

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,WIP1
endoplasmic reticulum unfolded protein response	10	1.58E-07	ASNS,ATF4,EIF2AK3,FKBP14,GFPT1,PDIA5,SEC31A,SYVN1,WFS1,WIP1
cellular response to unfolded protein	10	1.58E-07	ASNS,ATF4,EIF2AK3,FKBP14,GFPT1,PDIA5,SEC31A,SYVN1,WFS1,WIP1
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,WIP1
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,WIP1
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,WIP1
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,WIP1
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,WIP1

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
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,HSP95,KIAA1033,KIPNA2,LIN7C,MERT
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,DYNCL1L1,FABP5,FKBP4,G3BP1,GABARAPL2,H
1	nucleotide-sugar biosynthetic process	5	0.00117	GFP11,GMIPBP,PGM3,UAP1,UGDH
1	protein folding in endoplasmic reticulum	4	0.00129	CALR,DNAJC10,HSP90B1,HSP95
4	negative regulation of biological process	93	0.00153	AARS,ACPS,ALOX15B,ANG,ANKRD1,ASNS,ATP2A2,BANP,BCL2A1,C1D,C10,TNF1,CALR,CAPZ1,CAST,CCL23,CD164,CD276,CD36,CLIC2,CTNNB1,CTR9,CYP27B1,DDIT3,DERL2,DNA
1	cell redox homeostasis	8	0.00175	DDIT3,DNAJC10,EROC1LB,GOLC,PDIA4,PDIA6,SEL1
4	localization	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,DYNCL1L1,FAB
3	intrinsic apoptotic signaling pathway	12	0.00255	ADIT4,BCL2A1,DDIT3,DDIT4,DNAJC10,DYRK2,EIF2AK3,HTRA2,IER3,MSH2,SELK,TRIB3
1	transcription factor activity	11	0.00261	DDIT3,JD2,IRAK2,KLF4,NFKBIA,PEL1,SUMO1,TNFRSF4,TRIB1,WFS1,ZC3H12A
3	intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress	6	0.00261	ATF4,DDIT3,DNAJC10,EIF2AK3,SELK,TRIB3
3	regulation of apoptotic process	41	0.00262	AARS,ADA,ALK,ANKRD1,ASNS,ATF3,ATF4,BCL2A1,BEY2,CALR,CAST,CD38,CTNNB1,DDIT3,DUSP6,GDF15,HMG81,HSP90B1,HSP95,HSHP1,HTRA2,KLF4,LLGA,MERTK,MSH2,NFKBIA,
1	peptidyl-amino acid modification	30	0.00292	ALG13,ALK,CALR,CTR9,DYRK2,EIF2AK3,FKBP11,FKBP14,SYVN1,TA9,TCP1,TNFRSF4,TNFSF10,TOPORS,TRA1,WFS1
4	cellular amino acid metabolic process	17	0.00294	AARS,ADI1,ALDH1L2,ALDH5A1,ASNS,ATF4,CARS,CTNS,DYPD,EROC1LB,GOLC,GFP11,GPT2,PSAT1,SLC7A6,TARS,UPI1
4	response to biotic stimulus	26	0.0042	ACPS,ANKRD1,BATF,CD36,CTR9,CYP27B1,DDIT3,DDIT4,EIF2AK3,HSP5A,IER3,IRAK2,NFKBIA,PDE4B,PEL1,PIM2,PPP1R15B,PTGES,SERPINE1,SLFN11,TLR1,TMEM91,TRIB1,TRIB5,
4	cellular localization	54	0.00461	ABAT,ALDH5A1,ANP32A,APP,ASN1,ATP1B1,ATP2A2,BANP,CALR,CD36,CTNNB1,DDIT3,DERL2,EIF2AK3,GABARAPL2,HABP4,HERPUD1,HSP90B1,HSP95,KIAA1033,KIPNA2,LIN7C,MERTK,MSH2,NFKBIA,NFLOC4,PDIA4,PNP,RNF19B,ROCK1,RP11,RP1N1,RTP4,SAR1A,SEC11C,SEC31A,SEL1L,SEL1T,SERPINE1,SIL1,SLC17A9,SPCS2,SPCS3,SRSF11,SRSF3,SYVN1
3	regulation of cell death	42	0.00471	AARS,ADA,ALK,ANKRD1,ASNS,ATF3,ATF4,BCL2A1,BEY2,CALR,CAST,CD38,CTNNB1,DDIT3,DDIT4,DUSP6,GDF15,HMG81,HSP90B1,HSP95,HSHP1,HTRA2,KLF4,LLGA,MERTK,MSH2,NFKBIA,PIM2,PPP1R15B,PTGES,RAV9A,ROCK1,SDZL1,SERPINE1,SYVN1,TA9,TCP1,TNFRSF4,TNFSF10,TOPORS,TRA1,WFS1
4	negative regulation of cellular process	85	0.00601	AARS,ACPS,ALOX15B,ANG,ANKRD1,ASNS,ATF4,BCL2A1,C1D,C10,TNF1,CALR,CAPZ1,CAST,CCL23,CD164,CD276,CD36,CLIC2,CTNNB1,CTR9,CYP27B1,DDIT3,DERL2,DNAJA4,DNA
1	positive regulation of transcription from RNA polymerase II promoter in response to endoplasmic reticulum stress	4	0.00605	ATF3,ATF4,DDIT3,HSP45
1	single-organism carbohydrate metabolic process	23	0.00637	ALDH5A1,ATF3,ATF4,B3GNT5,CALR,EXH1,FABP5,GOLC,GFP11,GMIPBP,GOI1,MLEEC,OSTC,PC,PGM3,PPP1R15B,PTGES,SEC31A,STRGAL,NAC4,SYVN1,UAP1,UGDH
4	cellular metabolic process	152	0.00679	ACPS,ADI1,AGPAT9,ALDH1L2,ALK,ANG,ANKRD1,ANP32A,APP,ASN1,ASNS,ATF3,ATP2A2,ATMIN,ATXN3,B3GNT5,BANP,PCAS2,C12orf86,C1D,CALR,CARS,CD36,CHST2,CISD2,COM
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,FABP5,GABARAPL2,HERPUD1,HSP90B1,KIAA1033,LIN7C,MESD2A,NFKBIA,NIP1,LOC4,PDIA4,PNP,RNF198,RPL,P1,RTTP4,SAR1A,SEC11C,SEC24D,SEC31A,SEL,IL,SEL1,SIL1,SLC14A,SLC14A5,SLC22A1,6,SLC28A6,SLC35B1,SLC3A2,SLC37A1,SLC37A5,SFPCS2,SFPCS3,SRSF11,SRSF3,SYVN1,TCP1,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,C1D,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,FANCC,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,PDND2,PGM3,PIGA,PIW2,PP1G,PP1L1,PPP1CB,PPP4B,PSM06,PTMA,RAO9A,RNASE4,RNF198,ROCK1,RPL,P1,RP1,SPZL1,SEC24D,SEC31A,SEL,IL,SEL1,SERPINE1,SERTAD3,SIL1,SPOCD1,SRSF11,SRSF3,STREGALNAQC,SUMO1,SYVN1,TAJ9,TAJ9,TCF1,TPP2,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,RPL,P1,RPN1,SEC11C,SEC24D,SEC31A,SEL,IL,SFPCS2,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,TAJ9,TCF1,TPP2,TOFOR5,TRIB1,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,GGQC,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,C1D,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,RPL,P1,RP1,RTTP4,SAR1A,SEC11C,SEC24D,SEC31A,SEL,IL,SEL1,SIL1,SFPCS2,SFPCS3,SYVN1,TCP1,TMED7,TOB1,TRAM2,UFD1L,VPS28A,WFS1
2	B cell activation involved in immune response	5	0.0179	ADA,BATF,GRR183,LUG4,MSH2
2	response to molecule of bacterial origin	14	0.0187	ACPS,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,SLC37A5
1	positive regulation of protein metabolic process	38	0.0192	ALK,KANG,APP,ATXN3,C1GNTN1,CD276,CD36,CTNNB1,CTR9,EBI3,EIF2AK3,FAM129A,FR1,GQLC,GDF15,GRR183,HERPUD1,HMG81,HSPA6,HSPH1,HTRA2,IER3,IRAK2,KLF4,MNP17L2,NFKBIA,PEL1,PSM06,RAP1B,SUMO1,TLR1,TNFSF10,TOFOR5,TRIB1,TRIB3,TRIM5,WFS1,ZFAND2A
4	regulation of cellular catabolic process	24	0.0201	ATP1B1,ATXN3,C1SD2,DDI14,GABARAPL2,GQLC,HERPUD1,HTRA2,IER3,LARP1B,PIW2,PSM06,SLC17A9,SLC14A,SUMO1,TAJ9,TMED39A,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,CABLES2,CA LR,CARS,CAST,CCDC288,CCL23,CCL412,CD168,CD169,CD36,CDCA228P3,CHST2,CLIC2,COMMDD,CREL1,CTNNB1,CYB561,CYP27B1,CYP91A1,DDIT3,DDX17,DHS11,DNAAF1,DNAJB9,DYD,DITX3,DYRK2,EEF1B2,EEP1,EIF2AK3,ENTPD7,EVH5,EXT1,FAM129A,FANCE,FGFBP3,FICD,FKBP14,FKBP2,FKBP5,FNDC3A,FR1,FR3,IZO2,GABARAPL2,GAD,DM3G1P1,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,MSD2A,MIS12,MLEC,MPLKIP1,MV17L2,MSH2,MTT1H,MTM,MTTR1,MTHE,D2,NABP2,NDUFA5,NFKBIA,NFXL1,NIP1,LOC4,OSTC,PC,PDE4B,PDIA4,PDIA5,PDIA6,PDIA6,PNP,PP1G,PP1L1,PPP1CB,PPP4B,PSAT1,PSM06,PS1,PI2,PTMA,ROCK1,ROCK2,RNASE4,RNF198,ROCK1,RP1,P1,RTKN,RTTP4,SAR1A,SDF2L1,SEC31A,SELK,SEMA3A,SERPINE1,SIL1,SLA,SLC10A7,SLC17A9,SLC17A9,SLC17A9,SLC17A9,SLC22A16,SLC28A6,SLC35B1,SLC39A14,SLC3A2,SLC37A1,SLC7A5,SLE1N1,SP140,SRSF11,SRSF3,STREGALNAQC,SUMO1,SYVN1,TAJ9,TAJ9,TCF1,TPP2,TOFOR5,TRIB1,TRIB3,TRIM5,TSN,TUBA3D,TUBB8,UAP1,UBA5,UBE2T,UBXN1,UFD1L,USP18,V5X2,WFS1,WIP1,WIPAP,ZNF395,ZNF788
4	cell activation	22	0.0241	APP,BATF,CAST,CD276,CD36,CTNNB1,EBI3,GFP11,HABP4,HMG81,HSPA6,DI2,LUG4,MERTK,MSH2,MTM1G,RAIP1B,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,RPL,P1,RP1,RTTP4,SAR1A,SEC11C,SEC24D,SEC31A,SEL,IL,SEL1,SIL1,SFPCS2,SFPCS3,SYVN1,TCP1,TMED7,TOB1,TRAM2,UFD1L,VPS28A,WFS1
1	regulation of proteasomal protein catabolic process	12	0.0246	ATXN3,GABARAPL2,GQLC,HERPUD1,PSM06,SUMO1,TAJ9,TAJ9,TRIB1,TRIB3,UBXN1,USP18,ZFAND2A
2	immune response	36	0.0248	ADA,APP,BATF,CAPZ1,CCL23,CCL412,CD164,CD276,CD36,CTNNB1,CYP27B1,DUSP6,EBI3,GPR183,HMG81,IRAK2,LUG4,LV75,MATK,MSH2,NFKBIA,PEL1,PNP,PRKCGH,PSM06,RNF198,SLC28A6,SUMO1,TANK,TLR1,TNFRSF4,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,GMPPB,HABP4,HMG81,HRSF12,HSP90B1,HSPA5,HSPH1,HTRA2,HYOU1,IDD,IRAK2,KLF4,KPM2,LANC4,LMQ4,MATIK1,MBNL2,MERTK,MLIEC,MSH2,MTM4,NABP2,NFXL1,NPLOC4,OSTC,PDIA4,PDIA5,PDIA6,PELI1,PFND2,PGM3,PIGA,PIW2,PP1C,PPP1B,PPP4B,PSMOC6,PTM4,RAO9A,RNA52A,RNF199,ROCK1,ROP1,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,UFDH1,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,GMPPB,GFRT2,MTM4,MTM18,NPLOC4,PC,PGM3,PIGA,PMP,PSA1,PTGES,TRAM2,UAP1,UFD1L,UFDH1,UFB1
1	post-translational protein modification	15	0.0256	ALG13,B3GNT5,CALR,GFP1T,GMPPB,MLEC,PGM3,PIGA,PRKCSH,RPN1,SEC24D,SEC31A,ST6GALNA4C4,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,LYP1A1,NPLOC4,PPP2C8,PSMOC6,SDF2L1,SEL1L,SVVN1,TOPORS,UBXN1,UFD1L,USP18,WFS1
1	glycosylation	14	0.0281	B3GNT5,CALR,EXT1,GFP1T,GMPPB,MLEC,OSTC,PGM3,RPN1,SEC24D,SEC31A,ST6GALNA4C4,SVVN1,UAP1
1	regulation of protein metabolic process	56	0.0285	AARS,ALK,ANG,ATF3,ATXN3,BANP,CTOIN1,CALR,CD36,CTNNB1,CTR9,DDIT4,DERL2,DNAJC10,DUSP6,EBI3,EIF2AK3,FAM129A,FRP1,GABARAPL2,GGLC,GDF15,GPR183,HMG81,HSP90B1,HSPA5,HSPH1,HTRA2,IER3,IRAK2,KLF4,MAPV17L2,NFKBIA,PELI1,PPP1CB,PPP1R15B,PSMOC6,RAP1B,RGS2,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,UFB1
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,PNP,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,MTM4,PGM3,PIK3AP1,PNP,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,GFRT2,HERPUD1,HSP90B1,HSPA5,NPLOC4,PDE4B,PNP,PPP10B,PSMOC6,SDF2L1,SEL1L,SVVN1,UFD1L,UFB1,WPI1
4	small molecule biosynthetic process	16	0.0295	ABAT,ADP1,ALOX15B,ASNS,CYP27B1,CYP51A1,DPVD,ELOVL6,FABP5,GFRT2,MTM4,MTM18,USP18
1	negative regulation of protein metabolic process	30	0.0295	ANG,APP,ATF3,BANP,CALR,CD276,CTNNB1,DDIT4,DERL2,DNAJC10,DUSP6,EIF2AK3,FAM129A,GABARAPL2,GGLC,HERPUD1,HRSF12,HSPH1,KLF4,PPP1R15B,PSMOC6,SERPINE1,SPOCD1,TAJ9,TNFSF10,TOB1,TRIB1,TRIB3,UBXN1
4	anion transmembrane transport	13	0.0302	ASNA1,CD236,CLIC2,CTNS,GABRE,SLOC1A4,SLC17A5,SLC22A16,SLC26A6,SLC35B1,SLC32A2,SLC7A1,SLC7A5
3	negative regulation of apoptotic signaling pathway	11	0.0304	BCL2L1,CTNNB1,GGLC,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,GGLC,HTRA2,HYOU1,ILG4,MSH2,ROCK1,WFS1
4	single-organism intracellular transport	32	0.0315	APP,ATP1B1,ATP2A2,CALR,DDIT3,DERL2,GABARAPL2,HERPUD1,HSP90B1,KIAA1033,KIAA1279,KPNA2,NFKBIA,NPLOC4,PPP1R1,RPN1,RTD4,SEC11C,SEC24D,SEC31A,SEL1L,SPCS2,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,MERTK,MSH2,NFKBIA,PIW2,PSMOC6,ROCK1,SERPINE1,SVVN1,TAJ9,TNFSF10,TOPORS,WFS1
1	glycoprotein biosynthetic process	15	0.0333	ALG13,B3GNT5,CALR,EXT1,GFP1T,GMPPB,MLEC,OSTC,PGM3,RPN1,SEC24D,SEC31A,ST6GALNA4C4,SVVN1,UAP1
1	regulation of proteasomal ubiquitin-dependent protein catabolic process	9	0.0333	ATXN3,GGLC,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,GGLC,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,COTIN1,CALR,COG61,CD276,CD36,CD38,CTNNB1,CTR9,DDIT3,DDX17,DYRK2,EBI3,FAM129A,FRP1,FZD2,GGLC,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,ARHGAP10,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,GGLC,GDF15,GNL3,GPR183,HERPUD1,HMG81,HSPH1,HTRA2,IDD,IER3,IRAK2,KLF4,LARP1B,MAP,MEK21,MAPV17L2,MSH2,NFKBIA,PELI1,PIGA,PIW2,PSMOC6,RAP1B,ROCK1,RGS2,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,RP1P1,RPN1,RTT4,SAR1A,SEC11C,SEC24D,SEC31A,SELT1L,SELT1,SIL1,SPCS2,SPCS3,SYVIN1,TCOP1,TME07,TOB1,TOPORES,TRAM2,UFD1L,VPS26A,WFS1,WIP1
3	negative regulation of cell death	27	0.0389	AARS,ADA,ASNS,ATF4,BCL2L1,CAST,CD38,CTNNB1,EIF2AK3,HSP90B1,HSPA5,HSPH1,HTRA2,KLIF4,LIG4,MERTK,MSH2,NFKBIA,PNM2,PSMCG,ROCK1,SERPINE1,SYVIN1,TAIF9,TNFSF10,TOPORES,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,EEPDP1,ELOVL6,EXT1,FANCE,FICD,FKBP11,FKBP14,FKBP2,FKBP4,FKBP5,G3BP1,GADD45GIP1,GFP11,GMPFB,GP12,HABP4,HMG81,HRS,SP12,HSP90B1,HSPA5,HSPH1,HYOU1,HD,IRAK2,KLIF4,KPNA2,LIG4,LMO4,LYPLA1,MATK,MBNL2,ME,RTK,MLEC,MSH2,MTMR4,NABP2,NDUFA5,NFKX1,NPL0C4,OSTC,PC,PDE4B,PDIA4,PDIA5,PDIA6,PEL1,PFON2,PGM3,PIGA,PNM2,PNP,PP9G,PLP1,PPP1CB,PRPF4B,PSAT1,PSMCG,PTGES,PTMA,RAD9A,RNASE4,RNF19B,ROCK1,RP1P1,RPN1,SDFZL1,SEC24D,SEC31A,SELT1,SELT1,SERPINE1,SERTAD3,SIL1,SLC3A2,SLC7G5,SPOCD1,SRSF11,SRSF3,STB6GALNAO4,SUMO1,SYVIN1,TAIF9,TARS,TCOP1,TDP2,TNFSF10,TOPORES,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,SYVIN1,TAIF9,WFS1
4	regulation of sequence-specific DNA binding transcription factor activity	15	0.0409	ALK,DDIT3,FZD2,IRAK2,KLIF4,NFKBIA,PEL1,SUMO1,TNFRSF4,TRAF1,TRIB1,TRIM5,WFS1,ZC3H12A
1	intracellular protein transport	23	0.0485	ATP1B1,CALR,DERL2,HERPUD1,HSP90B1,KPNA2,NFKBIA,NPL0C4,RP1P1,RPN1,RTA4,SAR1A,SEC11C,SEC24D,SELT1,SIL1,SPCS2,SPCS3,SYVIN1,TOB1,UFD1L,VPS26A,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,DDC4ZEP3,GISD2,CLC2,CTNNB1,CTR9,DDIT4,DE,R2,DNAJB11,DNAJB9,DNAJC10,DUSP6,DYRK2,EBI3,EVL,EXT1,FKBP14,FKBP4,FKBP5,FKBP11,FKBP12,FKBP13,FKBP14,FKBP15,FKBP16,FKBP17,FKBP18,FKBP19,FKBP20,FKBP21,FKBP22,FKBP23,FKBP24,FKBP25,FKBP26,FKBP27,FKBP28,FKBP29,FKBP30,FKBP31,FKBP32,FKBP33,FKBP34,FKBP35,FKBP36,FKBP37,FKBP38,FKBP39,FKBP40,FKBP41,FKBP42,FKBP43,FKBP44,FKBP45,FKBP46,FKBP47,FKBP48,FKBP49,FKBP50,FKBP51,FKBP52,FKBP53,FKBP54,FKBP55,FKBP56,FKBP57,FKBP58,FKBP59,FKBP60,FKBP61,FKBP62,FKBP63,FKBP64,FKBP65,FKBP66,FKBP67,FKBP68,FKBP69,FKBP70,FKBP71,FKBP72,FKBP73,FKBP74,FKBP75,FKBP76,FKBP77,FKBP78,FKBP79,FKBP80,FKBP81,FKBP82,FKBP83,FKBP84,FKBP85,FKBP86,FKBP87,FKBP88,FKBP89,FKBP90,FKBP91,FKBP92,FKBP93,FKBP94,FKBP95,FKBP96,FKBP97,FKBP98,FKBP99,FKBP100,FKBP101,FKBP102,FKBP103,FKBP104,FKBP105,FKBP106,FKBP107,FKBP108,FKBP109,FKBP110,FKBP111,FKBP112,FKBP113,FKBP114,FKBP115,FKBP116,FKBP117,FKBP118,FKBP119,FKBP120,FKBP121,FKBP122,FKBP123,FKBP124,FKBP125,FKBP126,FKBP127,FKBP128,FKBP129,FKBP130,FKBP131,FKBP132,FKBP133,FKBP134,FKBP135,FKBP136,FKBP137,FKBP138,FKBP139,FKBP140,FKBP141,FKBP142,FKBP143,FKBP144,FKBP145,FKBP146,FKBP147,FKBP148,FKBP149,FKBP150,FKBP151,FKBP152,FKBP153,FKBP154,FKBP155,FKBP156,FKBP157,FKBP158,FKBP159,FKBP160,FKBP161,FKBP162,FKBP163,FKBP164,FKBP165,FKBP166,FKBP167,FKBP168,FKBP169,FKBP170,FKBP171,FKBP172,FKBP173,FKBP174,FKBP175,FKBP176,FKBP177,FKBP178,FKBP179,FKBP180,FKBP181,FKBP182,FKBP183,FKBP184,FKBP185,FKBP186,FKBP187,FKBP188,FKBP189,FKBP190,FKBP191,FKBP192,FKBP193,FKBP194,FKBP195,FKBP196,FKBP197,FKBP198,FKBP199,FKBP200,FKBP201,FKBP202,FKBP203,FKBP204,FKBP205,FKBP206,FKBP207,FKBP208,FKBP209,FKBP210,FKBP211,FKBP212,FKBP213,FKBP214,FKBP215,FKBP216,FKBP217,FKBP218,FKBP219,FKBP220,FKBP221,FKBP222,FKBP223,FKBP224,FKBP225,FKBP226,FKBP227,FKBP228,FKBP229,FKBP230,FKBP231,FKBP232,FKBP233,FKBP234,FKBP235,FKBP236,FKBP237,FKBP238,FKBP239,FKBP240,FKBP241,FKBP242,FKBP243,FKBP244,FKBP245,FKBP246,FKBP247,FKBP248,FKBP249,FKBP250,FKBP251,FKBP252,FKBP253,FKBP254,FKBP255,FKBP256,FKBP257,FKBP258,FKBP259,FKBP260,FKBP261,FKBP262,FKBP263,FKBP264,FKBP265,FKBP266,FKBP267,FKBP268,FKBP269,FKBP270,FKBP271,FKBP272,FKBP273,FKBP274,FKBP275,FKBP276,FKBP277,FKBP278,FKBP279,FKBP280,FKBP281,FKBP282,FKBP283,FKBP284,FKBP285,FKBP286,FKBP287,FKBP288,FKBP289,FKBP290,FKBP291,FKBP292,FKBP293,FKBP294,FKBP295,FKBP296,FKBP297,FKBP298,FKBP299,FKBP300,FKBP301,FKBP302,FKBP303,FKBP304,FKBP305,FKBP306,FKBP307,FKBP308,FKBP309,FKBP310,FKBP311,FKBP312,FKBP313,FKBP314,FKBP315,FKBP316,FKBP317,FKBP318,FKBP319,FKBP320,FKBP321,FKBP322,FKBP323,FKBP324,FKBP325,FKBP326,FKBP327,FKBP328,FKBP329,FKBP330,FKBP331,FKBP332,FKBP333,FKBP334,FKBP335,FKBP336,FKBP337,FKBP338,FKBP339,FKBP340,FKBP341,FKBP342,FKBP343,FKBP344,FKBP345,FKBP346,FKBP347,FKBP348,FKBP349,FKBP350,FKBP351,FKBP352,FKBP353,FKBP354,FKBP355,FKBP356,FKBP357,FKBP358,FKBP359,FKBP360,FKBP361,FKBP362,FKBP363,FKBP364,FKBP365,FKBP366,FKBP367,FKBP368,FKBP369,FKBP370,FKBP371,FKBP372,FKBP373,FKBP374,FKBP375,FKBP376,FKBP377,FKBP378,FKBP379,FKBP380,FKBP381,FKBP382,FKBP383,FKBP384,FKBP385,FKBP386,FKBP387,FKBP388,FKBP389,FKBP390,FKBP391,FKBP392,FKBP393,FKBP394,FKBP395,FKBP396,FKBP397,FKBP398,FKBP399,FKBP400,FKBP401,FKBP402,FKBP403,FKBP404,FKBP405,FKBP406,FKBP407,FKBP408,FKBP409,FKBP410,FKBP411,FKBP412,FKBP413,FKBP414,FKBP415,FKBP416,FKBP417,FKBP418,FKBP419,FKBP420,FKBP421,FKBP422,FKBP423,FKBP424,FKBP425,FKBP426,FKBP427,FKBP428,FKBP429,FKBP430,FKBP431,FKBP432,FKBP433,FKBP434,FKBP435,FKBP436,FKBP437,FKBP438,FKBP439,FKBP440,FKBP441,FKBP442,FKBP443,FKBP444,FKBP445,FKBP446,FKBP447,FKBP448,FKBP449,FKBP450,FKBP451,FKBP452,FKBP453,FKBP454,FKBP455,FKBP456,FKBP457,FKBP458,FKBP459,FKBP460,FKBP461,FKBP462,FKBP463,FKBP464,FKBP465,FKBP466,FKBP467,FKBP468,FKBP469,FKBP470,FKBP471,FKBP472,FKBP473,FKBP474,FKBP475,FKBP476,FKBP477,FKBP478,FKBP479,FKBP480,FKBP481,FKBP482,FKBP483,FKBP484,FKBP485,FKBP486,FKBP487,FKBP488,FKBP489,FKBP490,FKBP491,FKBP492,FKBP493,FKBP494,FKBP495,FKBP496,FKBP497,FKBP498,FKBP499,FKBP500,FKBP501,FKBP502,FKBP503,FKBP504,FKBP505,FKBP506,FKBP507,FKBP508,FKBP509,FKBP510,FKBP511,FKBP512,FKBP513,FKBP514,FKBP515,FKBP516,FKBP517,FKBP518,FKBP519,FKBP520,FKBP521,FKBP522,FKBP523,FKBP524,FKBP525,FKBP526,FKBP527,FKBP528,FKBP529,FKBP530,FKBP531,FKBP532,FKBP533,FKBP534,FKBP535,FKBP536,FKBP537,FKBP538,FKBP539,FKBP540,FKBP541,FKBP542,FKBP543,FKBP544,FKBP545,FKBP546,FKBP547,FKBP548,FKBP549,FKBP550,FKBP551,FKBP552,FKBP553,FKBP554,FKBP555,FKBP556,FKBP557,FKBP558,FKBP559,FKBP560,FKBP561,FKBP562,FKBP563,FKBP564,FKBP565,FKBP566,FKBP567,FKBP568,FKBP569,FKBP570,FKBP571,FKBP572,FKBP573,FKBP574,FKBP575,FKBP576,FKBP577,FKBP578,FKBP579,FKBP580,FKBP581,FKBP582,FKBP583,FKBP584,FKBP585,FKBP586,FKBP587,FKBP588,FKBP589,FKBP590,FKBP591,FKBP592,FKBP593,FKBP594,FKBP595,FKBP596,FKBP597,FKBP598,FKBP599,FKBP600,FKBP601,FKBP602,FKBP603,FKBP604,FKBP605,FKBP606,FKBP607,FKBP608,FKBP609,FKBP610,FKBP611,FKBP612,FKBP613,FKBP614,FKBP615,FKBP616,FKBP617,FKBP618,FKBP619,FKBP620,FKBP621,FKBP622,FKBP623,FKBP624,FKBP625,FKBP626,FKBP627,FKBP628,FKBP629,FKBP630,FKBP631,FKBP632,FKBP633,FKBP634,FKBP635,FKBP636,FKBP637,FKBP638,FKBP639,FKBP640,FKBP641,FKBP642,FKBP643,FKBP644,FKBP645,FKBP646,FKBP647,FKBP648,FKBP649,FKBP650,FKBP651,FKBP652,FKBP653,FKBP654,FKBP655,FKBP656,FKBP657,FKBP658,FKBP659,FKBP660,FKBP661,FKBP662,FKBP663,FKBP664,FKBP665,FKBP666,FKBP667,FKBP668,FKBP669,FKBP670,FKBP671,FKBP672,FKBP673,FKBP674,FKBP675,FKBP676,FKBP677,FKBP678,FKBP679,FKBP680,FKBP681,FKBP682,FKBP683,FKBP684,FKBP685,FKBP686,FKBP687,FKBP688,FKBP689,FKBP690,FKBP691,FKBP692,FKBP693,FKBP694,FKBP695,FKBP696,FKBP697,FKBP698,FKBP699,FKBP700,FKBP701,FKBP702,FKBP703,FKBP704,FKBP705,FKBP706,FKBP707,FKBP708,FKBP709,FKBP710,FKBP711,FKBP712,FKBP713,FKBP714,FKBP715,FKBP716,FKBP717,FKBP718,FKBP719,FKBP720,FKBP721,FKBP722,FKBP723,FKBP724,FKBP725,FKBP726,FKBP727,FKBP728,FKBP729,FKBP730,FKBP731,FKBP732,FKBP733,FKBP734,FKBP735,FKBP736,FKBP737,FKBP738,FKBP739,FKBP740,FKBP741,FKBP742,FKBP743,FKBP744,FKBP745,FKBP746,FKBP747,FKBP748,FKBP749,FKBP750,FKBP751,FKBP752,FKBP753,FKBP754,FKBP755,FKBP756,FKBP757,FKBP758,FKBP759,FKBP760,FKBP761,FKBP762,FKBP763,FKBP764,FKBP765,FKBP766,FKBP767,FKBP768,FKBP769,FKBP770,FKBP771,FKBP772,FKBP773,FKBP774,FKBP775,FKBP776,FKBP777,FKBP778,FKBP779,FKBP780,FKBP781,FKBP782,FKBP783,FKBP784,FKBP785,FKBP786,FKBP787,FKBP788,FKBP789,FKBP790,FKBP791,FKBP792,FKBP793,FKBP794,FKBP795,FKBP796,FKBP797,FKBP798,FKBP799,FKBP800,FKBP801,FKBP802,FKBP803,FKBP804,FKBP805,FKBP806,FKBP807,FKBP808,FKBP809,FKBP810,FKBP811,FKBP812,FKBP813,FKBP814,FKBP815,FKBP816,FKBP817,FKBP818,FKBP819,FKBP820,FKBP821,FKBP822,FKBP823,FKBP824,FKBP825,FKBP826,FKBP827,FKBP828,FKBP829,FKBP830,FKBP831,FKBP832,FKBP833,FKBP834,FKBP835,FKBP836,FKBP837,FKBP838,FKBP839,FKBP840,FKBP841,FKBP842,FKBP843,FKBP844,FKBP845,FKBP846,FKBP847,FKBP848,FKBP849,FKBP850,FKBP851,FKBP852,FKBP853,FKBP854,FKBP855,FKBP856,FKBP857,FKBP858,FKBP859,FKBP860,FKBP861,FKBP862,FKBP863,FKBP864,FKBP865,FKBP866,FKBP867,FKBP868,FKBP869,FKBP870,FKBP871,FKBP872,FKBP873,FKBP874,FKBP875,FKBP876,FKBP877,FKBP878,FKBP879,FKBP880,FKBP881,FKBP882,FKBP883,FKBP884,FKBP885,FKBP886,FKBP887,FKBP888,FKBP889,FKBP890,FKBP891,FKBP892,FKBP893,FKBP894,FKBP895,FKBP896,FKBP897,FKBP898,FKBP899,FKBP900,FKBP901,FKBP902,FKBP903,FKBP904,FKBP905,FKBP906,FKBP907,FKBP908,FKBP909,FKBP910,FKBP911,FKBP912,FKBP913,FKBP914,FKBP915,FKBP916,FKBP917,FKBP918,FKBP919,FKBP920,FKBP921,FKBP922,FKBP923,FKBP924,FKBP925,FKBP926,FKBP927,FKBP928,FKBP929,FKBP930,FKBP931,FKBP932,FKBP933,FKBP934,FKBP935,FKBP936,FKBP937,FKBP938,FKBP939,FKBP940,FKBP941,FKBP942,FKBP943,FKBP944,FKBP945,FKBP946,FKBP947,FKBP948,FKBP949,FKBP950,FKBP951,FKBP952,FKBP953,FKBP954,FKBP955,FKBP956,FKBP957,FKBP958,FKBP959,FKBP960,FKBP961,FKBP962,FKBP963,FKBP964,FKBP965,FKBP966,FKBP967,FKBP968,FKBP969,FKBP970,FKBP971,FKBP972,FKBP973,FKBP974,FKBP975,FKBP976,FKBP977,FKBP978,FKBP979,FKBP980,FKBP981,FKBP982,FKBP983,FKBP984,FKBP985,FKBP986,FKBP987,FKBP988,FKBP989,FKBP990,FKBP991,FKBP992,FKBP993,FKBP994,FKBP995,FKBP996,FKBP997,FKBP998,FKBP999,FKBP1000
4	carboxylic acid biosynthetic process	12	0.0486	ABAT,ADI1,ALOX15B,ASNS,DPVD,ELOVL6,GP12,MTDFD2,PSAT1,PTGES,UGDH,UPB1
3	negative regulation of intrinsic apoptotic signaling pathway	7	0.0486	BCL2L1,HERPUD1,HSPH1,HTRA2,SYVIN1,TAIF9,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,DNAAF1,DYRK2,EIF2AK3,EVL,HMG81,HSPA5,HSPH1,HTRA2,IER3,KCNK6,KLIF4,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,KLIF4,MAFM,ED21,MPV17L2,NFKBIA,PM2,PSMCG,SERPINE1,SERTAD3,TAIF9,TLR1,TOPORES,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)