF1,TRIB1,ZC3H12A
response to stress	20	0.00588	ANKRD1,BATF,CCL23,CCL4L2,CD163,CD38,CHST2,CYP27B1,DNAJA4,FKBP4,HSPH1,IER3,IRAK2,NFKBIA,PEL1,PTGES,RNF19B,SERPINE1,TNFRSF4,TRIB1
regulation of transport	14	0.00588	ADA,ALOX15B,ANKRD1,C1QTNF1,CD38,CLIC2,IER3,MERTK,NFKBIA,PDE4B,SERPINE1,SLAMF1,TNFRSF4,TNFRSF9
negative regulation of NF-kappaB transcription factor activity	4	0.00642	IRAK2,NFKBIA,PEL1,ZC3H12A
regulation of sequence-specific DNA binding transcription factor activity	7	0.00642	IRAK2,NFKBIA,PEL1,TNFRSF4,TRAF1,TRIB1,ZC3H12A
cellular response to stimulus	27	0.00642	ANKRD1,BATF,CCL23,CCL4L2,CD38,CLIC2,CYP27B1,EBI3,FPR1,FPR3,GPR132,GPR183,HSPH1,IER3,IRAK2,MT1G,MT1H,MT1M,NFKBIA,PDE4B,PTGES,SERPINE1,SLAMF1,TNFRSF4,TRAF1,TRIB1,ZC3H12A
immune response	12	0.00784	ADA,BATF,CCL23,CCL4L2,CYP27B1,EBI3,GPR183,IRAK2,NFKBIA,PEL1,RNF19B,TNFRSF4
response to oxygen-containing compound	12	0.00839	ADA,ANKRD1,CD38,CYP27B1,IRAK2,NFKBIA,PDE4B,PEL1,PTGES,SERPINE1,TRIB1,ZC3H12A
leukocyte activation	7	0.00922	BATF,EBI3,GPR183,MERTK,MT1G,SLAMF1,TNFRSF4
regulation of immune system process	12	0.00981	ADA,CD38,EBI3,GPR183,HSPH1,IRAK2,MERTK,PDE4B,SERPINE1,TNFRSF4,TRIB1,ZC3H12A
inflammatory response	7	0.015	CCL23,CCL4L2,CD163,CHST2,IRAK2,PTGES,TNFRSF4
B cell activation involved in immune response	3	0.0166	ADA,BATF,GPR183
response to chemical	20	0.0166	ADA,ANKRD1,CCL23,CCL4L2,CYP27B1,EBI3,FPR1,FPR3,HSPH1,IRAK2,MT1G,MT1H,MT1M,PDE4B,PEL1,PTGES,SERPINE1,TNFRSF4,TRIB1,ZC3H12A
cell activation	8	0.0219	BATF,EBI3,GPR183,MERTK,MT1G,SERPINE1,SLAMF1,TNFRSF4
lymphocyte activation	6	0.0263	BATF,EBI3,GPR183,MERTK,SLAMF1,TNFRSF4
response to stimulus	28	0.0263	ANKRD1,BATF,CCL23,CCL4L2,CD163,CHST2,CLIC2,CYP27B1,DNAJA4,EBI3,FPR1,FPR3,GPR132,GPR183,HSPH1,IER3,IRAK2,MT1G,MT1H,MT1M,NFKBIA,PDE4B,RNF19B,SERPINE1,SLAMF1,TRAF1,TRIB1,ZC3H12A
regulation of multicellular organismal process	15	0.03	ADA,ANKRD1,C1QTNF1,CD38,CLIC2,CYP27B1,EBI3,FKBP4,PDE4B,PEL1,SERPINE1,TNFRSF4,TNFRSF9,TRIB1,ZC3H12A
negative regulation of molecular function	10	0.0331	CCL23,CLIC2,CYP27B1,IRAK2,NFKBIA,PEL1,SERPINE1,TNFRSF4,TRIB1,ZC3H12A
regulation of molecular function	16	0.0347	ARHGEF10L,CCL23,CLIC2,CYP27B1,FPR1,HSPH1,IRAK2,NFKBIA,PDE4B,PEL1,SERPINE1,SLAMF1,TNFRSF4,TRAF1,TRIB1,ZC3H12A
positive regulation of multicellular organismal process	11	0.0377	ADA,ANKRD1,C1QTNF1,CD38,CYP27B1,EBI3,NFKBIA,PDE4B,PEL1,SERPINE1,TRIB1
positive regulation of cytokine production	6	0.0393	ALOX15B,EBI3,NFKBIA,PDE4B,PEL1,SERPINE1
negative regulation of growth	5	0.0393	ALOX15B,CYP27B1,MT1G,MT1H,MT1M
negative regulation of immune system process	6	0.041	ADA,MERTK,NFKBIA,PEL1,TRIB1,ZC3H12A
positive regulation of alpha-beta T cell activation	3	0.041	ADA,EBI3,HSPH1
response to organic substance	15	0.0423	ADA,ANKRD1,CD38,CYP27B1,EBI3,HSPH1,IRAK2,MT1G,PDE4B,PEL1,PTGES,SERPINE1,TNFRSF4,TRIB1,ZC3H12A
mature B cell differentiation involved in immune response	2	0.0449	ADA,GPR183





4	single-organism localization	74	0.000839	ABAT,ADA,ALDH5A1,APP,ASN1,ATP1B1,ATP2A2,CALR,CD36,CLIC2,CTNNB1,CTNS,CYB561,CYP27B1,DDIT3,DERL2,FABP6,FKBPA,GABARAPL2,GABRE,HABP4,HERPUD1,HIAT1,HS P90B1,HSP9A5,KONK6,KIAA1033,KIAA1279,KPNA2,LIN7C,MERTK,MFS2DA,MSTO1,NFKBIA,NPL,OC4,PDIA4,PNP,RNF198,RP1,RPN1,RTPA,SEC11C,SEC24D,SEC31A,SEL,IL,SEK,SE LT,SERPINE1,SLC17A9,SLC1A4,SLC1A5,SLC22A16,SLC28A6,SLC36B1,SLC39A14,SLC3A2,SLC7A1,SLC7A5,SPCS2,SPCS3,SRSF11,SRSF3,SYVN1,TMEM88B,TOB1,TOPORS UFDL1,UOQRH,VPS26A,WVF,WFS1,WIP1,XCR1
4	establishment of localization in cell	50	0.000925	ABAT,ALDH5A1,ANP32A,APP,ATP1B1,ATP2A2,CALR,CD36,CTNNB1,DDIT3,DERL2,EIF2AK3,GABARAPL2,HABP4,HERPUD1,HSP90B1,HSP9A5,KIAA1033,KIAA1279,KPNA2,LIN7C,MERT K,NFKBIA,NPL,OC4,PDIA4,PNP,RNF198,RP1,RPN1,RTPA,SAR1A,SEC11C,SEC31A,SEL,IL,SELT,SERPINE1,SLI,SLC17A9,SPCS2,SPCS3,SRSF11,SRSF3,SYVN1,TOB1,UFDL1,VPS26 A,WVF,WFS1,WIP1,XCR1
1	protein peptidyl-prolyl isomerization	7	0.000938	FKBP11,FKBP14,FKBP2,FKBP4,FKBP5,PRIG,PP1L1
1	transport	80	0.001	ABAT,ADA,ALDH5A1,ANP32A,APP,ASN1,ATP1B1,ATP2A2,CALR,CD163,CD36,CLIC2,CTNNB1,CTNS,CYB561,CYP27B1,DDIT3,DERL2,DYNCL11,FABP5,FKBP4,G3BP1,GABARAPL2,H ABP4,HERPUD1,HIAT1,HSP90B1,HSPH1,HYOU1,KONK6,KIAA1033,KIAA1279,LIN7C,LTY75,MERTK,MFS2DA,NFKBIA,NPL,OC4,PDIA4,PNP,RNF198,RP1,RPN1,RTPA,SAR1A,SEC11C, EC31A,SEL,IL,SEK,SELT,SERPINE1,SLI,SLC10A7,SLC17A9,SLC1A4,SLC1A5,SLC22A16,SLC26A6,SLC35B1,SLC39A14,SLC3A2,SLC7A1,SLC7A5,SPCS2,SPCS3,SRSF11,SRSF3,SYV N1,TCPI1,TMED7,TMEM88B,TOB1,TRAM2,UFDL1,UOQRH,VPS26A,WVF,WFS1,WIP1,XCR1
1	nucleotide-sugar biosynthetic process	5	0.00117	GFPT1,GMIPBP,PGM3,UAP1,UGDH
1	protein folding in endoplasmic reticulum	4	0.00129	CALR,DNAJC10,HSP90B1,HSP9A5
4	negative regulation of biological process	93	0.00153	AARS,ACPS,ALOX15B,ANG,ANKRD1,ASNS,ATP2A2,BANP,BC12A1,C1D,C10,TNF1,CALR,CAP2A1,CAST,CCL23,CD164,CD276,CD36,CLIC2,CTNNB1,CTR9,CYP27B1,DDIT3,DERL2,DNA JA4,DNAJB5,DNAJC10,DUSP6,DYRK2,EBI6,EV,FAI,MT29A,FGD,G3BP1,GABARAPL2,GADD45GIP1,GRR132,HMG81,HRSPT2,HSP90B1,HSPH1,HTRA2,IKAK2,KLF4,LLGA,LIAMA1,LYPL A1,MAF,MEZD1,MERTK,METRN,MSH2,MTG,MT1H,MT,MTM,MTMR4,NFKBIA,NFKL1,PC,PDE4B,PEL1,PKCZIP1,PMI2,PPP1CB,PPP1R15B,PSMCG,PTGES,RAD9A,RAPIB,RGSS2,RTKN,S ARIA,SEMA3A,SERPINE1,SERTAD3,SLFN11,SPOCD1,SUMO1,SYVN1,TAF9,TD2,TEJ5,TNFRSF4,TNFSF10,TOPORS,TRIB1,TRIB3,TRIM5,UBXN1,VSX2,WFS1,XCR1,ZC3H12A
1	cell redox homeostasis	8	0.00175	DDIT3,DNAJC10,EROC11B,GOLC,PDIA4,PDIA6,PDIA6,SELT
4	localization	4	0.00214	CALR,DDIT3,HSP90B1,HSP9A5
1	ATF6-mediated unfolded protein response	93	0.00255	ABAT,ADA,ALDH5A1,ANG,ANP32A,APP,ASN1,ATP1B1,ATP2A2,BANP,CALR,CCL23,CCL4L2,CD163,CD36,CLIC2,CTNNB1,CTNS,CYB561,CYP27B1,DDIT3,DDIT4,DERL2,DYNCL11,FAB P5,FKBP4,G3BP1,GABARAPL2,HABP4,HERPUD1,HIAT1,HMG81,HSP90B1,HSPH1,HIYOU1,KONK6,KIAA1033,KIAA1279,LIN7C,LTY75,MATK,MERTK,MFS2DA,MSTO1,NFKBIA,NPL,OC4,P DE4B,PDIA4,PNP,PTPIP2,PNP19B,ROCK1,RP1,RPN1,RTPA,SAR1A,SEC11C,SEC31A,SEL,IL,SEK,SELT,SEMA3A,SERPINE1,SLI,SLC10A7,SLC17A9,SLC1A4,SLC1A5,SLC22A16,S LC26A6,SLC35B1,SLC39A14,SLC3A2,SLC7A1,SLC26A6,SPCS2,SPCS3,SRSF11,SRSF3,SYVN1,TCPI1,TMED7,TMEM88B,TOB1,TOPORS,TRAM2,UFDL1,UOQRH,VPS26A,WVF,WFS1,WIP 11,XCR1
3	intrinsic apoptotic signaling pathway	12	0.00255	ADIT4,BCL2A1,DDIT3,DDIT4,DNAJC10,DYRK2,EIF2AK3,HTRA2,IER3,MSH2,SELT,TRIB3
1	negative regulation of sequence-specific DNA binding	11	0.00261	DDIT3,DDIT4,IRAK2,KLF4,NFKBIA,PEL1,SUMO1,TNFRSF4,TRIB1,WFS1,ZC3H12A
1	transcription factor activity	6	0.00261	ATF4,DDIT3,DNAJC10,EIF2AK3,SELT,TRIB3
3	intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress	41	0.00262	AARS,ADA,ALK,ANKRD1,ASNS,ATP2A2,BCL2A1,BEY2,CALR,CAST,CD38,CTNNB1,DDIT3,DUSP6,GF15,HMG81,HSP90B1,HSP9A5,HSPH1,HTRA2,KLF4,LLGA,LIAMA1,LYPL A1,MAF,MEZD1,MERTK,METRN,MSH2,MTG,MT1H,MT,MTM,MTMR4,NFKBIA,NFKL1,PC,PDE4B,PEL1,PKCZIP1,PMI2,PPP1CB,PPP1R15B,PSMCG,PTGES,RAD9A,RAPIB,RGSS2,RTKN,S ARIA,SEMA3A,SERPINE1,SERTAD3,SLFN11,SPOCD1,SUMO1,SYVN1,TAF9,TD2,TEJ5,TNFRSF4,TNFSF10,TOPORS,TRIB1,TRIB3,TRIM5,UBXN1,VSX2,WFS1,XCR1,ZC3H12A
3	regulation of apoptotic process	30	0.00292	ALG13,ALK,CALR,CTR9,DYRK2,EIF2AK3,FKBP11,FKBP14,SYVN1,TAF9,TCPI1,TNFRSF4,TNFSF10,TOPORS,TRAFF1,WFS1
1	peptidyl-amino acid modification	17	0.00294	AARS,ADH1,ALDH1L2,ALDH5A1,ASNS,ATP4,CARS,CTNS,DYPD,EROC11B,GOLC,GFPT1,GP2,PSAT1,SLC7A6,TARS,UPIB1
4	cellular amino acid metabolic process	26	0.0042	ACPS,ANKRD1,BATF,CD36,CTR9,CYP27B1,DDIT3,DDIT4,EIF2AK3,HSP9A5,IER3,IRAK2,NFKBIA,PDE4B,PEL1,PMI2,PPP1R15B,PTGES,SERPINE1,SLFN11,TLR1,TMEM81,TRIB1,TRIM5, WFS1,ZC3H12A
4	cellular localization	54	0.00461	ABAT,ALDH5A1,ANP32A,APP,ASN1,ATP1B1,ATP2A2,BANP,CALR,CD36,CTNNB1,DDIT3,DERL2,EIF2AK3,GABARAPL2,HABP4,HERPUD1,HSP90B1,HSP9A5,KIAA1033,KIAA1279,KPNA2, LIN7C,MERTK,MSTO1,NFKBIA,NPL,OC4,PDIA4,PNP,RNF198,RP1,RPN1,RTPA,SAR1A,SEC11C,SEC31A,SEL,IL,SELT,SERPINE1,SLI,SLC17A9,SPCS2,SPCS3,SRSF11,SRSF3,SYVN1 TOB1,TOPORS,UFDL1,VPS26A,WVF,WFS1,WIP1,XCR1
3	regulation of cell death	42	0.00471	AARS,ADA,ALK,ANKRD1,ASNS,ATP2A2,BCL2A1,BEY2,CALR,CAST,CD38,CTNNB1,DDIT3,DDIT4,DUSP6,GF15,HMG81,HSP90B1,HSP9A5,HSPH1,HTRA2,KLF4,LLGA,MERTK,MSH2,N FKBIA,PMI2,PPP1CB,PSMCG,RAD9A,ROCK1,SDZL1,SERPINE1,SYVN1,TAF9,TCPI1,TNFRSF4,TNFSF10,TOPORS,TRAFF1,WFS1
1	cellular amino acid biosynthetic process	8	0.00499	ABAT,ADH1,ASNS,DYPD,GP2,MTM,PSAT1,UPIB1
4	negative regulation of cellular process	85	0.00601	AARS,ACPS,ALOX15B,ANG,ANKRD1,ASNS,ATP4,BCL2A1,C1D,C10,TNF1,CALR,CAP2A1,CAST,CCL23,CD164,CD276,CD36,CLIC2,CTNNB1,CTR9,CYP27B1,DDIT3,DERL2,DNAJA4,DNA JB5,DNAJC10,DUSP6,DYRK2,EBI6,EV,FAI,MT29A,G3BP1,GABARAPL2,GADD45GIP1,GRR132,HMG81,HRSPT2,HSP90B1,HSPH1,HTRA2,IKAK2,KLF4,LLGA,LIAMA1,LYPLA,MAF,MEZD1 MERTK,MSH2,MTM,MTG,MT1H,MT,MTM,MTMR4,NFKBIA,NFKL1,PC,PDE4B,PEL1,PKCZIP1,PMI2,PPP1CB,PPP1R15B,PSMCG,PTGES,RAD9A,RAPIB,RGSS2,RTKN,SARIA,SEMA3A,SERPINE1, SERTAD3,SLFN11,SPOCD1,SUMO1,SYVN1,TAF9,TD2,TEJ5,TNFRSF4,TNFSF10,TOPORS,TRIB1,TRIB3,TRIM5,UBXN1,VSX2,WFS1,XCR1,ZC3H12A
1	positive regulation of transcription from RNA polymerase II promoter in response to endoplasmic reticulum stress	4	0.00605	ATF3,ATF4,DDIT3,HSPA5
1	single-organism carbohydrate metabolic process	23	0.00637	ALDH5A1,ATF3,ATF4,B3GNT5,CALR,EXH1,FABP5,GOLC,GFPT1,GMIPBP,GOI1,MLE,EC,OSTC,PC,PGM3,PPP1CB,RPN1,SEC24D,SEC31A,STRGAL,NAOC,SYVN1,UAP1,UGDH
4	cellular metabolic process	152	0.00679	ACPS,ADH1,AGPAT9,ALDH1L2,ALK,ANG,ANKRD1,ANP32A,APP,ASN1,ASNS,ATF3,ATP2A2,ATMIN,ATXN3,B3GNT5,BANP,BCAS2,C12orf86,C1D,CALR,CARS,CD36,CHSTZ,CISD2,COM MDS,CTNNB1,CTNS,CTR9,CYB561,CYP27B1,CYP9A1,DDIT3,DDX17,DERL2,DNAJA4,DNAJB5,DNAJB9,DNAJC10,DPYD,DTX3L,DUSP6,DYRK2,EEF1B2,EPHD1,ELOVL6,EXH1,FANCF, FGD,FKBP11,FKBP14,FKBP2,FKBP4,FKBP5,G3BP1,GABARAPL2,GADD45GIP1,GFPT1,GMIPBP,GND4,GNNG10,GP2,HABP4,HMG81,HRSPT2,HSP90B1,HSP9A5,HSPH1,HIYOU1,JD2,IRA K2,KLF4,KPNA2,LLGA,LMOC4,MAK7,MENL2,ME3,MERTK,MLEC,MSH2,MTFTR1,MTM,MTMR4,NFKBIA,NFKL1,NPL,OC4,OSTC,PDE4B,PDIA4,PDIA6,PDIA6,PEL1,PFNA2,PIA4, M2,PNP,PP1G,PLL1,PPP1CB,PRPF4B,PSAT1,PSMCG,PTGES,PTMA,RNASEH4,RNF198,ROCK1,RP1,RPN1,SDZL1,SEC24D,SEC31A,SEL,IL,SELT,SERPINE1,SERTAD3,SLI, SLC7A5,SPOCD1,SRSF11,SRSF3,STRGAL,NAOC,SUMO1,SYVN1,TAF9,TARS,TCPI1,TD2,TOPORS,TRIB1,TRIM5,TSN,TUBA3D,TUBB3,UAP1,UBA5,UBE2T,UBXN1,UFDL1,UGDH,UPIB1,U SPI8,VSX2,WFS1,WIP1,WTPA,ZC3H12A,ZNF396,ZNF788
1	positive regulation of proteasomal protein catabolic process	8	0.00679	ATXN3,GOLC,HERPUD1,PSMCG,SUMO1,TRIB1,TRIB3,ZFAND2A

1	ubiquitin-dependent protein catabolic process	19	0.00715	ATXN3,DDIT3,DERL2,DNAJB9,DNAJC10,HERPUD1,HSP90B1,HSPA6,NIP1,LOC4,PPP2C8,PSM06,SDF2L1,SEL,IL,SYVN1,TOFOR5,UBXN1,UFD1L,USP18,WFS1
4	organic substance transport	49	0.00742	ADA,ATP1B1,CALR,CD36,CTNS,DERL2,EIF2AK3,FAPB5,GABARAPL2,HERPUD1,HSP90B1,KIAA1033,LIN7C,MESD2A,NFKBIA,NIP1,LOC4,PDIA4,PNP,RNF198,RPLP1,RTTP4,SAR1A,SEC11C,SEC24D,SEC31A,SEL,IL,SELT,SIL1,SLC14A,SLC14A5,SLC22A1,6,SLC28A6,SLC35B1,SLC3A2,SLC37A1,SLC7A5,SFPCS2,SFPCS3,SRSF11,SRSF3,SYVN1,TCPI1,TMED7,TOB1,TRAM2,UFD1L,VPS28A,WFS1
1	UDP-N-acetylglucosamine biosynthetic process	3	0.00768	GFP11,PGM3,UAP1
1	protein glycosylation	15	0.00811	ALG13,B3GNT5,CALR,EXT1,GFP11,GMPPE,MLEC,OSTC,PGM8,RPN1,SEC24D,SEC31A,STREGALNAQC,SYVN1,UAP1
1	regulation of binding	14	0.00899	APP,CC23,CLC2,DDIT3,EIF2AK3,HABP4,HERPUD1,HMG81,HSPA5,DI2,NFKBIA,ROCK1,SUMO1,TRIB3
3	programmed cell death	33	0.0101	AFOX15B,APP,ATF4,BCL2A1,BEEX2,C10,CD38,CTNNB1,DDIT3,DDI1,DNAJC10,DYRK2,GQLC,HERPUD1,HMG81,HTRA2,KLF4,LUG4,MSH2,NFKBIA,PIW2,PPP2C8,PSM06,ROCK1,RTKN,SELK,SEMA3A,TNFRSF4,TNFRSF9,TNFSF10,TRAF1,TRIB3,ZC3H12A
4	cellular macromolecule metabolic process	127	0.0101	ALG13,ALK,ANG,ANKRD1,APP,ASNA1,ASNS,ATF3,ATF7IP2,ATMIN,ATXN3,B3GNT5,BANP,BCAS2,C12orf65,C1D,CALR,CARS,COMMDD,CTNNB1,CTR9,DDIT3,DDI1,DDX17,DERL2,DNAJ4,DNAJB5,DNAJB9,DNAJC10,DTX3L,DUSP6,DYRK2,EEF1B2,EEP1,EXT1,FANCF,FICD,FKBP14,FKBP14,FKBP2,FKBP4,FKBP5,GADD45G1P1,GFP11,GMPPE,HABP4,HMG81,1,HRS,P12,HSP90B1,HSPA5,HSPH1,HTRA2,HYOU1,DI2,IKK2,KLF4,KPN2A2,LGAL,LMOD4,LYPL1,1,MATK,MBNL1,MERTK,MLEC,MSH2,MTMR4,NFXL1,NIP1,LOC4,OSTC,PDIA4,PDIA5,PDIA6,PEL1,1,PEN2,PGM3,PIGA,PIW2,PIPG,PPL1,PPP1CB,PPP4B,PSM06,PTMA,RAO9A,RNASEH4,RNF198,ROCK1,RPLP1,RPNI,SPZL1,SEC24D,SEC31A,SEL,IL,SELT,SERPINE1,SERTAD3,SIL1,SPOCD1,SRSF11,SRSF3,STREGALNAQC,SUMO1,SYVN1,TAJ9,TAJ9,TCPI1,TOBP2,TOFOR5,TRIB1,TRIB3,TRIM5,TSN,TUBA3D,TUBB8,UAP1,UBA5,UBE2T,UBXN1,UFD1L,USP18,V5X2,WFS1,WIP1,WIPAP,ZNF395,ZNF788
3	1 regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway	5	0.0105	DDIT3,HERPUD1,HYOU1,SYVN1,WFS1
4	cytoplasmic transport	25	0.0113	ANP32A,ATP2A2,CALR,DDIT3,DERL2,HERPUD1,HSP90B1,KPNA2,NFKBIA,NIP1,OC4,RPLP1,RPN1,SEC11C,SEC24D,SEC31A,SEL,IL,SPCS2,SFPCS3,SRSF11,SRSF3,SYVN1,TOB1,UFD1L,WIP1,XCR1
1	cellular protein catabolic process	20	0.0131	ATXN3,DDIT3,DERL2,DNAJB9,DNAJC10,HERPUD1,HSP90B1,HSPA6,HTRA2,NIP1,LOC4,PPP2C8,PSM06,SDF2L1,SEL,IL,SYVN1,TOFOR5,UBXN1,UFD1L,USP18,WFS1
3	regulation of apoptotic signaling pathway	17	0.0137	ATF3,BCL2A1,CTNNB1,DDIT3,GQLC,HERPUD1,HSPH1,HTRA2,IER3,PPP1CB,RAD9A,SERPINE1,SYVN1,TAJ9,TNFSF10,TRAF1,WFS1
1	positive regulation of proteasomal ubiquitin-dependent protein catabolic process	7	0.0163	ATXN3,GQLC,HERPUD1,SUMO1,TRIB1,TRIB3,ZFAND2A
3	1 negative regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway	4	0.0163	HERPUD1,HYOU1,SYVN1,WFS1
1	negative regulation of response to endoplasmic reticulum stress	5	0.0163	DERL2,HERPUD1,HYOU1,PPP1R15B,SYVN1
2	idiolike receptor signaling pathway	9	0.0168	CD36,DUSP6,HSP90B1,IRAK2,NFKBIA,PEL1,PKC3AP1,TANK,TLR1
4	carbohydrate metabolic process	26	0.0171	ALDH4E1,AMY2B,ATF3,ATF4,B3GNT5,CALR,CHST2,EXT1,FAH,P5, GQLC,GFPT1,GMPPE,GOT1,MLEC,OSTC,PC,PGM3,PPP1CB,RPN1,SEC24D,SEC31A,SLC3A2,STREGALNAQC,SYVN1,UAP1,UGDH
3	apoptotic process	32	0.0171	AFOX15B,APP,ATF4,BCL2A1,BEEX2,C10,CD38,CTNNB1,DDIT3,DDI1,DNAJC10,DYRK2,GQLC,HERPUD1,HMG81,HTRA2,KLF4,LUG4,MSH2,NFKBIA,PIW2,PPP2C8,PSM06,ROCK1,RTKN,SELK,SEMA3A,TNFRSF9,TNFSF10,TRAF1,TRIB3,ZC3H12A
1	protein transport	35	0.0171	ATP1B1,CALR,CD36,DERL2,EIF2AK3,GABARAPL2,HERPUD1,HSP90B1,KIAA1033,LIN7C,NFKBIA,NIP1,LOC4,PDIA4,PNP,RNF198,RPLP1,RPNI,RTTP4,SAR1A,SEC11C,SEC24D,SEC31A,SEL,IL,SELT,SIL1,SPCS2,SFPCS3,SYVN1,TCPI1,TMED7,TOB1,TRAM2,UFD1L,VPS28A,WFS1
2	B cell activation involved in immune response	5	0.0179	ADA,BATF,GPR183,LUG4,MSH2
2	response to molecule of bacterial origin	14	0.0187	ACFS,ANKRD1,CD36,CTR9,CYP27B1,IRAK2,NFKBIA,PDE4B,PEL1,PTGES,SERPINE1,TLR1,TRIB1,ZC3H12A
4	organic acid transmembrane transport	9	0.0187	CD36,CTNS,SLC14A,SLC14A5,SLC22A16,SLC28A6,SLC3A2,SLC37A1,SLC7A5
1	positive regulation of protein metabolic process	38	0.0192	ALK,KANG,APP,ATXN3,CTQTN1,C,DD276,CD36,CTNNB1,CTR9,EBI3,EIF2AK3,FAM129A,FRP1,GQLC,GDF15,GPR183,HERPUD1,HMG81,HSPA6,HSPH1,HTRA2,IER3,IRAK2,KLF4,MNP17L2,NFKBIA,PEL1,PSM08,RAP1B,SUMO1,TLR1,TNFSF10,TOFOR5,TRIB1,TRIB3,TRIM5,WFS1,ZFAND2A
4	regulation of cellular catabolic process	24	0.0201	ATP1B1,ATXN3,CISD2,DDI14,GABARAPL2,GQLC,HERPUD1,HTRA2,IER3,LARP1B,PIW2,PSM06,SLC17A9,SLC14A,SUMO1,TAJ9,TMEM39A,TOB1,TRIB1,TRIB3,UBXN1,USP18,ZC3H12A,ZFAND2A
1	endoplasmic reticulum calcium ion homeostasis	4	0.0223	APP,ATP2A2,HERPUD1,WFS1
4	biological process	207	0.023	ACN9,ADP1,AGPAT9,ALDH1L2,ALK,AMY2B,ANG,ANKRD1,ANP32A,ARRHGFE10L,ASNA1,ATF4,ATF7IP2,ATL1,ATP1B1,ATP2A2,BANP,BCAS2,BCL2A1,BEEX2,BORA,C12orf65,CABLE32,CA LR,CARS,CAST,CCDC288,CCL23,CCL4L2,CD168,CD169,CD36,CDCA2,EP3,CHST2,CLIC2,COMMDD,CREL1,CTNNB1,CYB561,CYP27B1,CYP9A1A,DDIT3,DDX17,DHS11,DNAAF1,DNAJB9,DYD,DTX3L,DYRK2,EEF1B2,EEP1,EIF2AK3,ENTPD7,EVH1,EXT1,FAM129A,FANCE,FGFBP3,FICD,FKBP14,FKBP2,FKBP5,FNDC3A,FRP1,FR3,IZO2,GABARAPL2,GAD,DK3G1P1,GFP11,GMPPE,GNB4,GNL3,GPR132,GPR183,GPT2,HABP4,HCOS,HIAT1,HMG81,HSP90B1,HSPA6,HSPH1,DI2,IRAK2,ISOC2,KOTD15,KIAA1033,KIAA1279,KLF4,LARP1B,LAR P4,LUG4,LMNA1,LIN7C,LMPB3,LV75,LV9,LVPLA1,MANF,MATK,MBNL2,MEI1,MERTK,MLNRL,MSFSD2A,MIS22,MLEC,MPLKIP,MVF17L2,MSH2,MTI1H,MTM,MTTR1,MTHE,D2,NABP2,NDUFA5,NFKBIA,NFXL1,NIP1,LOC4,OSTC,PC,PDE4B,PDIA4,PDIA5,PDIA6,PIW2,PIGA,PNP,PPG,PPL1,1,PPP1CB,PPP4B,PSAT1,PSM06,PSYPI2,PTMA,ROCK1,ROG52,RNASE4,RNF198,ROCK1,RPPI1,RTKN,RTTP4,SAR1A,SDF2L1,SEC31A,SELK,SEMA3A,SERPINE1,SIL1,SLA,SLC10A7,SLC17A9,SLC17A9,SLC17A9,SLC17A9,SLC22A16,SLC28A6,SLC35B1,SLC39A14,SLC3A2,SLC37A1,SLC7A5,SLEFN1,SPH40,SRSF11,SRSF3,STREGALNAQC,SUMO1,SYVN1,TAJ9,TAJ9,TCPI1,TOBP2,TOFOR5,TRIM5,TNFSF10,TNFSF10,TNFSF10,TNFSF10,TNFSF10,TNFSF10,TNFSF10,TNFSF10,TRAM2,TRIB1,TRIB3,TRIM5,TSN,UAP1,UBA5,UBE2T,UBXN1,UFD1L,UGDH,UPB1,UOCOR1,USP18,VPS28A,V5X2,VWF,WFS1,WIP1,WIPAP,ZC3H12A,ZFAND2A,ZNF395,ZNF788
4	cell activation	22	0.0241	APP,BATF,CAST,CD276,CD36,CTNNB1,EBI3,GPR183,HABP4,HMG81,HSPA6,DI2,LUG4,MERTK,MSH2,MTI1,G,RAAP1B,SERPINE1,SLAMF1,TLR1,TNFRSF4,WVF
4	establishment of protein localization	36	0.0246	ASNA1,ATP1B1,CALR,CD36,DERL2,EIF2AK3,GABARAPL2,HERPUD1,HSP90B1,KIAA1033,LIN7C,NFKBIA,NIP1,LOC4,PDIA4,PNP,RNF198,RPLP1,RPNI,RTTP4,SAR1A,SEC11C,SEC24D,SEC31A,SEL,IL,SELT,SIL1,SPCS2,SFPCS3,SYVN1,TCPI1,TMED7,TOB1,TRAM2,UFD1L,VPS28A,WFS1
1	regulation of proteasomal protein catabolic process	12	0.0246	ATXN3,GABARAPL2,GQLC,HERPUD1,PSM06,SUMO1,TAJ9,TRIB1,TRIB3,UBXN1,USP18,ZFAND2A
2	immune response	36	0.0248	ADA,APP,BATF,CAPZ1,CCL23,CCL4L2,CD164,CD276,CD36,CTNNB1,CYP27B1,DUSP6,EBI3,GPR183,HMG81,IRAK2,LUG4,LV75,MATK,MSH2,NFKBIA,PEL1,PNP,PRKCGH,PSM06,RNF198,SLC28A6,SUMO1,TANK,TLR1,TNFSF4,TNFSF10,TRIB3,TRIM5,USP18

4	regulation of catabolic process	26	0.0248	ATP1B1,ATXN3,BANP,CISD2,DDIT4,DERL2,GABARAPL2,GQLC,HERPUD1,HTRA2,IER3,LARP1B,PIW2,PSMOC6,SLC17A4,SUMO1,TAE9,TM6M9A,TOB1,TRIB1,TRIB3,UBXN1,USP18,ZC3H12A,ZFAND2A
4	macromolecule metabolic process	133	0.0248	ALG13,ALK,ANG,ANKRD1,ANP32A,APP,ASNA1,ASNS,ATF3,ATF7IP2,ATMIN,B3GNT5,BANP,BCAS2,C12orf65,C1D,CALR,CARS,CHST2,COMMDB,CTNNB1,CTR9,DDIT3,DDIT4,DDX17,DERL2,DNAJA4,DNAJB5,DNAJB9,DNAJC10,DTXL,DDUSP6,DYRK2,EEF1B2,EERP1,EXT1,FANCE,FICD,FKBP11,FKBP14,FKBP2,FKBP4,FKBP5,G3BP1,GADD45GIP1,GFP1T,GMPFB,HABP4,HMG81,HRSF12,HSP90B1,HSPA5,HSPH1,HTRA2,HYOU1,IDD,IRAK2,KLF4,KPM2,LANC4,LMQ4,MATIK1,MENL2,MERTK,MLE,C,MSH2,MTM4,NABP2,NFXL1,NPLOC4,OSTC,PDIA4,PDIA5,PDIA6,PELI1,PFND2,PGM3,PIGA,PIW2,PP1C,PPP1B,PPP4B,PSMOC6,PTM,RAO9A,RNA52A,RNF199,ROCK1,RP1,RPN1,SDF2L1,SEC24D,SEC31A,SEL1L,SELT,SERPINE1,SERTAD3,SIL1,SPOCD1,SRSF11,SRSF3,STGALNA4C4,SUMO1,SVVN1,TAJ9,TARS,TOPI1,TPD2,TNFSF10,TOPORS,TRAM2,TRIB1,TRIB3,TRIM5,V5X2,WFS1,ZNF395,ZNF789,ZUBXN1,UFD1L,UGDH,USP18,V5X2,WVF1,WPI1,WTPA,ZC3H12A,ZNF395,ZNF789
3	negative regulation of neuron death	10	0.0248	AARS,ATF4,CTNNB1,GGLC,HTRA2,HYOU1,ILG4,MSH2,ROCK1,WFS1
4	single-organism biosynthetic process	36	0.0254	ABAT,ADP1,AGPAT9,ALOX15B,ANG,ASNS,ATF3,ATF4,B3GNT5,CHST2,CTNS,CYP27B1,CYP51A1,DPVD,ELOVL6,EXT1,FABP5,GADD45GIP1,GGLC,GFP1T,GMPFB,GF2T,MTM,MTM R4,NPLOC4,PC,PGM3,PIGA,PMP,PSA1,PTGES,TRAM2,UAP1,UFD1L,UGDH,UPEB1
1	post-translational protein modification	15	0.0256	ALG13,B3GNT5,CALR,GFP1T,GMPFB,MLEC,PGM3,PIGA,PRKCSH,RPN1,SEC24D,SEC31A,STGALNA4C4,SUMO1,UAP1
4	signal peptide processing	3	0.0263	SEC11C,SFCS2,SFCS3
1	protein catabolic process	20	0.0281	ATXN3,DDIT3,DERL2,DNAJB9,DNAJC10,HSP90B1,HSPA5,HTRA2,LYPLA1,NPLOC4,PPP2C8,PSMOC6,SDF2L1,SEL1L,SVVN1,TOPORS,UBXN1,UFD1L,USP18,WFS1
1	glycosylation	14	0.0281	B3GNT5,CALR,EXT1,GFP1T,GMPFB,MLEC,OSTC,PGM3,RPN1,SEC24D,SEC31A,STGALNA4C4,SVVN1,UAP1
1	regulation of protein metabolic process	56	0.0285	AARS,ALK,ANG,ATF3,ATXN3,BANP,CTNIN1,CTR9,DDIT4,DERL2,DNAJC10,DUSP6,EBI3,EIF2AK3,FAM129A,FRP1,GABARAPL2,GQLC,GDF15,GPR183,HMG81,HSP90B1,HSPA5,HSPH1,HTRA2,IER3,IRAK2,KLF4,MAPV17L2,NFKBIA,PELI1,PPP1CB,PPP1R15B,PSMOC6,RAP1B,RS2,SELT,SERPINE1,SPOOD1,SUMO1,TAJ9,TLR1,TNFSF10,TOB1,TOPORS,TRIB1,TRIB3,TRIM5,UBXN1,USP18,WFS1,ZFAND2A
4	cellular response to DNA damage stimulus	23	0.0289	ATMIN,ATXN3,BATF,BCL2A1,DDIT3,DDIT4,DTX3L,DYRK2,EERP1,FANCE,HMG81,HTRA2,IER3,ILG4,MSH2,NPLOC4,PSMOC6,RAD9A,SUMO1,TAJ9,TPP2,UBE2T,UFD1L
4	gamma-aminobutyric acid catabolic process	2	0.0289	ABAT,ALDH5A1
4	beta-alanine biosynthetic process	2	0.0289	DPVD,UPEB1
2	positive regulation of B cell proliferation	5	0.0289	ADA,CD38,GPR183,PELI1,TNFRSF4
2	positive regulation of lymphocyte proliferation	8	0.0289	ADA,CD276,CD38,EBI3,GPR183,PELI1,PMP,TNFRSF4
4	regulation of transcription from RNA polymerase II promoter in response to arsenic-containing substance	2	0.0289	ATF3,ATF4
2	cellular response to molecule of bacterial origin	9	0.0289	ANKRD1,CD36,CTR9,IRAK2,NFKBIA,PDE4B,SERPINE1,TLR1,ZC3H12A
1	regulation of ATF6-mediated unfolded protein response	2	0.0289	HSPA5,WFS1
2	immune system process	48	0.0292	APP,ATP1B1,BATF,CALR,CARZ1,CC123,CC142,CD164,CD276,CD38,CYP27B1,DDIT4,DUSP6,GPR183,HMG81,HSP90B1,IDD,IRAK2,KLF4,ILG4,LY75,MAPT,MSH2,MTM,PGM3,PIK3AP1,PMP,PRKCSH,PSMOC6,RNF199,ROCK1,SEC24D,SEC31A,SLAMF1,SLC26A6,SLC3A2,SLC7A5,SLFN11,SUMO1,TAK1,TM6M91,TNFRSF4,TNFSF10,TRIB3,TRIM5,USP18
4	single-organism catabolic process	27	0.0292	ABAT,ALDH1L2,ALDH5A1,CISD2,CYP27B1,DERL2,DNAJB9,DNAJC10,DPVD,FABP5,GABARAPL2,GFP1T,HERPUD1,HSP90B1,HSPA5,NPLOC4,PDE4B,PMP,PPP10B,PSMOC6,SDF2L1,SEL1L,SVVN1,UFD1L,UPEB1,WPI1
4	small molecule biosynthetic process	16	0.0295	ABAT,ADP1,ALOX15B,ASNS,CYP27B1,CYP51A1,DPVD,ELOVL6,FABP5,GF2T,MTM,FDZ,PMP,PSA1,PTGES,UGDH,UPEB1
1	negative regulation of protein metabolic process	30	0.0295	ANG,APP,ATF3,BANP,CALR,CD276,CTNNB1,DDIT4,DERL2,DNAJC10,DUSP6,EIF2AK3,FAM129A,GABARAPL2,GQLC,HERPUD1,HRSF12,HSPH1,KLF4,PPP1R15B,PSMOC6,RS2,SERPINE1,SPOCD1,TAJ9,TNFSF10,TOB1,TRIB1,TRIB3,UBXN1
4	anion transmembrane transport	13	0.0302	ASNA1,CD236,CLIC2,CTNS,GABRE,SLOC1A4,SLOC1A5,SLOC22A16,SLC26A6,SLC35B1,SLC3A2,SLC7A1,SLC7A5
3	negative regulation of apoptotic signaling pathway	11	0.0304	BCL2L1,CTNNB1,GQLC,HERPUD1,HSPH1,HTRA2,IER3,SERPINE1,SVVN1,TAJ9,WFS1
2	response to lipopolysaccharide	13	0.0315	ACPS,ANKRD1,CD36,CTR9,CYP27B1,IRAK2,NFKBIA,PDE4B,PELI1,PTGES,SERPINE1,TRIB1,ZC3H12A
3	regulation of neuron death	12	0.0315	AARS,ATF4,CTNNB1,DDIT3,DDIT4,GQLC,HTRA2,HYOU1,ILG4,MSH2,ROCK1,WFS1
4	single-organism intracellular transport	32	0.0315	APP,ATP1B1,ATP2A2,CALR,DDIT3,DERL2,GABARAPL2,HERPUD1,HSP90B1,KIAA1033,KIAA11279,KPNA2,NFKBIA,NPLOC4,RP1P1,RPN1,RTD4,SEC11C,SEC24D,SEC31A,SEL1L,SPC32,SPCS3,SRSF11,SRSF3,SVVN1,TOB1,UFD1L,VP526A,WFS1,WPI1,XCR1
1	protein maturation by protein folding	3	0.032	CALR,EROT1B,WFS1
3	negative regulation of apoptotic process	26	0.032	AARS,ADA,ASNS,BCL2A1,CAST,CD38,CTNNB1,EIF2AK3,HSP90B1,HSPA5,HSPH1,HTRA2,KLF4,ILG4,MSH2,NFKBIA,PIW2,PSMOC6,ROCK1,SERPINE1,SVVN1,TAJ9,TNFSF10,TOPORS,WFS1
1	glycoprotein biosynthetic process	15	0.0333	ALG13,B3GNT5,CALR,EXT1,GFP1T,GMPFB,MLEC,OSTC,PGM3,RPN1,SEC24D,SEC31A,STGALNA4C4,SVVN1,UAP1
1	regulation of proteasomal ubiquitin-dependent protein catabolic process	9	0.0333	ATXN3,GQLC,HERPUD1,SUMO1,TAJ9,TRIB1,TRIB3,UBXN1,ZFAND2A
4	positive regulation of macromolecule metabolic process	59	0.0351	ALK,ANG,ANKRD1,APP,ATF3,ATMIN,ATXN3,BANP,BATF,CALR,COG61,CD276,CD36,CD38,CTNNB1,CTR9,DDIT3,DDX17,DYRK2,EBI3,FAM129A,FRP1,FZD2,GQLC,GDF15,GNL3,GPR183,HERPUD1,HMG81,HSPH1,HTRA2,IDD,IER3,IRAK2,KLF4,LARP1B,MAP,MEK21,MAPV17L2,NFKBIA,PELI1,PIW2,PSMOC6,RAP1B,SERPINE1,SERTAD3,SUMO1,TAJ9,TLR1,TNFSF10,TOPORS,TRAF1,TRIB1,TRIB3,TRIM5,V5X2,WFS1,ZC3H12A,ZFAND2A
4	positive regulation of cellular metabolic process	62	0.0357	ALK,ANG,ANKRD1,APP,ATF3,ATMIN,ATP1B1,ATXN3,BANP,BATF,COTN1F,CALR,COG61,CD276,CD36,CD38,CTNNB1,CTR9,DDIT3,DDX17,DYRK2,EBI3,FAM129A,FRP1,FZD2,GQLC,GDF15,GNL3,GPR183,HERPUD1,HMG81,HSPH1,HTRA2,IDD,IER3,IRAK2,KLF4,LARP1B,MAP,MEK21,MAPV17L2,NFKBIA,PELI1,PIW2,PSMOC6,RAP1B,SERPINE1,SERTAD3,SLC14A4,SUMO1,TAJ9,TLR1,TM6M9A,TNFSF10,TOB1,TOPORS,TRAF1,TRIB1,TRIB3,TRIM5,V5X2,ZC3H12A,ZFAND2A
4	positive regulation of metabolic process	73	0.0364	ALK,ANG,ANKRD1,APP,ARHGEP10L,ATF3,ATMIN,ATP1B1,ATXN3,BANP,BATF,CALR,COG61,CD276,CD36,CD38,CDG4E29,CTNNB1,CTR9,CYP27B1,DDIT3,DDX17,DNAJC10,DYRK2,EBI3,EVL,FAM129A,FRP1,FZD2,GABARAPL2,GQLC,GDF15,GNL3,GPR183,HERPUD1,HMG81,HSPH1,HTRA2,IDD,IER3,IRAK2,KLF4,LARP1B,MAP,MEK21,MAPV17L2,MSH2,NFKBIA,PELI1,PIGA,PIW2,PSMOC6,RAP1B,ROCK1,RS2,SERPINE1,SERTAD3,SLC14A4,SUMO1,TAJ9,TLR1,TM6M9A,TNFSF10,TOB1,TOPORS,TRAF1,TRIB1,TRIB3,TRIM5,V5X2,WFS1,ZC3H12A,ZFAND2A



4	protein localization	42	0.0384	ASNA1,ATP1B1,BANP,CALR,CD36,CTNNB1,DERL2,EIF2AK3,FKBP4,GABARAPL2,HERPUD1,HSP90B1,HSPA5,KIAA1033,LIN7C,NFKBIA,NPL0C4,PDIA4,PNP,PNF19B,RP1,RPN1,RTT4,SAR1A,SEC11C,SEC24D,SEC31A,SELT,IL,SELT,SIL1,SPCS2,SPCS3,SYVN1,TCOP1,TIME07,TOB1,TOPOORS,TRAM2,UFD1L,VPS28A,WFS1,WIP1
3	negative regulation of cell death	27	0.0389	AARS,ADA,ASNS,ATF4,BCL2L1,CAST,CD38,CTNNB1,EIF2AK3,HSP90B1,HSPA5,HSPH1,HTRA2,KL,F4,LI,G4,MERTK,MSH2,NFKBIA,PNM2,PSMCG,ROCK1,SERPINE1,SYVN1,TA,F9,TNFSF10,TOPOORS,WFS1
4	primary metabolic process	148	0.0405	ADI1,AGPAT9,ALDH1L2,ALX,AMV,2B,ANG,ANKRD1,ANP32A,ASNA1,ASNS,ATF7IP2,ATMIN,B3GN15,BANP,BCAS2,C12orf65,C1D,CALR,CARS,CD36,CHST2,COMMD8,CTNNB1,CTNS,CTR9,CYP27B1,CYP51A1,DDIT3,DDIT4,DDX17,DERL2,DNAJA4,DNAJB5,DNAJB9,DNAJC10,DPVD,DTX3L,DUSP6,DYRK2,EEF1B2,EEPD1,ELOVL6,EXT1,FANCE,FICD,FKBP11,FKBP14,FKBP2,FKBP4,FKBP5,G3BP1,GADD45G,IP1,GFP11,GMPFB,GP12,HABP4,HMG81,HRS,SP12,HSP90B1,HSPA5,HSPH1,HYOU1,HD,IRAK2,KL,F4,KPNA2,LIG4,LMO4,LYPLA1,MATK,MBNL2,ME,RTK,MLEC,MSH2,MTMR4,NABP2,NDUFAG5,NFKL1,NPL0C4,OSTC,PC,PDE4B,PDIA4,PDIA5,PDIA6,PEL1,PFON2,PGM3,PIGA,PNM2,PNP,PP9G,PLL1,PPP1CB,PRPF4B,PSAT1,PSMCG,PTGES,PTMA,RAD9A,RNASE4,RNF19B,ROCK1,RP1,RPN1,SDFZL1,SEC24D,SEC31A,SELT,SERPINE1,SERTAD3,SIL1,SLC3A2,SLC7A5,SPOCD1,SRSF11,SRSF3,STB6GALNA,C4,SUMO1,SYVN1,TA,F9,TARS,TCOP1,TDP2,TNFSF10,TOPOORS,TRIB1,TRIM5,TSN,TUBA3D,TUBB3,UAP1,UBA5,UBE2T,UBXN1,UFD1L,UGDH,UPB1,USP18,V5X2,WVF,WFS1,WIP1,WTPA,Z,CH12A,ZNF395,ZNF768
3	regulation of intrinsic apoptotic signaling pathway	9	0.0405	BCL2L1,DDIT3,HERPUD1,HSPH1,HTRA2,RAD9A,SYVN1,TA,F9,WFS1
4	regulation of sequence-specific DNA binding transcription factor activity	15	0.0409	ALK,DDIT3,FZD2,IRAK2,KL,F4,NFKBIA,PEL1,SUMO1,TNFRSF4,TRAF1,TRIB1,TRIM5,WFS1,ZC3H12A
1	intracellular protein transport	23	0.0485	ATP1B1,CALR,DERL2,HERPUD1,HSP90B1,KPNA2,NFKBIA,NPL0C4,RP1,RPN1,RTA4,SAR1A,SEC11C,SEC24D,SELT,SIL1,SPCS2,SPCS3,SYVN1,TOB1,UFD1L,VPS28A,WFS1
4	cell communication	97	0.0486	AARS,ABAT,ALDH9A1,ALK,ANG,ANP32A,APP,ASNA1,ASNS,ATP1B1,ATP2A2,ATXN3,BATF,BCL2L1,CALR,CCL23,CD164,CD36,CD38,DDC4,ZEP3,GSD2,CLC2,CTNNB1,CTR9,DDIT4,DE,R2,DNAJB11,DNAJB9,DNAJC10,DUSP6,DYRK2,EBI3,EVL,EXT1,FKBP14,FKBP4,FKBP5,FKBP11,FKBP13,G3BP1,GABARAPL2,GABRE,GDF15,GFP11,GNB4,GPR132,GPR183,HERPUD1,HSP90B1,HSPA5,HTRA2,HYOU1,IER3,IRAK2,KCNK6,KL,F4,KPNA2,LIN7C,MATK,MSH2,MTMR4,PDE4B,PDIA5,PDIA6,PIK3AP1,PPP1CB,PPP1R15B,PPP2C8B,PRKCSH,PSMCG,PTGES,ROCK1,RTKN,SEC31A,SELT,SELK,SELT,SEMA3A,SERPINE1,SLAMF1,SLC1A4,SLC2B6A,SRSF3,SUMO1,SYVN1,TDP2,TNFRSF4,TNFSF10,TOB1,TRAF1,TRIB1,TRIB3,TRIM5,USP18,WFS1,WIP1,XCR1
4	carboxylic acid biosynthetic process	12	0.0486	ABAT,ADI1,ALOX15B,ASNS,DPVD,ELOVL6,GPT2,MTHFD2,PSAT1,PTGES,UGDH,UPB1
3	negative regulation of intrinsic apoptotic signaling pathway	7	0.0486	BCL2L1,HERPUD1,HSPH1,HTRA2,SYVN1,TA,F9,WFS1
4	regulation of localization	52	0.0489	ABAT,ADA,ALOX15B,ANG,ANKRD1,ATF4,ATP1B1,ATP2A2,BORA,C10orf11,CALR,CDZ76,CD36,CD38,CLC2,CTNNB1,DDIT3,DERL2,DNAJF1,DYRK2,EIF2AK3,EVL,HMG81,HSPA5,HSPH1,HTRA2,IER3,KCNK6,KL,F4,LYPLA1,MERTK,NFKBIA,PDE4B,RAIP1B,ROCK1,SAR1A,SEC11C,SERPINE1,SLAMF1,SLC17A9,SLC26A6,SPCS2,SPCS3,SUMO1,TLR1,TNFRSF4,TNFRSF9,TRIB1,TRIB3,WFS1,XCR1,ZC3H12A
4	positive regulation of macromolecule biosynthetic process	40	0.0494	ALK,ANKRD1,APP,ATF3,ATMIN,BANP,BATF,CALR,CCPG1,CD276,CD38,CTNNB1,CTR9,DDIT3,DDX17,DYRK2,EBB,FAM129A,FZD2,GNL3,HMG81,HSPA5,HSPH1,HD,IRAK2,KL,F4,MAFM,ED21,MPV17L2,NFKBIA,PM2,PSMCG,SERPINE1,SERTAD3,TA,F9,TLR1,TOPOORS,TRAF1,TRIM5,V5X2

Pathway association denoted by colour as follows: UPR only (Blue), Inflammation only (Green), Cell survival (Red), UPR and Inflammation (Purple), General cell process (Grey)