

subset	ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	geneID
Up dcSsc	GO:0006958	complement activation, classical pathway	34/1134	137/18670	1.06E-12	5.13E-09	IGHV3-21/IGHV4-59/IGLC3/IGLV2-23/IGHA1/IGHV4-34/IGKV1-16/IGLV2-14/IGLV1-47/IGHG3/IGKV3-15/IGHV3-48/IGLV1-44/IGLV3-1/IGHV2-26/IGLC2/IGKC/IGKV1-17/CR2/IGLL5/IGHM/IGKV3D-20/IGHA2/IGLV1-40/C1S/IGKV4-1/IGHV1-69-2/IGHV3-11/IGHD/IGHG1/IGKV3-20/IGHV4-31/IGKV1-5/IGHV3-20
Up dcSsc	GO:0042113	B cell activation	54/1134	310/18670	1.90E-12	5.13E-09	NBN/IGHV3-21/IGHV4-59/IGLC3/TP53/IGHA1/IGHV4-34/IGHG3/PRKDC/IGHV3-48/TNFRSF13C/DOCK11/IGHV2-26/IGLC2/ADAM17/IGKC/CR2/IGLL5/IGHM/MZB1/NCKAP1L/CD19/TXNA/TXNA2/CIRG1/IGHA2/TLR4/IKZF3/IRS2/ZFP36L2/SWAP70/BATF/MS4A1/HSPD1/FCRL1/PAWR/MIR17HG/BST2/JAK3/ATP11C/IGHV1-69-2/IGHV3-11/SKAP2/CD79B/TNFAIP3/IGHD/CD79A/IGHG1/IL7/PCID2/TNFRSF13B/FCRL3/IGHV4-31/BLNK/IGHV3-20
Up dcSsc	GO:0002455	humoral immune response mediated by circulating immunoglobulin	35/1134	150/18670	3.41E-12	6.14E-09	IGHV3-21/IGHV4-59/IGLC3/IGLV2-23/IGHA1/IGHV4-34/IGKV1-16/IGLV2-14/IGLV1-47/IGHG3/IGKV3-15/IGHV3-48/IGLV1-44/IGLV3-1/IGHV2-26/IGLC2/IGKC/IGKV1-17/CR2/IGLL5/IGHM/IGKV3D-20/IGHA2/IGLV1-40/C1S/IGKV4-1/IGHV1-69-2/IGHV3-11/IGHD/IGHG1/FCER2/IGKV3-20/IGHV4-31/IGKV1-5/IGHV3-20
Up dcSsc	GO:0006909	phagocytosis	57/1134	369/18670	6.80E-11	6.46E-08	IGHV3-21/IGHV4-59/DYSF/IGLC3/IGLV2-23/IGHA1/PRTN3/IGHV4-34/IGKV1-16/IGLV2-14/LYAR/PTEN/IGLV1-47/SYT11/IGHG3/IGKV3-15/STAP1/PTK2/IGHV3-48/IGLV1-44/IGLV3-1/UNC13D/IGHV2-26/IGLC2/RAB27A/SPG11/IGKC/IGKV1-17/CORO1C/IGLL5/MYH9/IGHM/NCKAP1L/IGKV3D-20/CD93/IGHA2/IGLV1-40/TLR4/FCGR3A/ANXA3/IGKV4-1/ITGAV/WAS/IGHV1-69-2/IGHV3-11/RAB14/TLR2/IGHD/IGHG1/FPR2/IGKV3-20/IGHV4-31/IGKV1-5/IGHV3-20/TXNDC5/CALR/NCF2
Up dcSsc	GO:0043312	neutrophil degranulation	68/1134	485/18670	8.38E-11	6.46E-08	IDH1/APAF1/COPB1/PRTN3/CAND1/PYGB/BPI/CLEC12A/PSMC2/METTL7A/PSEN1/RAB44/MMP8/ADAM10/IQGAP2/UNC13D/RAB27A/RNASE2/PSMA2/CAPN1/IGLB1/LTF/DNAJC13/PSMD1/S100A8/ENPP4/MCEMP1/SIGLEC9/HPSE/NCKAP1L/LRG1/RAB10/DYNLT1/RETN/CD93/MAPK14/TCIRG1/CD53/ANXA3/CRISPLD2/ITGAV/BST2/XRCC5/IQGAP1/GNS/PLGYP1/SERPINB10/DYNC1H1/PSMD11/S100A9/DSP/RAB14/CXCR2/SLC15A4/TLR2/CTSD/FPR2/CEACAM1/CCT2/SLPI/ARSB/RAB6A/CD63/DIAPH1/CRISP3/TXNDC5/HP/SLCO4C1
Up dcSsc	GO:0002283	neutrophil activation involved in immune response	68/1134	488/18670	1.10E-10	6.55E-08	IDH1/APAF1/COPB1/PRTN3/CAND1/PYGB/BPI/CLEC12A/PSMC2/METTL7A/PSEN1/RAB44/MMP8/ADAM10/IQGAP2/UNC13D/RAB27A/RNASE2/PSMA2/CAPN1/IGLB1/LTF/DNAJC13/PSMD1/S100A8/ENPP4/MCEMP1/SIGLEC9/HPSE/NCKAP1L/LRG1/RAB10/DYNLT1/RETN/CD93/MAPK14/TCIRG1/CD53/ANXA3/CRISPLD2/ITGAV/BST2/XRCC5/IQGAP1/GNS/PLGYP1/SERPINB10/DYNC1H1/PSMD11/S100A9/DSP/RAB14/CXCR2/SLC15A4/TLR2/CTSD/FPR2/CEACAM1/CCT2/SLPI/ARSB/RAB6A/CD63/DIAPH1/CRISP3/TXNDC5/HP/SLCO4C1
Up dcSsc	GO:0002446	neutrophil mediated immunity	69/1134	499/18670	1.13E-10	6.55E-08	IDH1/APAF1/COPB1/PRTN3/CAND1/PYGB/BPI/CLEC12A/PSMC2/METTL7A/PSEN1/RAB44/MMP8/ADAM10/IQGAP2/UNC13D/RAB27A/ADAM17/RNASE2/PSMA2/CAPN1/IGLB1/LTF/DNAJC13/PSMD1/S100A8/ENPP4/MCEMP1/SIGLEC9/HPSE/NCKAP1L/LRG1/RAB10/DYNLT1/RETN/CD93/MAPK14/TCIRG1/CD53/ANXA3/CRISPLD2/ITGAV/BST2/XRCC5/IQGAP1/GNS/PLGYP1/SERPINB10/DYNC1H1/PSMD11/S100A9/DSP/RAB14/CXCR2/SLC15A4/TLR2/CTSD/FPR2/CEACAM1/CCT2/SLPI/ARSB/RAB6A/CD63/DIAPH1/CRISP3/TXNDC5/HP/SLCO4C1
Up dcSsc	GO:0002429	immune response-activating cell surface receptor signaling pathway	66/1134	473/18670	1.97E-10	9.65E-08	IGHV3-21/IGHV4-59/IGLC3/IGLV2-23/IGHA1/IGHV4-34/PRKACB/IGKV1-16/IGLV2-14/MAP3K7/IGLV1-47/IGHG3/IGKV3-15/PSMC2/PSEN1/STAP1/PTK2/IGHV3-48/IGLV1-44/IGLV3-1/MUC1/IGHV2-26/IGLC2/PSMA2/IGKC/IGKV1-17/CR2/LIME1/IGLL5/CMKLR1/IGHM/PSMD1/PAX5/NCKAP1L/GPR33/CD19/PRK2/IGKV3D-20/IGHA2/IGLV1-40/DUSP3/FCGR3A/UBE2N/MS4A1/IGKV4-1/PAWR/MUCA/WAS/CACNB3/IGHV1-69-2/IGHV3-11/PSMD11/CD79B/IGHD/CD79A/IGHG1/CLEC4E/FPR2/CEACAM1/IGKV3-20/FCRL3/IGHV4-31/IGKV1-5/IGHV3-20/BLK/CLEC6A
Up dcSsc	GO:0042119	neutrophil activation	68/1134	498/18670	2.69E-10	1.21E-07	IDH1/APAF1/COPB1/PRTN3/CAND1/PYGB/BPI/CLEC12A/PSMC2/METTL7A/PSEN1/RAB44/MMP8/ADAM10/IQGAP2/UNC13D/RAB27A/RNASE2/PSMA2/CAPN1/IGLB1/LTF/DNAJC13/PSMD1/S100A8/ENPP4/MCEMP1/SIGLEC9/HPSE/NCKAP1L/LRG1/RAB10/DYNLT1/RETN/CD93/MAPK14/TCIRG1/CD53/ANXA3/CRISPLD2/ITGAV/BST2/XRCC5/IQGAP1/GNS/PLGYP1/SERPINB10/DYNC1H1/PSMD11/S100A9/DSP/RAB14/CXCR2/SLC15A4/TLR2/CTSD/FPR2/CEACAM1/CCT2/SLPI/ARSB/RAB6A/CD63/DIAPH1/CRISP3/TXNDC5/HP/SLCO4C1
Up dcSsc	GO:0048194	Golgi vesicle budding	22/1134	80/18670	1.29E-09	4.63E-07	USO1/NSF/SEC23IP/GOLPH3L/MIA3/PREB/CUL3/SEC22B/SEC24C/PEF1/F5/GBF1/LMAN1/SEC23B/RAB1A/ANKRD28/PRKCI/GOLPH3/SEC16A/SEC24A/SEC24D/MAPK15
Up dcSsc	GO:0050864	regulation of B cell activation	35/1134	184/18670	1.37E-09	4.64E-07	IGHV3-21/IGHV4-59/IGLC3/IGHA1/IGHV4-34/IGHG3/IGHV3-48/TNFRSF13C/IGHV2-26/IGLC2/IGKC/IGLL5/IGHM/MZB1/NCKAP1L/CD19/IGHA2/TLR4/IKZF3/IRS2/ZFP36L2/PAWR/MIR17HG/ATP11C/IGHV1-69-2/IGHV3-11/TNFAIP3/IGHD/IGHG1/IL7/PCID2/TNFRSF13B/FCRL3/IGHV4-31/IGHV3-20
Up dcSsc	GO:0002449	lymphocyte mediated immunity	52/1134	352/18670	2.34E-09	7.43E-07	NBN/IGHV3-21/IGHV4-59/IGLC3/IGLV2-23/IGHA1/IGHV4-34/IGKV1-16/CLEC12B/IGLV2-14/MAP3K7/SCART1/IGLV1-47/IGHG3/IGKV3-15/IGHV3-48/IGLV1-44/IGLV3-1/UNC13D/IGHV2-26/IGLC2/RAB27A/IGKC/SLAMF6/IGKV1-17/CR2/FADD/IGLL5/IGHM/CD19/IGKV3D-20/TCIRG1/IGHA2/IGLV1-40/SWAP70/C1S/BATF/HSPD1/FBXO38/IGKV4-1/WAS/IGHV1-69-2/IGHV3-11/IGHD/IGHG1/FCER2/CEACAM1/IGKV3-20/IGHV4-31/KDELRL1/IGKV1-5/IGHV3-20
Up dcSsc	GO:0006900	vesicle budding from membrane	24/1134	102/18670	7.09E-09	2.13E-06	USO1/NSF/SEC23IP/GOLPH3L/MIA3/PREB/CUL3/SEC22B/SEC24C/PEF1/F5/GBF1/LMAN1/SEC23B/RAB1A/AP3D1/ANKRD28/PRKCI/ANXA2P2/GOLPH3/SEC16A/SEC24A/SEC24D/MAPK15
Up dcSsc	GO:0016050	vesicle organization	48/1134	325/18670	9.73E-09	2.75E-06	USO1/NSF/SEC23IP/GOLPH3L/ANKFY1/DYSF/MIA3/EP15/VPS4B/PREB/ANXA8/CUL3/SEC22B/CHMP7/SEC24C/RAB27A/SPG11/CORO1C/SCARB2/AGFG1/DNAJC13/PEF1/VPS39/SORT1/C2CD5/AKTIP/F5/PI4K2B/GBF1/LMAN1/SEC23B/VPS41/RAB1A/AP3D1/TSG101/RAB14/ANKRD28/PRKCI/GRIKS/TAPBP/ANXA2P2/GOLPH3/SEC16A/HOOK3/SEC24A/SEC24D/MAPK15/CALR
Up dcSsc	GO:0072376	protein activation cascade	35/1134	198/18670	1.02E-08	2.75E-06	IGHV3-21/IGHV4-59/IGLC3/IGLV2-23/IGHA1/IGHV4-34/IGKV1-16/IGLV2-14/IGLV1-47/IGHG3/IGKV3-15/IGHV3-48/IGLV1-44/IGLV3-1/IGHV2-26/IGLC2/IGKC/IGKV1-17/CR2/IGLL5/IGHM/CD19/IGKV3D-20/IGHA2/IGLV1-40/C1S/IGKV4-1/IGHV1-69-2/IGHV3-11/IGHD/IGHG1/IGKV3-20/IGHV4-31/IGKV1-5/IGHV3-20
Up dcSsc	GO:0050900	leukocyte migration	64/1134	499/18670	1.12E-08	2.88E-06	IGHV4-59/DYSF/IGLC3/IGLV2-23/IGHA1/PRTN3/IGHV4-34/MIA3/IGKV1-16/SOS1/IGLV2-14/NLRP12/IGLV1-47/SLC16A8/IGKV3-15/ADAM10/STAP1/IGHV3-48/ECM1/IGLV1-44/IGLV3-1/IGLC2/ADAM17/ITGB7/IGKC/IGKV1-17/FADD/MYH9/TNFRSF11A/CMKLR1/IGHM/S100A8/NCKAP1L/IGKV3D-20/MAPK14/CCL17/IGHA2/IGLV1-40/GBF1/ITGA9/SWAP70/IGKV4-1/ITGAV/CH25H/IGHV3-11/S100A9/RAC2/CXCR2/CCL22/CXCR1/VPREB3/CCR1/FPR2/CEACAM1/IGKV3-20/CNR2/GOLPH3/THBS4/IGKV1-5/DBH/CCL24/CALR/IL6R/HOXA7
Up dcSsc	GO:0030449	regulation of complement activation	25/1134	115/18670	1.93E-08	4.73E-06	IGHV4-59/IGLC3/IGLV2-23/IGHV4-34/IGKV1-16/IGLV2-14/IGLV1-47/IGHG3/IGKV3-15/IGHV3-48/IGLV1-44/IGLV3-1/IGLC2/IGKC/IGKV1-17/CR2/CD19/IGKV3D-20/IGLV1-40/C1S/IGKV4-1/IGHV3-11/IGHG1/IGKV3-20/IGKV1-5
Up dcSsc	GO:2000257	regulation of protein activation cascade	25/1134	116/18670	2.32E-08	5.44E-06	IGHV4-59/IGLC3/IGLV2-23/IGHV4-34/IGKV1-16/IGLV2-14/IGLV1-47/IGHG3/IGKV3-15/IGHV3-48/IGLV1-44/IGLV3-1/IGLC2/IGKC/IGKV1-17/CR2/CD19/IGKV3D-20/IGLV1-40/C1S/IGKV4-1/IGHV3-11/IGHG1/IGKV3-20/IGKV1-5
Up dcSsc	GO:0048193	Golgi vesicle transport	50/1134	368/18670	7.50E-08	1.69E-05	USO1/NSF/SEC23IP/GOLPH3L/ANKFY1/CAPZA1/NBAS/COPB2/COPB1/PGAP1/MIA3/PREPL/COPA/EP15/PREB/CUL3/SEC22B/SEC24C/OSBPL5/PEF1/RAB10/SORT1/ACS13/COPG1/KDELRL2/F5/GBF1/AMN/VPS54/LMAN1/KIF3C/PITPNB/TMED6/SEC23B/RAB1A/AP3D1/DYNC1H1/RAB14/ANKRD28/PRKCI/CP2/TAPBP/GOLPH3/SEC16A/RAB6A/KDELRL1/SEC24A/SEC24D/MAPK15/CAPZA2
Up dcSsc	GO:0002920	regulation of humoral immune response	26/1134	134/18670	1.17E-07	2.34E-05	IGHV4-59/IGLC3/IGLV2-23/IGHV4-34/IGKV1-16/IGLV2-14/IGLV1-47/IGHG3/IGKV3-15/IGHV3-48/IGLV1-44/IGLV3-1/IGLC2/IGKC/IGKV1-17/CR2/CD19/IGKV3D-20/IGLV1-40/C1S/IGKV4-1/IGHV3-11/IGHG1/FCER2/IGKV3-20/IGKV1-5
Down dcSsc	GO:0006613	cotranslational protein targeting to membrane	68/859	109/18670	2.64E-63	1.26E-59	RPL6/RPL37/RP58/RPL35A/RPL11/RPL4/RPL34/RPL30/RPL13A/RPL14/RPL13A/RPL19/RPL32/RPL26/RPS6/RPL27/RPL3/RPS29/UBA52/RPL7A/RPL31/RPL23/RPS3A/RPS27A/RPL10/RPL24/RPL22/RPS10/RPS17/RPL10A/RPS19/RPS11/RPL37A/RPL5/RPL35/RPL39/RPS21/RPS2/RPL15/RPL18/RPS25/RPL38/RPL18A/RPS16/RPL12/RPS15A/RPL14/RPS12/RPL36/RPS5/RPLP2/RPLP0/RPL23A/RPL27A/RPS3/RPS20/RPL17/RPS15/RPL8/RPL1/RPS14/RPL13/RPS27/RPS24/RPL7/SSR1/SSR2/RPS18
Down dcSsc	GO:0072599	establishment of protein localization to endoplasmic reticulum	68/859	122/18670	1.50E-58	1.79E-55	RPL6/RPL37/RP58/RPL35A/RPL11/RPL4/RPL34/RPL30/RPL13A/RPL14/RPL13A/RPL19/RPL32/RPL26/RPS6/RPL27/RPL3/RPS29/UBA52/PMM1/RPL7A/RPL31/RPL23/RPS3A/RPS27A/RPL10/RPL24/RPL22/RPS10/RPS17/RPL10A/RPS19/RPS11/RPL37A/RPL5/RPL35/RPL39/RPS21/RPS2/RPL15/RPL18/RPS25/RPL38/RPL18A/RPS16/RPL12/RPS15A/RPL14/RPS12/RPL36/RPS5/RPLP2/RPLP0/RPL23A/RPL27A/RPS3/RPS20/RPL17/RPS15/RPL8/RPL1/RPS14/RPL13/RPS27/RPS24/RPL7/CHMP4A/RPS18

Down dcSSc	GO:000184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	67/859	120/18670	9.11E-58	8.72E-55	RPL6/RPL37/RPS8/RPL35A/RPL11/RPL4/RPL34/RPL30/RPL13A/RPL19/RPL41/RPL29/RPL32/RPL26/RPS6/RPL27/RPL3/RPS29/UBA52/RPL7A/RPL31/RPL23/RPS3A/RPS27A/RPL10/RPL24/RPL22/RPS10/RPS17/RPL10A/RPS19/RPS11/RPL37A/RPL5/RPL35/RPL39/RPS21/RPS2/RPL15/RPL18/RPS25/RPL38/RPL18A/RPS16/RPL12/RPS15A/RPL14/RPS12/RPL36/RPS5/RPL2/RPLP0/RPL23A/RPL27A/RPS3/RPS20/RPL17/RPS15/RPL8/RPLP1/EIF3E/RPS14/RPL13/RPS27/RPS24/RPL7/RPS18
Down dcSSc	GO:0006413	translational initiation	81/859	193/18670	6.20E-57	4.95E-54	RPL6/RPL37/RPS8/RPL35A/RPL11/RPL4/RPL34/RPL30/RPL13A/RPL19/RPL41/RPL29/RPL32/RPL26/RPS6/RPL27/RPL3/EIF3L/RPS29/UBA52/RPL7A/RPL31/RPL23/RPS3A/RPS27A/RPL10/RPL24/RPL22/RPS10/RPS17/RPL10A/RPS19/RPS11/RPL37A/RPL5/RPL35/RPL39/RPS21/ATF4/RPS2/EIF1/RPL15/RPL18/RPS25/RPL38/RPL18A/EIF3I/RPS16/RPL12/RPS15A/RPL14/RPS12/EIF3H/RPL36/CCL5/RBM4/RPS5/RPLP2/RPLP0/RPL23A/RPL27A/YTHDF3/RPS3/RPS20/RPL17/EIF2D/IMPACT/RPS15/RPL8/RPLP1/EIF3E/RPS14/EIF4B/RPL13/RPS27/RPS24/EIF3G/EIF3K/RPL7/EIF3F/RPS18
Down dcSSc	GO:0019080	viral gene expression	78/859	191/18670	9.69E-54	6.62E-51	RPL6/RPL37/RPS8/RPL35A/RPL11/RPL4/RPL34/RPL30/RPL13A/RPL19/RPL41/RPL29/RPL32/RPL26/RPS6/RPL27/RPL3/EIF3L/RPS29/UBA52/RPL7A/RPL31/RPL23/RPS3A/RPS27A/RPL10/RPL24/RPL22/RPS10/CCNT1/RPS17/RPL10A/RPS19/RPS11/RPL37A/RPL5/RPL35/SUPT4H1/RPL39/RPS21/RPS2/RPL15/RPL18/CDK9/RPS25/RPL38/RPL18A/RPS16/RPL12/RPS15A/RPL14/RPS12/RPL36/CCL5/RPS5/RPLP2/RPLP0/CCL4/RPL23A/RPL27A/RPS3/RPS20/RPL17/EIF2D/RPS15/RPL8/RPL1/RPL11/USF2/POLR2J/RPS14/RPL13/RPS27/RPS24/EIF3G/RPL7/RSF1/EIF3F/RPS18
Down dcSSc	GO:0019083	viral transcription	74/859	177/18670	6.75E-52	4.04E-49	RPL6/RPL37/RPS8/RPL35A/RPL11/RPL4/RPL34/RPL30/RPL13A/RPL19/RPL41/RPL29/RPL32/RPL26/RPS6/RPL27/RPL3/RPS29/UBA52/RPL7A/RPL31/RPL23/RPS3A/RPS27A/RPL10/RPL24/RPL22/RPS10/CCNT1/RPS17/RPL10A/RPS19/RPS11/RPL37A/RPL5/RPL35/SUPT4H1/RPL39/RPS21/RPS2/RPL15/RPL18/CDK9/RPS25/RPL38/RPL18A/RPS16/RPL12/RPS15A/RPL14/RPS12/RPL36/CCL5/RPS5/RPLP2/RPLP0/CCL4/RPL23A/RPL27A/RPS3/RPS20/RPL17/RPS15/RPL8/RPL1/USF2/POLR2J/RPS14/RPL13/RPS27/RPS24/RPL7/RSF1/RPS18
Down dcSSc	GO:0042255	ribosome assembly	20/859	63/18670	3.00E-12	8.46E-10	RPL6/RPL11/RPL3/RPL10/RPL24/RPS10/RPS19/SBDS/RPL5/RPL38/RPL12/RPLP0P6/RPS5/RPLP0/RPL23A/MTERF4/RPS15/RPS14/RPS27/MRPL11
Down dcSSc	GO:0042273	ribosomal large subunit biogenesis	20/859	71/18670	3.54E-11	9.42E-09	RPL6/RPL35A/RPL11/RPL26/RPL3/RPL7A/RPL10/RPL24/RPL10A/RPL5/RPL35/RPL38/RPL12/RPL14/RPLP0P6/RPLP0/RPL23A/RSL1D1/RPL7/MRPL11
Down dcSSc	GO:0071826	ribonucleoprotein complex subunit organization	39/859	291/18670	2.00E-09	4.56E-07	RPL6/RPL11/RPL13A/CIRBP/RPL3/EIF3L/RPL10/RPL24/RPS10/RPS19/SBDS/RPL5/RNVU1-6/RPL38/EIF3I/RPL12/EIF3H/RPLP0P6/RPS5/SNRPD2/RPLP0/RPL23A/MTERF4/LSM4/EIF2D/RPS15/EIF3E/RPS14/EIF4B/RNU4ATAC/RPS27/ZFAND1/EIF3G/EIF3K/MRP L11/PRPF18/GEMIN4/EIF3F/SNRPE
Down dcSSc	GO:0006364	rRNA processing	30/859	214/18670	5.27E-08	1.10E-05	RPS8/RPL35A/RPL11/RPL26/RPS6/RPL27/RPL7A/RPS17/RPL10A/RPS19/SBDS/FBL/RPL5/RPL35/RPS21/RPS2/RPS16/RPL14/NSA2/SUV39H1/RSL1D1/MTERF4/RPS15/RPS14/RPS27/RPS24/RBFA/RPL7/METT16/GEMIN4
Down dcSSc	GO:0090200	positive regulation of release of cytochrome c from mitochondria	9/859	30/18670	5.29E-06	0.000938357	BMF/CHCHD10/FAM162A/PLAUR/PMAIP1/BCL2L11/BAX/BAD/BID
Down dcSSc	GO:0097711	ciliary basal body-plasma membrane docking	16/859	95/18670	6.39E-06	0.00109231	TTBK2/HAUS7/TCTN1/PCNT/CC2D2A/TUBA1A/SSNA1/HAUS5/CDK5RAP2/OFD1/MAPRE1/PLK4/CSNK1E/TMEM67/SDCCAG8/NPHP4
Down dcSSc	GO:1904666	regulation of ubiquitin protein ligase activity	7/859	22/18670	3.96E-05	0.006110243	RPL11/RPL23/UBE2S/RPL5/MAD2L2/CDC14B/FZR1
Down dcSSc	GO:1903708	positive regulation of hemopoiesis	21/859	185/18670	0.000126535	0.015943419	CD4/NFKBID/CD83/PRMT1/TAL1/GNAS/TNFSF9/ZBTB46/EGR3/CD74/BAD/INHBA/CTNNBIP1/TNFSF4/FAM210B/IL1RL2/RUNX3/ID2/ZFP36L1/HMGB1/DUSP10
Down dcSSc	GO:0002262	myeloid cell homeostasis	18/859	147/18670	0.000145046	0.017807193	RPS6/RPS17/RPS19/DMTN/PRMT1/TAL1/SH2B3/PDE4B/BCL2L11/BAX/INHBA/RPS14/FAM210B/ID2/SP3/RPS24/ZFP36L1/HMGB1
Down dcSSc	GO:1903039	positive regulation of leukocyte cell-cell adhesion	23/859	218/18670	0.000186759	0.022355059	CD4/HLA-DPB1/NFKBID/HLA-DPA1/CD83/NR4A3/TNFSF9/GRAP2/CCL5/EGR3/ICAM1/CD74/BAD/RPS3/PDPK1/TNFSF4/IL1RL2/RUNX3/HLA-DMB/AIF1/IL1B/HMGB1/DUSP10
Down dcSSc	GO:0042110	T cell activation	39/859	464/18670	0.000220979	0.025806037	RPS6/CD4/HLA-DPB1/NFKBID/RPL22/HLA-DPA1/CD83/HLA-DOA/HFE/PTGER4/TNFSF9/GRAP2/CCL5/BAX/NRARP/CLEC4A/EGR3/ICAM1/CD74/BAD/RPS3/NCAPH2/PDPK1/PRDX2/TNFSF4/IL1RL2/RUNX3/SP3/SLA2/RELB/ZFP36L1/HLA-DMB/AIF1/IL1B/NFATC2/SH3RF1/HMGB1/GSN/DUSP10
Down dcSSc	GO:0045619	regulation of lymphocyte differentiation	19/859	169/18670	0.000295168	0.033649155	NFKBID/CD83/HLA-DOA/TNFSF9/NRARP/EGR3/CD74/BAD/INHBA/PRDX2/TNFSF4/IL1RL2/RUNX3/ID2/ZFP36L1/NFATC2/SH3RF1/HMGB1/DUSP10
Down dcSSc	GO:0001844	protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	7/859	30/18670	0.000342209	0.036411064	BMF/SFN/PMAIP1/BCL2L11/BAX/BAD/BID
Down dcSSc	GO:0071470	cellular response to osmotic stress	8/859	40/18670	0.000402592	0.041013014	PTGS2/SLC2A1/MBIP/BAD/MYLK/RELB/ZFP36L1/AKR1B1
Up eaSSc	GO:0000280	nuclear division	58/861	407/18670	1.62E-14	4.01E-11	SPAG5/SMC4/MYBL2/USP16/KIFC1/SPHK1/ANAPC4/CDC45/CDC20/TTN/CEP192/PLK1/TOP2A/KNTC1/TTK/PDS5B/CUL3/KIF23/MKI67/NUSAP1/CLASP2/VPS4B/CCN A1/KIF2C/MUS81/NCAPG/RGCC/POG2/SIRT7/NDC80/CENPK/MASTL/CENPE/CHK1/NCAPH/WNT4/EDN1/SLX4/GEN1/ASPM/TOP2B/SEH1/DLGAP5/KIF18B/PTTG2/BIRC5/FANCM/PHF13/FZR1/CDKN1C/HSPA2/CENPF/FGF8/CDC27/ANLN/KIF11/RAD51C
Up eaSSc	GO:0006260	DNA replication	46/861	274/18670	2.17E-14	4.01E-11	CHTF18/POLE2/MCM8/CDK1/POLQ/DONSON/TOP1/THOC1/TSPYL2/RECQL/WHDH3/CD45/ATR/LIG1/ORC6/NUP98/MCM7/RECQL4/PNKP/DNAJC2/POLE/INGS/AC HE/DTL/MCM4/BRCA2/CHEK1/REV3L/POLD1/POLG2/MSH6/MCM10/RRM2/SLX4/IGHMBP2/GEN1/TOP3A/HUS1/SIN3A/EXO1/E2F8/FANCM/ORC2/TICRR/CCNA2/N BN
Up eaSSc	GO:0140014	mitotic nuclear division	45/861	264/18670	2.37E-14	4.01E-11	SPAG5/SMC4/MYBL2/USP16/KIFC1/SPHK1/ANAPC4/CDC45/CDC20/TTN/CEP192/PLK1/KNTC1/TTK/PDS5B/CUL3/KIF23/MKI67/NUSAP1/CLASP2/VPS4B/KIF2C/NCAP G/RGCC/POG2/SIRT7/NDC80/CENPK/CENPE/CHK1/NCAPH/EDN1/GEN1/SEH1/DLGAP5/KIF18B/PTTG2/BIRC5/PHF13/CDKN1C/CENPF/FGF8/CDC27/ANLN/KIF11
Up eaSSc	GO:1901987	regulation of cell cycle phase transition	62/861	480/18670	1.87E-13	1.82E-10	PCM1/ANAPC4/PSME4/RINT1/DCUN1D3/DYRK3/CDC45/CDC20/USP47/BRD4/CEP192/CEP152/CDK1/PLK1/KNTC1/TTK/WNT10B/DONSON/CUL3/CSNK1D/VPS4B/MI R221/CD45/SF1/RGCC/NDC80/E2F1/RCC2/CENPE/DTL/CCND2/CHEK1/ZNF655/DACT1/GPR132/MECP2/GEN1/TPRA1/GTSE1/PAFAH1B1/EP300/CDK5RAP3/D LGAP5/HUS1/SIN3A/GIGYF2/YWHAG/E2F8/FZR1/CDKN1C/TICRR/FBXO7/HSPA2/CENPF/CDC27/ANLN/NBN/EZH2/CDK10/RAD51C/RIPK1
Up eaSSc	GO:0000075	cell cycle checkpoint	39/861	216/18670	1.95E-13	1.82E-10	RINT1/CDC20/CDK1/PLK1/TOP2A/KNTC1/TTK/DONSON/THOC1/CCAR2/CDC45/ATR/MUS81/WDR76/CDC5L/RGCC/NDC80/E2F1/DTL/CHEK1/DDX39B/DLG1/NSUN2/INTS7/GEN1/GTSE1/TOP2B/EP300/CDK5RAP3/DOT1L/HUS1/GIGYF2/MDC1/E2F8/USP28/FZR1/TICRR/CENPF/NBN
Up eaSSc	GO:1901990	regulation of mitotic cell cycle phase transition	59/861	444/18670	2.15E-13	1.82E-10	PCM1/ANAPC4/PSME4/RINT1/DCUN1D3/CDC45/CDC20/USP47/BRD4/CEP192/CEP152/CDK1/PLK1/KNTC1/TTK/WNT10B/DONSON/CUL3/CSNK1D/VPS4B/MI R221/C DC45/SF1/RGCC/NDC80/E2F1/RCC2/CENPE/DTL/CCND2/ZNF655/DACT1/GPR132/MECP2/GEN1/TPRA1/GTSE1/PAFAH1B1/EP300/CDK5RAP3/DLGAP5/HUS1/SIN3A/ GIGYF2/YWHAG/E2F8/FZR1/CDKN1C/TICRR/FBXO7/HSPA2/CENPF/CDC27/ANLN/NBN/EZH2/CDK10/RAD51C/RIPK1
Up eaSSc	GO:0044839	cell cycle G2/M phase transition	42/861	266/18670	2.46E-12	1.56E-09	PCM1/PSME4/RINT1/DYRK3/USP47/BRD4/CEP192/CEP152/CDK1/PLK1/WNT10B/DONSON/CSNK1D/PPP1CB/VPS4B/SF1/TAF2/RCC2/MASTL/BACH1/DTL/CHEK1/AB CB1/GPR132/MECP2/GTSE1/PAFAH1B1/CDK5RAP3/CIT/HUS1/SIN3A/PPP2R2A/YWHAG/MELK/FBXL18/FZR1/TICRR/HSPA2/CCNA2/CENPF/NBN/RAD51C
Up eaSSc	GO:0000819	sister chromatid segregation	34/861	189/18670	7.69E-12	3.90E-09	SPAG5/SMC4/KIFC1/ANAPC4/CDC45/CDC20/TTN/PLK1/TOP2A/TTK/SFPQ/PDS5B/CUL3/KIF23/NUSAP1/VPS4B/KIF2C/NCAPG/POG2/NDC80/CENPK/CENPE/NCAPH/C TNNB1/GEN1/TOP2B/SEH1/DLGAP5/KIF18B/PTTG2/PHF13/CENPF/CDC27/RAD51C

Up eaSSc	GO:0033044	regulation of chromosome organization	46/861	342/18670	6.72E-11	2.28E-08	ANAPC4/CDC45/CDC20/BRD4/SUPT6H/PLK1/TOP2A/ATAD2/TTK/TRIP12/SFPQ/FMR1/XRN1/CUL3/MKI67/ZNF335/CDC45/ATR/NDC80/PNKP/DHX36/CENPE/CHEK1/FOX3/PAF1/MECP2/PHF1/ATAD2B/RIF1/CTNNB1/VEGFA/SLX4/GEN1/CCT2/EED/DLGAP5/SIN3A/USP7/PTTG2/SKI/YLPM1/CENPF/CDC27/NBN/SMG1/MAP3K4
Up eaSSc	GO:0000077	DNA damage checkpoint	27/861	145/18670	4.94E-10	1.39E-07	RINT1/CDK1/PLK1/DONSON/THOC1/CCAR2/ATR/MUS81/WDR76/CDC5L/RGCC/E2F1/DTL/CHEK1/DDX39B/INTS7/GTSE1/EP300/CDK5RAP3/DOT1L/HUS1/GIGYF2/MDC1/E2F8/USP28/FZR1/NBN
Up eaSSc	GO:0016569	covalent chromatin modification	51/861	474/18670	1.69E-08	3.44E-06	PRMT9/USP36/USP16/CHD1/BRD4/SUPT6H/CDK1/TRIP12/RLF/SFPQ/FMR1/HELLS/KDM6B/YEATS2/LDB1/KANSL3/MORF4L2/ZNF335/JMJD1C/SIRT7/KDM3B/HCF1/ING5/PER2/BRCA2/ING3/CHEK1/FOX3/KMT2C/PAF1/MECP2/UHRF1/PRDM2/PHF1/RIF1/CTNNB1/VEGFA/GTF2B/EP300/EED/DOT1L/SIN3A/HR/USP7/JMJD6/SKI/PRMT3/BAZ1B/BEND3/CCNA2/EZH2
Up eaSSc	GO:0016570	histone modification	49/861	454/18670	2.94E-08	5.33E-06	PRMT9/USP36/USP16/BRD4/SUPT6H/CDK1/TRIP12/RLF/SFPQ/FMR1/KDM6B/YEATS2/LDB1/KANSL3/MORF4L2/ZNF335/JMJD1C/SIRT7/KDM3B/HCF1/ING5/PER2/BRCA2/ING3/CHEK1/FOX3/KMT2C/PAF1/MECP2/UHRF1/PRDM2/PHF1/RIF1/CTNNB1/VEGFA/GTF2B/EP300/EED/DOT1L/SIN3A/HR/USP7/JMJD6/SKI/PRMT3/BAZ1B/BEND3/CCNA2/EZH2
Up eaSSc	GO:0045930	negative regulation of mitotic cell cycle	39/861	338/18670	1.36E-07	2.17E-05	PSME4/RINT1/DCUN1D3/CDC20/USP47/CDK1/PLK1/TOP2A/KNTC1/TTK/DONSON/TNF/MUS81/RGCC/NDC80/E2F1/CHEK1/ZNF655/DLG1/DACT1/GPR132/CTNNB1/GEN1/TPRA1/GTSE1/TOP2B/EP300/CDK5RAP3/HUS1/GIGYF2/MDC1/PTTG2/E2F8/TICRR/FBXO7/CENPF/NBN/EZH2/RIPK1
Up eaSSc	GO:0007088	regulation of mitotic nuclear division	25/861	164/18670	1.38E-07	2.17E-05	SPHK1/ANAPC4/CDC45/CDC20/PLK1/KNTC1/TTK/CUL3/MKI67/NUSAP1/VPS4B/RGCC/NDC80/CENPE/CHEK1/EDN1/GEN1/DLGAP5/PTTG2/CDKN1C/CENPF/FGF8/CD27/ANLN/KIF11
Up eaSSc	GO:0006406	mRNA export from nucleus	20/861	111/18670	1.53E-07	2.17E-05	RANBP2/NUP54/DHX38/SUPT6H/NUP153/THOC1/YTHDC1/NUP155/NUP107/NUP160/CPSF2/NUP98/DDX39B/POM121/AGFG1/SEH1L/SRSF11/EIF4E/NCBP2/SMG1
Up eaSSc	GO:0071427	mRNA-containing ribonucleoprotein complex export from nucleus	20/861	111/18670	1.53E-07	2.17E-05	RANBP2/NUP54/DHX38/SUPT6H/NUP153/THOC1/YTHDC1/NUP155/NUP107/NUP160/CPSF2/NUP98/DDX39B/POM121/AGFG1/SEH1L/SRSF11/EIF4E/NCBP2/SMG1
Up eaSSc	GO:0051783	regulation of nuclear division	27/861	188/18670	1.54E-07	2.17E-05	SPHK1/ANAPC4/CDC45/CDC20/PLK1/KNTC1/TTK/CUL3/MKI67/NUSAP1/VPS4B/RGCC/NDC80/CENPE/CHEK1/WNT4/EDN1/GEN1/DLGAP5/PTTG2/FZR1/CDKN1C/CENPF/FGF8/CD27/ANLN/KIF11
Up eaSSc	GO:0007093	mitotic cell cycle checkpoint	25/861	165/18670	1.55E-07	2.17E-05	RINT1/CDC20/CDK1/PLK1/TOP2A/KNTC1/TTK/DONSON/MUS81/RGCC/NDC80/E2F1/DLG1/GEN1/GTSE1/TOP2B/EP300/CDK5RAP3/HUS1/GIGYF2/MDC1/E2F8/TICRR/CENPF/NBN
Up eaSSc	GO:0044766	multi-organism transport	16/861	73/18670	1.62E-07	2.17E-05	RANBP2/NUP54/NUP153/FMR1/THOC1/NUP155/NUP107/NUP160/NUP98/UBAP1/KPNA2/DDX39B/VPS37B/POM121/SEH1L/TSG101
Up eaSSc	GO:1902579	multi-organism localization	16/861	73/18670	1.62E-07	2.17E-05	RANBP2/NUP54/NUP153/FMR1/THOC1/NUP155/NUP107/NUP160/NUP98/UBAP1/KPNA2/DDX39B/VPS37B/POM121/SEH1L/TSG101
Down eaSSc	GO:0006613	cotranslational protein targeting to membrane	68/723	109/18670	1.72E-68	3.74E-65	RPL6/RPL11/RPL22/RPL37/RPL4/RPL3/RPL7A/RPS25/RPL30/RPL32/RPS8/RPL19/RPL26/RPS17/UBA52/RPS20/RPL35A/RPL24/RPL34/RPL41/RPL15/RPS12/RPL10A/RP S6/RPL29/RPS2/RPL27/RPL13A/RPL23/RPL35/RPS27A/RPL5/RPL10/RPL31/RPL23A/RPL37A/RPS29/RPL12/RPS11/RPL38/RPLP0/RPS3/RPLP1/RPLP2/RPL14/RPS14/RP L18A/RPS15A/RPS24/RPL36/SRP14/RPL18/RPS16/RPS10/RPS15/RPS21/RPL8/SSR2/RPS19/RPS23/RPS27/RPL13/RPS3A/RPS26/RPS18/RPS5/RPL27A/RPS9
Down eaSSc	GO:0006614	SRP-dependent cotranslational protein targeting to membrane	67/723	105/18670	1.76E-68	3.74E-65	RPL6/RPL11/RPL22/RPL37/RPL4/RPL3/RPL7A/RPS25/RPL30/RPL32/RPS8/RPL19/RPL26/RPS17/UBA52/RPS20/RPL35A/RPL24/RPL34/RPL41/RPL15/RPS12/RPL10A/RP S6/RPL29/RPS2/RPL27/RPL13A/RPL23/RPL35/RPS27A/RPL5/RPL10/RPL31/RPL23A/RPL37A/RPS29/RPL12/RPS11/RPL38/RPLP0/RPS3/RPLP1/RPLP2/RPL14/RPS14/RP L18A/RPS15A/RPS24/RPL36/SRP14/RPL18/RPS16/RPS10/RPS15/RPS21/RPL8/RPS19/RPS23/RPS27/RPL13/RPS3A/RPS26/RPS18/RPS5/RPL27A/RPS9
Down eaSSc	GO:0072599	establishment of protein localization to endoplasmic reticulum	69/723	122/18670	3.07E-65	3.26E-62	RPL6/RPL11/RPL22/RPL37/RPL4/RPL3/RPL7A/RPS25/RPL30/RPL32/RPS8/RPL19/RPL26/RPS17/UBA52/RPS20/RPL35A/RPL24/RPL34/RPL41/RPL15/RPS12/RPL10A/RP S6/RPL29/RPS2/RPL27/RPL13A/RPL23/RPL35/RPS27A/RPL5/RPL10/RPL31/RPL23A/RPL37A/RPS29/RPL12/RPS11/RPL38/RPLP0/RPS3/RPLP1/RPLP2/RPL14/RPS14/RP L18A/RPS15A/RPS24/RPL36/SRP14/RPL18/RPS16/RPS10/RPS15/RPS21/RPL8/RPS19/RPS23/SPCS1/RPS27/RPL13/RPS3A/RPS26/RPS18/RPS5/RPL27A/RPS9/PMM1
Down eaSSc	GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	68/723	120/18670	2.24E-64	1.90E-61	RPL6/RPL11/RPL22/RPL37/RPL4/RPL3/RPL7A/RPS25/RPL30/RPL32/RPS8/RPL19/RPL26/RPS17/UBA52/RPS20/RPL35A/RPL24/RPL34/RPL41/RPL15/RPS12/RPL10A/RP S6/RPL29/RPS2/RPL27/RPL13A/RPL23/RPL35/RPS27A/RPL5/RPL10/RPL31/RPL23A/EIF3E/RPL37A/RPS29/RPL12/RPS11/RPL38/RPLP0/RPS3/RPLP1/RPLP2/RPL14/RPS 14/RPL18A/RPS15A/RPS24/RPL36/RPL18/RPS16/RPS10/RPS15/RPS21/RPL8/RPS19/RPS23/RPS27/RPL13/RPS3A/RPS26/RPS18/RPS5/RPL27A/RPS9/DCP1B
Down eaSSc	GO:0006413	translational initiation	82/723	193/18670	2.85E-64	2.02E-61	RPL6/RPL11/RPL22/EIF31/RPL37/RPL4/RPL3/RPL7A/RPS25/RPL30/RPL32/RPS8/RPL19/RPL26/RPS17/UBA52/RPS20/RPL35A/RPL24/EIF3L/RPL34/RPL41/RPL15/RPS12 /RPL10A/EIF3H/RPS6/RPL29/RPS2/RPL27/RPL13A/RPL23/RPL35/RPS27A/RPL5/RPL10/RPL31/RPL23A/EIF3E/RPL37A/RPS29/RPL12/RPS11/RPL38/RPLP0/RPS3/RPLP1 /RPLP2/RPL14/RPS14/RPL18A/NCK2/RPS15A/RPS24/RPL36/RPL18/EIF3G/RPS16/RPS10/EIF3D/RPS15/RPS21/RPL8/RPS19/CCL5/RPS23/EIF2D/EIF2S2/RPS27/R PL13/RPS3A/RPS26/RPS18/RPS5/RPL27A/EIF3M/RPS9/IMPACT/EIF2AK1/POLR2G/EIF2A
Down eaSSc	GO:0019080	viral gene expression	74/723	191/18670	1.81E-54	9.60E-52	RPL6/RPL11/RPL22/RPL37/RPL4/RPL3/RPL7A/RPS25/RPL30/RPL32/RPS8/RPL19/RPL26/RPS17/UBA52/RPS20/RPL35A/RPL24/EIF3L/RPL34/RPL41/RPL15/RPS12/RPL1 0A/RPS6/RPL29/RPS2/RPL27/RPL13A/RPL23/RPL35/RPS27A/RPL5/RPL10/RPL31/RPL23A/RPL37A/RPS29/RPL12/RPS11/RPL38/RPLP0/RPS3/RPLP1/RPLP2/RPL14/RPS 14/RPL18A/RPS15A/RPS24/RPL36/RPL18/EIF3G/RPS16/RPS10/EIF3D/RPS15/RPS21/RPL8/RPS19/CCL5/RPS23/EIF2D/RPS27/RPL13/HDAC1/RPS3A/RPS26/RPS18/RPS 5/SUPT4H1/RPL27A/RPS9/POLR2G
Down eaSSc	GO:0019083	viral transcription	70/723	177/18670	2.84E-52	1.20E-49	RPL6/RPL11/RPL22/RPL37/RPL4/RPL3/RPL7A/RPS25/RPL30/RPL32/RPS8/RPL19/RPL26/RPS17/UBA52/RPS20/RPL35A/RPL24/RPL34/RPL41/RPL15/RPS12/RPL10A/RP S6/RPL29/RPS2/RPL27/RPL13A/RPL23/RPL35/RPS27A/RPL5/RPL10/RPL31/RPL23A/RPL37A/RPS29/RPL12/RPS11/RPL38/RPLP0/RPS3/RPLP1/RPLP2/RPL14/RPS14/RP L18A/RPS15A/RPS24/RPL36/RPL18/RPS16/RPS10/RPS15/RPS21/RPL8/RPS19/CCL5/RPS23/RPS27/RPL13/HDAC1/RPS3A/RPS26/RPS18/RPS5/SUPT4H1/RPL27A/RPS9 /POLR2G
Down eaSSc	GO:0042254	ribosome biogenesis	52/723	297/18670	3.60E-20	9.00E-18	RPL6/RPL11/RPL3/RPL7A/FBL/RPS8/RPL26/RPS17/RPL35A/RPL24/RPL10A/C1QB/MRPL11/RPS2/RPL27/RPL35/RPL5/RPL10/RPL23A/RPL12/RPL38/RPLP0/RPL 14/RPLP0P6/RPS14/RSL1D1/ZNHIT3/RPS24/RPS16/RPS10/RPS15/RPS21/RPS19/NSA2/EXOSC5/RPS27/NHP2/IMP4/NIP7/RPS5/RPS9/PA2G4/RSL24D1/EXOSC7/RRP3 6/MRPL20/NOP16/NUDT16/TRMT112/MRPS2/EIF2A
Down eaSSc	GO:0022618	ribonucleoprotein complex assembly	49/723	277/18670	2.89E-19	6.82E-17	RPL6/RPL11/EIF31/RPL3/RPL24/EIF3L/SNRPD3/EIF3H/C1QB/MRPL11/RPL13A/RPL5/SNRPF/RPL10/RPL23A/EIF3E/SNRPC/SNRPD2/RPL12/RPL38/CLNS1A/RPLP0/RPL P0P6/RPS14/ZNHIT3/EIF3K/EIF3G/RPS10/EIF3D/RPS15/STYXL1/RPS19/RPS23/EIF2D/EIF2S2/GEMIN7/RUVBL1/RPS27/TXNL4A/NIP7/SNRPD1/SNRPE/RPS5/EIF3M/RS L24D1/LSM4/MRPL20/MRPS2/EIF2A
Down eaSSc	GO:0071826	ribonucleoprotein complex subunit organization	50/723	291/18670	4.48E-19	1.00E-16	RPL6/RPL11/EIF31/RPL3/RPL24/EIF3L/SNRPD3/EIF3H/C1QB/MRPL11/RPL13A/RPL5/SNRPF/RPL10/RPL23A/EIF3E/SNRPC/SNRPD2/RPL12/RPL38/CLNS1A/RPLP0/RPL P0P6/RPS14/ZNHIT3/EIF3K/EIF3G/RPS10/EIF3D/RPS15/STYXL1/RPS19/RPS23/EIF2D/EIF2S2/GEMIN7/RUVBL1/RPS27/TXNL4A/NIP7/SNRPD1/SNRPE/RPS5/E IF3M/RSL24D1/LSM4/MRPL20/MRPS2/EIF2A
Down eaSSc	GO:0042775	mitochondrial ATP synthesis coupled electron transport	28/723	97/18670	2.57E-17	4.96E-15	UQCRC1/COX7C/UQCRCB/COX6C/COX5A/COX6A1/NDUFS4/NDUFAB1/UQCRC10/NDUFA6/COX6B1/NDUFC1/COX7A2L/NDUFC2/NDUFB4/NDUFS2/COX411/UQCRCQ/UQ CRC2/SDHA/NDUFB5/NDUFV1/COQ9/UQCRCR/NDUFA1/COX5B/SDHC/NDUFB2
Down eaSSc	GO:0022904	respiratory electron transport chain	29/723	117/18670	6.26E-16	1.11E-13	UQCRC1/COX7C/UQCRCB/COX6C/COX5A/COX6A1/NDUFS4/NDUFAB1/UQCRC10/NDUFA6/COX6B1/NDUFC1/COX7A2L/NDUFC2/SDHB/NDUFB4/NDUFS2/COX411/UQC RQ/UQCRC2/SDHA/NDUFB5/NDUFV1/COQ9/UQCRCR/NDUFA1/COX5B/SDHC/NDUFB2
Down eaSSc	GO:0006364	rRNA processing	33/723	214/18670	1.12E-11	1.53E-09	RPL11/RPL7A/FBL/RPL26/RPS17/RPL35A/RPL10A/RPS6/RPS2/RPL27/RPL35/RPL5/RPL14/RPS14/RSL1D1/ZNHIT3/RPS24/RPS16/RPS15/RPS21/RPS19/NSA2/EX OSC5/RPS27/NHP2/IMP4/RPS9/PA2G4/EXOSC7/RRP36/NUDT16/TRMT112

Down eaSSc	GO:0009144	purine nucleoside triphosphate metabolic process	38/723	342/18670	5.56E-09	6.21E-07	UQCR11/COX7C/UQCRB/COX6C/COX5A/COX6A1/NDUF54/GAPDH/NDUFAB1/UQCR10/NDUFA6/COX6B1/NDUFC1/COX7A2L/NDUFC2/NDUFB4/NDUFS2/COX41/IMPDH2/UQCRQ/NDME1/UQCRC2/TREX1/ADK/SDHA/NDUFB5/NDUFV1/COQ9/UQCRH/NDUFA1/COX5B/NUDT16/SDHC/NDUFB2/TMSB4X/ENO4/MOCS2/PGAM1
Down eaSSc	GO:0140053	mitochondrial gene expression	23/723	162/18670	7.28E-08	6.45E-06	MRPS33/C1QBP/MRPL11/RPUSD3/MRPL16/MRPL15/MRPL37/DAP3/MRPL21/OXA1L/MRPL34/MRPL18/MRPL24/MRPS15/MRPL28/MRPL33/MRPL40/MRPL20/MRPS2/MRPL51/MRPS16/MRPL45/MRPL43
Down eaSSc	GO:0033108	mitochondrial respiratory chain complex assembly	17/723	96/18670	1.46E-07	1.22E-05	UQCRB/NDUF54/NDUFAB1/UQCR10/NDUFA6/NDUFC1/NDUFC2/NDUFB4/NDUFS2/OXA1L/SMIM20/NDUFB5/NDUFV1/TIMMDC1/NDUFA1/PET117/NDUFB2
Down eaSSc	GO:0042119	neutrophil activation	43/723	498/18670	8.27E-07	6.25E-05	PSMB7/SERPINB6/PGRMC1/LAMTOR2/ALAD/TRAPPC1/EEF1A1/FOLR3/LILRA2/SRP14/GSTP1/DDOST/VAMP8/PRDX6/CCL5/RAB3D/NDUFC2/PGM2/TIMP2/CAP1/EEF2/HEBP2/IMPDH2/HMOX2/PRDX4/ATP6AP2/DNASE1L3/QPCT/SYNGR1/GMFG/RAB5B/PA2G4/HLA-H/GLB1/PYCARD/APRT/SERPINB1/MMP25/CEACAM3/VCL/PGAM1/OSTF1/IL18
Down eaSSc	GO:0043624	cellular protein complex disassembly	25/723	217/18670	1.17E-06	8.43E-05	MRPS33/MRPL11/DMTN/C12orf65/MRPL16/MRPL15/MRPL37/CAPZB/DAP3/MRPL21/OXA1L/MRPL34/MRPL18/MRPL24/MRPS15/MRPL28/MRPL33/MRPL40/MRPL20/TRMT112/MRPS2/MRPL51/MRPS16/MRPL45/MRPL43
Down eaSSc	GO:0002283	neutrophil activation involved in immune response	41/723	488/18670	2.96E-06	0.000206438	PSMB7/SERPINB6/PGRMC1/LAMTOR2/ALAD/TRAPPC1/EEF1A1/FOLR3/LILRA2/SRP14/GSTP1/DDOST/VAMP8/PRDX6/RAB3D/NDUFC2/PGM2/TIMP2/CAP1/EEF2/HEBP2/IMPDH2/HMOX2/PRDX4/ATP6AP2/DNASE1L3/QPCT/SYNGR1/GMFG/RAB5B/PA2G4/HLA-H/GLB1/PYCARD/APRT/SERPINB1/MMP25/CEACAM3/VCL/PGAM1/OSTF1
Down eaSSc	GO:0002446	neutrophil mediated immunity	40/723	499/18670	1.20E-05	0.000807639	PSMB7/SERPINB6/PGRMC1/LAMTOR2/ALAD/TRAPPC1/EEF1A1/FOLR3/SRP14/GSTP1/DDOST/VAMP8/PRDX6/RAB3D/NDUFC2/PGM2/TIMP2/CAP1/EEF2/HEBP2/IMPDH2/HMOX2/PRDX4/ATP6AP2/DNASE1L3/QPCT/SYNGR1/GMFG/RAB5B/PA2G4/HLA-H/GLB1/PYCARD/APRT/SERPINB1/MMP25/CEACAM3/VCL/PGAM1/OSTF1
Up lcSSc	GO:0048285	organelle fission	54/824	449/18670	2.16E-11	1.02E-07	PEX11B/TTK/RMI1/TTN/KNTC1/HORMAD1/CDC20/SEH1L/BIRC5/CEP192/ASPM/FANCM/PCID2/ANAPC4/FANCD2/FIGNL1/CLASP2/BRIP1/KIFC1/NDC80/TOP2A/SMC4/GEN1/SYCP2/CENPE/KIF14/KIF18B/CDC45/NUSAP1/MYBL2/C11orf80/VPS4B/BUB3/CENPK/CIAO1/MEI1/SPAG5/TUBG1/KIF23
Up lcSSc	GO:0007059	chromosome segregation	41/824	321/18670	9.72E-10	1.53E-06	TTK/RMI1/TTN/HORMAD1/CDC20/SEH1L/BIRC5/FANCM/PCID2/ANAPC4/FANCD2/ESCO2/BRIP1/KIFC1/NDC80/TOP2A/SMC4/GEN1/SYCP2/PUM2/SMC6/CENPE/KIF14/KIF18B/CDC45/NUSAP1/MKI67/CDC26/NUP37/KNSTRN/ECT2/SMC2/PTTG2/VPS4B/BUB3/CENPK/CIAO1/MEI1/SPAG5/TUBG1/KIF23
Up lcSSc	GO:0000070	mitotic sister chromatid segregation	25/824	151/18670	1.09E-08	1.03E-05	TTK/TTN/CDC20/SEH1L/PCID2/ANAPC4/KIFC1/NDC80/SMC4/GEN1/CENPE/KIF14/KIF18B/CDC45/NUSAP1/CDC26/KNSTRN/SMC2/PTTG2/VPS4B/BUB3/CENPK/SPAG5/TUBG1/KIF23
Up lcSSc	GO:0006260	DNA replication	35/824	274/18670	1.64E-08	1.23E-05	RMI1/SLFN11/FANCM/TBRG1/ORC6/POLE2/RECQL/CDK1/POLQ/ESCO2/WDHD1/NBN/BRIP1/MAP2K4/DONSON/PCNA/THOC1/WRN/GEN1/ATR/ZMPSTE24/GMNN/ORC2/RAD51/CCNA2/CDC45/E2F7/NUGGC/RFC3/RPAIN/ORC1/POLG2/RBBP7/POLI/RRM2
Up lcSSc	GO:0140014	mitotic nuclear division	34/824	264/18670	2.14E-08	1.26E-05	TTK/TTN/KNTC1/CDC20/SEH1L/BIRC5/CEP192/PCID2/ANAPC4/CLASP2/KIFC1/NDC80/SMC4/GEN1/CENPE/KIF14/KIF18B/CDC45/NUSAP1/MYBL2/MKI67/CDC26/KNSTRN/SMC2/PTTG2/KIF11/VPS4B/BUB3/CENPK/USP16/SPAG5/FGF8/TUBG1/KIF23
Up lcSSc	GO:0006403	RNA localization	29/824	230/18670	3.65E-07	0.00015651	CPSF2/NUP107/NUP160/NUP205/SEH1L/AGFG1/SRSF11/PCID2/XPO5/SHQ1/TCP1/DHX38/THOC1/CETN3/ATR/NUP133/NUP188/TSC1/FMR1/NUP54/NCBP1/NUP37/DHX36/CCT2/RBM26/SMG1/EXOSC10/NCBP2/KIF5C
Up lcSSc	GO:0051983	regulation of chromosome segregation	18/824	103/18670	5.38E-07	0.000211293	TTK/HORMAD1/CDC20/PCID2/ANAPC4/NDC80/GEN1/PUM2/SMC6/CENPE/CDC45/MKI67/CDC26/KNSTRN/ECT2/PTTG2/BUB3/SPAG5
Up lcSSc	GO:0031503	protein-containing complex localization	32/824	281/18670	9.33E-07	0.000338403	CPSF2/NUP107/NUP160/NUP205/LCA5/SEH1L/GRIPAP1/BIRC5/AGFG1/SRSF11/PCID2/STX7/ICK/TTC30B/DHX38/THOC1/ATR/NUP133/NUP188/TSC1/HSPB11/VPS35/NUP54/NCBP1/PCM1/CEP72/NUP37/ARHGAP44/SMG1/SYJN2BP/NCBP2/KIF5C
Up lcSSc	GO:0006405	RNA export from nucleus	20/824	135/18670	1.95E-06	0.000657521	CPSF2/NUP107/NUP160/NUP205/SEH1L/AGFG1/SRSF11/PCID2/XPO5/DHX38/THOC1/NUP133/NUP188/TSC1/NUP54/NCBP1/NUP37/RBM26/SMG1/NCBP2
Up lcSSc	GO:1901990	regulation of mitotic cell cycle phase transition	42/824	444/18670	2.96E-06	0.000931009	TTK/KNTC1/CDC20/SLFN11/CEP192/PCID2/ANAPC4/FAM107A/CDK1/CNOT6/NBN/CEP78/DONSON/PCNA/NDC80/PSMA3/GEN1/SFI1/CENPE/PSMD14/KIF14/PSME4/PCBP4/CDK5RAP3/CDC45/WNT10B/CNOT11/CDC26/PCM1/UBD/CDC45/CEP72/CNOT11/E2F7/CENPJ/VPS4B/BUB3/PKIA/TMOD3/ORC1/TUBG1/HYAL1
Up lcSSc	GO:0007051	spindle organization	22/824	170/18670	6.02E-06	0.001514295	TTK/CDC20/BIRC5/CEP192/ASPM/CLASP2/NEK7/GPSM2/KIFC1/NDC80/CENPE/MYBL2/CEP72/KNSTRN/CLTC/KIF11/VPS4B/TUBGCP5/SAC3D1/SPAG5/TUBG1/KIF23
Up lcSSc	GO:0071427	mRNA-containing ribonucleoprotein complex export from nucleus	17/824	111/18670	7.18E-06	0.001612556	CPSF2/NUP107/NUP160/NUP205/SEH1L/AGFG1/SRSF11/PCID2/DHX38/THOC1/NUP133/NUP188/NUP54/NCBP1/NUP37/SMG1/NCBP2
Up lcSSc	GO:0071166	ribonucleoprotein complex localization	18/824	128/18670	1.32E-05	0.002488175	CPSF2/NUP107/NUP160/NUP205/SEH1L/AGFG1/SRSF11/PCID2/DHX38/THOC1/NUP133/NUP188/TSC1/NUP54/NCBP1/NUP37/SMG1/NCBP2
Up lcSSc	GO:0051321	meiotic cell cycle	27/824	249/18670	1.60E-05	0.002702056	TTK/RMI1/HORMAD1/CDC20/ASPM/FANCM/FANCD2/FIGNL1/NBN/BRIP1/PRKACB/TOP2A/NPPC/SMC4/SYCP2/C11orf80/RAD51/WNT4/CNTD1/SMC2/PTTG2/NSUN2/BUB3/TUBGCP5/MEI1/RAD54L/TUBG1
Up lcSSc	GO:0033044	regulation of chromosome organization	33/824	342/18670	2.25E-05	0.00366235	TTK/CTR9/CDC20/PCID2/ANAPC4/ATAD2/TRIP12/NEK7/NBN/PYGO2/NDC80/TOP2A/TCP1/GEN1/CENPE/ATR/ZMPSTE24/CDC45/FMR1/MKI67/CDC26/CDC45/RNF20/DHX36/PTTG2/CCT2/BUB3/ZNF451/PRKD1/OGT/SMG1/EXOSC10/LRRK2
Up lcSSc	GO:0007093	mitotic cell cycle checkpoint	20/824	165/18670	4.12E-05	0.005885022	TTK/KNTC1/CDC20/PCID2/CDK1/CNOT6/NBN/DONSON/PCNA/NDC80/TOP2A/MSH2/GEN1/PCBP4/CDK5RAP3/CNOT11/CNOT1/E2F7/BUB3/ORC1
Up lcSSc	GO:0000077	DNA damage checkpoint	18/824	145/18670	7.19E-05	0.009383219	MAPK14/CDK1/CNOT6/NBN/BRIP1/DONSON/PCNA/THOC1/MSH2/ATR/PCBP4/CDK5RAP3/WDR76/TIPRL/CNOT11/CNOT1/E2F7/INTS7
Up lcSSc	GO:0140013	meiotic nuclear division	20/824	172/18670	7.44E-05	0.009383219	TTK/RMI1/HORMAD1/CDC20/ASPM/FANCM/FANCD2/FIGNL1/BRIP1/TOP2A/SMC4/SYCP2/C11orf80/RAD51/WNT4/CNTD1/SMC2/PTTG2/MEI1/RAD54L
Up lcSSc	GO:0044766	multi-organism transport	12/824	73/18670	7.76E-05	0.009383219	NUP107/NUP160/NUP205/SEH1L/TCP1/THOC1/NUP133/NUP188/KPNA1/FMR1/NUP54/NUP37
Up lcSSc	GO:1902579	multi-organism localization	12/824	73/18670	7.76E-05	0.009383219	NUP107/NUP160/NUP205/SEH1L/TCP1/THOC1/NUP133/NUP188/KPNA1/FMR1/NUP54/NUP37
Down lcSSc	GO:0019080	viral gene expression	39/655	191/18670	2.80E-19	1.19E-15	EIF3G/RPL29/RPL13A/RPL6/USF2/TRIM8/RPL3/RPS9/RPL35/RPL11/RPL14/RPL19/EIF3D/EIF2D/RPL8/RPL4/RPL7A/NELFE/RSF1/RPL13/POLR21/CCL4/RPL36/POLR2E/FURIN/RPL24/RPL15/RPS15/SUPT4H1/RPL18A/RPL1/RPL35A/CCL5/RPL18/CCNT1/RPS19/PCBP2/RPS8/POLR2L
Down lcSSc	GO:0006413	translational initiation	36/655	193/18670	1.46E-16	3.09E-13	EIF3G/EIF3/RPL29/RPL13A/RPL6/RPL3/RPS9/ATF4/RPL35/RPL11/RPL14/KHDRBS1/RPL19/EIF3D/EIF4H/EIF1/EIF2D/RPL8/RPL4/RPL7A/PABPC1/RPL13/EIF3H/RPL36/EIF3K/RPL24/RPL15/RPS15/RPL18A/RPL1/RPL35A/CCL5/RPL18/EIF4B/RPS19/RPS8
Down lcSSc	GO:0019083	viral transcription	34/655	177/18670	4.07E-16	5.75E-13	RPL29/RPL13A/RPL6/USF2/TRIM8/RPL3/RPS9/RPL35/RPL11/RPL14/RPL19/RPL8/RPL4/RPL7A/NELFE/RSF1/RPL13/POLR21/CCL4/RPL36/POLR2E/RPL24/RPL15/RPS15/SUPT4H1/RPL18A/RPL1/RPL35A/CCL5/RPL18/CCNT1/RPS19/RPS8/POLR2L
Down lcSSc	GO:0006614	SRP-dependent cotranslational protein targeting to membrane	23/655	105/18670	1.39E-12	1.18E-09	RPL29/RPL13A/RPL6/RPL3/RPS9/RPL35/RPL11/RPL14/RPL19/RPL8/RPL4/RPL7A/RPL13/RPL36/RPL24/RPL15/RPS15/RPL18A/RPL1/RPL35A/RPL18/RPS19/RPS8
Down lcSSc	GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	24/655	120/18670	3.66E-12	1.94E-09	RPL29/RPL13A/RPL6/RPL3/RPS9/RPL35/RPL11/RPL14/RPL19/RPL8/RPL4/RPL7A/PABPC1/RPL13/RPL36/RPL24/RPL15/RPS15/RPL18A/RPL1/RPL35A/RPL18/RPS19/RPS8
Down lcSSc	GO:0072599	establishment of protein localization to endoplasmic reticulum	24/655	122/18670	5.32E-12	2.51E-09	RPL29/RPL13A/RPL6/RPL3/RPS9/RPL35/RPL11/RPL14/RPL19/RPL8/RPL4/RPL7A/RPL13/RPL36/RPL24/RPL15/RPS15/RPL18A/RPL1/RPL35A/RPL18/RPS19/RPS8
Down lcSSc	GO:0042273	ribosomal large subunit biogenesis	16/655	71/18670	2.33E-09	7.08E-07	RSL1D1/RPL6/RPL3/MRPL11/RPL35/RPL11/RPL14/RSL24D1/RPL7A/NLE1/ZNHIT3/BRIX1/RPL24/NHP2/RPL35A/GTF3A

Down lcSSc	GO:0042255	ribosome assembly	14/655	63/18670	2.84E-08	6.35E-06	RPL6/RPL3/MRPL11/RPL11/RSL24D1/MRPS11/NLE1/BRIX1/RPL24/C1QBP/RPS15/SBDS/ABT1/RPS19
Down lcSSc	GO:0071826	ribonucleoprotein complex subunit organization	29/655	291/18670	4.63E-07	9.36E-05	EIF3G/EIF3I/RPL13A/RPL6/RPL3/MRPL11/RPL11/EIF3D/EIF4H/EIF2D/RSL24D1/MRPS11/SNRPD2/NLE1/EIF3H/ZNHIT3/BRIX1/EIF3K/RUVBL2/RPL24/USP39/C1QBP/RPS15/PRPF18/SART1/SBDS/ABT1/EIF4B/RPS19
Down lcSSc	GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	34/655	379/18670	5.80E-07	0.000107062	YBX1/HNRNPA0/PCBP1/KHDRBS1/SNRPA/RBM15B/LSM7/SF3B2/SYF2/PABPC1/PQBP1/SNRPD2/POLR2I/NSRP1/POLR2E/HNRNPUL1/USP39/ALYREF/SCNM1/HNRNPL/SF3B5/C1QBP/CDK13/PRPF18/SART1/HNRNPM/SNRPN/PCBP2/METTL6/PPIL3/ZMAT2/POLR2L/SNIP1/PRDX6
Down lcSSc	GO:0000398	mRNA splicing, via spliceosome	34/655	379/18670	5.80E-07	0.000107062	YBX1/HNRNPA0/PCBP1/KHDRBS1/SNRPA/RBM15B/LSM7/SF3B2/SYF2/PABPC1/PQBP1/SNRPD2/POLR2I/NSRP1/POLR2E/HNRNPUL1/USP39/ALYREF/SCNM1/HNRNPL/SF3B5/C1QBP/CDK13/PRPF18/SART1/HNRNPM/SNRPN/PCBP2/METTL6/PPIL3/ZMAT2/POLR2L/SNIP1/PRDX6
Down lcSSc	GO:0006119	oxidative phosphorylation	16/655	145/18670	5.09E-05	0.007197812	SURF1/NDUFA2/UQCRC1/NDUFB10/CYC1/COX5A/UQCRCF51/PPIF/COX6A1/SLC25A33/NDUFB7/NDUFS7/NDUFS8/NDUFA6/CHCHD10/NDUFA1
Down lcSSc	GO:0006098	pentose-phosphate shunt	5/655	15/18670	0.000117276	0.015245683	PGLS/PGAM1/RBKS/PGM2/TKT
Down lcSSc	GO:0033238	regulation of cellular amine metabolic process	11/655	81/18670	0.000118574	0.015245683	COMT/OAZ1/ODC1/ITGB2/PSMB7/PSMD4/PSMD8/PSMC5/PSMB2/OAZ3/PNKD
Down lcSSc	GO:0042119	neutrophil activation	34/655	498/18670	0.000178416	0.019838415	SYNGR1/ALAD/LILRA2/EEF2/RAP2B/FOLR3/ITGB2/PSMB7/PTPN6/PGRMC1/HLA-H/GLIPR1/PGAM1/BCR/FTH1/GMFG/PLAUR/PGM2/DDOST/ACAA1/ARL8A/ACTR1B/IMPDH1/CDK13/PDAP1/MAN2B1/DOCK2/PECAM1/CTSZ/CCL5/PLAU/GHDC/COTL1/PRDX6
Down lcSSc	GO:0051156	glucose 6-phosphate metabolic process	6/655	25/18670	0.000182347	0.019838415	PGLS/PGAM1/RBKS/PGM2/TKT/G6PC3
Down lcSSc	GO:0001836	release of cytochrome c from mitochondria	9/655	59/18670	0.000199443	0.021155956	GPX1/BAD/PLAUR/TIMM50/PPIF/PMAIP1/FIS1/BMF/CHCHD10
Down lcSSc	GO:0022904	respiratory electron transport chain	13/655	117/18670	0.000235604	0.024382183	NDUFA2/UQCRC1/NDUFB10/CYC1/COX5A/SDHB/UQCRCF51/COX6A1/NDUFB7/NDUFS7/NDUFS8/NDUFA6/NDUFA1
Down lcSSc	GO:0002283	neutrophil activation involved in immune response	33/655	488/18670	0.000263084	0.026577717	SYNGR1/ALAD/LILRA2/EEF2/RAP2B/FOLR3/ITGB2/PSMB7/PTPN6/PGRMC1/HLA-H/GLIPR1/PGAM1/BCR/FTH1/GMFG/PLAUR/PGM2/DDOST/ACAA1/ARL8A/ACTR1B/IMPDH1/CDK13/PDAP1/MAN2B1/DOCK2/PECAM1/CTSZ/PLAU/GHDC/COTL1/PRDX6
Down lcSSc	GO:0070126	mitochondrial translational termination	11/655	89/18670	0.00027734	0.027366409	MRPL28/AURKAI1/MRPL11/MRPL55/MRPS11/MRPL34/MTRF1L/MRPS34/OXA1L/MRPL4/MRPL16
Up ncSSc	GO:0042113	B cell activation	24/517	310/18670	6.27E-06	0.028037426	MIR17HG/PCID2/TNFRSF4/SWAP70/THOC1/IL6/HSPD1/RBP1/CHRN2/CD19/PAWR/MS4A1/IGHV3-33/TNFRSF13C/MALT1/IGHV2-70/FCRL1/CXCR5/FZD9/CD180/NBN/CD79B/PPP2R3C/IGHV3-11
Up ncSSc	GO:0044766	multi-organism transport	10/517	73/18670	3.16E-05	0.041913325	TSG101/NUP107/CAV1/THOC1/SEH1L/RANBP2/NUP54/VPS37B/FMR1/NUP88
Up ncSSc	GO:1902579	multi-organism localization	10/517	73/18670	3.16E-05	0.041913325	TSG101/NUP107/CAV1/THOC1/SEH1L/RANBP2/NUP54/VPS37B/FMR1/NUP88
Up ncSSc	GO:0046794	transport of virus	9/517	60/18670	3.76E-05	0.041913325	TSG101/NUP107/CAV1/SEH1L/RANBP2/NUP54/VPS37B/FMR1/NUP88
Up ncSSc	GO:0019058	viral life cycle	23/517	328/18670	4.69E-05	0.041913325	TSG101/ZNF502/NUP107/TNFRSF4/RAB1A/CAV1/DDX5/SEH1L/SLC10A1/RANBP2/EFNB2/NUP54/RNASEL/VPS37B/ITGAV/LAMTOR5/TOP2A/FMR1/MIR221/CD86/C HMP7/SLPI/NUP88
Up ncSSc	GO:0015682	ferric iron transport	7/517	38/18670	7.18E-05	0.044980462	TF/ATP6V1C1/ATP6V1E1/STEAP4/CLTC/ATP6V1D/ATP6V1A
Up ncSSc	GO:0072512	trivalent inorganic cation transport	7/517	38/18670	7.18E-05	0.044980462	TF/ATP6V1C1/ATP6V1E1/STEAP4/CLTC/ATP6V1D/ATP6V1A
Up ncSSc	GO:0000070	mitotic sister chromatid segregation	14/517	151/18670	8.04E-05	0.044980462	SPAG5/PCID2/CDC45/SEH1L/ANAPC4/KIFC1/DLGA5/KIF23/CENPK/CDC26/KIF18B/CENPE/CHMP7/TTN
Up ncSSc	GO:0051249	regulation of lymphocyte activation	29/517	485/18670	9.29E-05	0.045390335	PTPN22/MIR17HG/ZBTB16/PCID2/TNFRSF4/CAV1/PLA2G2F/THOC1/IL6/CD24/SOCS1/HSPD1/CHRN2/CD19/PAWR/TNFRSF18/IGHV3-33/EFNB2/TNFRSF13C/MALT1/IGHV2-70/AP1G1/DLG1/HES1/LAG3/HAVCR2/CD86/PPP2R3C/IGHV3-11
Up ncSSc	GO:0006607	NLS-bearing protein import into nucleus	5/517	18/18670	0.000101476	0.045390335	RGPD3/CBLB/RANBP2/NUP54/RGPD2
Down ncSSc	GO:0019080	viral gene expression	25/421	191/18670	1.42E-12	3.50E-09	CCL5/RPL14/RPL13A/TRIM8/RPL35/RPS15/RPL28/RPL29/RPL6/RPL3/RPL36/RPS19/RPL18A/EIF3G/RPL19/TRIM11/RPL1/RPL4/USF2/RPS9/RPL18/REST/RPL35A/RPL10A/TRIM62
Down ncSSc	GO:0019083	viral transcription	24/421	177/18670	1.85E-12	3.50E-09	CCL5/RPL14/RPL13A/TRIM8/RPL35/RPS15/RPL28/RPL29/RPL6/RPL3/RPL36/RPS19/RPL18A/RPL19/TRIM11/RPL1/RPL4/USF2/RPS9/RPL18/REST/RPL35A/RPL10A/T RIM62
Down ncSSc	GO:0045047	protein targeting to ER	19/421	118/18670	1.82E-11	1.99E-08	RPL14/RPL13A/RPL35/RPS15/RPL28/RPL29/RPL6/RPL3/RPL36/RPS19/RPL18A/RPL19/PMM1/RPL1/RPL4/RPS9/RPL18/RPL35A/RPL10A
Down ncSSc	GO:0006614	SRP-dependent cotranslational protein targeting to membrane	18/421	105/18670	2.10E-11	1.99E-08	RPL14/RPL13A/RPL35/RPS15/RPL28/RPL29/RPL6/RPL3/RPL36/RPS19/RPL18A/RPL19/RPL1/RPL4/RPS9/RPL18/RPL35A/RPL10A
Down ncSSc	GO:0072599	establishment of protein localization to endoplasmic reticulum	19/421	122/18670	3.33E-11	2.10E-08	RPL14/RPL13A/RPL35/RPS15/RPL28/RPL29/RPL6/RPL3/RPL36/RPS19/RPL18A/RPL19/PMM1/RPL1/RPL4/RPS9/RPL18/RPL35A/RPL10A
Down ncSSc	GO:0006413	translational initiation	23/421	193/18670	7.90E-11	3.73E-08	NCK2/CCL5/RPL14/RPL13A/RPL35/RPS15/RPL28/RPL29/RPL6/RPL3/RPL36/RPS19/RPL18A/KHDRBS1/EIF3G/RPL19/RPL1/RPL4/RPS9/DHX33/RPL18/RPL35A/RPL10A
Down ncSSc	GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	18/421	120/18670	2.09E-10	8.78E-08	RPL14/RPL13A/RPL35/RPS15/RPL28/RPL29/RPL6/RPL3/RPL36/RPS19/RPL18A/RPL19/RPL1/RPL4/RPS9/RPL18/RPL35A/RPL10A
Down ncSSc	GO:0030168	platelet activation	15/421	153/18670	2.01E-06	0.000543591	DMTN/SH2B3/VWF/GNAS/SELP/GP1BA/GP6/APOE/ALOX12/FYN/TREM1/CSR1/ITGA2B/GNG2/TLN1
Down ncSSc	GO:0034109	homotypic cell-cell adhesion	9/421	81/18670	8.60E-05	0.017107301	DMTN/SH2B3/CCL5/GNAS/GP1BA/ALOX12/CSR1/ITGA2B/TLN1
Down ncSSc	GO:0032897	negative regulation of viral transcription	5/421	24/18670	0.000169829	0.03209776	CCL5/TRIM8/TRIM11/REST/TRIM62