Tissue: Heart_Left_Ventricle=>Adipose_Subcutaneous Type: asymmetric

SourceGene: CRABP1(ENSG00000166426.7)

TargetGeneSet: RP11 SRGAP2P2 CDC42SE1 PMVK PTPN7 MRPL33
SGOL2 PHLDB2 COX17 PSAPL1 C4orf3 NDUFC1 NDUFS4 COX7C FAM65B RPS6KA2
MRPS24 TP53TG1 SGK196 TMEM67 COX6C DEPTOR FAM27E2 CNTRL QSOX2 FBXW5
ZNF215 TBC1D10C TMEM106C DNAJC14 TMEM198B PARP4 ELF1
FLVCR2 NDUFB1 MOK NDUFB10 GABARAPL2 MAP1LC3B IL17C SCIMP
NLRP1 CBX1 UQCR11 S1PR4 PRR22 HSH2D FKBP8 C19orf54 SAMHD1
NCOA3 ZBP1 RP4 ATP5J HSF2BP TTC38

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0022904	5.98E-10	34.25119617	0.305584389	8	96	respiratory electron transport chain
GO:0022900	8.59E-09	23.85797828	0.426544876	8	134	electron transport chain
GO:0045333	1.36E-08	22.42105263	0.452010242	8	142	cellular respiration
GO:0015980	4.90E-06	9.932054216	0.977233409	8	307	energy derivation by oxidation of organic compounds
GO:0006120	4.91E-06	42.77678571	0.114594146	4	36	"mitochondrial electron transport, NADH to ubiquinone"

GO:0006091 6.71E-06 8.119331742 1.362397066 9 428 generation of precursor metabolites and energy

GO:0042773 1.45E-05 31.80952381 0.149609024 4 47 ATP synthesis coupled electron transport

GO:0042775 1.45E-05 31.80952381 0.149609024 4 47 mitochondrial ATP synthesis coupled electron transport

Tissue: Adipose_Subcutaneous=>Heart_Left_Ventricle Type: asymmetric

SourceGene: CTD-2184D3.7(ENSG00000259709.1) Novel antisense

TargetGeneSet: RPL11 IPO9-AS1 RP11 RAB1A FAHD2B KANSL1L RPL37A MME-AS1 RPL39P3 PDAP1 TAS2R5 RPL30 PTCH1 RPL35 TOR1B EIF5AL1 RPLP2 RPS25 ERH SLIRP SRP14 MAP2K5 WHAMM MYL12B RPL36 CDC37 EEF1B2P3 6-Sep

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0006414	1.09E-14	111.984375	0.152584596	9	105	translational elongation
GO:0006415	3.44E-13	106.3725672	0.132239983	8	91	translational termination
GO:0006612	3.48E-13	74.40625	0.222337554	9	153	protein targeting to membrane
GO:0006614	1.11E-12	90.93100714	0.152584596	8	105	SRP-dependent cotranslational protein targeting to membrane

GO:0006613	1.20E-12	89.99686028	0.154037783	8	106	cotranslational protein targeting to membrane
GO:0045047	1.20E-12	89.99686028	0.154037783	8	106	protein targeting to ER
GO:0072599	1.20E-12	89.99686028	0.154037783	8	106	establishment of protein localization to endoplasmic reticulum
GO:0070972	2.89E-12	80.11188811	0.171476022	8	118	protein localization to endoplasmic reticulum
GO:0043624	2.38E-11	60.62599469	0.222337554	8	153	cellular protein complex disassembly
GO:0043241	3.08E-11	58.58461538	0.229603488	8	158	protein complex disassembly
GO:0034623	6.69E-11	52.87859129	0.252854474	8	174	cellular macromolecular complex disassembly
GO:0032984	8.40E-11	51.31443995	0.260120407	8	179	macromolecular complex disassembly
GO:0000184	2.27E-10	63.91964286	0.172929209	7	119	"nuclear-transcribed mRNA catabolic process, nonsense-mediated decay"
GO:0072594	2.39E-10	44.69073783	0.296450073	8	204	establishment of protein localization to organelle
GO:0006605	3.35E-10	27.36285266	0.688810463	10	474	protein targeting
GO:0019080	1.22E-09	49.60416667	0.219431181	7	151	viral genome expression
GO:0019083	1.22E-09	49.60416667	0.219431181	7	151	

viral transcription

GO:0006413	1.27E-09	49.25862069	0.220884368	7	152	translational initiation
GO:0000956	2.68E-09	44.03703704	0.245588541	7	169	nuclear-transcribed mRNA catabolic process
GO:0071845	3.29E-09	31.55852843	0.412705003	8	284	cellular component disassembly at cellular level
GO:0022411	3.67E-09	31.0989011	0.41851775	8	288	cellular component disassembly
GO:0006402	3.84E-09	41.69298246	0.25866722	7	178	mRNA catabolic process
GO:0006401	1.03E-08	35.93939394	0.297903259	7	205	RNA catabolic process
GO:0019058	2.34E-08	31.70982143	0.335686112	7	231	viral infectious cycle
GO:0022415	5.28E-08	28.01778656	0.377828524	7	260	viral reproductive process
GO:0033365	1.74E-07	18.48138958	0.687357276	8	473	protein localization to organelle
GO:0016032	2.19E-06	15.75	0.65538717	7	451	viral reproduction

Tissue: Heart_Left_Ventricle=>Adipose_Subcutaneous	Type:	asymmetric

SourceGene: CTD-2290C23.1(ENSG00000224282.3)

TargetGeneSet: MTND1P23 RP11 TNFRSF4 KCNAB2 C1QC C1QB ARID1A
C1orf38 CSF3R C1orf162 ADORA3 RP4 SRGAP2P2 C1orf56 SLAMF8 PIGM
CD84 CEP350 PTPRC BIRC6 ITGB6 PDCD1 BRK1 UBE2E2 STAB1 FAM208A PHC3
MFSD7 SH3TC1 BOD1L TXK PDGFRA BMP2K RPS3A FYB EMB SKP1
DDX46 CSF1R DOCK2 ATF6B GPSM3 CUTA FGD2 WDR11 RP3 MPLKIP
CCL24 IFRD1 TFEC TBXAS1 PRSS1 SLA SYK WDFY4 RPS3AP5 PNLIPRP2
MS4A6A MS4A7 FERMT3 BAD RNASEH2C BCRP1 RHOD AIP SLCO2B1
MYO7A ATM UBE4A KCNJ5 CD4 PTPN6 CD163 C3AR1 ITPR2 ALG10B MLL4
NCKAP1L RBMS1P1 SELPLG GIT2 MED13L LACC1 MYCBP2-AS1 SLC7A7 FANCM
VTI1B SIVA1 FMN1 USP8 STUB1 MEFV SLC7A6 ARRB2 POLR2A TMEM106A
TMEM106A-AS1 RHBDF2 TNRC6C C19orf35 CLEC4G CD209 EIF3G GMIP
TYROBP RASGRP4 JOSD2 LILRA1 SIGLEC1 ADAMTS1 TRPM2 MCM3AP EP300 C22orf32
NFAM1 WAS CACNA1F VSIG4 BTK DDX26B MPP1

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0002253	1.53E-08	8.129535604	2.048370355	14	299	activation of immune response
GO:0046649	3.70E-08	6.441882638	2.966369109	16	433	lymphocyte activation

GO:0051249	6.51E-08	7.883979328	1.938758563	13	283	regulation of lymphocyte activation
GO:0050864	7.76E-08	17.19584525	0.554909695	8	81	regulation of B cell activation
GO:0045577	7.90E-08	63.56382979	0.116462529	5	17	regulation of B cell differentiation
GO:0050865	8.49E-08	7.020275344	2.349802782	14	343	regulation of cell activation
GO:0050851	1.59E-07	12.48947368	0.842640648	9	123	antigen receptor-mediated signaling pathway

GO:0050778	1.76E-07	6.589176471	2.493668258	14	364	positive regulation of immune response
GO:0045579	2.54E-07	120.8168421	0.061656633	4	9	positive regulation of B cell differentiation
GO:0042110	2.61E-07	6.938668491	2.185385094	13	319	T cell activation
GO:0002694	2.80E-07	6.892630625	2.199086568	13	321	regulation of leukocyte activation
GO:0002429	3.10E-07	11.47419355	0.911148017	9	133	immune response-activating cell surface receptor signaling pathway

GO:0002768	6.09E-07	10.53111111	0.986506124	9	144	immune response-regulating cell surface receptor signaling pathway
GO:0002521	1.02E-06	6.6882283	2.068922566	12	302	leukocyte differentiation
GO:0030098	1.32E-06	8.199930499	1.397550343	10	204	lymphocyte differentiation
GO:0050853	1.42E-06	31.75531915	0.198671372	5	29	B cell receptor signaling pathway

GO:0050871	1.76E-06	19.22580645	0.369939797	6	54	positive regulation of B cell activation
GO:0002757	4.69E-06	7.054681648	1.609923189	10	235	immune response-activating signal transduction
GO:0050900	5.87E-06	6.868524734	1.651027611	10	241	leukocyte migration
GO:0001817	6.09E-06	5.566928351	2.459414573	12	359	regulation of cytokine production
GO:0030183	6.89E-06	14.86992716	0.465850114	6	68	B cell differentiation

GO:0002764	7.55E-06	6.663204608	1.698982769	10	248	
immune response-regulating signaling pathway						
GO:0042113	9.97E-06	8.613565745	1.048162757	8	153	B
cell activation						
GO:0002252	1.27E-05	5.155080214	2.644384472	12	386	
immune effector process						
GO:0006954	1.56E-05	4.680659864	3.165040482	13	462	
inflammatory response						
GO:0030097	1.59E-05	4.669922481	3.171891219	13	463	
hemopoiesis						

GO:0001816	1.59E-05	5.03070136	2.706041104	12	395	cytokine production
GO:0042098	1.62E-05	9.761750881	0.808386963	7	118	T cell proliferation
GO:0051251	1.64E-05	6.866990291	1.472908449	9	215	positive regulation of lymphocyte activation

Tissue: Heart_Left_Ventricle=>Adipose_Subcutaneous Type: cluster

SourceGene: CTD-2290C23.1(ENSG00000224282.3)

TargetGeneSet: MTND1P23 RP11 TNFRSF4 KCNAB2 C1QC C1QB ARID1A C1orf38 CSF3R C1orf162 ADORA3 RP4 SRGAP2P2 C1orf56 SLAMF8 PIGM CD84 CEP350 PTPRC BIRC6 ITGB6 PDCD1 BRK1 UBE2E2 STAB1 FAM208A PHC3 MFSD7 SH3TC1 BOD1L TXK PDGFRA BMP2K RPS3A FYB EMB SKP1 DDX46 CSF1R DOCK2 ATF6B GPSM3 CUTA FGD2 WDR11 RP3 MPLKIP CCL24 IFRD1 TFEC TBXAS1 PRSS1 SLA SYK WDFY4 RPS3AP5 PNLIPRP2 MS4A6A MS4A7 FERMT3 BAD RNASEH2C BCRP1 RHOD AIP SLCO2B1 MYO7A ATM UBE4A KCNJ5 CD4 PTPN6 CD163 C3AR1 ITPR2 ALG10B MLL4 NCKAP1L RBMS1P1 SELPLG GIT2 MED13L LACC1 MYCBP2-AS1 SLC7A7 FANCM VTI1B SIVA1 FMN1 USP8 STUB1 MEFV SLC7A6 ARRB2 POLR2A TMEM106A TMEM106A-AS1 RHBDF2 TNRC6C C19orf35 CLEC4G CD209 EIF3G GMIP TYROBP RASGRP4 JOSD2 LILRA1 SIGLEC1 ADAMTS1 TRPM2 MCM3AP EP300 C22orf32 NFAM1 WAS CACNA1F VSIG4 BTK DDX26B MPP1

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0002253	1.53E-08	8.129535604	2.048370355	14	299	activation of immune response
GO:0046649	3.70E-08	6.441882638	2.966369109	16	433	lymphocyte activation
GO:0051249	6.51E-08	7.883979328	1.938758563	13	283	regulation of lymphocyte activation

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GO:0050864      7.76E-08        17.19584525     0.554909695     8       81
regulation of B cell activation
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GO:0045577      7.90E-08        63.56382979     0.116462529     5       17
regulation of B cell differentiation
```

```
GO:0050865      8.49E-08        7.020275344     2.349802782     14      343
regulation of cell activation
```

```
GO:0050851      1.59E-07        12.48947368     0.842640648     9       123
antigen receptor-mediated signaling pathway
```

GO:0050778	1.76E-07	6.589176471	2.493668258	14	364	positive regulation of immune response
GO:0045579	2.54E-07	120.8168421	0.061656633	4	9	positive regulation of B cell differentiation
GO:0042110	2.61E-07	6.938668491	2.185385094	13	319	T cell activation
GO:0002694	2.80E-07	6.892630625	2.199086568	13	321	regulation of leukocyte activation
GO:0002429	3.10E-07	11.47419355	0.911148017	9	133	immune response-activating cell surface receptor signaling pathway

GO:0002768	6.09E-07	10.53111111	0.986506124	9	144	immune response-regulating cell surface receptor signaling pathway
GO:0002521	1.02E-06	6.6882283	2.068922566	12	302	leukocyte differentiation
GO:0030098	1.32E-06	8.199930499	1.397550343	10	204	lymphocyte differentiation
GO:0050853	1.42E-06	31.75531915	0.198671372	5	29	B cell receptor signaling pathway
GO:0050871	1.76E-06	19.22580645	0.369939797	6	54	positive regulation of B cell activation

GO:0002757	4.69E-06	7.054681648	1.609923189	10	235		immune response-activating signal transduction
GO:0050900	5.87E-06	6.868524734	1.651027611	10	241		leukocyte migration
GO:0001817	6.09E-06	5.566928351	2.459414573	12	359		regulation of cytokine production
GO:0030183	6.89E-06	14.86992716	0.465850114	6	68	B	cell differentiation
GO:0002764	7.55E-06	6.663204608	1.698982769	10	248		immune response-regulating signaling pathway

GO:0042113 cell activation	9.97E-06	8.613565745	1.048162757	8	153	B
GO:0002252 immune effector process	1.27E-05	5.155080214	2.644384472	12	386	
GO:0006954 inflammatory response	1.56E-05	4.680659864	3.165040482	13	462	
GO:0030097 hemopoiesis	1.59E-05	4.669922481	3.171891219	13	463	
GO:0001816 cytokine production	1.59E-05	5.03070136	2.706041104	12	395	

GO:0042098	1.62E-05	9.761750881	0.808386963	7	118	T cell proliferation
GO:0051251	1.64E-05	6.866990291	1.472908449	9	215	positive regulation of lymphocyte activation

Tissue: Heart_Left_Ventricle=>Adipose_Subcutaneous Type: asymmetric

SourceGene: ENSG00000228649.1

TargetGeneSet: TRIM63 ACTA1 NEB XIRP2 KBTBD10 TTN MYL1 WDR48 ODZ1 RP11 CMYA5 SRPK1 LMOD2 ANKRD2 NRAP RPL23AP64 RP3 POU5F1P3 MYL2 OAS3 MYH7 ATP2A1 MYLPF ENO3 MYH2 MYH1 SPAG9 CACNG1 FOXJ1 CKM TNNT1 C20orf85 EEF1A2 PVALB APOBEC3H

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0006936	2.68E-16	51.03650442	0.479620787	13	239	muscle contraction
GO:0003012	1.08E-15	45.50321146	0.533803889	13	266	muscle system process

GO:0030049	5.39E-15	176.8479263	0.07826448	8	39
muscle filament sliding					
GO:0033275	5.39E-15	176.8479263	0.07826448	8	39
actin-myosin filament sliding					
GO:0070252	1.03E-14	161.210084	0.084284825	8	42
actin-mediated cell contraction					
GO:0030048	1.89E-13	107.3464052	0.118400111	8	59
actin filament-based movement					
GO:0006941	1.08E-10	67.1644385	0.150508615	7	75
striated muscle contraction					
GO:0030029	6.19E-09	17.46071339	0.866929624	10	432
actin filament-based process					
GO:0003010	2.90E-08	1663.961538	0.008027126	3	4
voluntary skeletal muscle contraction					
GO:0014721	2.90E-08	1663.961538	0.008027126	3	4
twitch skeletal muscle contraction					
GO:0061061	6.47E-08	15.77475	0.820773649	9	409
muscle structure development					
GO:0007517	9.97E-08	18.24309927	0.608054806	8	303
muscle organ development					
GO:0010927	4.15E-06	25.25423729	0.246834129	5	123
cellular component assembly involved in morphogenesis					
GO:0003009	6.89E-06	103.8894231	0.038128849	3	19
skeletal muscle contraction					

GO:0045071	1.09E-05	87.46761134	0.044149194	3	22	negative regulation of viral genome replication
GO:0048525	1.09E-05	87.46761134	0.044149194	3	22	negative regulation of viral reproduction
GO:0050879	1.83E-05	72.23578595	0.05217632	3	26	multicellular organismal movement
GO:0050881	1.83E-05	72.23578595	0.05217632	3	26	musculoskeletal movement

Tissue: Heart_Left_Ventricle=>Adipose_Subcutaneous Type: asymmetric

SourceGene: ENSG00000231536.1 antisense RNA

TargetGeneSet: RPS8 ADORA3 FCGR2A NEURL1B RP11 CTB RP4 RSPH9 STK3 RPL8 RP1 PNLIPRP3 NCKAP1L RPL18AP3 TERF1P5 RPL4 RPL13 RPS15 ELAVL1 RPL18A SSBP4 ETV2 RPL18 LILRA1 RPS4X

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0006415	3.44E-13	106.3725672	0.132239983	8	91	translational termination
GO:0006414	1.11E-12	90.93100714	0.152584596	8	105	translational elongation
GO:0006614	1.11E-12	90.93100714	0.152584596	8	105	SRP-dependent cotranslational protein targeting to membrane
GO:0006613	1.20E-12	89.99686028	0.154037783	8	106	cotranslational protein targeting to membrane
GO:0045047	1.20E-12	89.99686028	0.154037783	8	106	

```
protein targeting to ER


GO:0072599      1.20E-12        89.99686028     0.154037783     8       106
establishment of protein localization to endoplasmic reticulum



GO:0070972      2.89E-12        80.11188811     0.171476022     8       118
protein localization to endoplasmic reticulum



GO:0000184      3.10E-12        79.38461538     0.172929209     8       119
"nuclear-transcribed mRNA catabolic process, nonsense-mediated decay"



GO:0019080      2.14E-11        61.48251748     0.219431181     8       151
viral genome expression


GO:0019083      2.14E-11        61.48251748     0.219431181     8       151
viral transcription


GO:0006413      2.26E-11        61.05128205     0.220884368     8       152
translational initiation



GO:0006612      2.38E-11        60.62599469     0.222337554     8       153
protein targeting to membrane



GO:0043624      2.38E-11        60.62599469     0.222337554     8       153
cellular protein complex disassembly



GO:0043241      3.08E-11        58.58461538     0.229603488     8       158
protein complex disassembly



GO:0000956      5.30E-11        54.53989489     0.245588541     8       169
nuclear-transcribed mRNA catabolic process



GO:0034623      6.69E-11        52.87859129     0.252854474     8       174
cellular macromolecular complex disassembly



GO:0006402      8.03E-11        51.6199095      0.25866722      8       178     mRNA
catabolic process


GO:0032984      8.40E-11        51.31443995     0.260120407     8       179
macromolecular complex disassembly
```

GO:0072594	2.39E-10	44.69073783	0.296450073	8	204	establishment of protein localization to organelle
GO:0006401	2.49E-10	44.46075752	0.297903259	8	205	RNA catabolic process
GO:0019058	6.43E-10	39.20524319	0.335686112	8	231	viral infectious cycle
GO:0022415	1.64E-09	34.62271062	0.377828524	8	260	viral reproductive process
GO:0071845	3.29E-09	31.55852843	0.412705003	8	284	cellular component disassembly at cellular level
GO:0022411	3.67E-09	31.0989011	0.41851775	8	288	cellular component disassembly
GO:0016032	1.20E-07	19.42976211	0.65538717	8	451	viral reproduction
GO:0033365	1.74E-07	18.48138958	0.687357276	8	473	protein localization to organelle
GO:0006605	1.76E-07	18.44040938	0.688810463	8	474	protein targeting

Tissue: Heart_Left_Ventricle=>Adipose_Subcutaneous Type: asymmetric

SourceGene: FAM124B(ENSG00000124019.9)

TargetGeneSet: WASF2 RP4 KIF2C DDAH1 RP11 UGGT1 CDCA7 KLF7 ARPC4 FANCD2 CENPE BRCC3 KIF20A ANLN PBK PTP4A3 NAPRT1 MELK E2F7 BUB1B OIP5 CCNB2 PLK1 HIC1 BIRC5 TYMS NDC80 LIG1 E2F1 C22orf29 MT

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term

GO:0000087	4.56E-11	24.64231137	0.722441354	11	360	M phase of mitotic cell cycle
GO:0051301	5.17E-10	19.37402368	0.907065255	11	452	cell division
GO:0000280	8.13E-10	21.79876161	0.702373538	10	350	nuclear division
GO:0007067	8.13E-10	21.79876161	0.702373538	10	350	mitosis
GO:0048285	1.39E-09	20.55847953	0.742509169	10	370	organelle fission
GO:0000236	1.48E-08	47.36268575	0.170576431	6	85	mitotic prometaphase
GO:0051329	7.65E-06	12.01735093	0.760570203	7	379	interphase of mitotic cell cycle
GO:0051325	8.77E-06	11.7576555	0.776624455	7	387	interphase

Tissue: Heart_Left_Ventricle=>Adipose_Subcutaneous   Type: cluster

SourceGene: GABRA1(ENSG00000022355.10)

TargetGeneSet: PANK4 KCNAB2 ESPN C1QC C1QB FUCA1 UBXN11 CD52 FGR
C1orf38 RAB42 LAPTM5 BRD8 SLC6A9 CD53 C1orf88 C1orf162 ADORA3
APH1A CTSS ARHGAP30 FCER1G FAM20B NPL PRG4 PTPRC RP11 CR1
RCOR3 CDC42BPA DISC1 NID1 GPR137B VAMP8 BDP1 KYNU RPE
C2orf62 SLC11A1 ARL4C FANCD2 CMTM7 HCLS1 CD86 CTBP1 RBPJ TBC1D1
CCDC109B FYB ITGA1 HEXB PAPD4 CTNNA1 GPX3 DOCK2 MGAT1
KIF13A C2 UNC5CL ZC3H12D WTAP AVL9 PILRA PMPCB TFEC TBXAS1 CTSB
MSR1 PREX2 SLA KIAA1432 TLN1 FAM27E2 SYK COL15A1 DAB2IP RSU1
VSTM4 HPSE2 COMMD9 PRG2 SERPING1 LPXN MS4A6A MS4A7 UNC93B1
ALDH3B1 ANO1 ANO1-AS1 NEU3 IL10RA PTPN6 C1S CD163 DAZAP2 BIN2
PRR13 IL23A TMEM55B SLC7A7 LTB4R NPC2 FLVCR2 GALC FAM98B UBR1
UNC13C FAM96A HEXA ADPGK SLC5A11 APOBR ZDHHC7 CYBA ARRB2 SCIMP CD68
PIK3R5 PMP22 MPRIP ABHD15 SSH2 RNF135 EVI2B EVI2A FMNL1 RP13
MPPE1 CABYR TCF4 STXBP2 NOTCH3 IFI30 TYROBP ZNF527 PSG5 PLAUR
C5AR1 CA11 SIGLEC9 SIGLEC7 OSCAR LILRB2 SIRPG SIRPB1 HCK C20orf111
TTPAL PLTP DNAJC28 ARVCF HPS4 GPR143 TLR8 PIGA WAS VSIG4 RP1
SASH3 RAP2C

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0050778	1.46E-11	7.708769994	3.324891011	21	364	positive regulation of immune response
GO:0002252	4.38E-11	7.232728619	3.525845962	21	386	immune effector process

GO:0002443 leukocyte mediated immunity	8.56E-11	9.990450928	1.927340668	16	211
GO:0002253 activation of immune response	1.87E-09	7.358279371	2.731160473	17	299
GO:0002250 adaptive immune response	3.44E-09	9.114314665	1.808594561	14	198

GO:0002449	4.02E-09	10.04829204	1.525430766	13	167	lymphocyte mediated immunity
GO:0002697	4.18E-09	8.966192332	1.835997509	14	201	regulation of immune effector process
GO:0002460	9.78E-08	8.372781065	1.65331119	12	181	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains
GO:0002703	1.54E-07	12.55010285	0.840357069	9	92	regulation of leukocyte mediated immunity

GO:0046479	8.09E-07	89.4625	0.082208844	4	9	glycosphingolipid catabolic process
GO:0006956	1.63E-06	14.263	0.575461906	7	63	complement activation
GO:0002283	2.09E-06	63.89285714	0.100477476	4	11	neutrophil activation involved in immune response
GO:0002764	2.83E-06	5.967372881	2.265310359	12	248	immune response-regulating signaling pathway

GO:0006689	2.96E-06	332.9767442	0.036537264	3	4
ganglioside catabolic process					
GO:0019377	3.11E-06	55.90234375	0.109611792	4	12
glycolipid catabolic process					
GO:0006958	5.92E-06	15.4491342	0.456715798	6	50
"complement activation, classical pathway"					

GO:0016064	7.86E-06	8.904478547	1.013909072	8	111		immunoglobulin mediated immune response
GO:0019724	9.57E-06	8.650639075	1.04131202	8	114	B	cell mediated immunity
GO:0072376	9.73E-06	10.63552	0.749013909	7	82		protein activation cascade
GO:0043304	1.11E-05	37.2578125	0.146149055	4	16		regulation of mast cell degranulation

GO:0042098	1.23E-05	8.33372434	1.077849284	8	118	T cell proliferation
GO:0033006	1.44E-05	34.38942308	0.155283371	4	17	regulation of mast cell activation involved in immune response
GO:0002263	1.67E-05	7.96858345	1.123520864	8	123	cell activation involved in immune response
GO:0002366	1.67E-05	7.96858345	1.123520864	8	123	leukocyte activation involved in immune response

```
GO:0031347      1.89E-05        4.248616618     3.681129334     14      403
regulation of defense response

Tissue: Adipose_Subcutaneous=>Heart_Left_Ventricle      Type:   asymmetric

SourceGene:     HIRA(ENSG00000100084.9) histone cell cycle regulator

TargetGeneSet:  TTLL10  C1QA    C1QB    E2F2    CLSPN   CDCA8   TMEM125 CDC20
FAM72D  PRPF3   GPR161  NEK2    C1orf148        FTH1P2  NCAPH   CKAP2L  PSD4
RABL2A  MARCO   HJURP   OXTR    KIF15   CAMK2N2 RP11    SLC39A8 CENPE   BRCC3
CCNB1   HMMR    RMND5B  DHX16   SLC25A27        FKBP1C  RNASET2 RPL23P8 CHN2    ANLN
MELK    ZNF658B SAPCD2  CDK1    C10orf116       AGAP11  CEP55   PIK3AP1 MKI67
RIC8A   EHF     MPP2    EEF1A1P33       ESPL1   CSRP2   EP400NL DLGAP5  XRCC3
SIVA1   BUB1B   NUSAP1  CCNB2   E4F1    FLYWCH1 CLDN9   ANKS3   CTRB2   AURKB
TOP2A   KIF18B  BRIP1   BIRC5   TYMS    NDC80   ZNF562  ZNF653  ASF1B   LRRC25  TPX2
PI3     UBE2C   CTSZ    RP1     APOBEC3B        CTA     TMEM27  KIF4A   RP13
FAM199X

GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
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GO:0000280	2.14E-19	20.49376988	1.646944848	22	350	nuclear division
GO:0007067	2.14E-19	20.49376988	1.646944848	22	350	mitosis
GO:0000087	3.92E-19	19.8732956	1.694000415	22	360	M phase of mitotic cell cycle
GO:0048285	7.07E-19	19.28848076	1.741055982	22	370	organelle fission
GO:0051301	7.66E-16	14.46374093	2.126911632	21	452	cell division
GO:0010564	4.01E-13	12.71545455	1.948100477	18	414	regulation of cell cycle process

GO:0007059	1.94E-12	23.86439732	0.658777939	12	140	chromosome segregation
GO:0000819	2.05E-12	50.87110761	0.244688949	9	52	sister chromatid segregation
GO:0007346	7.69E-12	13.85121855	1.425783683	15	303	regulation of mitotic cell cycle
GO:0007017	2.67E-11	11.4311365	1.849283787	16	393	microtubule-based process
GO:0000070	6.08E-11	46.64065041	0.230572279	8	49	mitotic sister chromatid segregation
GO:0007051	3.49E-09	26.50185185	0.376444537	8	80	spindle organization

GO:0000236	5.68E-09	24.77229437	0.39997232	8	85	mitotic prometaphase
GO:0000086	2.25E-08	16.09943503	0.677600166	9	144	G2/M transition of mitotic cell cycle
GO:0000226	4.54E-08	10.56541548	1.265794755	11	269	microtubule cytoskeleton organization
GO:0007088	1.75E-07	20.26189031	0.41408899	7	88	regulation of mitosis
GO:0051783	1.75E-07	20.26189031	0.41408899	7	88	regulation of nuclear division
GO:0030261	2.58E-07	45.58095238	0.141166701	5	30	chromosome condensation
GO:0071156	4.00E-07	9.59068694	1.242266971	10	264	regulation of cell cycle arrest

GO:0051656	4.52E-07	17.44384374	0.475261228	7	101	establishment of organelle localization
GO:0008608	1.02E-06	69.08653846	0.079994464	4	17	attachment of spindle microtubules to kinetochore
GO:0007050	1.08E-06	7.560276389	1.736350426	11	369	cell cycle arrest
GO:0051329	1.40E-06	7.349590008	1.783405993	11	379	interphase of mitotic cell cycle
GO:0031577	1.48E-06	30.77220077	0.197633382	5	42	spindle checkpoint
GO:0051313	1.65E-06	59.86666667	0.089405577	4	19	attachment of spindle microtubules to chromosome

GO:0030071	1.67E-06	29.96031746	0.202338938	5	43	regulation of mitotic metaphase/anaphase transition
GO:0051325	1.72E-06	7.189109742	1.821050446	11	387	interphase
GO:0000075	1.86E-06	9.263839383	1.138744724	9	242	cell cycle checkpoint
GO:0034501	1.97E-06	221.2307692	0.02823334	3	6	protein localization to kinetochore
GO:0007091	2.10E-06	28.45833333	0.211750052	5	45	mitotic metaphase/anaphase transition
GO:0031145	2.46E-06	17.97989108	0.390561207	6	83	anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process

GO:0050000	2.53E-06	52.81617647	0.098816691	4	21	chromosome localization
GO:0051303	2.53E-06	52.81617647	0.098816691	4	21	establishment of chromosome localization
GO:0007093	3.89E-06	12.38909588	0.654072383	7	139	mitotic cell cycle checkpoint
GO:0051983	4.44E-06	44.884375	0.112933361	4	24	regulation of chromosome segregation
GO:0000910	5.10E-06	15.72030792	0.442322331	6	94	cytokinesis
GO:0045786	5.53E-06	6.322666996	2.056328282	11	437	negative regulation of cell cycle

GO:0051640 6.44E-06 11.42726126 0.705833506 7 150 organelle localization

GO:0006323 7.34E-06 11.19009656 0.719950176 7 153 DNA packaging

GO:0045787 8.19E-06 14.40221774 0.479966784 6 102 positive regulation of cell cycle

GO:0007052 1.66E-05 30.93534483 0.155283371 4 33 mitotic spindle organization

Tissue: Adipose_Subcutaneous=>Heart_Left_Ventricle Type: asymmetric

SourceGene: HSPD1P16(ENSG00000218792.2) HSPD1P16 heat shock 60kDa protein 1 (chaperonin) pseudogene 16

TargetGeneSet: ARHGEF19 CAPZB RAB42 MPL RP11 MCOLN2 GORAB METTL13 TRMT1L IPO9-AS1 ARL8A ARHGEF33 RPL37A TMIE CTD PPP1R2P3 C6orf195 C8orf59 RPL30 RPL8 NOL8 RPLP2 RPL27A ZNF408 MEN1 RPS25 ANKRD13A MPHOSPH9 UFM1 ARHGEF40 RPL36A NDUFB1 CCDC78 FBXL19-AS1 RPL17 RPL19 HEXIM2 RPL38 SIRT7 CDC37 ATP13A1 IGSF23 LZTR1

GOBPID Pvalue OddsRatio ExpCount Count Size Term

GO:0006415	2.59E-13	68.41622481	0.201508546	9	91	translational termination
GO:0043624	6.95E-13	45.37825811	0.338800083	10	153	cellular protein complex disassembly
GO:0043241	9.61E-13	43.82985258	0.349871981	10	158	protein complex disassembly
GO:0006414	9.72E-13	58.38179348	0.232509861	9	105	translational elongation
GO:0006614	9.72E-13	58.38179348	0.232509861	9	105	SRP-dependent cotranslational protein targeting to membrane
GO:0006613	1.06E-12	57.77588525	0.234724241	9	106	cotranslational protein targeting to membrane
GO:0045047	1.06E-12	57.77588525	0.234724241	9	106	protein targeting to ER
GO:0072599	1.06E-12	57.77588525	0.234724241	9	106	establishment of protein localization to endoplasmic reticulum
GO:0034623	2.53E-12	39.5094235	0.385302055	10	174	cellular macromolecular complex disassembly
GO:0070972	2.84E-12	51.37215796	0.261296796	9	118	protein localization to endoplasmic reticulum

GO:0000184	3.07E-12	50.90158103	0.263511176	9	119	"nuclear-transcribed mRNA catabolic process, nonsense-mediated decay"
GO:0032984	3.37E-12	38.32705756	0.396373953	10	179	macromolecular complex disassembly
GO:0019080	2.67E-11	39.34262094	0.334371324	9	151	viral genome expression
GO:0019083	2.67E-11	39.34262094	0.334371324	9	151	viral transcription
GO:0006413	2.83E-11	39.06476133	0.336585703	9	152	translational initiation
GO:0006612	3.01E-11	38.79076087	0.338800083	9	153	protein targeting to membrane
GO:0000956	7.36E-11	34.87255435	0.374230157	9	169	nuclear-transcribed mRNA catabolic process
GO:0006402	1.17E-10	32.99459738	0.394159574	9	178	mRNA catabolic process
GO:0071845	3.23E-10	23.46549436	0.628883814	10	284	cellular component disassembly at cellular level
GO:0022411	3.71E-10	23.12132112	0.637741333	10	288	cellular component disassembly

GO:0072594	3.95E-10	28.54314381	0.451733444	9	204	establishment of protein localization to organelle
GO:0006401	4.13E-10	28.39551908	0.453947824	9	205	RNA catabolic process
GO:0019058	1.19E-09	25.02408931	0.511521694	9	231	viral infectious cycle
GO:0022415	3.36E-09	22.0876494	0.575738703	9	260	viral reproductive process
GO:0006605	4.42E-08	13.67065047	1.049615944	10	474	protein targeting
GO:0016032	3.84E-07	12.37389337	0.998685212	9	451	viral reproduction
GO:0033365	5.73E-07	11.76864693	1.047401564	9	473	protein localization to organelle

Tissue: Heart_Left_Ventricle=>Adipose_Subcutaneous Type: asymmetric

SourceGene: IFIT1(ENSG00000185745.8) interferon-induced protein with tetratricopeptide repeats 1

```
TargetGeneSet:  EIF1AX  RCN3    SLC30A2 HMGN2   FGR     CDC20   STIL    RP11    MCL1
FCRLA   RASAL2  KIF14   PPP2R5A ANGEL2  CENPF   ODC1    RHOB    XPO1    SH3RF3
LINC00116       BUB1    CCNT2   SGOL2   COPS8   SGOL1   LZTFL1  FAM116A PHLDB2  BOC
BZW1P2  CCNL1   CCRL1   GUF1    CORIN   PLK4    HMGB2   POLK    GPR150  FSTL4
KIF20A  PCYOX1L HMMR    TRIM41  C6orf62 FKBP5   KCTD20  UBR2    SLC29A1 ANKRD6
ZNF259P1        MAN1A1  STEAP1B ANLN    LAMB1   KCND2   FAM40B  CDCA2   PBK
TMEM67  MPDZ    MELK    KLF9    KLF4    GBGT1   SYT15   CEP55   PHBP9   LZTS2
ZNF215  KIF18A  CAT     RPLP0P2 PELI3   AASDHPPT        MPP2    GRIN2B  TMEM106C
TROAP   DNAJC14 TMEM198B        SDSL    CAMKK2  GTF2H3  DIAPH3  DLGAP5  RHOJ    FCF1
OIP5    NUSAP1  ATP8B4  LARP6   PAQR4   HMOX2   PLK1    SHCBP1  ORC6    CDT1
ZBTB4   SPAG5   PNMT    VAT1    MPP3    KIF18B  H3F3B   BIRC5   TYMS    RNF125
SLC25A23        KANK2   ZNF441  FKBP8   CEACAM4 ZNF665  TPX2    SAMHD1  UBE2C
TIAM1   PKNOX1  CDC45   ZNF74   SAMM50  ARHGAP6 FIGF

GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term



GO:0000087      5.68E-16        11.95300445     2.565912394     23      360     M
phase of mitotic cell cycle



GO:0000280      3.75E-15        11.60945498     2.494637049     22      350
nuclear division



GO:0007067      3.75E-15        11.60945498     2.494637049     22      350
mitosis
```

GO:0048285	1.18E-14	10.92663545	2.637187738	22	370	organelle fission
GO:0051301	7.49E-14	9.328001166	3.221645561	23	452	cell division
GO:0010564	6.88E-10	7.460962567	2.950799253	18	414	regulation of cell cycle process
GO:0000236	8.75E-09	17.97984323	0.605840426	9	85	mitotic prometaphase
GO:0007059	5.78E-08	11.76013234	0.99785482	10	140	

						chromosome segregation
GO:0007346	2.31E-07	7.002068966	2.159642931	13	303	regulation of mitotic cell cycle
GO:0030071	5.57E-07	23.92477013	0.30648398	6	43	regulation of mitotic metaphase/anaphase transition
GO:0007091	7.36E-07	22.69468676	0.320739049	6	45	mitotic metaphase/anaphase transition
GO:0071156	2.78E-06	6.661153119	1.881669089	11	264	regulation of cell cycle arrest

```
GO:0007088      3.01E-06        12.8432356      0.62722303      7       88
regulation of mitosis

GO:0051783      3.01E-06        12.8432356      0.62722303      7       88
regulation of nuclear division

GO:0007017      4.26E-06        5.309473684     2.80112103      13      393
microtubule-based process

GO:0000910      4.69E-06        11.95246648     0.669988236     7       94
cytokinesis

GO:0010948      5.39E-06        11.68223315     0.684243305     7       96
negative regulation of cell cycle process
```

GO:0000086	8.57E-06	8.8	1.026364957	8	144	G2/M transition of mitotic cell cycle
GO:0000075	8.69E-06	6.542454579	1.724863331	10	242	cell cycle checkpoint
GO:0031577	1.15E-05	19.73386652	0.299356446	5	42	spindle checkpoint
GO:0051488	1.21E-05	107.58	0.049892741	3	7	activation of anaphase-promoting complex activity
GO:0050000	1.33E-05	34.06060606	0.149678223	4	21	chromosome localization

GO:0051303	1.33E-05	34.06060606	0.149678223	4	21
establishment of chromosome localization

GO:0051329	1.59E-05	5.023564991	2.701335548	12	379
interphase of mitotic cell cycle

GO:0051325	1.95E-05	4.913582418	2.758355823	12	387
interphase

Tissue: Heart_Left_Ventricle=>Adipose_Subcutaneous	Type:	asymmetric

SourceGene:	LAD1(ENSG00000159166.9) ladinin 1

TargetGeneSet: CDCA8 PGCP1 ASPM KIF14 CENPF RAB3GAP2 TCEB1P21
BUB1 IHH PASK KIF15 RP11 TACC3 CENPE FBXO4 CTA C9orf174
ZWINT CEP55 HELLS MKI67 CDCA5 CDCA3 RNASE13 CBLN3 BUB1B KIAA0101
WDR73 PKMYT1 SHCBP1 ORC6 FAM64A AURKB TOP2A KIF18B PCTP NDC80
UHRF1 ZNF490 DHPS STX10 PARP4P3 CLTCL1 CDC45 GTSE1 MBTPS2 FAM122C MT

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0000280	2.36E-18	35.94249249	0.896131756	17	350	nuclear division
GO:0007067	2.36E-18	35.94249249	0.896131756	17	350	mitosis
GO:0000087	3.81E-18	34.86982507	0.92173552	17	360	M phase of mitotic cell cycle
GO:0048285	6.05E-18	33.85793201	0.947339284	17	370	organelle fission
GO:0051301	1.06E-13	21.80726025	1.157290153	15	452	cell division
GO:0000236	3.44E-11	51.36408419	0.217631998	8	85	mitotic prometaphase
GO:0007059	1.93E-09	29.84743992	0.358452702	8	140	chromosome segregation
GO:0010564	4.09E-09	14.70900935	1.059995848	11	414	regulation of cell cycle process

GO:0007017	3.57E-08	13.56832028	1.006227943	10	393	microtubule-based process
GO:0000075	1.40E-07	16.71676982	0.6196111	8	242	cell cycle checkpoint
GO:0000819	1.98E-07	47.76263298	0.133139575	5	52	sister chromatid segregation
GO:0071156	2.72E-07	15.25646552	0.675939381	8	264	regulation of cell cycle arrest
GO:0007346	7.75E-07	13.20303916	0.775794063	8	303	regulation of mitotic cell cycle
GO:0007093	1.29E-06	20.78243997	0.355892326	6	139	mitotic cell cycle checkpoint
GO:0007051	1.74E-06	29.87291667	0.204830116	5	80	spindle organization
GO:0051640	2.02E-06	19.18010753	0.384056467	6	150	organelle localization
GO:0007050	3.38E-06	10.73875251	0.944778908	8	369	cell cycle arrest

```
GO:0034508      5.52E-06        115.5320856     0.03584527      3       14
centromere complex assembly

GO:0000070      7.10E-06        38.7043771      0.125458446     4       49
mitotic sister chromatid segregation

GO:0051310      1.03E-05        90.75630252     0.0435264       3       17
metaphase plate congression

GO:0045786      1.17E-05        8.992846234     1.118884506     8       437
negative regulation of cell cycle

GO:0050000      1.99E-05        70.56862745     0.053767905     3       21
chromosome localization

GO:0051303      1.99E-05        70.56862745     0.053767905     3       21
establishment of chromosome localization

Tissue: Heart_Left_Ventricle=>Adipose_Subcutaneous      Type:   asymmetric

SourceGene:     NT5C2(ENSG00000076685.13)       "5'-nucleotidase, cytosolic II"

TargetGeneSet:  PUSL1   MIB2    RP11    PGCP1   SLAMF8  DUSP27  NLRC4   FBXO48
TCEB1P21        RHOQP2  NEB     XIRP2   KBTBD10 TTN     MYL1    TMEM169 CMYA5
TMEM232 LMOD2   MYOM2   ENDOG   TMEM141 FAS     NRAP    C11orf73        DDN
LINC00464       BUB1B   RBFOX1  ATP2A1  MYLPF   MYH2    MYH1    CCR10   PSMA8   RYR1
CKM     SNORD33 MYBPC2  EEF1A2  PI4KAP2 SMPX    HMGN1P26
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GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term



GO:0006936      1.28E-11        34.43474042     0.46308214      10      239
muscle contraction



GO:0003012      3.70E-11        30.74435764     0.515396858     10      266
muscle system process



GO:0030049      1.03E-08        92.00127877     0.075565705     5       39
muscle filament sliding



GO:0033275      1.03E-08        92.00127877     0.075565705     5       39
actin-myosin filament sliding



GO:0070252      1.52E-08        84.52408931     0.081378451     5       42
actin-mediated cell contraction



GO:0030048      8.73E-08        57.84621578     0.114317348     5       59
actin filament-based movement



GO:0006941      2.95E-07        44.57453416     0.145318663     5       75
striated muscle contraction



Tissue: Adipose_Subcutaneous=>Heart_Left_Ventricle      Type:   asymmetric
SourceGene:     RP11-439A17.9(ENSG00000233029.2)
TargetGeneSet:  AURKAIP1        SPEN    ARHGEF19        MINOS1  RP11    ZSCAN20
MRPS15  FAM151A RPL5    FAM212B LYSMD1  SNRPE   SRGAP3  ZNF513  NFU1    COX5B   TSPO
SF3B3   EEF1B2  CAPN7   UBE2E1  RPL18AP7        GORASP1 LIMD1   ZNF717  YEATS2  MRAP
CNO     NDUFC1  COX7C   ARAP3   NSD1    TMEM14B CCNC    HEBP2   AGPAT4  MRPS24  SRI
TECPR1  ZKSCAN5 FIS1    TNPO3   C7orf73 PRKDC   RPS20   C8orf59 RPL30   COX6C
TMEM65  SPATC1  RPL8    C9orf46 RPS6    ALDH1A1 POLR3A  RPL27A  NDUFS3  FAU
RPS25   PFDN5   C12orf51        GCN1L1  GTF3A   MED4    MRPL52  U2      SLIRP   MGA
TPM1    RPL4    MYO9A   NDUFAB1 FAM65A  7SK     WDR81   METTL16 PSMB6   GABARAP CTD
RPL26   TMEM220 TRIM16  RPS7P1  RPL23A  CCL2    RPL19   DCAF7   NDUFV2  TXNL4A
ATP5D   OAZ1    C19orf70        CDC37   C19orf53        NDUFB7  BRD4    MAST3
COX6B1  RPS11   ZNF808  ZNF341  PLCG1   NCOA3   APOL2   TNRC6B  PPARA   PNPLA4
EEF1B2P3        FUNDC1  COX7B   BCORL1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
```

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GO:0006414      3.69274637378678e-15    28.1420118343195        0.668465850114179
14      105     translational elongation
GO:0006415      1.50203658113874e-14    30.1286919831224        0.579337070098955
13      91      translational termination
GO:0006614      1.01827296410455e-13    25.518849752339 0.668465850114179       13
105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.15469488928884e-13    25.2426840887437        0.674832191543838
13      106     cotranslational protein targeting to membrane
GO:0045047      1.15469488928884e-13    25.2426840887437        0.674832191543838
13      106     protein targeting to ER
GO:0072599      1.15469488928884e-13    25.2426840887437        0.674832191543838
13      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      4.74744411074256e-13    22.3389993972272        0.751228288699744
13      118     protein localization to endoplasmic reticulum
GO:0000184      5.30249188814586e-13    22.1267016957249        0.757594630129403
13      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      1.15437991848963e-11    16.9577141808842        0.961317555878486
13      151     viral genome expression
GO:0019083      1.15437991848963e-11    16.9577141808842        0.961317555878486
13      151     viral transcription
GO:0006413      1.25589680093365e-11    16.8345323741007        0.967683897308145
13      152     translational initiation
GO:0006612      1.36550618939728e-11    16.7131103074141        0.974050238737804
13      153     protein targeting to membrane
GO:0043624      1.36550618939728e-11    16.7131103074141        0.974050238737804
13      153     cellular protein complex disassembly
GO:0043241      2.05652439826081e-11    16.1311217808817        1.0058819458861 13
158     protein complex disassembly
GO:0022904      2.13412240890585e-11    22.8052287581699        0.611168777247249
11      96      respiratory electron transport chain
GO:0072594      3.82294072612714e-11    13.385020242915 1.2987336516504 14      204
establishment of protein localization to organelle
GO:0000956      4.82346741374753e-11    14.9820675105485        1.07591170161235
13      169     nuclear-transcribed mRNA catabolic process
GO:0034623      6.96470222143446e-11    14.5116754461829        1.10774340876064
13      174     cellular macromolecular complex disassembly
GO:0006402      9.26646282702262e-11    14.1558879938627        1.13320877447927
13      178     mRNA catabolic process
GO:0032984      9.94107155620554e-11    14.0696202531646        1.13957511590893
13      179     macromolecular complex disassembly
GO:0019058      2.00447753500612e-10    11.697270471464 1.47062487025119        14
231     viral infectious cycle
GO:0006401      5.37465029970302e-10    12.1420754219409        1.30509999308006
13      205     RNA catabolic process
GO:0022900      8.17322226875273e-10    15.7177556960755        0.853089751574286
11      134     electron transport chain
GO:0022415      9.47557506538276e-10    10.2971648947259        1.6552487717113 14
260     viral reproductive process
GO:0045333      1.52063803221109e-09    14.7495994722458        0.904020483011556
11      142     cellular respiration
GO:0016032      3.06268020579448e-09    7.2726574500768 2.87121998477614        17
451     viral reproduction
GO:0006605      6.45100649366348e-09    6.89522975929978        3.01764583765829
17      474     protein targeting
GO:0071845      2.76755982344779e-08    8.55453314026811        1.80804096602311
13      284     cellular component disassembly at cellular level
GO:0022411      3.26461497070382e-08    8.42771001150748        1.83350633174175
13      288     cellular component disassembly
GO:0033365      2.75047658881905e-07    5.91263539953496        3.01127949622863
15      473     protein localization to organelle
GO:0006119      1.7511410088196e-06     19.1954382826476        0.369247802920213
6       58      oxidative phosphorylation
GO:0006120      3.02300201070875e-06    26.5628476084538        0.229188291467718
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5       36      mitochondrial electron transport, NADH to ubiquinone
GO:0015980      3.87136211202597e-06    6.45199366032699        1.95446681890527
11      307     energy derivation by oxidation of organic compounds
GO:0042773      1.16400533956989e-05    19.5908593322386        0.299218047193966
5       47      ATP synthesis coupled electron transport
GO:0042775      1.16400533956989e-05    19.5908593322386        0.299218047193966
5       47      mitochondrial ATP synthesis coupled electron transport
GO:0006091      1.66141261505467e-05    5.02752403846154        2.72479413189399
12      428     generation of precursor metabolites and energy
Tissue: Adipose_Subcutaneous=>Heart_Left_Ventricle      Type:   cluster
SourceGene:     RP11-439A17.9(ENSG00000233029.2)
TargetGeneSet:  AURKAIP1        SPEN    ARHGEF19        MINOS1  RP11    ZSCAN20
MRPS15  FAM151A RPL5    FAM212B LYSMD1  SNRPE   SRGAP3  ZNF513  NFU1    COX5B   TSPO
SF3B3   EEF1B2  CAPN7   UBE2E1  RPL18AP7        GORASP1 LIMD1   ZNF717  YEATS2  MRAP
CNO     NDUFC1  COX7C   ARAP3   NSD1    TMEM14B CCNC    HEBP2   AGPAT4  MRPS24  SRI
TECPR1  ZKSCAN5 FIS1    TNPO3   C7orf73 PRKDC   RPS20   C8orf59 RPL30   COX6C
TMEM65  SPATC1  RPL8    C9orf46 RPS6    ALDH1A1 POLR3A  RPL27A  NDUFS3  FAU
RPS25   PFDN5   C12orf51        GCN1L1  GTF3A   MED4    MRPL52  U2      SLIRP   MGA
TPM1    RPL4    MYO9A   NDUFAB1 FAM65A  7SK     WDR81   METTL16 PSMB6   GABARAP CTD
RPL26   TMEM220 TRIM16  RPS7P1  RPL23A  CCL2    RPL19   DCAF7   NDUFV2  TXNL4A
ATP5D   OAZ1    C19orf70        CDC37   C19orf53        NDUFB7  BRD4    MAST3
COX6B1  RPS11   ZNF808  ZNF341  PLCG1   NCOA3   APOL2   TNRC6B  PPARA   PNPLA4
EEF1B2P3        FUNDC1  COX7B   BCORL1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      3.69274637378678e-15    28.1420118343195        0.668465850114179
14      105     translational elongation
GO:0006415      1.50203658113874e-14    30.1286919831224        0.579337070098955
13      91      translational termination
GO:0006614      1.01827296410455e-13    25.518849752339 0.668465850114179       13
105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.15469488928884e-13    25.2426840887437        0.674832191543838
13      106     cotranslational protein targeting to membrane
GO:0045047      1.15469488928884e-13    25.2426840887437        0.674832191543838
13      106     protein targeting to ER
GO:0072599      1.15469488928884e-13    25.2426840887437        0.674832191543838
13      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      4.74744411074256e-13    22.3389993972272        0.751228288699744
13      118     protein localization to endoplasmic reticulum
GO:0000184      5.30249188814586e-13    22.1267016957249        0.757594630129403
13      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      1.15437991848963e-11    16.9577141808842        0.961317555878486
13      151     viral genome expression
GO:0019083      1.15437991848963e-11    16.9577141808842        0.961317555878486
13      151     viral transcription
GO:0006413      1.25589680093365e-11    16.8345323741007        0.967683897308145
13      152     translational initiation
GO:0006612      1.36550618939728e-11    16.7131103074141        0.974050238737804
13      153     protein targeting to membrane
GO:0043624      1.36550618939728e-11    16.7131103074141        0.974050238737804
13      153     cellular protein complex disassembly
GO:0043241      2.05652439826081e-11    16.1311217808817        1.0058819458861 13
158     protein complex disassembly
GO:0022904      2.13412240890585e-11    22.8052287581699        0.611168777247249
11      96      respiratory electron transport chain
GO:0072594      3.82294072612714e-11    13.385020242915 1.2987336516504 14      204
establishment of protein localization to organelle
GO:0000956      4.82346741374753e-11    14.9820675105485        1.07591170161235
13      169     nuclear-transcribed mRNA catabolic process
GO:0034623      6.96470222143446e-11    14.5116754461829        1.10774340876064
13      174     cellular macromolecular complex disassembly
GO:0006402      9.26646282702262e-11    14.1558879938627        1.13320877447927
13      178     mRNA catabolic process
GO:0032984      9.94107155620554e-11    14.0696202531646        1.13957511590893
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13      179     macromolecular complex disassembly
GO:0019058      2.00447753500612e-10    11.697270471464 1.47062487025119        14
231     viral infectious cycle
GO:0006401      5.37465029970302e-10    12.1420754219409        1.30509999308006
13      205     RNA catabolic process
GO:0022900      8.17322226875273e-10    15.7177556960755        0.853089751574286
11      134     electron transport chain
GO:0022415      9.47557506538276e-10    10.2971648947259        1.6552487717113 14
260     viral reproductive process
GO:0045333      1.52063803221109e-09    14.7495994722458        0.904020483011556
11      142     cellular respiration
GO:0016032      3.06268020579448e-09    7.2726574500768 2.87121998477614        17
451     viral reproduction
GO:0006605      6.45100649366348e-09    6.89522975929978        3.01764583765829
17      474     protein targeting
GO:0071845      2.76755982344779e-08    8.55453314026811        1.80804096602311
13      284     cellular component disassembly at cellular level
GO:0022411      3.26461497070382e-08    8.42771001150748        1.83350633174175
13      288     cellular component disassembly
GO:0033365      2.75047658881905e-07    5.91263539953496        3.01127949622863
15      473     protein localization to organelle
GO:0006119      1.7511410088196e-06     19.1954382826476        0.369247802920213
6       58      oxidative phosphorylation
GO:0006120      3.02300201070875e-06    26.5628476084538        0.229188291467718
5       36      mitochondrial electron transport, NADH to ubiquinone
GO:0015980      3.87136211202597e-06    6.45199366032699        1.95446681890527
11      307     energy derivation by oxidation of organic compounds
GO:0042773      1.16400533956989e-05    19.5908593322386        0.299218047193966
5       47      ATP synthesis coupled electron transport
GO:0042775      1.16400533956989e-05    19.5908593322386        0.299218047193966
5       47      mitochondrial ATP synthesis coupled electron transport
GO:0006091      1.66141261505467e-05    5.02752403846154        2.72479413189399
12      428     generation of precursor metabolites and energy
Tissue: Heart_Left_Ventricle=>Adipose_Subcutaneous      Type:   asymmetric
SourceGene:     RP11-655M14.13(ENSG00000255318.1)
TargetGeneSet:  CSMD2   RPS8    RPL5    RP11    SRGAP2P2        PSMB4   RPS7    NFU1
ANKRD36 BRK1    RPL15   RAD54L2 KCTD6   ZBTB20  GYG1    MRPS18C ADH5    SMARCA5-AS1
RPS3A   CTD     BTF3    SKP1    PCDHGA4 CTB     MSX2    CUTA    WDR11   ABRACL
RPS3AP26        BRAF    ZNF484  C10orf31        ADRA2A  RPS24   RPS3AP5 DNMBP-AS1
TMEM126B        IFT46   PHB2    MLL4    RPL6    RPSAP54 STARD13-AS1     ESD     MED4
PSMA3   SQRDL   RPS3AP6 FAM108C1        ADCY7   KARS    RPL26   STX8    RPS7P1
RPS7P11 TUBD1   PSMG2   CHMP4B
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      1.45666516821016e-10    41.8459291712304        0.258182824718013
8       91      translational termination
GO:0006414      4.64438735855612e-10    35.7713214620431        0.297903259290015
8       105     translational elongation
GO:0006614      4.64438735855612e-10    35.7713214620431        0.297903259290015
8       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      5.01328235068794e-10    35.4038342609771        0.300740433188015
8       106     cotranslational protein targeting to membrane
GO:0045047      5.01328235068794e-10    35.4038342609771        0.300740433188015
8       106     protein targeting to ER
GO:0072599      5.01328235068794e-10    35.4038342609771        0.300740433188015
8       106     establishment of protein localization to endoplasmic reticulum
GO:0070972      1.18662231122188e-09    31.5151515151515        0.334786519964016
8       118     protein localization to endoplasmic reticulum
GO:0000184      1.26955061819192e-09    31.2290472290472        0.337623693862016
8       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      8.41804379915956e-09    24.1864801864802        0.428413258598021
8       151     viral genome expression
GO:0019083      8.41804379915956e-09    24.1864801864802        0.428413258598021
8       151     viral transcription
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GO:0006413      8.86757287242486e-09    24.016835016835 0.431250432496021       8
152     translational initiation
GO:0006612      9.33771581822956e-09    23.8495297805643        0.434087606394021
8       153     protein targeting to membrane
GO:0043624      9.33771581822956e-09    23.8495297805643        0.434087606394021
8       153     cellular protein complex disassembly
GO:0043241      1.20261549553799e-08    23.0464646464646        0.448273475884022
8       158     protein complex disassembly
GO:0000956      2.03875613063529e-08    21.4552983248635        0.479482388762023
8       169     nuclear-transcribed mRNA catabolic process
GO:0034623      2.56067776833948e-08    20.8017524644031        0.493668258252024
8       174     cellular macromolecular complex disassembly
GO:0006402      3.05762649345097e-08    20.3065953654189        0.505016953844025
8       178     mRNA catabolic process
GO:0032984      3.19413302749748e-08    20.1864256601099        0.507854127742025
8       179     macromolecular complex disassembly
GO:0016032      3.28582059199147e-08    11.6416666666667        1.27956542799806
11      451     viral reproduction
GO:0072594      8.80848819809488e-08    17.5807050092764        0.578783475192028
8       204     establishment of protein localization to organelle
GO:0006401      9.14744595825104e-08    17.4902322719582        0.581620649090028
8       205     RNA catabolic process
GO:0019058      2.29018273477018e-07    15.4227476559315        0.655387170438032
8       231     viral infectious cycle
GO:0022415      5.63551274443617e-07    13.6200096200096        0.737665213480036
8       260     viral reproductive process
GO:0071845      1.0973138698979e-06     12.4145805884936        0.805757387032039
8       284     cellular component disassembly at cellular level
GO:0022411      1.21888515040308e-06    12.2337662337662        0.81710608262404
8       288     cellular component disassembly
GO:0033365      5.50598763044479e-06    8.45325969827586        1.34198325375407
9       473     protein localization to organelle
GO:0006605      5.60114799230724e-06    8.43447580645161        1.34482042765207
9       474     protein targeting
GO:0006364      1.06890887301401e-05    20.0771604938272        0.295066085392014
5       104     rRNA processing
GO:0016072      1.40496412678571e-05    18.9219576719577        0.312089128780015
5       110     rRNA metabolic process
GO:0042274      1.67934151149249e-05    75.7631578947368        0.0510691301640025
3       18      ribosomal small subunit biogenesis
GO:0034470      1.95796569622906e-05    12.5620029455081        0.567434779600028
6       200     ncRNA processing
Tissue: Adipose_Subcutaneous=>Heart_Left_Ventricle      Type:   asymmetric




SourceGene:     ST3GAL5(ENSG00000115525.11)     "ST3 beta-galactoside
alpha-2,3-sialyltransferase 5"
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TargetGeneSet:  RP11     MRPL20   DNAJC16 EIF1AX   RPRD2    ILDR2    TGFB2    LYPLAL1
CICP5    RAB4A    RPS7     NBAS     MRPL33  MORN2    UBC      CCDC142 SNRNP200
TNFAIP6 CIDEC    HIGD1A   ADIPOQ   LETM1    MRAP     RPS3A    NDUFAF2 MTND5P11
TMEM14B RPS10    PGM3     HEBP2    MAGI2-AS3         ZKSCAN5 GS1      MEPCE    PNPLA8
ADCK2    RPL30    FBXO32   FAM49B   EEF1D    RPL8     LURAP1L RPS6     DCTN3    HABP4
TRIM32   CDK5RAP2          RPL35    GTF3C4   UPF2     DCLRE1C TMEM180 RPLP2    RPL27A   FAR1
RP4      HYLS1    CACNA1C-IT3       REP15    RAP1B    GLIPR1   RPL18AP3          ANKRD13A
FAM179B MAPK1IP1L          VTI1B    PLDN     ZFAND6   C17orf50          RPL19    C17orf53
SRSF1    SRSF2    CABYR    MOB3A    ALKBH7   ZNF490   ZNF829   SPRED3   AURKC    CSRP2BP RBL1
PCK1     SMPX     DYNLT3   ACSL4    FAM127A EMD

GOBPID   Pvalue   OddsRatio         ExpCount          Count    Size     Term

GO:0006414       1.47E-14          37.64845293      0.443221922      12       105
translational elongation

GO:0000184       6.85E-14          32.6904444       0.502318179      12       119
"nuclear-transcribed mRNA catabolic process, nonsense-mediated decay"

GO:0006415       1.07E-13          39.3525 0.384125666      11       91
translational termination

GO:0006614       5.39E-13          33.4587234       0.443221922      11       105
SRP-dependent cotranslational protein targeting to membrane
```

GO:0006613	6.00E-13	33.10421053	0.447443084	11	106	cotranslational protein targeting to membrane
GO:0045047	6.00E-13	33.10421053	0.447443084	11	106	protein targeting to ER
GO:0072599	6.00E-13	33.10421053	0.447443084	11	106	establishment of protein localization to endoplasmic reticulum
GO:0006413	1.32E-12	24.9271137	0.641616497	12	152	translational initiation
GO:0070972	1.99E-12	29.36691589	0.498097018	11	118	protein localization to endoplasmic reticulum
GO:0000956	4.68E-12	22.20148187	0.713376237	12	169	nuclear-transcribed mRNA catabolic process
GO:0006402	8.66E-12	20.98450947	0.751366687	12	178	mRNA catabolic process

GO:0019080	3.00E-11	22.39285714	0.637395336	11	151	viral genome expression
GO:0019083	3.00E-11	22.39285714	0.637395336	11	151	viral transcription
GO:0006612	3.46E-11	22.0743662	0.645837658	11	153	protein targeting to membrane
GO:0043624	3.46E-11	22.0743662	0.645837658	11	153	cellular protein complex disassembly
GO:0072594	4.30E-11	18.10969388	0.861116878	12	204	establishment of protein localization to organelle
GO:0006401	4.56E-11	18.01459237	0.865338039	12	205	RNA catabolic process

GO:0043241	4.91E-11	21.31605442	0.666943464	11	158	protein complex disassembly
GO:0034623	1.39E-10	19.20208589	0.734482043	11	174	cellular macromolecular complex disassembly
GO:0032984	1.89E-10	18.62404762	0.755587849	11	179	macromolecular complex disassembly
GO:0019058	2.84E-09	14.17	0.975088229	11	231	viral infectious cycle
GO:0033365	7.35E-09	9.040652668	1.996609231	14	473	protein localization to organelle
GO:0006605	7.56E-09	9.020351526	2.000830392	14	474	protein targeting

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GO:0022415      9.77E-09        12.49405622     1.097501903     11      260
viral reproductive process




GO:0071845      2.43E-08        11.376337       1.198809771     11      284
cellular component disassembly at cellular level




GO:0022411      2.81E-08        11.20888087     1.215694416     11      288
cellular component disassembly




GO:0016032      3.21E-07        7.782622844     1.903743686     12      451
viral reproduction




Tissue: Heart_Left_Ventricle=>Adipose_Subcutaneous      Type:   asymmetric
SourceGene:     VDAC1P2(ENSG00000213856.3)
TargetGeneSet:  RP11    TCEB1P21        NEB     XIRP2   KBTBD10 TTN     MYL1
KBTBD5  CMYA5   HCG16   RP1     CTB     LMOD2   YWHAZP3 DYDC2   OR52E8  CSRP3   MYL2
THSD1P1 MYH7    CTD     ATP2A1  MYH2    MYH1    FOXJ1   TMEM161A        CKM
COX6CP2 PVALB   LGALS1  RP13
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006936      6.37191302025124e-12    55.5730434782609        0.314234309044357
9       239     muscle contraction
GO:0030049      6.82931318946151e-12    201.384615384615        0.0512767282541001
6       39      muscle filament sliding
GO:0033275      6.82931318946151e-12    201.384615384615        0.0512767282541001
6       39      actin-myosin filament sliding
GO:0070252      1.09550346103916e-11    184.564102564103        0.0552210919659539
6       42      actin-mediated cell contraction
GO:0003012      1.66726778779246e-11    49.6400778210117        0.349733582451041
9       266     muscle system process
GO:0030048      9.28670025034424e-11    125.216255442671        0.0775724863331257
6       59      actin filament-based movement
```

```
GO:0006941      4.09911483040142e-10    96.0735785953177        0.0986090927963463
6       75      striated muscle contraction
GO:0030029      3.38449798682131e-08    24.0274442538593        0.567988374506954
8       432     actin filament-based process
GO:0061061      5.18891587400419e-07    20.3586235489221        0.537748252716075
7       409     muscle structure development
GO:0007517      1.74331969548227e-06    21.965811965812 0.398380734897239       6
303     muscle organ development
GO:0007507      3.51644406305201e-06    19.3626373626374        0.449657463151339
6       342     heart development
GO:0003010      9.81137925112146e-06    848.823529411765        0.00525915161580513
2       4       voluntary skeletal muscle contraction
GO:0014721      9.81137925112146e-06    848.823529411765        0.00525915161580513
2       4       twitch skeletal muscle contraction
GO:0048738      1.34512757015315e-05    34.4048048048048        0.151200608954398
4       115     cardiac muscle tissue development
GO:0003015      1.3920077546574e-05     34.0952380952381        0.152515396858349
4       116     heart process
GO:0060047      1.3920077546574e-05     34.0952380952381        0.152515396858349
4       116     heart contraction
Tissue: Muscle_Skeletal=>Adipose_Subcutaneous   Type:   asymmetric





SourceGene:     ARGLU1(ENSG00000134884.8)       arginine and glutamate rich 1
```

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TargetGeneSet:  RP11    CEP104  RPL22   VPS13D  RP1     UBR4    HSPG2   RPL11
ARID1A  EPB41   PUM1    KPNA7   ZBTB8OS 7SK     MFI2    MACF1   SZT2    PTPRF
KDM4A   DPH5    HIPK1   MRPS21  ADAR    ASH1L   ARHGEF11        DCAF8   EDEM3
LPGAT1  URB2    ADAM18  TTC32   ASXL2   SOS1-IT1        CCDC104 USP34   AAK1
ALMS1   TET3    RETSAT  TMEM131 HOXD-AS2        NBEAL1  FARP2   BRK1    NR2C2
GOLGA4  ZNF621  USP19   USP4    RNF123  VPRBP   RAD54L2 APPL1   PCNP    ZBTB11
KPNA1   CNBP    H1FX    EIF4G1  CTBP1-AS1       NOP14   DANCR   WDFY3-AS1
RPL34   MAML3   NIPBL   CTD     TAF9    BDP1    DMXL1   RAD50   AFF4    HSPA4
CTNNA1  RPS14   SLC2A3P1        HRH2    NSD1    DHX16   DDX39B  SRPK1   ZFAND3  CUL9
XPO5    TMEM63B KIAA1919        RP3     C6orf99 TNRC18  FBXL18  PLEKHA8 TRRAP   CUX1
COG5    TNPO3   MLL3    POLR3D  KIAA1967        KAT6A   RPS20   NIPAL2  VPS13B
EIF3H   EIF2C2  HEATR7A KCNV2   KIAA2026        SNAPC3  BICD2   SETX    BRD3
SEC16A  NOTCH1  EHMT1   HK1     SEC24C  FUT11   KIAA0913        TNKS2   IDE
DNMBP-AS1       CHUK    PPRC1   GBF1    EIF6    PDDC1   CARS-AS1        RPL27A
DNAJC24 TNKS1BP1        KDM2A   LRP5    PPP6R3  UBE4A   DDX6    SRPR    ERC1
SCAF11  CCDC65  MLL4    PFDN5   ANKRD52 PPTC7   ATXN2   C12orf47        MLXIP
SBNO1   EP400   ZDHHC20 DGKH    MYCBP2-AS1      TEP1    ARHGEF40        HNRNPC
C14orf21        STRN3   NIN     EXOC5   EXD2    CCNK    DYNC1H1 TECPR2  CDC42BPB
KIAA0284        CYFIP1  HERC2   TYRO3   MGA     GANC    CCNDBP1 TP53BP1 USP8
CCPG1   RPS3AP6 MYO9A   SIN3A   SEC11A  ZNF592  POLG    NME3    ZNF598  TSC2    PKD1
PDPK1   SLX4    CREBBP  RPS15A  SMG1    GTF3C1  SRCAP   RNF40   RAB43P1 VPS35
LONP2   ADCY7   AARS    ZNF778  RP13    ZZEF1   RAI1    TOM1L2  LLGL1   FLII
KIAA0100        RPL23A  NUFIP2  TAOK1   RPL19   CDK12   NKIRAS2 KPNB1   CLTC
DCAF7   ERN1    CEP95   UBE2O   PGS1    CSNK1D  FOXK2   ZNF236  NFIC    ZBTB7A
PLIN4   RANBP3  KHSRP   CARM1   SMARCA4 C19orf43        BRD4    UPF1    ARHGAP35
RPS11   PRR12   CNOT3   U2AF2   ATRN    RNF24   RRBP1   NCOA6   SOGA1   RALGAPB
STAU1   ADRM1   RP4     ZGPAT   DNAJC5  SCAF4   SON     CBR3-AS1        AGPAT3
UBE2G2  MCM3AP  DSTNP1  ZNF70   C22orf45        CTA     SYN3    EIF3L   SMCR7L
EP300   TCF20   ZBED4   SBF1    CDKL5   UXT     KDM5C   HUWE1   GNL3L   RRAGB
FAM123B RPS4X   RBM41

GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
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GO:0000956	6.11E-10	7.914936525	2.52605356	17	169	nuclear-transcribed mRNA catabolic process
GO:0006402	1.37E-09	7.467711227	2.660577123	17	178	mRNA catabolic process
GO:0000184	2.70E-09	9.326732673	1.778700436	14	119	"nuclear-transcribed mRNA catabolic process, nonsense-mediated decay"

GO:0006614	5.39E-09	9.844666952	1.569441561	13	105
SRP-dependent cotranslational protein targeting to membrane					
GO:0006613	6.06E-09	9.738121723	1.584388624	13	106
cotranslational protein targeting to membrane					

GO:0045047	6.06E-09	9.738121723	1.584388624	13	106	protein targeting to ER
GO:0072599	6.06E-09	9.738121723	1.584388624	13	106	establishment of protein localization to endoplasmic reticulum

GO:0006413	8.40E-09	7.679485783	2.271953498	15	152	translational initiation
GO:0006415	1.02E-08	10.54058079	1.360182686	12	91	translational termination
GO:0006401	1.18E-08	6.382951994	3.06414781	17	205	RNA catabolic process

GO:0016570	1.35E-08	5.576771406	3.901183309	19	261
histone modification					
GO:0016569	1.95E-08	5.439516129	3.990865684	19	267
covalent chromatin modification					

GO:0070972	2.26E-08	8.617874736	1.763753373	13	118	protein localization to endoplasmic reticulum
GO:0033365	4.25E-08	4.028082928	7.069960556	25	473	protein localization to organelle

GO:0006605	4.43E-08	4.018820182	7.084907619	25	474	protein targeting
GO:0006612	7.00E-08	7.028420828	2.286900561	14	153	protein targeting to membrane
GO:0072594	7.04E-08	5.977446809	3.049200747	16	204	establishment of protein localization to organelle

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GO:0034623      3.47E-07        6.096844059     2.600788873     14      174
cellular macromolecular complex disassembly
```

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GO:0022415      3.76E-07        4.918915565     3.886236247     17      260
viral reproductive process
```

GO:0019058	3.87E-07	5.216744186	3.452771435	16	231	viral infectious cycle
GO:0019080	4.23E-07	6.541764832	2.257006436	13	151	viral genome expression

GO:0019083	4.23E-07	6.541764832	2.257006436	13	151
viral transcription					
GO:0006414	4.70E-07	8.072184743	1.569441561	11	105
translational elongation					
GO:0032984	4.91E-07	5.909990999	2.675524185	14	179
macromolecular complex disassembly					

GO:0016568	1.30E-06	3.744066486	6.262819182	21	419	chromatin modification
GO:0006397	2.35E-06	3.730547628	5.963877932	20	399	mRNA processing

GO:0043624	3.18E-06	5.879849812	2.286900561	12	153
cellular protein complex disassembly					
GO:0043241	4.45E-06	5.676470588	2.361635873	12	158
protein complex disassembly					

GO:0071845	5.81E-06	4.169253731	4.244965746	16	284
cellular component disassembly at cellular level

GO:0022411	6.94E-06	4.106764706	4.304753996	16	288
cellular component disassembly

Tissue: Muscle_Skeletal=>Adipose_Subcutaneous	Type:	cluster
SourceGene:	ARGLU1(ENSG00000134884.8)
TargetGeneSet:	RP11	CEP104	RPL22	VPS13D	RP1	UBR4	HSPG2	RPL11
ARID1A	EPB41	PUM1	KPNA7	ZBTB8OS	7SK	MFI2	MACF1	SZT2	PTPRF

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KDM4A   DPH5    HIPK1   MRPS21  ADAR    ASH1L   ARHGEF11        DCAF8   EDEM3
LPGAT1  URB2    ADAM18  TTC32   ASXL2   SOS1-IT1        CCDC104 USP34   AAK1
ALMS1   TET3    RETSAT  TMEM131 HOXD-AS2        NBEAL1  FARP2   BRK1    NR2C2
GOLGA4  ZNF621  USP19   USP4    RNF123  VPRBP   RAD54L2 APPL1   PCNP    ZBTB11
KPNA1   CNBP    H1FX    EIF4G1  CTBP1-AS1       NOP14   DANCR   WDFY3-AS1
RPL34   MAML3   NIPBL   CTD     TAF9    BDP1    DMXL1   RAD50   AFF4    HSPA4
CTNNA1  RPS14   SLC2A3P1        HRH2    NSD1    DHX16   DDX39B  SRPK1   ZFAND3  CUL9
XPO5    TMEM63B KIAA1919        RP3     C6orf99 TNRC18  FBXL18  PLEKHA8 TRRAP   CUX1
COG5    TNPO3   MLL3    POLR3D  KIAA1967        KAT6A   RPS20   NIPAL2  VPS13B
EIF3H   EIF2C2  HEATR7A KCNV2   KIAA2026        SNAPC3  BICD2   SETX    BRD3
SEC16A  NOTCH1  EHMT1   HK1     SEC24C  FUT11   KIAA0913        TNKS2   IDE
DNMBP-AS1       CHUK    PPRC1   GBF1    EIF6    PDDC1   CARS-AS1        RPL27A
DNAJC24 TNKS1BP1        KDM2A   LRP5    PPP6R3  UBE4A   DDX6    SRPR    ERC1
SCAF11  CCDC65  MLL4    PFDN5   ANKRD52 PPTC7   ATXN2   C12orf47        MLXIP
SBNO1   EP400   ZDHHC20 DGKH    MYCBP2-AS1      TEP1    ARHGEF40        HNRNPC
C14orf21        STRN3   NIN     EXOC5   EXD2    CCNK    DYNC1H1 TECPR2  CDC42BPB
KIAA0284        CYFIP1  HERC2   TYRO3   MGA     GANC    CCNDBP1 TP53BP1 USP8
CCPG1   RPS3AP6 MYO9A   SIN3A   SEC11A  ZNF592  POLG    NME3    ZNF598  TSC2    PKD1
PDPK1   SLX4    CREBBP  RPS15A  SMG1    GTF3C1  SRCAP   RNF40   RAB43P1 VPS35
LONP2   ADCY7   AARS    ZNF778  RP13    ZZEF1   RAI1    TOM1L2  LLGL1   FLII
KIAA0100        RPL23A  NUFIP2  TAOK1   RPL19   CDK12   NKIRAS2 KPNB1   CLTC
DCAF7   ERN1    CEP95   UBE2O   PGS1    CSNK1D  FOXK2   ZNF236  NFIC    ZBTB7A
PLIN4   RANBP3  KHSRP   CARM1   SMARCA4 C19orf43        BRD4    UPF1    ARHGAP35
RPS11   PRR12   CNOT3   U2AF2   ATRN    RNF24   RRBP1   NCOA6   SOGA1   RALGAPB
STAU1   ADRM1   RP4     ZGPAT   DNAJC5  SCAF4   SON     CBR3-AS1        AGPAT3
UBE2G2  MCM3AP  DSTNP1  ZNF70   C22orf45        CTA     SYN3    EIF3L   SMCR7L
EP300   TCF20   ZBED4   SBF1    CDKL5   UXT     KDM5C   HUWE1   GNL3L   RRAGB
FAM123B RPS4X   RBM41
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0000956      6.10642257567849e-10    7.91493652472891        2.52605356030725
17      169     nuclear-transcribed mRNA catabolic process
GO:0006402      1.36881264877844e-09    7.46771122694216        2.66057712269047
17      178     mRNA catabolic process
GO:0000184      2.7035754699696e-09     9.32673267326733        1.77870043595599
14      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006614      5.39080792717484e-09    9.84466695223817        1.56944156113764
13      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      6.06420928503676e-09    9.73812172254886        1.58438862362466
13      106     cotranslational protein targeting to membrane
GO:0045047      6.06420928503676e-09    9.73812172254886        1.58438862362466
13      106     protein targeting to ER
GO:0072599      6.06420928503676e-09    9.73812172254886        1.58438862362466
13      106     establishment of protein localization to endoplasmic reticulum
GO:0006413      8.40146687823775e-09    7.67948578276501        2.27195349802782
15      152     translational initiation
GO:0006415      1.02439993812341e-08    10.5405807892777        1.36018268631929
12      91      translational termination
GO:0006401      1.1782094541953e-08     6.38295199401262        3.06414780984015
17      205     RNA catabolic process
GO:0016570      1.35055073605818e-08    5.57677140579771        3.90118330911356
19      261     histone modification
GO:0016569      1.95220980776489e-08    5.43951612903226        3.99086568403571
19      267     covalent chromatin modification
GO:0070972      2.26458106688009e-08    8.61787473610134        1.76375337346896
13      118     protein localization to endoplasmic reticulum
GO:0033365      4.24816230312305e-08    4.02808292819746        7.06996055636288
25      473     protein localization to organelle
GO:0006605      4.42651014331273e-08    4.01882018213832        7.08490761884991
25      474     protein targeting
GO:0006612      6.99926641472807e-08    7.02842082769428        2.28690056051484
14      153     protein targeting to membrane
GO:0072594      7.03581564956439e-08    5.97744680851064        3.04920074735312
16      204     establishment of protein localization to organelle
```

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GO:0034623      3.46922599961797e-07    6.09684405940594        2.60078887274237
14      174     cellular macromolecular complex disassembly
GO:0022415      3.76483983363389e-07    4.91891556548173        3.88623624662653
17      260     viral reproductive process
GO:0019058      3.87360169100841e-07    5.21674418604651        3.4527714345028 16
231     viral infectious cycle
GO:0019080      4.22788759172526e-07    6.54176483186978        2.25700643554079
13      151     viral genome expression
GO:0019083      4.22788759172526e-07    6.54176483186978        2.25700643554079
13      151     viral transcription
GO:0006414      4.69793777412849e-07    8.07218474312403        1.56944156113764
11      105     translational elongation
GO:0032984      4.90505725544315e-07    5.90999099909991        2.6755241851775 14
179     macromolecular complex disassembly
GO:0016568      1.29733854344659e-06    3.74406648627754        6.26281918206352
21      419     chromatin modification
GO:0006397      2.34560710933339e-06    3.73054762802218        5.96387793232302
20      399     mRNA processing
GO:0043624      3.18160741122279e-06    5.87984981226533        2.28690056051484
12      153     cellular protein complex disassembly
GO:0043241      4.44707132878579e-06    5.67647058823529        2.36163587294997
12      158     protein complex disassembly
GO:0071845      5.81404164814309e-06    4.16925373134328        4.24496574631513
16      284     cellular component disassembly at cellular level
GO:0022411      6.94154593913884e-06    4.10676470588235        4.30475399626323
16      288     cellular component disassembly
Tissue: Muscle_Skeletal=>Adipose_Subcutaneous   Type:   asymmetric




SourceGene:     CTD-2089O24.1(ENSG00000248966.1)        This is an expressed
pseudogene. What does this mean? How high is its expression?




TargetGeneSet:  RP1     RPS8    RPL5    RP11    DDIT3   UBC     CCDC115 EEF1B2
SETD5   RPL15   RPL10AP6        AIMP1   RPS3A   CCNO    NDUFAF2 TAF9    BTF3    CTB
NPM1    RPL15P3 ABT1    RPL10A  DAAM2   TBCC    EEF1A1  HOXA-AS3        SSBP1   CTD
RPL7    PABPC1  EIF3H   RPS6    RPL12   EEF1A1P5        RPL7A   RPS24   TCTN3
MORN4   C11orf46        EIF3M   PHB2    CDK4    NAP1L1  RPL18AP3        DGKH    TPT1
WDFY2   TPPP2   RSL24D1 RPS17L  MEF2A   RSL1D1  RPL26   RPL23A  TAOK1   RPL19
PSMG2   RPL17   AKAP8L  RPL18   RPL13A  RPS9    RPS5    RPL12P4 YDJC    EIF3L
RPSAP9  RPL10

GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term




GO:0006414      2.57E-36        133.8487805     0.385094457     23      105
translational elongation
```

GO:0006413	3.18E-36	100.3304274	0.557470071	25	152	translational initiation
GO:0006415	1.38E-33	134.325	0.33374853	21	91	translational termination
GO:0000184	6.77E-33	104.6298637	0.436440385	22	119	"nuclear-transcribed mRNA catabolic process, nonsense-mediated decay"
GO:0006614	3.86E-32	111.828125	0.385094457	21	105	SRP-dependent cotranslational protein targeting to membrane
GO:0006613	4.81E-32	110.5047794	0.388762023	21	106	cotranslational protein targeting to membrane
GO:0045047	4.81E-32	110.5047794	0.388762023	21	106	protein targeting to ER
GO:0072599	4.81E-32	110.5047794	0.388762023	21	106	establishment of protein localization to endoplasmic reticulum

GO:0070972	5.61E-31	96.75289948	0.432772818	21	118	protein localization to endoplasmic reticulum
GO:0000956	2.60E-29	68.80008778	0.619818698	22	169	nuclear-transcribed mRNA catabolic process
GO:0006402	8.62E-29	64.78990902	0.652826794	22	178	mRNA catabolic process
GO:0019080	1.43E-28	72.02596154	0.553802505	21	151	viral genome expression
GO:0019083	1.43E-28	72.02596154	0.553802505	21	151	viral transcription
GO:0006612	1.92E-28	70.92471591	0.561137638	21	153	protein targeting to membrane
GO:0043624	1.92E-28	70.92471591	0.561137638	21	153	cellular protein complex disassembly
GO:0043241	3.91E-28	68.3122719	0.579475469	21	158	protein complex disassembly

GO:0006401	2.19E-27	55.12603561	0.751851083	22	205	RNA catabolic process
GO:0034623	3.27E-27	61.09987745	0.638156529	21	174	cellular macromolecular complex disassembly
GO:0032984	6.09E-27	59.14556962	0.65649436	21	179	macromolecular complex disassembly
GO:0072594	1.05E-25	50.97592213	0.748183517	21	204	establishment of protein localization to organelle
GO:0019058	1.53E-24	44.3375	0.847207806	21	231	viral infectious cycle
GO:0022415	1.92E-23	38.87800732	0.953567227	21	260	viral reproductive process
GO:0071845	1.25E-22	35.27031844	1.041588817	21	284	cellular component disassembly at cellular level

GO:0022411	1.68E-22	34.7320927	1.056259082	21	288	cellular component disassembly
GO:0016032	8.54E-20	23.10835401	1.654072383	22	451	viral reproduction
GO:0033365	5.07E-18	20.24792588	1.73475884	21	473	protein localization to organelle
GO:0006605	5.30E-18	20.2017798	1.738426406	21	474	protein targeting
GO:0042254	1.34E-10	23.85644972	0.546467373	10	149	ribosome biogenesis
GO:0022613	4.38E-10	17.35914553	0.825202408	11	225	ribonucleoprotein complex biogenesis
GO:0071843	8.32E-10	16.27715121	0.876548336	11	239	cellular component biogenesis at cellular level
GO:0006364	9.58E-08	22.43545495	0.381426891	7	104	rRNA

```
processing




GO:0016072      1.41E-07        21.11967075     0.403432288     7       110     rRNA
metabolic process




GO:0042274      4.75E-07        83.87172012     0.066016193     4       18
ribosomal small subunit biogenesis




GO:0034470      7.87E-06        11.20015769     0.733513252     7       200
ncRNA processing




GO:0034660      8.51E-06        9.062815884     1.045256384     8       285
ncRNA metabolic process




GO:0042273      1.00E-05        95.92666667     0.044010795     3       12
ribosomal large subunit biogenesis




Tissue: Muscle_Skeletal=>Adipose_Subcutaneous   Type:   cluster
SourceGene:     CTD-2089O24.1(ENSG00000248966.1)
TargetGeneSet:  RP1     RPS8    RPL5    RP11    DDIT3   UBC     CCDC115 EEF1B2
SETD5   RPL15   RPL10AP6        AIMP1   RPS3A   CCNO    NDUFAF2 TAF9    BTF3    CTB
NPM1    RPL15P3 ABT1    RPL10A  DAAM2   TBCC    EEF1A1  HOXA-AS3        SSBP1   CTD
RPL7    PABPC1  EIF3H   RPS6    RPL12   EEF1A1P5        RPL7A   RPS24   TCTN3
MORN4   C11orf46        EIF3M   PHB2    CDK4    NAP1L1  RPL18AP3        DGKH    TPT1
WDFY2   TPPP2   RSL24D1 RPS17L  MEF2A   RSL1D1  RPL26   RPL23A  TAOK1   RPL19
PSMG2   RPL17   AKAP8L  RPL18   RPL13A  RPS9    RPS5    RPL12P4 YDJC    EIF3L
RPSAP9  RPL10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      2.57316855367557e-36    133.848780487805        0.385094457130994
23      105     translational elongation
GO:0006413      3.18438255427382e-36    100.330427446569        0.557470071275344
```

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25      152     translational initiation
GO:0006415      1.37683091113982e-33    134.325 0.333748529513528       21      91
translational termination
GO:0000184      6.76824231087336e-33    104.62986365148 0.43644038474846        22
119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006614      3.86335117243005e-32    111.828125      0.385094457130994       21
105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      4.80757453431886e-32    110.504779411765        0.388762023389385
21      106     cotranslational protein targeting to membrane
GO:0045047      4.80757453431886e-32    110.504779411765        0.388762023389385
21      106     protein targeting to ER
GO:0072599      4.80757453431886e-32    110.504779411765        0.388762023389385
21      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      5.60861412618874e-31    96.7528994845361        0.43277281849007
21      118     protein localization to endoplasmic reticulum
GO:0000956      2.60238859680657e-29    68.8000877770463        0.619818697667981
22      169     nuclear-transcribed mRNA catabolic process
GO:0006402      8.6246094938347e-29     64.7899090157155        0.652826793993495
22      178     mRNA catabolic process
GO:0019080      1.43194412988401e-28    72.0259615384615        0.553802505016954
21      151     viral genome expression
GO:0019083      1.43194412988401e-28    72.0259615384615        0.553802505016954
21      151     viral transcription
GO:0006612      1.91761007854905e-28    70.9247159090909        0.561137637533735
21      153     protein targeting to membrane
GO:0043624      1.91761007854905e-28    70.9247159090909        0.561137637533735
21      153     cellular protein complex disassembly
GO:0043241      3.90934916237724e-28    68.3122718978102        0.579475468825687
21      158     protein complex disassembly
GO:0006401      2.19300724539094e-27    55.1260356072625        0.751851082970037
22      205     RNA catabolic process
GO:0034623      3.27259657214294e-27    61.0998774509804        0.638156528959934
21      174     cellular macromolecular complex disassembly
GO:0032984      6.08849197704669e-27    59.1455696202532        0.656494360251886
21      179     macromolecular complex disassembly
GO:0072594      1.04927189093189e-25    50.9759221311475        0.748183516711646
21      204     establishment of protein localization to organelle
GO:0019058      1.53164327185711e-24    44.3375 0.847207805688188       21      231
viral infectious cycle
GO:0022415      1.920198072866e-23      38.8780073221757        0.95356722718151
21      260     viral reproductive process
GO:0071845      1.25135930369499e-22    35.2703184410646        1.04158881738288
21      284     cellular component disassembly at cellular level
GO:0022411      1.68221806922201e-22    34.7320926966292        1.05625908241644
21      288     cellular component disassembly
GO:0016032      8.54399763582425e-20    23.1083540115798        1.65407238253408
22      451     viral reproduction
GO:0033365      5.07474222486416e-18    20.2479258849558        1.73475884021867
21      473     protein localization to organelle
GO:0006605      5.2984331346356e-18     20.2017798013245        1.73842640647706
21      474     protein targeting
GO:0042254      1.33696473540869e-10    23.8564497239418        0.546467372500173
10      149     ribosome biogenesis
GO:0022613      4.38238687051113e-10    17.3591455273698        0.825202408137845
11      225     ribonucleoprotein complex biogenesis
GO:0071843      8.31956408197553e-10    16.2771512113617        0.876548335755311
11      239     cellular component biogenesis at cellular level
GO:0006364      9.57804202948499e-08    22.4354549529359        0.381426890872604
7       104     rRNA processing
GO:0016072      1.41089845216968e-07    21.1196707471507        0.403432288422946
7       110     rRNA metabolic process
GO:0042274      4.74914639992733e-07    83.8717201166181        0.0660161926510276
4       18      ribosomal small subunit biogenesis
```

```
GO:0034470      7.87291764517478e-06    11.2001576931741        0.733513251678085
7       200     ncRNA processing
GO:0034660      8.51423230299042e-06    9.06281588447653        1.04525638364127
8       285     ncRNA metabolic process
GO:0042273      1.00118700227926e-05    95.9266666666667        0.0440107951006851
3       12      ribosomal large subunit biogenesis
Tissue: Muscle_Skeletal=>Adipose_Subcutaneous   Type:   asymmetric
```

```
SourceGene:     ENSG00000229344.1       Also an expressed pseudogene?
```

```
TargetGeneSet:  MTND2P28        RPL22   ICMT    CLSTN1  NMNAT1  DFFA    MFN2
VPS13D  DDI2    SPEN    UBR4    KIAA0090        LDLRAD2 HSPG2   RPL11   ARID1A
WASF2   KPNA7   ZMYM4   THRAP3  MEAF6   MFI2    MACF1   RP1     SZT2    RPS8
RPS15AP10       TM2D1   RP4     FAM73A  GNG5    RPL5    RP11    SORT1   ATP5F1
HIPK1   NBPF16  HIST2H2BD       RPRD2   JTB     RPS27   ASH1L   MIR555  SSR2
MEF2D   ARHGEF11        COPA    POU2F1  PRRC2C  CEP350  ARPC5   RPS7    ADAM18  NBAS
ASXL2   PPP1CB  DHX57   RHOQ    UBC     USP34   C1D     AAK1    TET3    DCTN1
TMEM131 EIF5B   RANBP2  UGGT1   MZT2B   MLK7-AS1        SENP2   PLEKHM3 GIGYF2
SETD5   RPL32   NR2C2   RPL15   MAP4    CELSR3  LAMB2   RAD54L2 RPL29   DNAH1
APPL1   KCTD6   PCNP    RPL24   CNBP    NME9    PDCD10  PHC3    DNAJC19 PSMD2
EIF4G1  CPN2    HTT     BOD1L   RELL1   COPS4   UBE2D3  AIMP1   RPL34   RPS3A
NIPBL   CTD     MRPS36  TAF9    TBCA    ARSB    ERAP1   MAN2A1  APC     HINT1   AFF4
SKP1    CTB     MTND5P11        KDM3B   PAIP2   PCDHGB3 PCDHGB6 RPS14   RPL15P3 NOL7
DEK     GPLD1   ABT1    PPP1R10 TAPBP   RPS10   RPL10A  C6orf89 MTRNR2L9
WDR11   ASCC3   MRPS12  PHACTR2 IGF2R   FOXK1   PHF14   MPLKIP  CHCHD2  LMTK2
RPS3AP26        TRRAP   GNB2    CUX1    SLC26A4 TNPO3   HIPK2   MLL3    KAT6A
HOOK3   RPS20   ASPH    RBM12B  RPL30   POLR2K  TRAPPC9 HEATR7A VPS28   RPL8    RPS6
TLN1    CLTA    CNN2P4  HSD17B3 XPA     NIPSNAP3A       TMEM245 FKBP15  ATP6V1G1
RPL35   RPL12   NUP188  SETX    RPL7A   COMMD3  PRINS   FUT11   KIAA0913
RPS24   GBF1    ARL3    EIF6    RPL27A  MTRNR2L8        TSG101  CKAP5   C1QTNF4
C11orf31        DDB1    GANAB   FAU     PACS1   PPP6R3  TMEM126B        TMEM126A
SDHD    BACE1   UBE4A   ATP5L   DDX6    RPL23AP64       VPS11   SIAE    KDM5A   ERC1
USP5    C12orf57        FGFR1OP2        SCAF11  MLL4    PFDN5   BAZ2A   LRP1
TMBIM4  RBMS1P1 EEA1    APAF1   RPL18AP3        VPS29   ACAD10  SBNO1   ZC3H13  ESD
RPL13AP25       COMMD6  DNAJC3  HMGB3P4 CCNB1IP1        CHD8    C14orf119
C14orf21        STRN3   FNTB    MED6    YLPM1   SEL1L   C14orf102       CCNK
DYNC1H1 CYFIP1  HERC2   HERC2P10        RPAP1   VPS39   CCNDBP1 DUT     USP8
CCPG1   RPS3AP6 LRRC49  SIN3A   C15orf40        SEC11A  IQGAP1  MEF2A   JMJD8   NME3
SPSB3   NDUFB10 ECI1    MGRN1   NOMO1   RPS15A  ZNF771  SRCAP   ZNF629  CES1P2
NFATC3  AARS    GABARAPL2       CDYL2   HSBP1   RPL13   VPS53   RP13    METTL16
ZZEF1   SLC35G6 RPL26   TOM1L2  RPS7P1  PIGS    SUPT6H  RPL23A  TAOK1   CPD
TAF15   RPL19   CDK12   WIPF2   NKIRAS2 STAT5A  AOC3    RPL27   NMT1    CLTC
HEATR6  DCAF7   COG1    NT5C    TNRC6C  RPTOR   ROCK1P1 C18orf21        C18orf32
RPL17   ZNF407  TPGS1   ATP5D   RPS15   RPL36   TRAPPC5 ZNF121  LPHN1   BRD4
YJEFN3  RPS19   POU2F2  MEGF8   SNRPD2  ARHGAP35        RPL18   NUCB1   RPL13A
MYH7B   RPS9    ZNF587  RPS5    ATRN    KIF3B   NCOA6   SCAND1  RALGAPB NCOA3   ADNP
PSMD10P1        TSHZ2   RPL12P4 SON     PCBP3   PI4KA   YDJC    FAM211B CTA     MPST
APOBEC3C        RPL3    TNRC6B  EP300   TCF20   VCX3B   TMSB4X  RPL9P7  DYNLT3
USP9X   CDK16   KDM5C   HUWE1   GNL3L   CBX1P1  RPS4X   APOOL   RPL39   THOC2
HCFC1   RPL10

GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
```

GO:0006415	1.18E-50	52.83744681	1.851359767	44	91
translational termination					

GO:0006614	2.09E-50	44.32121378	2.136184347	46	105	SRP-dependent cotranslational protein targeting to membrane
GO:0006613	3.63E-50	43.57943548	2.15652896	46	106	cotranslational protein targeting to membrane

```
GO:0045047      3.63E-50        43.57943548     2.15652896      46      106
protein targeting to ER
```

```
GO:0072599      3.63E-50        43.57943548     2.15652896      46      106
establishment of protein localization to endoplasmic reticulum
```

GO:0070972	1.64E-47	36.28528226	2.400664314	46	118
protein localization to endoplasmic reticulum					
GO:0006414	3.78E-47	40.67042623	2.136184347	44	105
translational elongation					

```
GO:0000184      9.27E-46        34.39352003     2.421008927     45      119
"nuclear-transcribed mRNA catabolic process, nonsense-mediated decay"
```

GO:0006612	3.01E-44	26.11289199	3.112725763	48	153	protein targeting to membrane
GO:0006413	5.47E-43	25.4653557	3.09238115	47	152	translational initiation

GO:0019080	9.76E-42	24.82304147	3.072036537	46	151
viral genome expression					
GO:0019083	9.76E-42	24.82304147	3.072036537	46	151
viral transcription					

GO:0043624	4.65E-40	23.50903614	3.112725763	45	153
cellular protein complex disassembly					
GO:0043241	2.34E-39	22.46081672	3.214448827	45	158
protein complex disassembly					

GO:0000956	3.16E-39	21.16325728	3.438239568	46	169	nuclear-transcribed mRNA catabolic process

```
GO:0072594	6.75E-39	18.06709677	4.150301017	49	204
establishment of protein localization to organelle
```

```
GO:0034623	1.37E-38	20.32932208	3.539962632	46	174
cellular macromolecular complex disassembly
```

GO:0006402	4.30E-38	19.70766129	3.621341084	46	178	mRNA catabolic process
GO:0032984	5.68E-38	19.55808877	3.641685696	46	179	macromolecular complex disassembly

GO:0022415	5.99E-37	14.41012397	5.289599336	52	260
viral reproductive process					
GO:0019058	4.17E-36	15.35714286	4.699605564	49	231
viral infectious cycle					

GO:0006401	4.47E-35	16.32958004	4.17064563	46	205	RNA catabolic process

```
GO:0016032      3.33E-32        9.027477212     9.175420386     60      451
viral reproduction
```

```
GO:0071845      1.69E-29        11.17613898     5.777870044     47      284
cellular component disassembly at cellular level
```

GO:0022411	3.23E-29	10.98748467	5.859248495	47	288	cellular component disassembly
GO:0033365	2.82E-28	7.944224684	9.623001868	57	473	protein localization to organelle

GO:0006605	3.15E-28	7.924597031	9.643346481	57	474	protein targeting
GO:0042274	3.53E-08	31.36585366	0.366203031	7	18	ribosomal small subunit biogenesis

GO:0022613	1.73E-07	4.679064431	4.577537887	19	225	ribonucleoprotein complex biogenesis

GO:0071843	4.42E-07	4.376909091	4.862362466	19	239
cellular component biogenesis at cellular level					
GO:0042254	2.12E-06	5.193333333	3.031347312	14	149
ribosome biogenesis					

GO:0006364	8.53E-06	5.87803488	2.115839734	11	104	rRNA processing
GO:0016072	1.46E-05	5.519434629	2.237907411	11	110	rRNA metabolic process

```
Tissue: Muscle_Skeletal=>Adipose_Subcutaneous   Type:   cluster
SourceGene:     ENSG00000229344.1
TargetGeneSet:  MTND2P28        RPL22   ICMT    CLSTN1  NMNAT1  DFFA    MFN2
VPS13D  DDI2    SPEN    UBR4    KIAA0090        LDLRAD2 HSPG2   RPL11   ARID1A
WASF2   KPNA7   ZMYM4   THRAP3  MEAF6   MFI2    MACF1   RP1     SZT2    RPS8
RPS15AP10       TM2D1   RP4     FAM73A  GNG5    RPL5    RP11    SORT1   ATP5F1
HIPK1   NBPF16  HIST2H2BD       RPRD2   JTB     RPS27   ASH1L   MIR555  SSR2
MEF2D   ARHGEF11        COPA    POU2F1  PRRC2C  CEP350  ARPC5   RPS7    ADAM18  NBAS
ASXL2   PPP1CB  DHX57   RHOQ    UBC     USP34   C1D     AAK1    TET3    DCTN1
TMEM131 EIF5B   RANBP2  UGGT1   MZT2B   MLK7-AS1        SENP2   PLEKHM3 GIGYF2
SETD5   RPL32   NR2C2   RPL15   MAP4    CELSR3  LAMB2   RAD54L2 RPL29   DNAH1
APPL1   KCTD6   PCNP    RPL24   CNBP    NME9    PDCD10  PHC3    DNAJC19 PSMD2
EIF4G1  CPN2    HTT     BOD1L   RELL1   COPS4   UBE2D3  AIMP1   RPL34   RPS3A
NIPBL   CTD     MRPS36  TAF9    TBCA    ARSB    ERAP1   MAN2A1  APC     HINT1   AFF4
SKP1    CTB     MTND5P11        KDM3B   PAIP2   PCDHGB3 PCDHGB6 RPS14   RPL15P3 NOL7
DEK     GPLD1   ABT1    PPP1R10 TAPBP   RPS10   RPL10A  C6orf89 MTRNR2L9
WDR11   ASCC3   MRPS12  PHACTR2 IGF2R   FOXK1   PHF14   MPLKIP  CHCHD2  LMTK2
RPS3AP26        TRRAP   GNB2    CUX1    SLC26A4 TNPO3   HIPK2   MLL3    KAT6A
HOOK3   RPS20   ASPH    RBM12B  RPL30   POLR2K  TRAPPC9 HEATR7A VPS28   RPL8    RPS6
TLN1    CLTA    CNN2P4  HSD17B3 XPA     NIPSNAP3A       TMEM245 FKBP15  ATP6V1G1
RPL35   RPL12   NUP188  SETX    RPL7A   COMMD3  PRINS   FUT11   KIAA0913
RPS24   GBF1    ARL3    EIF6    RPL27A  MTRNR2L8        TSG101  CKAP5   C1QTNF4
C11orf31        DDB1    GANAB   FAU     PACS1   PPP6R3  TMEM126B        TMEM126A
SDHD    BACE1   UBE4A   ATP5L   DDX6    RPL23AP64       VPS11   SIAE    KDM5A   ERC1
USP5    C12orf57        FGFR1OP2        SCAF11  MLL4    PFDN5   BAZ2A   LRP1
TMBIM4  RBMS1P1 EEA1    APAF1   RPL18AP3        VPS29   ACAD10  SBNO1   ZC3H13  ESD
RPL13AP25       COMMD6  DNAJC3  HMGB3P4 CCNB1IP1        CHD8    C14orf119
C14orf21        STRN3   FNTB    MED6    YLPM1   SEL1L   C14orf102       CCNK
DYNC1H1 CYFIP1  HERC2   HERC2P10        RPAP1   VPS39   CCNDBP1 DUT     USP8
CCPG1   RPS3AP6 LRRC49  SIN3A   C15orf40        SEC11A  IQGAP1  MEF2A   JMJD8   NME3
SPSB3   NDUFB10 ECI1    MGRN1   NOMO1   RPS15A  ZNF771  SRCAP   ZNF629  CES1P2
NFATC3  AARS    GABARAPL2       CDYL2   HSBP1   RPL13   VPS53   RP13    METTL16
ZZEF1   SLC35G6 RPL26   TOM1L2  RPS7P1  PIGS    SUPT6H  RPL23A  TAOK1   CPD
TAF15   RPL19   CDK12   WIPF2   NKIRAS2 STAT5A  AOC3    RPL27   NMT1    CLTC
HEATR6  DCAF7   COG1    NT5C    TNRC6C  RPTOR   ROCK1P1 C18orf21        C18orf32
RPL17   ZNF407  TPGS1   ATP5D   RPS15   RPL36   TRAPPC5 ZNF121  LPHN1   BRD4
YJEFN3  RPS19   POU2F2  MEGF8   SNRPD2  ARHGAP35        RPL18   NUCB1   RPL13A
MYH7B   RPS9    ZNF587  RPS5    ATRN    KIF3B   NCOA6   SCAND1  RALGAPB NCOA3   ADNP
PSMD10P1        TSHZ2   RPL12P4 SON     PCBP3   PI4KA   YDJC    FAM211B CTA     MPST
APOBEC3C        RPL3    TNRC6B  EP300   TCF20   VCX3B   TMSB4X  RPL9P7  DYNLT3
USP9X   CDK16   KDM5C   HUWE1   GNL3L   CBX1P1  RPS4X   APOOL   RPL39   THOC2
HCFC1   RPL10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      1.18091173108757e-50    52.8374468085106        1.85135976749014
```

```
44      91      translational termination
GO:0006614      2.09172658551235e-50    44.3212137780208        2.13618434710401
46      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      3.63289544301091e-50    43.579435483871 2.15652895993357        46
106     cotranslational protein targeting to membrane
GO:0045047      3.63289544301091e-50    43.579435483871 2.15652895993357        46
106     protein targeting to ER
GO:0072599      3.63289544301091e-50    43.579435483871 2.15652895993357        46
106     establishment of protein localization to endoplasmic reticulum
GO:0070972      1.64396294360088e-47    36.2852822580645        2.40066431388831
46      118     protein localization to endoplasmic reticulum
GO:0006414      3.78449564522234e-47    40.6704262295082        2.13618434710401
44      105     translational elongation
GO:0000184      9.27350257945361e-46    34.3935200260501        2.42100892671787
45      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006612      3.00677485738495e-44    26.1128919860627        3.11272576292298
48      153     protein targeting to membrane
GO:0006413      5.46614409583205e-43    25.4653556969346        3.09238115009342
47      152     translational initiation
GO:0019080      9.75572766221803e-42    24.8230414746544        3.07203653726386
46      151     viral genome expression
GO:0019083      9.75572766221803e-42    24.8230414746544        3.07203653726386
46      151     viral transcription
GO:0043624      4.65270176117719e-40    23.5090361445783        3.11272576292298
45      153     cellular protein complex disassembly
GO:0043241      2.34166071234943e-39    22.4608167182002        3.21444882707079
45      158     protein complex disassembly
GO:0000956      3.15866900736828e-39    21.1632572777341        3.43823956819597
46      169     nuclear-transcribed mRNA catabolic process
GO:0072594      6.74610504771765e-39    18.0670967741935        4.15030101723064
49      204     establishment of protein localization to organelle
GO:0034623      1.37459865525761e-38    20.3293220766129        3.53996263234378
46      174     cellular macromolecular complex disassembly
GO:0006402      4.29525212359941e-38    19.7076612903226        3.62134108366203
46      178     mRNA catabolic process
GO:0032984      5.68264718768384e-38    19.5580887703129        3.64168569649159
46      179     macromolecular complex disassembly
GO:0022415      5.99138943130968e-37    14.4101239669421        5.28959933568611
52      260     viral reproductive process
GO:0019058      4.17095704564696e-36    15.3571428571429        4.69960556362881
49      231     viral infectious cycle
GO:0006401      4.47343411260268e-35    16.3295800365186        4.1706456300602 46
205     RNA catabolic process
GO:0016032      3.32587370046433e-32    9.02747721162043        9.17542038613245
60      451     viral reproduction
GO:0071845      1.68874570139949e-29    11.1761389842669        5.7778700435956 47
284     cellular component disassembly at cellular level
GO:0022411      3.22850201111655e-29    10.9874846708216        5.85924849491385
47      288     cellular component disassembly
GO:0033365      2.81601968032666e-28    7.9442246835443 9.62300186838281        57
473     protein localization to organelle
GO:0006605      3.14776323708927e-28    7.92459703123577        9.64334648121237
57      474     protein targeting
GO:0042274      3.52846334098024e-08    31.3658536585366        0.366203030932115
7       18      ribosomal small subunit biogenesis
GO:0022613      1.72939544098139e-07    4.67906443071492        4.57753788665144
19      225     ribonucleoprotein complex biogenesis
GO:0071843      4.41698210520289e-07    4.37690909090909        4.86236246626531
19      239     cellular component biogenesis at cellular level
GO:0042254      2.11823520481386e-06    5.19333333333333        3.03134731160473
14      149     ribosome biogenesis
GO:0006364      8.53332664867264e-06    5.87803487974467        2.11583973427444
11      104     rRNA processing
```

GO:0016072 1.46426333350594e-05 5.51943462897527 2.23790741125182 11 110 rRNA metabolic process

Tissue: Muscle_Skeletal=>Adipose_Subcutaneous Type: asymmetric

SourceGene: EPCAM(ENSG00000119888.6) epithelial cell adhesion molecule (disease associations)

TargetGeneSet: C1orf200 TRAPPC3 ATRX NUF2 ASPM RRM2 HJURP DNAJC19 CENPE ANLN ESCO2 PAG1 PAPPA CEP55 MKI67 FAM111B CDCA5 ATP5L MPP2 CDCA3 RP11 TROAP HMGA2 CPM SKA3 DIAPH3 BUB1B CASC5 CCNB2 SNAPC5 POLR3K IFT140 PKMYT1 GABARAPL2 SDR42E1 CDT1 FANCA FAM64A SNORA48 TOP2A KIF18B TK1 BIRC5 CTD LINGO3 ASF1B ZNF576 TRPM4 SHANK1 UBE2C

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0000280	1.46E-15	24.97050344	1.041450419	16	350	nuclear division
GO:0007067	1.46E-15	24.97050344	1.041450419	16	350	mitosis
GO:0000087	2.27E-15	24.22739018	1.071206145	16	360	M phase of mitotic cell cycle
GO:0048285	3.49E-15	23.52626072	1.100961871	16	370	organelle fission
GO:0051301	7.88E-14	18.99014611	1.344958826	16	452	cell division

GO:0010564	1.79E-09	13.48675975	1.231887067	12	414	regulation of cell cycle process
GO:0007059	6.91E-09	24.72034632	0.416580167	8	140	chromosome segregation
GO:0071156	6.48E-08	14.6916955	0.785551173	9	264	regulation of cell cycle arrest
GO:0000086	2.01E-07	20.25486618	0.428482458	7	144	G2/M transition of mitotic cell cycle
GO:0000075	4.82E-07	13.84517705	0.720088575	8	242	cell cycle checkpoint
GO:0007050	1.10E-06	10.32941176	1.097986299	9	369	cell cycle arrest
GO:0071103	1.27E-06	15.19871795	0.562383226	7	189	DNA conformation change
GO:0051329	1.37E-06	10.04308426	1.127742025	9	379	interphase of mitotic cell cycle
GO:0051325	1.63E-06	9.824929972	1.151546606	9	387	interphase

```
GO:0007346      2.61E-06        10.93501211     0.901598505     8       303
regulation of mitotic cell cycle



GO:0045786      4.40E-06        8.646234195     1.300325237     9       437
negative regulation of cell cycle



GO:0000236      5.05E-06        23.56578947     0.252923673     5       85
mitotic prometaphase



GO:0007096      5.30E-06        119.9916667     0.035706871     3       12
regulation of exit from mitosis



GO:0006323      5.63E-06        15.73193602     0.455262612     6       153     DNA
packaging



GO:0031577      7.01E-06        38.7854251      0.12497405      4       42
spindle checkpoint



GO:0010458      1.34E-05        83.04807692     0.047609162     3       16      exit
from mitosis



Tissue: Muscle_Skeletal=>Adipose_Subcutaneous   Type:   asymmetric




SourceGene:     GEN1(ENSG00000178295.9) GEN1 Holliday junction 5' flap endonuclease
```

TargetGeneSet: RPL22 FBXO6 RPL5 RP11 PPM1J RP1 GAS5 GEN1
SLC40A1 FAM126B NBEAL1 RPL32 RPL15 RPL14 APPL1 RAB6B GRK7 RPS3A TAF9
SMN1 BTF3 CAMLG CTNNA1 CTB SRPK1 IGFBP3 C7orf57 RPS3AP26
PTCD1 RPL30 RPS3AP5 RPP30 RPL27A PFDN5 CDK2 ARPC3 DGKH ATP7B
RAB15 EXD2 PSMC1 TYRO3 TP53BP1 ATP8B4 RPS3AP6 FURIN SGSM2 RPL26
MPRIP RPL23A RPL19 AOC3 PGS1 CTD RPL17 RPL36 PRKACA RPL13A
RPS11 ASMT UXT RPS4X RBM41 RPL10

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0006415	6.62E-26	99.73751024	0.314857103	17	91	translational termination
GO:0006414	9.16E-25	83.78822314	0.363296658	17	105	translational elongation
GO:0006614	9.16E-25	83.78822314	0.363296658	17	105	SRP-dependent cotranslational protein targeting to membrane
GO:0006613	1.09E-24	82.84099421	0.366756626	17	106	cotranslational protein targeting to membrane
GO:0045047	1.09E-24	82.84099421	0.366756626	17	106	protein targeting to ER
GO:0072599	1.09E-24	82.84099421	0.366756626	17	106	establishment of protein localization to endoplasmic reticulum

GO:0070972	7.59E-24	72.93729373	0.408276244	17	118
protein localization to endoplasmic reticulum					
GO:0000184	8.84E-24	72.21717172	0.411736212	17	119
"nuclear-transcribed mRNA catabolic process, nonsense-mediated decay"					
GO:0019080	6.16E-22	54.84825871	0.522455193	17	151
viral genome expression					
GO:0019083	6.16E-22	54.84825871	0.522455193	17	151
viral transcription					
GO:0019058	6.90E-22	41.02115033	0.799252647	19	231
viral infectious cycle					
GO:0006413	6.92E-22	54.43815937	0.525915162	17	152
translational initiation					
GO:0006612	7.76E-22	54.03409091	0.52937513	17	153
protein targeting to membrane					
GO:0043624	7.76E-22	54.03409091	0.52937513	17	153
cellular protein complex disassembly					

GO:0043241	1.37E-21	52.09972061	0.546674971	17	158	protein complex disassembly
GO:0000956	4.45E-21	48.29206539	0.58473462	17	169	nuclear-transcribed mRNA catabolic process
GO:0022415	6.71E-21	36.01124347	0.899591724	19	260	viral reproductive process
GO:0034623	7.41E-21	46.73769543	0.602034461	17	174	cellular macromolecular complex disassembly
GO:0006402	1.10E-20	45.56371165	0.615874334	17	178	mRNA catabolic process
GO:0032984	1.21E-20	45.27927422	0.619334302	17	179	macromolecular complex disassembly
GO:0072594	1.17E-19	39.15702479	0.705833506	17	204	establishment of protein localization to organelle
GO:0006401	1.27E-19	38.94600258	0.709293475	17	205	RNA

						catabolic process
GO:0016032	4.42E-19	23.52774659	1.560445644	21	451	viral reproduction
GO:0071845	1.15E-18	29.89074248	0.98263096	18	284	cellular component disassembly at cellular level
GO:0022411	1.47E-18	29.43958333	0.996470832	18	288	cellular component disassembly
GO:0006605	9.61E-15	17.20189145	1.640024912	18	474	protein targeting
GO:0033365	1.55E-13	15.75392079	1.636564944	17	473	protein localization to organelle
GO:0042273	8.39E-06	102.070922	0.041519618	3	12	ribosomal large subunit biogenesis

Tissue: Muscle_Skeletal=>Adipose_Subcutaneous Type: asymmetric

SourceGene: IGKJ5(ENSG00000211593.2) immunoglobulin kappa joining 5

```
TargetGeneSet:  RP1     RP11    UBC     RPL31   SENP2   C2orf54 RPL32   RPL35A
RPL34   NSA2    RPL10A  RPL39P3 C8orf59 RPL30   TPT1    COMMD6  RPS3AP6 RPL36

GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term


GO:0006415      5.26E-15        230.5863454     0.088159989     8       91
translational termination


GO:0006414      1.72E-14        197.1134021     0.101723064     8       105
translational elongation


GO:0006614      1.72E-14        197.1134021     0.101723064     8       105
SRP-dependent cotranslational protein targeting to membrane


GO:0006613      1.86E-14        195.0884354     0.102691855     8       106
cotranslational protein targeting to membrane


GO:0045047      1.86E-14        195.0884354     0.102691855     8       106
protein targeting to ER


GO:0072599      1.86E-14        195.0884354     0.102691855     8       106
establishment of protein localization to endoplasmic reticulum


GO:0070972      4.48E-14        173.6606061     0.114317348     8       118
protein localization to endoplasmic reticulum


GO:0000184      4.80E-14        172.0840841     0.115286139     8       119
"nuclear-transcribed mRNA catabolic process, nonsense-mediated decay"


GO:0019080      3.36E-13        133.2773893     0.146287454     8       151
viral genome expression


GO:0019083      3.36E-13        133.2773893     0.146287454     8       151
viral transcription


GO:0006413      3.54E-13        132.3425926     0.147256245     8       152
translational initiation


GO:0006612      3.74E-13        131.4206897     0.148225036     8       153
protein targeting to membrane


GO:0043624      3.74E-13        131.4206897     0.148225036     8       153
cellular protein complex disassembly


GO:0043241      4.85E-13        126.9955556     0.153068992     8       158
protein complex disassembly


GO:0000956      8.38E-13        118.2277433     0.163725694     8       169
```

```
nuclear-transcribed mRNA catabolic process


GO:0034623      1.06E-12        114.626506      0.168569649     8       174
cellular macromolecular complex disassembly


GO:0006402      1.28E-12        111.8980392     0.172444814     8       178     mRNA
catabolic process


GO:0032984      1.34E-12        111.2358674     0.173413605     8       179
macromolecular complex disassembly


GO:0072594      3.84E-12        96.87755102     0.197633382     8       204
establishment of protein localization to organelle


GO:0006401      3.99E-12        96.37901861     0.198602173     8       205     RNA
catabolic process


GO:0019058      1.04E-11        84.98654709     0.223790741     8       231
viral infectious cycle


GO:0022415      2.70E-11        75.05291005     0.251885683     8       260
viral reproductive process


GO:0071845      5.47E-11        68.41062802     0.275136669     8       284
cellular component disassembly at cellular level


GO:0022411      6.12E-11        67.41428571     0.279011833     8       288
cellular component disassembly


GO:0016032      2.16E-09        42.11888638     0.43692478      8       451
viral reproduction


GO:0033365      3.14E-09        40.06308244     0.458238184     8       473
protein localization to organelle


GO:0006605      3.19E-09        39.97424893     0.459206975     8       474
protein targeting


Tissue: Muscle_Skeletal=>Adipose_Subcutaneous   Type:   cluster
SourceGene:     MTND1P23(ENSG00000225972.1)
TargetGeneSet:  MTND1P23        MTND2P28        UBR4    KPNA7   RP4     THRAP3  RP1
ATP5F1  HIPK1   CSDE1   ADAR    ASH1L   MIR555  TKT     PRRC2C  RP11    CEP350  LAD1
LPGAT1  ASXL2   RHOQ    UBC     COMMD1  AAK1    TET3    EIF5B   UGGT1   MZT2B
RHOQP3  RHOQP2  MZT2A   GULP1   HDLBP   IL17RC  MAP4    RAD54L2 PCNP    RPL24
PDCD10  DNAJC19 IQCG    RELL1   CISD2   RPL34   RPS3A   CTD     MRPS36  TBCA    ARSB
ERAP1   MAN2A1  HINT1   AFF4    CTB     MTND5P11        RPS14   NOL7    GPLD1
HLA-H   TAPBP   C6orf89 ZFAND3  MTRNR2L9        BCKDHB  SNHG5   MRPS12  PHACTR2 RP3
IGF2R   FOXK1   CHCHD2  CUX1    TRBV6-5 HOOK3   RBM12B  TG      CLTA    CBWD3   XPA
ATP6V1G1        SETX    RPL7A   SSNA1   COMMD3  FUT11   RPL27A  MTRNR2L8
CCDC85B PACS1   SDHD    UBE4A   ATP5L   DDX6    RPL23AP64       ERC1    C12orf57
```

```
MLL4    PFDN5   HMGB1   NKX2-1  FKBP3   C14orf1 C14orf102       DUT     RAB11A
KIAA1199        SEC11A  NME3    ECI1    ZNF771  SRCAP   FBXL19-AS1      RPL13
VPS53   RPL26   TOM1L2  RPS2P48 NT5C    C17orf99        ANKRD12 GNAL    C18orf32
GCDH    BRD4    ARHGAP35        RPL18   ZNF551  ZNF587  RPS5    KIF3B   ADNP
ATP9A   TSHZ2   RPL12P4 YDJC    HMGB1P10        MPST    RPL3    RP6     USP9X
HUWE1   GNL3L   COX7B   RPL39   HCFC1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006614      2.85187993110751e-14    23.8361204013378        0.770188914261989
14      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      3.2662520390078e-14     23.5753780718336        0.77752404677877
14      106     cotranslational protein targeting to membrane
GO:0045047      3.2662520390078e-14     23.5753780718336        0.77752404677877
14      106     protein targeting to ER
GO:0072599      3.2662520390078e-14     23.5753780718336        0.77752404677877
14      106     establishment of protein localization to endoplasmic reticulum
GO:0006415      9.97513105924338e-14    25.5681003584229        0.667497059027057
13      91      translational termination
GO:0070972      1.50034564504427e-13    20.8375836120401        0.86554563698014
14      118     protein localization to endoplasmic reticulum
GO:0006612      3.3319676772627e-13     16.9696607740086        1.12227527506747
15      153     protein targeting to membrane
GO:0006414      6.67721192852802e-13    21.65603085554  0.770188914261989       13
105     translational elongation
GO:0072594      1.66474874630968e-12    13.3872340425532        1.49636703342329
16      204     establishment of protein localization to organelle
GO:0000184      3.43323659244544e-12    18.7773382024751        0.872880769496921
13      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006413      5.1002164221504e-12     15.6661940768746        1.11494014255069
14      152     translational initiation
GO:0000956      2.16589459825813e-11    13.9312762973352        1.23963739533596
14      169     nuclear-transcribed mRNA catabolic process
GO:0006402      4.3664296916785e-11     13.1584040296925        1.30565358798699
14      178     mRNA catabolic process
GO:0019080      7.26080401728964e-11    14.3907589216145        1.10760501003391
13      151     viral genome expression
GO:0019083      7.26080401728964e-11    14.3907589216145        1.10760501003391
13      151     viral transcription
GO:0043624      8.57319919396345e-11    14.1831797235023        1.12227527506747
13      153     cellular protein complex disassembly
GO:0043241      1.28533505959621e-10    13.689284390063 1.15895093765137        13
158     protein complex disassembly
GO:0006401      2.87805973677657e-10    11.2768040063738        1.50370216594007
14      205     RNA catabolic process
GO:0034623      4.29033958791117e-10    12.3149669404929        1.27631305791987
13      174     cellular macromolecular complex disassembly
GO:0032984      6.09615116983799e-10    11.9398238113745        1.31298872050377
13      179     macromolecular complex disassembly
GO:0071845      2.27349123483779e-09    8.62535234282446        2.08317763476576
15      284     cellular component disassembly at cellular level
GO:0022411      2.75236896680963e-09    8.49655838666828        2.11251816483288
15      288     cellular component disassembly
GO:0022415      6.35358966199288e-09    8.72154471544715        1.90713445436302
14      260     viral reproductive process
GO:0033365      9.09854180531894e-09    6.24425574425574        3.46951768043734
18      473     protein localization to organelle
GO:0019058      1.3585501099947e-08     9.05844924533886        1.69441561137638
13      231     viral infectious cycle
GO:0006605      5.84999051009004e-08    5.80473532810464        3.47685281295412
17      474     protein targeting
GO:0016032      9.88474098314292e-07    5.25846859562456        3.30814476506816
15      451     viral reproduction
Tissue: Muscle_Skeletal=>Adipose_Subcutaneous   Type:   asymmetric
```

SourceGene: MTND2P28(ENSG00000225630.1) pseudogene

TargetGeneSet: MTND1P23 MTND2P28 RPL22 DFFA VPS13D DDI2
C1orf134 UBR4 ARID1A KPNA7 THRAP3 MFI2 RP1 RPS8 RPS15AP10
RPL5 RP11 SORT1 HIPK1 NBPF16 JTB RPS27 ASH1L POU2F1 PRRC2C
CEP350 LPGAT1 KIDINS220 NBAS ASXL2 PPP1CB RHOQ UBC USP34 AAK1
TET3 DCTN1 COA5 EIF5B RANBP2 UGGT1 MZT2B RHOQP3 RHOQP2 PLEKHM3
HDLBP NR2C2 RPL15 MAP4 LAMB2 RAD54L2 RN5S132 RPL29 SEMA3G CTD PCNP
RPL24 DNAJC13 PDCD10 PHC3 DNAJC19 EIF4G1 HTT RP13 RELL1 OCIAD1
COPS4 AIMP1 RPL34 RPS3A NIPBL MRPS36 TBCA ARSB ERAP1 MAN2A1 APC
HINT1 AFF4 SKP1 CTB MTND5P11 KDM3B PCDHGA6 PCDHGC5 RPS14 NOL7
GPLD1 HLA-H TAPBP RPS10 RPL10A ZFAND3 DST MTRNR2L9 WDR11
SNHG5 ASCC3 MRPS12 PHACTR2 RP3 IGF2R FOXK1 PHF14 THSD7A MALSU1
CHCHD2 LMTK2 RPS3AP26 BUD31 SPDYE2 TNPO3 HIPK2 MLL3 KAT6A
HOOK3 RPS20 ASPH RPL30 TG TRAPPC9 NFIB TLN1 CLTA XPA
RPL12 SETX RPL7A FAM208B COMMD3 PRINS FUT11 RPS24 EIF6 CD151
RPL27A MTRNR2L8 TSG101 C11orf31 GANAB PACS1 PPP6R3 TMEM126B

TMEM126A UBE4A DDX6 RPL23AP64 APPL2 KDM5A ERC1 C12orf57
PHB2 SCAF11 MLL4 PFDN5 TMBIM4 RBMS1P1 C12orf73 ACAD10 RPL6
SBNO1 GOLGA3 ESD COMMD6 HMGB3P4 CHD8 NKX2-1 NIN C14orf102
CYFIP1 HERC2 HERC2P10 C15orf40 SEC11A LRRK1 JMJD8 NME3
SPSB3 ECI1 MGRN1 EMP2 RPS15A ZNF771 SRCAP ATXN1L CDYL2 BANP
VPS53 METTL16 ZZEF1 ALOX12 SLC35G6 RPL26 SUPT6H RPL23A TAOK1 TAF15
ZNHIT3 RPL19 CDK12 WIPF2 RPL27 ANKRD40 CLTC MED13 TNRC6C ROCK1P1
ANKRD12 C18orf21 C18orf32 RPL17 ZNF407 ZBTB7A ZNF121 HNRNPA1P10
BRD4 RPSAP58 ARHGAP35 RPL18 RPL13A MYH7B ZNF587 ZNF8 RPS5 HM13
KIF3B NCOA6 RALGAPB NCOA3 ADNP TSHZ2 RPL12P4 PCMTD2 SON PEX26
PI4KA YDJC CTA HMGB1P10 MPST RPL3 TNRC6B EP300 VCX3B
USP9X HUWE1 GNL3L RPS4X APOOL RPL39 THOC2 XIAP HCFC1 RPL10

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0006415	3.38E-39	50.17851788	1.221645561	33	91	translational termination

```
GO:0006614      2.14E-38        42.45809859     1.409591032     34      105
SRP-dependent cotranslational protein targeting to membrane
```

```
GO:0006613      3.11E-38        41.86545139     1.423015708     34      106
cotranslational protein targeting to membrane
```

```
GO:0045047      3.11E-38        41.86545139     1.423015708     34      106
protein targeting to ER
```

```
GO:0072599      3.11E-38        41.86545139     1.423015708     34      106
establishment of protein localization to endoplasmic reticulum
```

```
GO:0006414      8.90E-37        40.38172878     1.409591032     33      105
translational elongation
```

```
GO:0070972      2.06E-36        35.85431548     1.584111826     34      118
protein localization to endoplasmic reticulum
```

```
GO:0000184      2.85E-36        35.43   1.597536503     34      119
"nuclear-transcribed mRNA catabolic process, nonsense-mediated decay"
```

```
GO:0006612      5.07E-35        27.53651412     2.053975503     36      153
protein targeting to membrane
```

GO:0006413	1.07E-33	26.60323604	2.040550827	35	152
translational initiation					
GO:0019080	2.21E-32	25.68162393	2.02712615	34	151
viral genome expression					

GO:0019083	2.21E-32	25.68162393	2.02712615	34	151
viral transcription					
GO:0043624	3.58E-32	25.24642857	2.053975503	34	153
cellular protein complex disassembly					
GO:0000956	5.79E-32	23.20027222	2.268770327	35	169
nuclear-transcribed mRNA catabolic process					

```
GO:0043241      1.16E-31        24.21985887     2.121098886     34      158
protein complex disassembly
```

```
GO:0072594      1.54E-31        19.88367215     2.738634005     37      204
establishment of protein localization to organelle
```

GO:0034623	1.71E-31	22.35781186	2.33589371	35	174	cellular macromolecular complex disassembly
GO:0006402	3.96E-31	21.72626116	2.389592416	35	178	mRNA catabolic process
GO:0032984	4.87E-31	21.5738557	2.403017092	35	179	macromolecular complex disassembly

GO:0006401	6.84E-29	18.24065853	2.752058681	35	205	RNA catabolic process
GO:0022415	9.58E-29	15.39991915	3.490415888	38	260	viral reproductive process

```
GO:0019058      4.85E-27        15.79177898     3.10110027      35      231
viral infectious cycle
```

```
GO:0033365      6.50E-26        9.758279496     6.349871981     45      473
protein localization to organelle
```

```
GO:0071845      4.98E-25        12.87066149     3.812608124     36      284
cellular component disassembly at cellular level
```

GO:0022411	8.16E-25	12.66274864	3.86630683	36	288
cellular component disassembly					
GO:0006605	6.46E-24	9.135047095	6.363296658	43	474
protein targeting					

```
GO:0016032      7.82E-23        9.050326797     6.054529098     41      451
viral reproduction
```

```
Tissue: Muscle_Skeletal=>Adipose_Subcutaneous   Type:   cluster
SourceGene:     MTND2P28(ENSG00000225630.1)
TargetGeneSet:  MTND1P23        MTND2P28        RPL22   DFFA    VPS13D  DDI2
C1orf134        UBR4    ARID1A  KPNA7   THRAP3  MFI2    RP1     RPS8    RPS15AP10
RPL5    RP11    SORT1   HIPK1   NBPF16  JTB     RPS27   ASH1L   POU2F1  PRRC2C
CEP350  LPGAT1  KIDINS220       NBAS    ASXL2   PPP1CB  RHOQ    UBC     USP34   AAK1
TET3    DCTN1   COA5    EIF5B   RANBP2  UGGT1   MZT2B   RHOQP3  RHOQP2  PLEKHM3
HDLBP   NR2C2   RPL15   MAP4    LAMB2   RAD54L2 RN5S132 RPL29   SEMA3G  CTD     PCNP
RPL24   DNAJC13 PDCD10  PHC3    DNAJC19 EIF4G1  HTT     RP13    RELL1   OCIAD1
COPS4   AIMP1   RPL34   RPS3A   NIPBL   MRPS36  TBCA    ARSB    ERAP1   MAN2A1  APC
HINT1   AFF4    SKP1    CTB     MTND5P11        KDM3B   PCDHGA6 PCDHGC5 RPS14   NOL7
GPLD1   HLA-H   TAPBP   RPS10   RPL10A  ZFAND3  DST     MTRNR2L9        WDR11
SNHG5   ASCC3   MRPS12  PHACTR2 RP3     IGF2R   FOXK1   PHF14   THSD7A  MALSU1
CHCHD2  LMTK2   RPS3AP26        BUD31   SPDYE2  TNPO3   HIPK2   MLL3    KAT6A
HOOK3   RPS20   ASPH    RPL30   TG      TRAPPC9 NFIB    TLN1    CLTA    XPA
RPL12   SETX    RPL7A   FAM208B COMMD3  PRINS   FUT11   RPS24   EIF6    CD151
RPL27A  MTRNR2L8        TSG101  C11orf31        GANAB   PACS1   PPP6R3  TMEM126B
TMEM126A        UBE4A   DDX6    RPL23AP64       APPL2   KDM5A   ERC1    C12orf57
PHB2    SCAF11  MLL4    PFDN5   TMBIM4  RBMS1P1 C12orf73        ACAD10  RPL6
SBNO1   GOLGA3  ESD     COMMD6  HMGB3P4 CHD8    NKX2-1  NIN     C14orf102
CYFIP1  HERC2   HERC2P10        C15orf40        SEC11A  LRRK1   JMJD8   NME3
SPSB3   ECI1    MGRN1   EMP2    RPS15A  ZNF771  SRCAP   ATXN1L  CDYL2   BANP
VPS53   METTL16 ZZEF1   ALOX12  SLC35G6 RPL26   SUPT6H  RPL23A  TAOK1   TAF15
ZNHIT3  RPL19   CDK12   WIPF2   RPL27   ANKRD40 CLTC    MED13   TNRC6C  ROCK1P1
ANKRD12 C18orf21        C18orf32        RPL17   ZNF407  ZBTB7A  ZNF121  HNRNPA1P10
BRD4    RPSAP58 ARHGAP35        RPL18   RPL13A  MYH7B   ZNF587  ZNF8    RPS5    HM13
KIF3B   NCOA6   RALGAPB NCOA3   ADNP    TSHZ2   RPL12P4 PCMTD2  SON     PEX26
PI4KA   YDJC    CTA     HMGB1P10        MPST    RPL3    TNRC6B  EP300   VCX3B
USP9X   HUWE1   GNL3L   RPS4X   APOOL   RPL39   THOC2   XIAP    HCFC1   RPL10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      3.37848132117428e-39    50.1785178839152        1.22164556086084
33      91      translational termination
GO:0006614      2.13651690835942e-38    42.4580985915493        1.40959103176251
34      105     SRP-dependent cotranslational protein targeting to membrane
```

```
GO:0006613      3.11137614749354e-38    41.8654513888889        1.42301570825548
34      106     cotranslational protein targeting to membrane
GO:0045047      3.11137614749354e-38    41.8654513888889        1.42301570825548
34      106     protein targeting to ER
GO:0072599      3.11137614749354e-38    41.8654513888889        1.42301570825548
34      106     establishment of protein localization to endoplasmic reticulum
GO:0006414      8.9001924638916e-37     40.3817287784679        1.40959103176251
33      105     translational elongation
GO:0070972      2.06153783064841e-36    35.8543154761905        1.5841118261712 34
118     protein localization to endoplasmic reticulum
GO:0000184      2.85488460075027e-36    35.43   1.59753650266418        34      119
nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006612      5.06588451374648e-35    27.5365141187926        2.05397550342537
36      153     protein targeting to membrane
GO:0006413      1.07329332825106e-33    26.6032360371983        2.04055082693239
35      152     translational initiation
GO:0019080      2.21174037966493e-32    25.6816239316239        2.02712615043942
34      151     viral genome expression
GO:0019083      2.21174037966493e-32    25.6816239316239        2.02712615043942
34      151     viral transcription
GO:0043624      3.5839345031581e-32     25.2464285714286        2.05397550342537
34      153     cellular protein complex disassembly
GO:0000956      5.78680390021384e-32    23.2002722237867        2.26877032731299
35      169     nuclear-transcribed mRNA catabolic process
GO:0043241      1.16020677849e-31       24.2198588709677        2.12109888589025
34      158     protein complex disassembly
GO:0072594      1.54032264360333e-31    19.8836721461536        2.73863400456716
37      204     establishment of protein localization to organelle
GO:0034623      1.70970250788406e-31    22.3578118637166        2.33589370977787
35      174     cellular macromolecular complex disassembly
GO:0006402      3.96285383659401e-31    21.7262611602234        2.38959241574977
35      178     mRNA catabolic process
GO:0032984      4.87277837579616e-31    21.573855695318 2.40301709224275        35
179     macromolecular complex disassembly
GO:0006401      6.84005738847217e-29    18.240658527562 2.75205868106013        35
205     RNA catabolic process
GO:0022415      9.58139378065215e-29    15.3999191499191        3.49041588817383
38      260     viral reproductive process
GO:0019058      4.85276860766041e-27    15.7917789757412        3.10110026987752
35      231     viral infectious cycle
GO:0033365      6.50112578404979e-26    9.75827949570344        6.34987198117777
45      473     protein localization to organelle
GO:0071845      4.98394237888988e-25    12.8706614944875        3.81260812400526
36      284     cellular component disassembly at cellular level
GO:0022411      8.16468621454925e-25    12.6627486437613        3.86630682997716
36      288     cellular component disassembly
GO:0006605      6.45691417132307e-24    9.13504709515834        6.36329665767075
43      474     protein targeting
GO:0016032      7.82496057998823e-23    9.05032679738562        6.0545290983323 41
451     viral reproduction
Tissue: Muscle_Skeletal=>Adipose_Subcutaneous   Type:   cluster
```

SourceGene: MTRNR2L8(ENSG00000255823.1) humanin-like protein 8

TargetGeneSet: MTND2P28 NMNAT1 RP4 THRAP3 RPS8 RPS15AP10 RPL5
RP11 ASH1L PRRC2C CEP350 RPS7 ADAM18 EIF5B MAP4K4 UGGT1 MZT2B
RHOQP3 GIGYF2 RPL15 MAP4 RAD54L2 RPL29 APPL1 RPL10AP6 TMF1 PCNP
RPL24 C3orf15 PHC3 DNAJC19 LMLN-AS1 HTT BOD1L RELL1 ZBTB12B
RPL34 CTD ERAP1 PTMAP2 AFF4 CTB MTND5P11 RPL15P3 TAPBP
ZFAND3 MTRNR2L9 WDR11 IYD IGF2R STARD3NL RPS3AP26
TNPO3 TRPV6 MLL3 DRP2 HMBOX1 HOOK3 ARFGEF1 RBM12B TG NIPSNAP3A
SETX EEF1A1P5 RPL7A RPS24 RPS3AP5 EMX2 RPL27A MTRNR2L8
CKAP5 TMEM126B UBE4A DDX6 SIAE C12orf57 SCAF11 MLL4
PFDN5 TMBIM4 EEA1 RP3 RPL6 RP1 SBNO1 RPSAP54 LATS2 MRP63
GTF3A DIS3 HMGB3P4 CCNB1IP1 C14orf21 YLPM1 CCNK HERC2P10
CALML4 MYO9A SEC11A ASB9P1 LRRK1 MPG NME3 NDUFB10 RPS15A LONP2
NFATC3 RPL13 VPS53 WDR81 RPL26 TOM1L2 RPS7P1 SUPT6H RPL23A TAOK1
NKIRAS2 STAT5A RPL27 RPS7P11 NFE2L1 CLTC MED13 GPR142 TNRC6C FN3KRP
ROCK1P1 ANKRD12 FAM108A1 ZNF121 BRD4 RPSAP58 C19orf54 RPL18
NUCB1 ZNF587 RPS5 REM1 KIF3B NCOA3 TSHZ2 RPL12P4 UBE2G2 FAM108A5P
HMGB1P10 MPST UQCRFS1P1 TNRC6B DYNLT3 USP9X GNL3L COX7B
PGAM4 RPL39

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0006614	3.61E-23	38.56389452	0.777454847	20	105	SRP-dependent cotranslational protein targeting to membrane

GO:0006613	4.43E-23	38.11280406	0.784859179	20	106	cotranslational protein targeting to membrane
GO:0045047	4.43E-23	38.11280406	0.784859179	20	106	protein targeting to ER
GO:0072599	4.43E-23	38.11280406	0.784859179	20	106	establishment of protein localization to endoplasmic reticulum
GO:0006415	7.32E-23	42.7979798	0.673794201	19	91	translational termination

GO:0070972	4.34E-22	33.41778091	0.873711162	20	118
protein localization to endoplasmic reticulum					
GO:0006414	1.36E-21	35.79571882	0.777454847	19	105
translational elongation					
GO:0000184	1.68E-20	30.75409091	0.881115494	19	119
"nuclear-transcribed mRNA catabolic process, nonsense-mediated decay"					
GO:0000956	3.16E-20	23.4220616	1.251332088	21	169
nuclear-transcribed mRNA catabolic process					

GO:0006413 8.40E-20 24.75095785 1.125458446 20 152
translational initiation

GO:0072594 8.52E-20 20.13988365 1.510483704 22 204
establishment of protein localization to organelle

GO:0006402 9.54E-20 22.06539772 1.317971075 21 178 mRNA
catabolic process

GO:0006612 9.61E-20 24.56313197 1.132862778 20 153
protein targeting to membrane

GO:0019080	1.80E-18	23.24621212	1.118054114	19	151	viral genome expression
GO:0019083	1.80E-18	23.24621212	1.118054114	19	151	viral transcription
GO:0006401	1.87E-18	18.7917088	1.517888035	21	205	RNA catabolic process
GO:0043624	2.32E-18	22.89603121	1.132862778	19	153	

cellular protein complex disassembly					
GO:0043241	4.32E-18	22.06466645	1.169884437	19	158
protein complex disassembly					
GO:0034623	2.74E-17	19.76473607	1.288353747	19	174
cellular macromolecular complex disassembly					
GO:0032984	4.69E-17	19.14034091	1.325375407	19	179
macromolecular complex disassembly					

GO:0033365	5.60E-16	9.979341011	3.502248979	26	473
protein localization to organelle					
GO:0019058	5.53E-15	14.39258148	1.710400664	19	231
viral infectious cycle					
GO:0006605	5.81E-15	9.434923135	3.509653311	25	474
protein targeting					
GO:0022415	4.81E-14	12.63471332	1.925126289	19	260
viral reproductive process					

GO:0071845	2.37E-13	11.47088336	2.102830254	19	284
cellular component disassembly at cellular level					
GO:0022411	3.05E-13	11.29710206	2.132447581	19	288
cellular component disassembly					
GO:0016032	7.29E-10	6.953072391	3.339353678	19	451
viral reproduction					
GO:0022613	8.53E-07	7.565712617	1.665974673	11	225
ribonucleoprotein complex biogenesis					

```
GO:0071843      1.54E-06        7.094115497     1.769635319     11      239
cellular component biogenesis at cellular level
```

```
GO:0042254      1.46E-05        8.139838097     1.10324545      8       149
ribosome biogenesis
```

```
Tissue: Muscle_Skeletal=>Adipose_Subcutaneous   Type:   asymmetric
SourceGene:     RP1-199J3.5(ENSG00000219755.1)
TargetGeneSet:  EIF3I   NFYC    GAS5    EIF3FP3 HAT1    RPL24   EIF2S1  RP11
RIOK2   GNB2L1  RPL15P3 CYC1    STOML2  FXN     SNORA65 RPL7A   MMS19   BCCIP   PHB2
PPP1CC  RP13    RPS15A  KARS    RPS7P1  RPL19   RPS2P48 MRPL38  TIMM21  RPL18   CA11
RPL13A  PCMTD2  C21orf59        EIF3L   RPL3    RP3     PQBP1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006413      3.51044963663819e-14    67.0610328638498        0.262957580790257
10      152     translational initiation
GO:0006415      1.36125432420966e-10    66.3981481481482        0.157428551657325
7       91      translational termination
GO:0006414      3.76966412411771e-10    56.8571428571429        0.181648328835375
7       105     translational elongation
GO:0006614      3.76966412411771e-10    56.8571428571429        0.181648328835375
7       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      4.03178584212367e-10    56.2789001122334        0.183378312919521
7       106     cotranslational protein targeting to membrane
GO:0045047      4.03178584212367e-10    56.2789001122334        0.183378312919521
7       106     protein targeting to ER
GO:0072599      4.03178584212367e-10    56.2789001122334        0.183378312919521
7       106     establishment of protein localization to endoplasmic reticulum
GO:0070972      8.60841328508279e-10    50.1526526526527        0.204138121929278
7       118     protein localization to endoplasmic reticulum
GO:0000184      9.13641681991106e-10    49.7013888888889        0.205868106013425
7       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0072594      1.21023242562198e-09    34.1656662665066        0.352916753165871
8       204     establishment of protein localization to organelle
GO:0019080      4.85655971717182e-09    38.5702160493827        0.26122759670611
```

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7       151     viral genome expression
GO:0019083      4.85655971717182e-09    38.5702160493827        0.26122759670611
7       151     viral transcription
GO:0006612      5.32340134246467e-09    38.0365296803653        0.264687564874403
7       153     protein targeting to membrane
GO:0043624      5.32340134246467e-09    38.0365296803653        0.264687564874403
7       153     cellular protein complex disassembly
GO:0043241      6.66046984147184e-09    36.7641648270787        0.273337485295135
7       158     protein complex disassembly
GO:0000956      1.0634672804538e-08     34.241426611797 0.292367310220746       7
169     nuclear-transcribed mRNA catabolic process
GO:0034623      1.30186743611952e-08    33.2045908183633        0.301017230641478
7       174     cellular macromolecular complex disassembly
GO:0006402      1.52391365969805e-08    32.4187784275504        0.307937166978064
7       178     mRNA catabolic process
GO:0032984      1.58419103619109e-08    32.2280361757106        0.30966715106221
7       179     macromolecular complex disassembly
GO:0006401      4.03930072703358e-08    27.9450056116723        0.354646737250017
7       205     RNA catabolic process
GO:0019058      9.16197193198717e-08    24.65625        0.399626323437824       7
231     viral infectious cycle
GO:0022415      2.05171463523108e-07    21.7854633289416        0.449795861878071
7       260     viral reproductive process
GO:0071845      3.73284780332888e-07    19.8642198154834        0.491315479897585
7       284     cellular component disassembly at cellular level
GO:0022411      4.10292613740075e-07    19.5759193357058        0.498235416234171
7       288     cellular component disassembly
GO:0033365      8.22122464461807e-07    14.1287792536369        0.818282471801259
8       473     protein localization to organelle
GO:0006605      8.35341126315392e-07    14.0974501388538        0.820012455885406
8       474     protein targeting
GO:0016032      8.12287569685107e-06    12.2464964964965        0.780222821950038
7       451     viral reproduction
Tissue: Muscle_Skeletal=>Adipose_Subcutaneous   Type:   asymmetric
```

```
SourceGene:     RP11-10B2.1(ENSG00000230916.1)  agan a processed expressed
pseudogene
```

```
TargetGeneSet:  MTND1P23        MTND2P28        NMNAT1  DFFA    UBR4    LDLRAD2
HSPG2   KPNA7   THRAP3  RPS8    RPS15AP10       CCBL2   RPL5    RP11    ATP5F1
RPS27   ASH1L   MEF2D   COPA    PRRC2C  CEP350  NBAS    PPP1CB  UBC     C1D     AAK1
DCTN1   EIF5B   MAP4K4  IL1RL2  RANBP2  UGGT1   MZT2B   HAT1    HDLBP   CRELD1
RPL15   MAP4    USP4    RAD54L2 RPL29   TMF1    PCNP    RPL24   CNBP    PDCD10
DNAJC19 AFAP1   BOD1L   RELL1   CISD2   RPL34   RPS3A   NIPBL   CTD     MRPS36
ERAP1   AFF4    SKP1    CTB     MTND5P11        CTNNA1  PCDHGC5 TRIM41  GNB2L1
TMEM14C RPL15P3 DEK     GPLD1   RPS10   RPL10A  ZFAND3  MTRNR2L9        WDR11
BCKDHB  PHACTR2 IGF2R   FOXK1   PHF14   YWHAG   CACNA2D1        RPS3AP26
TNPO3   MLL3    DRP2    HOOK3   RPS20   PAG1    RBM12B  POLR2K  TG      TLN1    CLTA
XPA     ATP6V1G1        RPL35   SETX    RPL7A   SEC16A  PRINS   FUT11   KIAA0913
RPS24   RPS3AP5 MRPL43  ARL3    SFR1    EIF6    CD151   RPL27A  MTRNR2L8
CKAP5   C1QTNF4 GANAB   PACS1   TMEM126B        UBE4A   ATP5L   DDX6    ERC1
C12orf57        PHB2    SCAF11  PFDN5   LRP1    APAF1   RPL18AP3        VPS29
SBNO1   GOLGA3  HMGB1   ZC3H13  ESD     ITM2B   CCNB1IP1        TEP1    DNAL1
SEL1L   DYNC1H1 MYO9A   SEC11A  MPG     SPSB3   NDUFB10 PGPEP1  MGRN1   ABCC1
RPS15A  NFATC3  CDYL2   RPL13   VPS53   RP13    TLCD2   WDR81   RPL26   TOM1L2
SUPT6H  RPL23A  TAOK1   TAF15   RPL19   CDK12   NKIRAS2 RPL27   NMT1    RPS7P11 CLTC
SUMO2   ANKRD12 C18orf32        RPL17   TPGS1   RPS15   NFIC    LONP1   HNRNPA1P10
BRD4    RPL18   NUCB1   RPL13A  ZNF587  RPS5    RRBP1   REM1    HM13    KIF3B
SCAND1  RALGAPB NCOA3   ADNP    TSHZ2   RPL12P4 UBE2G2  HMGB1P10        RP3     MPST
TNRC6B  TCF20   VCX3B   USP9X   GNL3L   RPS4X   COX7B   APOOL   RPL39   THOC2   XIAP
HCFC1

GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term

GO:0006415      1.69E-34        47.85437456     1.057919867     29      91
translational termination
```

GO:0006614	4.91E-34	41.1826087	1.22067677	30	105
SRP-dependent cotranslational protein targeting to membrane					
GO:0006613	6.78E-34	40.63787185	1.232302263	30	106
cotranslational protein targeting to membrane					
GO:0045047	6.78E-34	40.63787185	1.232302263	30	106
protein targeting to ER					

GO:0072599	6.78E-34	40.63787185	1.232302263	30	106
establishment of protein localization to endoplasmic reticulum					
GO:0006414	1.98E-32	39.00066263	1.22067677	29	105
translational elongation					
GO:0070972	2.52E-32	35.0666996	1.371808179	30	118
protein localization to endoplasmic reticulum					

```
GO:0000184	1.14E-30	32.90143885	1.383433672	29	119
"nuclear-transcribed mRNA catabolic process, nonsense-mediated decay"
```

```
GO:0006612	4.58E-30	26.26486778	1.778700436	31	153
protein targeting to membrane
```

```
GO:0019080	7.80E-29	25.44376572	1.75544945	30	151
viral genome expression
```

GO:0019083	7.80E-29	25.44376572	1.75544945	30	151
viral transcription					
GO:0006413	9.63E-29	25.23342837	1.767074943	30	152
translational initiation					
GO:0072594	2.63E-27	19.30369357	2.371600581	32	204
establishment of protein localization to organelle					

GO:0000956	2.74E-27	22.12073819	1.964708325	30	169	nuclear-transcribed mRNA catabolic process
GO:0043624	2.93E-27	23.82287074	1.778700436	29	153	cellular protein complex disassembly
GO:0043241	7.82E-27	22.8914171	1.836827901	29	158	protein complex disassembly

GO:0006402	1.39E-26	20.76233843	2.069337762	30	178	mRNA catabolic process
GO:0034623	1.44E-25	20.34244604	2.02283579	29	174	cellular macromolecular complex disassembly
GO:0032984	3.36E-25	19.65741007	2.080963255	29	179	macromolecular complex disassembly

GO:0022415	4.37E-25	15.1361723	3.022628192	33	260	viral reproductive process
GO:0006401	1.07E-24	17.52546584	2.383226074	30	205	RNA catabolic process
GO:0019058	2.47E-24	15.93332117	2.685488894	31	231	viral infectious cycle

GO:0016032	2.38E-22	9.816725647	5.243097364	38	451
viral reproduction					
GO:0071845	1.37E-21	12.54810883	3.301640025	31	284
cellular component disassembly at cellular level					
GO:0022411	2.08E-21	12.34928569	3.348141997	31	288

cellular component disassembly

GO:0033365	1.19E-20	8.97014847	5.498858211	37	473

protein localization to organelle

GO:0006605	1.28E-20	8.948975492	5.510483704	37	474

protein targeting

GO:0022613	2.26E-06	5.566737675	2.615735935	13	225

ribonucleoprotein complex biogenesis

GO:0071843 4.39E-06 5.216699971 2.778492838 13 239
cellular component biogenesis at cellular level

Tissue: Muscle_Skeletal=>Adipose_Subcutaneous Type: cluster
SourceGene: RP11-10B2.1(ENSG00000230916.1)
TargetGeneSet: MTND1P23 MTND2P28 NMNAT1 DFFA UBR4 LDLRAD2
HSPG2 KPNA7 THRAP3 RPS8 RPS15AP10 CCBL2 RPL5 RP11 ATP5F1
RPS27 ASH1L MEF2D COPA PRRC2C CEP350 NBAS PPP1CB UBC C1D AAK1
DCTN1 EIF5B MAP4K4 IL1RL2 RANBP2 UGGT1 MZT2B HAT1 HDLBP CRELD1
RPL15 MAP4 USP4 RAD54L2 RPL29 TMF1 PCNP RPL24 CNBP PDCD10
DNAJC19 AFAP1 BOD1L RELL1 CISD2 RPL34 RPS3A NIPBL CTD MRPS36
ERAP1 AFF4 SKP1 CTB MTND5P11 CTNNA1 PCDHGC5 TRIM41 GNB2L1
TMEM14C RPL15P3 DEK GPLD1 RPS10 RPL10A ZFAND3 MTRNR2L9 WDR11
BCKDHB PHACTR2 IGF2R FOXK1 PHF14 YWHAG CACNA2D1 RPS3AP26
TNPO3 MLL3 DRP2 HOOK3 RPS20 PAG1 RBM12B POLR2K TG TLN1 CLTA
XPA ATP6V1G1 RPL35 SETX RPL7A SEC16A PRINS FUT11 KIAA0913
RPS24 RPS3AP5 MRPL43 ARL3 SFR1 EIF6 CD151 RPL27A MTRNR2L8
CKAP5 C1QTNF4 GANAB PACS1 TMEM126B UBE4A ATP5L DDX6 ERC1
C12orf57 PHB2 SCAF11 PFDN5 LRP1 APAF1 RPL18AP3 VPS29
SBNO1 GOLGA3 HMGB1 ZC3H13 ESD ITM2B CCNB1IP1 TEP1 DNAL1
SEL1L DYNC1H1 MYO9A SEC11A MPG SPSB3 NDUFB10 PGPEP1 MGRN1 ABCC1
RPS15A NFATC3 CDYL2 RPL13 VPS53 RP13 TLCD2 WDR81 RPL26 TOM1L2
SUPT6H RPL23A TAOK1 TAF15 RPL19 CDK12 NKIRAS2 RPL27 NMT1 RPS7P11 CLTC
SUMO2 ANKRD12 C18orf32 RPL17 TPGS1 RPS15 NFIC LONP1 HNRNPA1P10
BRD4 RPL18 NUCB1 RPL13A ZNF587 RPS5 RRBP1 REM1 HM13 KIF3B

SCAND1 RALGAPB NCOA3 ADNP TSHZ2 RPL12P4 UBE2G2 HMGB1P10 RP3 MPST TNRC6B TCF20 VCX3B USP9X GNL3L RPS4X COX7B APOOL RPL39 THOC2 XIAP HCFC1

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0006415	1.69315822596365e-34	47.8543745648642	1.05791986713722	29	91	translational termination
GO:0006614	4.90507034226677e-34	41.1826086956522	1.22067676977372	30	105	SRP-dependent cotranslational protein targeting to membrane
GO:0006613	6.77765453932191e-34	40.6378718535469	1.23230226281918	30	106	cotranslational protein targeting to membrane
GO:0045047	6.77765453932191e-34	40.6378718535469	1.23230226281918	30	106	protein targeting to ER
GO:0072599	6.77765453932191e-34	40.6378718535469	1.23230226281918	30	106	establishment of protein localization to endoplasmic reticulum
GO:0006414	1.98171925672855e-32	39.0006626277925	1.22067676977372	29	105	translational elongation
GO:0070972	2.51687126500944e-32	35.0666996047431	1.37180817936475	30	118	protein localization to endoplasmic reticulum
GO:0000184	1.13652656807989e-30	32.9014388489209	1.38343367241021	29	119	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006612	4.57834943264373e-30	26.2648677755175	1.77870043595599	31	153	protein targeting to membrane
GO:0019080	7.79920054782776e-29	25.4437657204456	1.75544944986506	30	151	viral genome expression
GO:0019083	7.79920054782776e-29	25.4437657204456	1.75544944986506	30	151	viral transcription
GO:0006413	9.62642535139002e-29	25.2334283677833	1.76707494291053	30	152	translational initiation
GO:0072594	2.63344945567504e-27	19.3036935704514	2.37160058127465	32	204	establishment of protein localization to organelle
GO:0000956	2.74432847515856e-27	22.1207381920551	1.96470832468341	30	169	nuclear-transcribed mRNA catabolic process
GO:0043624	2.92947177317936e-27	23.8228707356695	1.77870043595599	29	153	cellular protein complex disassembly
GO:0043241	7.81569614070746e-27	22.891417098879	1.83682790118331	29	158	protein complex disassembly
GO:0006402	1.38563776211798e-26	20.7623384253819	2.06933776209259	30	178	mRNA catabolic process
GO:0034623	1.44028660172029e-25	20.3424460431655	2.02283578991073	29	174	cellular macromolecular complex disassembly
GO:0032984	3.3615600053829e-25	19.6574100719424	2.08096325513805	29	179	macromolecular complex disassembly
GO:0022415	4.36523592449143e-25	15.1361722956437	3.02262819182064	33	260	viral reproductive process
GO:0006401	1.06582774776324e-24	17.5254658385093	2.38322607432012	30	205	RNA catabolic process
GO:0019058	2.47279703702292e-24	15.9333211678832	2.68548889350218	31	231	viral infectious cycle
GO:0016032	2.38073510689295e-22	9.81672564723412	5.24309736350426	38	451	viral reproduction
GO:0071845	1.36745321225318e-21	12.5481088254811	3.30164002491177	31	284	cellular component disassembly at cellular level
GO:0022411	2.08232852202989e-21	12.3492856939987	3.34814199709363	31	288	cellular component disassembly
GO:0033365	1.19041863769823e-20	8.9701484697808	5.49885821050446	37	473	protein localization to organelle
GO:0006605	1.27947337289121e-20	8.94897549216553	5.51048370354993	37	474	protein targeting
GO:0022613	2.25613810346652e-06	5.56673767498478	2.6157359352294	13	225	ribonucleoprotein complex biogenesis
GO:0071843	4.3887913331541e-06	5.21669997145304	2.77849283786589	13	239	cellular component biogenesis at cellular level

Tissue: Muscle_Skeletal=>Adipose_Subcutaneous Type: asymmetric

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SourceGene:     RP11-809N8.5(ENSG00000256148.1)
TargetGeneSet:  MTND1P23        MTND2P28        DFFA    HSPG2   WASF2   THRAP3  MFI2
SZT2    RPS8    RPL5    RP11    ATP5F1  RPS27   ASH1L   PRRC2C  CEP350  CICP13
CDC42BPA        ADAM18  NBAS    ASXL2   AAK1    DCTN1   EIF5B   RANBP2  UGGT1
MZT2B   ANKRD44 FAM126B NBEAL1  COL4A4  NR2C2   RPL15   MAP4    USP4    RAD54L2
RPL29   PCNP    PHC3    DNAJC19 HTT     BOD1L   RELL1   DANCR   CISD2   RPL34
RPS3A   NIPBL   CTD     ERAP1   MAN2A1  AFF4    CTB     MTND5P11        RPS14
TRIM41  RPL15P3 DDX39B  ZFAND3  MTRNR2L9        WDR11   PHACTR2 IGF2R   FOXK1
HNRNPA1P8       RPS3AP26        TNPO3   MLL3    DRP2    HOOK3   RPS20   ARFGEF1 PAG1
RBM12B  SETX    RPL7A   SEC16A  PRINS   FUT11   KIAA0913        GBF1    CD151
RPL27A  MTRNR2L8        CKAP5   C1QTNF4 DDB1    PPP6R3  UBE4A   ATP5L   DDX6
KDM5A   ERC1    C12orf57        RECQL   SCAF11  MLL4    PFDN5   TMBIM4  SBNO1
GOLGA3  ZC3H13  COL4A2  COL4A2-AS1      CCNB1IP1        TEP1    C14orf21
STRN3   NIN     YLPM1   SEL1L   CCNK    CDC42BPB        BAHD1   MYO9A   SEC11A  NME3
NDUFB10 TSC2    RPS15A  CDYL2   RPL13   GAS8    VPS53   WDR81   ZZEF1   RPL26
TOM1L2  SUPT6H  RPL23A  TAOK1   CDK12   NKIRAS2 RPS7P11 CLTC    SUMO2   FN3KRP
ROCK1P1 ANKRD12 HNRNPA1P10      BRD4    RPSAP58 RPL18   RPL13A  ZNF587  REM1
KIF3B   RALGAPB NCOA3   RPL12P4 UBE2G2  HMGB1P10        MPST    EIF3L   USP9X
KDM5C   HUWE1   GNL3L   RPS4X   COX7B   RPL39   HCFC1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006614      4.92329849393982e-22    33.185789167152 0.879177911563214       20
105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      6.02762935647183e-22    32.7976053419295        0.887551034530482
20      106     cotranslational protein targeting to membrane
GO:0045047      6.02762935647183e-22    32.7976053419295        0.887551034530482
20      106     protein targeting to ER
GO:0072599      6.02762935647183e-22    32.7976053419295        0.887551034530482
20      106     establishment of protein localization to endoplasmic reticulum
GO:0006415      8.71361094645675e-22    36.8875272331155        0.761954190021452
19      91      translational termination
GO:0070972      5.84034084046466e-21    28.757324712063 0.988028510137707       20
118     protein localization to endoplasmic reticulum
GO:0006414      1.60244186277121e-20    30.8522571819425        0.879177911563214
19      105     translational elongation
GO:0006413      4.88828125182033e-20    22.7617557251908        1.27271469102484
21      152     translational initiation
GO:0000184      1.95056941221635e-19    26.506862745098 0.996401633104975       19
119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006612      1.25287033764925e-18    21.1374972083675        1.28108781399211
20      153     protein targeting to membrane
GO:0000956      9.3458581385066e-18     18.8464349790684        1.41505778146841
20      169     nuclear-transcribed mRNA catabolic process
GO:0019080      2.02829989637344e-17    20.0357991681521        1.26434156805757
19      151     viral genome expression
GO:0019083      2.02829989637344e-17    20.0357991681521        1.26434156805757
19      151     viral transcription
GO:0072594      2.44165470363414e-17    16.234262295082 1.70811708532281        21
204     establishment of protein localization to organelle
GO:0043624      2.61108758813079e-17    19.7339771729587        1.28108781399211
19      153     cellular protein complex disassembly
GO:0006402      2.64029367412081e-17    17.7616242636922        1.49041588817383
20      178     mRNA catabolic process
GO:0043241      4.83217148446209e-17    19.017421357032 1.32295342882845        19
158     protein complex disassembly
GO:0034623      3.01775072241743e-16    17.0351043643264        1.45692339630475
19      174     cellular macromolecular complex disassembly
GO:0006401      4.3132110232671e-16     15.1404870216751        1.71649020829008
20      205     RNA catabolic process
GO:0032984      5.14684970725644e-16    16.4969362745098        1.4987890111411 19
179     macromolecular complex disassembly
GO:0033365      1.52662954937172e-15    8.94160862513119        3.9604871635181 27
473     protein localization to organelle
GO:0022415      3.46075199164941e-15    12.3812133891213        2.17701197148986
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21      260     viral reproductive process
GO:0006605      1.42515940146057e-14    8.48054511278196        3.96886028648536
26      474     protein targeting
GO:0019058      5.78076611768289e-14    12.4048279689234        1.93419140543907
19      231     viral infectious cycle
GO:0071845      2.25182775650332e-13    10.5505550555056        2.37796692270431
20      284     cellular component disassembly at cellular level
GO:0022411      2.9273467923705e-13     10.3901285650953        2.41145941457339
20      288     cellular component disassembly
GO:0016032      2.00252277318165e-11    7.2007252007252 3.77627845823818        22
451     viral reproduction
GO:0022613      1.92112304952327e-05    5.91451917033312        1.88395266763546
10      225     ribonucleoprotein complex biogenesis
Tissue: Muscle_Skeletal=>Adipose_Subcutaneous   Type:   cluster
SourceGene:     RP11-809N8.5(ENSG00000256148.1)
TargetGeneSet:  MTND1P23        MTND2P28        DFFA    HSPG2   WASF2   THRAP3  MFI2
SZT2    RPS8    RPL5    RP11    ATP5F1  RPS27   ASH1L   PRRC2C  CEP350  CICP13
CDC42BPA        ADAM18  NBAS    ASXL2   AAK1    DCTN1   EIF5B   RANBP2  UGGT1
MZT2B   ANKRD44 FAM126B NBEAL1  COL4A4  NR2C2   RPL15   MAP4    USP4    RAD54L2
RPL29   PCNP    PHC3    DNAJC19 HTT     BOD1L   RELL1   DANCR   CISD2   RPL34
RPS3A   NIPBL   CTD     ERAP1   MAN2A1  AFF4    CTB     MTND5P11        RPS14
TRIM41  RPL15P3 DDX39B  ZFAND3  MTRNR2L9        WDR11   PHACTR2 IGF2R   FOXK1
HNRNPA1P8       RPS3AP26        TNPO3   MLL3    DRP2    HOOK3   RPS20   ARFGEF1 PAG1
RBM12B  SETX    RPL7A   SEC16A  PRINS   FUT11   KIAA0913        GBF1    CD151
RPL27A  MTRNR2L8        CKAP5   C1QTNF4 DDB1    PPP6R3  UBE4A   ATP5L   DDX6
KDM5A   ERC1    C12orf57        RECQL   SCAF11  MLL4    PFDN5   TMBIM4  SBNO1
GOLGA3  ZC3H13  COL4A2  COL4A2-AS1      CCNB1IP1        TEP1    C14orf21
STRN3   NIN     YLPM1   SEL1L   CCNK    CDC42BPB        BAHD1   MYO9A   SEC11A  NME3
NDUFB10 TSC2    RPS15A  CDYL2   RPL13   GAS8    VPS53   WDR81   ZZEF1   RPL26
TOM1L2  SUPT6H  RPL23A  TAOK1   CDK12   NKIRAS2 RPS7P11 CLTC    SUMO2   FN3KRP
ROCK1P1 ANKRD12 HNRNPA1P10      BRD4    RPSAP58 RPL18   RPL13A  ZNF587  REM1
KIF3B   RALGAPB NCOA3   RPL12P4 UBE2G2  HMGB1P10        MPST    EIF3L   USP9X
KDM5C   HUWE1   GNL3L   RPS4X   COX7B   RPL39   HCFC1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006614      4.92329849393982e-22    33.185789167152 0.879177911563214       20
105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      6.02762935647183e-22    32.7976053419295        0.887551034530482
20      106     cotranslational protein targeting to membrane
GO:0045047      6.02762935647183e-22    32.7976053419295        0.887551034530482
20      106     protein targeting to ER
GO:0072599      6.02762935647183e-22    32.7976053419295        0.887551034530482
20      106     establishment of protein localization to endoplasmic reticulum
GO:0006415      8.71361094645675e-22    36.8875272331155        0.761954190021452
19      91      translational termination
GO:0070972      5.84034084046466e-21    28.757324712063 0.988028510137707       20
118     protein localization to endoplasmic reticulum
GO:0006414      1.60244186277121e-20    30.8522571819425        0.879177911563214
19      105     translational elongation
GO:0006413      4.88828125182033e-20    22.7617557251908        1.27271469102484
21      152     translational initiation
GO:0000184      1.95056941221635e-19    26.506862745098 0.996401633104975       19
119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006612      1.25287033764925e-18    21.1374972083675        1.28108781399211
20      153     protein targeting to membrane
GO:0000956      9.3458581385066e-18     18.8464349790684        1.41505778146841
20      169     nuclear-transcribed mRNA catabolic process
GO:0019080      2.02829989637344e-17    20.0357991681521        1.26434156805757
19      151     viral genome expression
GO:0019083      2.02829989637344e-17    20.0357991681521        1.26434156805757
19      151     viral transcription
GO:0072594      2.44165470363414e-17    16.234262295082 1.70811708532281        21
204     establishment of protein localization to organelle
GO:0043624      2.61108758813079e-17    19.7339771729587        1.28108781399211
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19      153     cellular protein complex disassembly
GO:0006402      2.64029367412081e-17    17.7616242636922        1.49041588817383
20      178     mRNA catabolic process
GO:0043241      4.83217148446209e-17    19.017421357032 1.32295342882845        19
158     protein complex disassembly
GO:0034623      3.01775072241743e-16    17.0351043643264        1.45692339630475
19      174     cellular macromolecular complex disassembly
GO:0006401      4.3132110232671e-16     15.1404870216751        1.7164902082900 8
20      205     RNA catabolic process
GO:0032984      5.14684970725644e-16    16.4969362745098        1.4987890111411 19
179     macromolecular complex disassembly
GO:0033365      1.52662954937172e-15    8.94160862513119        3.9604871635181 27
473     protein localization to organelle
GO:0022415      3.46075199164941e-15    12.3812133891213        2.17701197148986
21      260     viral reproductive process
GO:0006605      1.42515940146057e-14    8.48054511278196        3.96886028648536
26      474     protein targeting
GO:0019058      5.78076611768289e-14    12.4048279689234        1.93419140543907
19      231     viral infectious cycle
GO:0071845      2.25182775650332e-13    10.5505550555056        2.37796692270431
20      284     cellular component disassembly at cellular level
GO:0022411      2.9273467923705e-13     10.3901285650953        2.41145941457339
20      288     cellular component disassembly
GO:0016032      2.00252277318165e-11    7.2007252007252 3.77627845823818        22
451     viral reproduction
GO:0022613      1.92112304952327e-05    5.91451917033312        1.88395266763546
10      225     ribonucleoprotein complex biogenesis
Tissue: Adipose_Subcutaneous=>Nerve_Tibial      Type:   asymmetric
SourceGene:     ALDH1B1(ENSG00000137124.5)
TargetGeneSet:  RPL11   RPS27   PKLR    GAS5    RPL14   CADM2-AS1       RP11
SCRG1   RPS10   RPS20   RPL30   RPL12   RPL7A   PCBD1   RPL6    RPL7AP6 SNRPN
GOLGA6L4        RPL26   ACACA   RPL19   NETO1   HPN     NKG7    RPL28   LSS
EIF3L   GPC4    RPL10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      2.36525599733211e-23    217.409090909091        0.151131409591032
13      91      translational termination
GO:0006414      1.70532207841082e-22    184.145256916996        0.17438239568196
13      105     translational elongation
GO:0006614      1.70532207841082e-22    184.145256916996        0.17438239568196
13      105     SRP-dependent cotranslational protein targeting to membrane
GO:0019080      1.79407676843101e-22    146.029197080292        0.250778492837866
14      151     viral genome expression
GO:0019083      1.79407676843101e-22    146.029197080292        0.250778492837866
14      151     viral transcription
GO:0006613      1.94231758806374e-22    182.152492668622        0.17604318040274
13      106     cotranslational protein targeting to membrane
GO:0045047      1.94231758806374e-22    182.152492668622        0.17604318040274
13      106     protein targeting to ER
GO:0072599      1.94231758806374e-22    182.152492668622        0.17604318040274
13      106     establishment of protein localization to endoplasmic reticulum
GO:0006413      1.97479609705954e-22    144.960869565217        0.252439277558646
14      152     translational initiation
GO:0070972      8.41874403674507e-22    161.2   0.195972597052107       13      118
protein localization to endoplasmic reticulum
GO:0000184      9.44450207397793e-22    159.668096054889        0.197633381772888
13      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006612      2.82503658286128e-20    120.604545454545        0.254100062279427
13      153     protein targeting to membrane
GO:0043624      2.82503658286128e-20    120.604545454545        0.254100062279427
13      153     cellular protein complex disassembly
GO:0043241      4.34944305560692e-20    116.405015673981        0.26240398588333
13      158     protein complex disassembly
GO:0019058      8.15435952605171e-20    91.6774193548387        0.383641270500311
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14      231     viral infectious cycle
GO:0000956      1.07082145951018e-19    108.113636363636        0.280672617811916
13      169     nuclear-transcribed mRNA catabolic process
GO:0034623      1.58064540448204e-19    104.719367588933        0.288976541415819
13      174     cellular macromolecular complex disassembly
GO:0006402      2.14045600967934e-19    102.152066115702        0.295619680298941
13      178     mRNA catabolic process
GO:0032984      2.30643262079744e-19    101.529572836802        0.297280465019722
13      179     macromolecular complex disassembly
GO:0022415      4.38531556145992e-19    80.7048780487805        0.431804027402948
14      260     viral reproductive process
GO:0072594      1.3107907802754e-18     88.0856734888148        0.338800083039236
13      204     establishment of protein localization to organelle
GO:0006401      1.39854045986023e-18    87.6207386363636        0.340460867760017
13      205     RNA catabolic process
GO:0071845      1.53203446987607e-18    73.4066666666667        0.471662860701682
14      284     cellular component disassembly at cellular level
GO:0022411      1.86706634090778e-18    72.314598540146 0.478305999584804       14
288     cellular component disassembly
GO:0016032      1.00514907255067e-15    44.8192219679634        0.749013909072037
14      451     viral reproduction
GO:0033365      7.55931581953024e-14    35.8835968379447        0.785551172929209
13      473     protein localization to organelle
GO:0006605      7.76682818723057e-14    35.8031946361664        0.78721195764999
13      474     protein targeting
GO:0042273      8.76835229964862e-07    228.857142857143        0.0199294166493668
3       12      ribosomal large subunit biogenesis
Tissue: Adipose_Subcutaneous=>Nerve_Tibial      Type:   asymmetric
SourceGene:     CNN1(ENSG00000130176.2)
TargetGeneSet:  RPL11   RP11    RPS27   BCL11A  RPL14   EPB41L4A        FAM135A
MRPS12  RPS20   OTUD6B  RPL30   TATDN1  KLC2    VWA5A   CTD     ALDH3A1 ACACA
RPL17   RPL19   RSL24D1P11      UBA52   RPL28   PCBP3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      2.42067264909835e-16    196.90243902439 0.107051415126981       9
91      translational termination
GO:0006414      9.216208669879e-16      168.0234375     0.123520863608055       9
105     translational elongation
GO:0006614      9.216208669879e-16      168.0234375     0.123520863608055       9
105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.00662717500152e-15    166.279639175258        0.124697252785274
9       106     cotranslational protein targeting to membrane
GO:0045047      1.00662717500152e-15    166.279639175258        0.124697252785274
9       106     protein targeting to ER
GO:0072599      1.00662717500152e-15    166.279639175258        0.124697252785274
9       106     establishment of protein localization to endoplasmic reticulum
GO:0070972      2.72424673952409e-15    147.849770642202        0.138813922911909
9       118     protein localization to endoplasmic reticulum
GO:0000184      2.94566104471822e-15    146.495454545455        0.139990312089129
9       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      2.64338118996e-14       113.228873239437        0.177634765760155
9       151     viral genome expression
GO:0019083      2.64338118996e-14       113.228873239437        0.177634765760155
9       151     viral transcription
GO:0006413      2.80833544815286e-14    112.429195804196        0.178811154937375
9       152     translational initiation
GO:0006612      2.98235641610268e-14    111.640625      0.179987544114594       9
153     protein targeting to membrane
GO:0043624      2.98235641610268e-14    111.640625      0.179987544114594       9
153     cellular protein complex disassembly
GO:0043241      4.00419344287656e-14    107.856543624161        0.185869490000692
9       158     protein complex disassembly
GO:0000956      7.41056323208651e-14    100.3640625     0.198809770950107       9
169     nuclear-transcribed mRNA catabolic process
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GO:0034623      9.67098404549803e-14    97.2886363636364        0.204691716836205
9       174     cellular macromolecular complex disassembly
GO:0006402      1.1899244880822e-13     94.9593195266272        0.209397273545083
9       178     mRNA catabolic process
GO:0032984      1.25228968636938e-13    94.3941176470588        0.210573662722303
9       179     macromolecular complex disassembly
GO:0072594      4.11396147908514e-13    82.1480769230769        0.239983392152792
9       204     establishment of protein localization to organelle
GO:0006401      4.3006982319074e-13     81.7232142857143        0.241159781330012
9       205     RNA catabolic process
GO:0019058      1.26875360582069e-12    72.0202702702703        0.271745899937721
9       231     viral infectious cycle
GO:0022415      3.68969869097354e-12    63.5692231075697        0.305861186077088
9       260     viral reproductive process
GO:0071845      8.16598085479159e-12    57.9231818181818        0.334094526330358
9       284     cellular component disassembly at cellular level
GO:0022411      9.25924200927783e-12    57.0766129032258        0.338800083039236
9       288     cellular component disassembly
GO:0016032      5.05270111811315e-10    35.6131221719457        0.530551518926026
9       451     viral reproduction
GO:0033365      7.69883716810493e-10    33.8712284482759        0.556432080824856
9       473     protein localization to organelle
GO:0006605      7.84382676642097e-10    33.7959677419355        0.557608470002076
9       474     protein targeting
Tissue: Nerve_Tibial=>Adipose_Subcutaneous      Type:   asymmetric
SourceGene:     ENSG00000231312.2
TargetGeneSet:  AGRN    RPL11   MED8    PRPF38A STXBP3  RP11    PFDN2   TOMM20
NRBP1   UBC     RPL37A  DNPEP   RPL32   RPL14   SS18L2  RTP3    RPL24   RPL35A
MRPS30  BTF3    TBCA    HDAC3   MRPL22  TDP2    COX11P1 LY6G6C  LYPLA2P1
MRPS12  PSMB1   DGKB    RP1     TMEM68  RPS20   RPL30   LURAP1L RPS6    CCDC107
PSMB7   RPL35   RPL12   WDR5    EIF3M   POLR2G  LTBP2   OVOL1   RPS25   KCNA5
RPL41   NUP37   C12orf73        RFXAP   MED6    DEGS2   NOP10   CDAN1   PARP16
RPL35AP32       AAGAB   RPS17L  NTRK3   PDIA2   CCP110  LCMT1   ZFHX3   AATF
RPL17   RPL19   KRT23   DNAJC7  UTP18   PTPN2   CASP14  SBSN    KLK7    LINC00493
U2AF1   COL18A1 MTMR3   PLA2G3  DRG1    NHP2L1  RPS4X   IGSF1   MOSPD1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      7.30962476000486e-25    67.8461538461538        0.440799944640509
18      91      translational termination
GO:0070972      2.11551730701453e-24    53.7448999801941        0.571586741401979
19      118     protein localization to endoplasmic reticulum
GO:0006414      1.18173310704828e-23    56.8726790450928        0.508615320739049
18      105     translational elongation
GO:0006614      1.18173310704828e-23    56.8726790450928        0.508615320739049
18      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.4185688397062e-23     56.222465034965 0.513459276174659       18
106     cotranslational protein targeting to membrane
GO:0045047      1.4185688397062e-23     56.222465034965 0.513459276174659       18
106     protein targeting to ER
GO:0072599      1.4185688397062e-23     56.222465034965 0.513459276174659       18
106     establishment of protein localization to endoplasmic reticulum
GO:0000184      1.29820820228028e-22    48.9413556740289        0.576430696837589
18      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      2.90784919987631e-22    40.2155377302436        0.731437270777109
19      151     viral genome expression
GO:0019083      2.90784919987631e-22    40.2155377302436        0.731437270777109
19      151     viral transcription
GO:0006413      3.31201462109142e-22    39.9103641456583        0.736281226212719
19      152     translational initiation
GO:0006612      3.76883575150336e-22    39.6097453906936        0.741125181648329
19      153     protein targeting to membrane
GO:0043624      1.45617067757464e-20    36.5282051282051        0.741125181648329
18      153     cellular protein complex disassembly
GO:0043241      2.64230363399189e-20    35.2112637362637        0.765344958826379
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18      158     protein complex disassembly
GO:0000956      9.14426211627071e-20    32.6209882832399        0.818628468618089
18      169     nuclear-transcribed mRNA catabolic process
GO:0072594      1.01281337619908e-19    28.58759936407  0.988166908864438       19
204     establishment of protein localization to organelle
GO:0034623      1.56212869138555e-19    31.564349112426 0.842848245796139       18
174     cellular macromolecular complex disassembly
GO:0006402      2.36916065429315e-19    30.7665865384615        0.862224067538579
18      178     mRNA catabolic process
GO:0032984      2.6249639709827e-19     30.5733397037745        0.867068022974189
18      179     macromolecular complex disassembly
GO:0022415      4.40429713301696e-19    23.5683333333333        1.2594284132586 20
260     viral reproductive process
GO:0019058      1.08752417944434e-18    24.8992785793563        1.11895370562591
19      231     viral infectious cycle
GO:0006401      3.09399941062075e-18    26.2743726861374        0.993010864300048
18      205     RNA catabolic process
GO:0016032      6.20298111973668e-18    15.9534201630543        2.18462390146011
23      451     viral reproduction
GO:0071845      1.03446605192964e-15    18.3682764603817        1.37568334371324
18      284     cellular component disassembly at cellular level
GO:0022411      1.32254325251912e-15    18.0910256410256        1.39505916545568
18      288     cellular component disassembly
GO:0006605      3.8290047218012e-15     13.1769157994324        2.29603487647914
21      474     protein targeting
GO:0033365      4.76779668040605e-14    12.2984547461369        2.29119092104353
20      473     protein localization to organelle
GO:0042254      2.34275810998796e-09    17.0767386091127        0.721749359905889
10      149     ribosome biogenesis
GO:0022613      9.86397295395444e-09    12.3425471249802        1.08988997301225
11      225     ribonucleoprotein complex biogenesis
GO:0071843      1.84432686540542e-08    11.5732233125186        1.15770534911079
11      239     cellular component biogenesis at cellular level
GO:0006364      6.74004146267171e-07    16.3619702176403        0.503771365303439
7       104     rRNA processing
GO:0016072      9.86739548870654e-07    15.4023732470334        0.532835097917099
7       110     rRNA metabolic process
GO:0000028      2.15448756952043e-06    214.597014925373        0.02906373261366
3       6       ribosomal small subunit assembly
Tissue: Nerve_Tibial=>Adipose_Subcutaneous      Type:   asymmetric
SourceGene:     ENSG00000233702.1
TargetGeneSet:  RPL22   DLEU2L  DPYD    RTCD1   GNRHR2  RP11    RPL37A  RPL32
PTPN23  SLC52A1 PVRL3-AS1       RPL35A  NKX3-2  EEF1A1P19       RPS14   EEF1A1
HOXA13  PEG10   AHCYL2  RPS20   RPL30   TATDN1  NELL1   RPS13   WNK1    ATN1
PRPF40B RPL41   RPL14P1 CAMTA2  CEP95   SMARCA4 ARHGEF1 SNRPD2  RPS11   PI4KA
TMEM184B        UBA1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      8.48006399289468e-17    88.2402015677492        0.21797799460245
11      105     translational elongation
GO:0006415      1.59771081355511e-15    88.5185185185185        0.18891426198879
10      91      translational termination
GO:0019080      5.16753494456863e-15    59.0567669172932        0.313473116047332
11      151     viral genome expression
GO:0019083      5.16753494456863e-15    59.0567669172932        0.313473116047332
11      151     viral transcription
GO:0006614      7.04569488407382e-15    75.4    0.21797799460245        10      105
SRP-dependent cotranslational protein targeting to membrane
GO:0006613      7.76977716994345e-15    74.609375       0.220053975503425       10
106     cotranslational protein targeting to membrane
GO:0045047      7.76977716994345e-15    74.609375       0.220053975503425       10
106     protein targeting to ER
GO:0072599      7.76977716994345e-15    74.609375       0.220053975503425       10
106     establishment of protein localization to endoplasmic reticulum
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GO:0070972      2.34128555621209e-14    66.2638888888889        0.244965746315134
10      118     protein localization to endoplasmic reticulum
GO:0034623      2.51352674312269e-14    50.6419115272845        0.361220676769774
11      174     cellular macromolecular complex disassembly
GO:0000184      2.55284572541155e-14    65.651376146789 0.24704172721611        10
119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0032984      3.44329372861052e-14    49.1174812030075        0.371600581274652
11      179     macromolecular complex disassembly
GO:0006413      3.08501908715246e-13    50.2781690140845        0.315549096948308
10      152     translational initiation
GO:0006612      3.29656753823955e-13    49.9230769230769        0.317625077849284
10      153     protein targeting to membrane
GO:0043624      3.29656753823955e-13    49.9230769230769        0.317625077849284
10      153     cellular protein complex disassembly
GO:0043241      4.56222333399732e-13    48.2195945945946        0.328004982354162
10      158     protein complex disassembly
GO:0019058      5.73980054119701e-13    37.3710526315789        0.479551588125389
11      231     viral infectious cycle
GO:0000956      8.99047406816903e-13    44.8490566037736        0.350840772264895
10      169     nuclear-transcribed mRNA catabolic process
GO:0006402      1.51432237195242e-12    42.4196428571429        0.369524600373677
10      178     mRNA catabolic process
GO:0022415      2.09096768632073e-12    32.9511731135067        0.539755034253685
11      260     viral reproductive process
GO:0071845      5.46196938724066e-12    30.0034702139965        0.589578575877102
11      284     cellular component disassembly at cellular level
GO:0072594      5.92154903042295e-12    36.6675257731959        0.423500103799045
10      204     establishment of protein localization to organelle
GO:0006401      6.21729949789748e-12    36.4769230769231        0.425576084700021
10      205     RNA catabolic process
GO:0022411      6.35672814117802e-12    29.5618468554057        0.597882499481005
11      288     cellular component disassembly
GO:0016032      7.74981439820864e-10    18.3960526315789        0.936267386340046
11      451     viral reproduction
GO:0033365      2.14146811280286e-08    15.07343412527  0.981938966161511       10
473     protein localization to organelle
GO:0006605      2.18479789659218e-08    15.0398706896552        0.984014947062487
10      474     protein targeting
Tissue: Nerve_Tibial=>Adipose_Subcutaneous      Type:   asymmetric
SourceGene:     FAM179A(ENSG00000189350.7)
TargetGeneSet:  RPL22   RPL11   WDR65   RPS8    RPL5    RP11    SSR2    NENF    MYCN
FAM179A RPLP0P6 UBC     RPL31   CLASP1  LIMS2   MAP2    SPAG16  RPL37A  RPL32
RPL15   RPL14   ZNF90P1 RPL24   PVRL3-AS1       RPL35A  MSANTD1 RPL34   EEF1A1P19
CTD     BTF3    RPS14   CCNG1   TMEM14C RPS10   RPL10A  EEF1A1  MRPS12  TNRC18
HOXA13  RABL5   PPAPDC1B        RPS20   RPL30   EIF3H   CPSF1   RABGAP1 RPL7A
RPS24   C10orf32        PNLIPRP3        OR51C1P RPS13   RIMKLB  PFDN5   RPL41   NACA
RPL6    TPT1    SLC25A21        CNIH    TIMM9   RSL24D1 RPL4    SKOR1   RPS15A
RPL23A  RPL17   RPL19   ROCK1   ELP2    SMARCA4 NOTCH3  RPL18A  ARHGEF1 SNRPD2
RPL18   RPS11   C20orf96        EBF4    LINC00493       RP4     DRG1    EIF3L
RPS4X   RPSAP9  RPL10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      1.6459967607858e-57     188.263157894737        0.530413120199294
35      105     translational elongation
GO:0006415      1.70215030519587e-55    203.689655172414        0.459691370839388
33      91      translational termination
GO:0006614      2.97791640187156e-55    175.672806067172        0.530413120199294
34      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      4.37258017281276e-55    173.220797720798        0.535464673725002
34      106     cotranslational protein targeting to membrane
GO:0045047      4.37258017281276e-55    173.220797720798        0.535464673725002
34      106     protein targeting to ER
GO:0072599      4.37258017281276e-55    173.220797720798        0.535464673725002
34      106     establishment of protein localization to endoplasmic reticulum
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GO:0070972      3.19846385812202e-53    148.350427350427        0.596083316033493
34      118     protein localization to endoplasmic reticulum
GO:0006413      5.33433800978301e-51    112.266081871345        0.76783613590755
35      152     translational initiation
GO:0000184      6.31192773072493e-51    137.103488372093        0.6011348695592 33
119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006612      6.8986947491144e-51     111.306868867083        0.772887689433257
35      153     protein targeting to membrane
GO:0019080      4.50595972262906e-49    106.262108262108        0.762784582381842
34      151     viral genome expression
GO:0019083      4.50595972262906e-49    106.262108262108        0.762784582381842
34      151     viral transcription
GO:0043624      7.42318269568848e-49    104.461538461538        0.772887689433257
34      153     cellular protein complex disassembly
GO:0034623      1.01940428041778e-48    94.3515713744794        0.878970313473116
35      174     cellular macromolecular complex disassembly
GO:0043241      2.50444397395419e-48    100.214226633581        0.798145457061795
34      158     protein complex disassembly
GO:0032984      3.0282059262799e-48     91.0434941520468        0.904228081101654
35      179     macromolecular complex disassembly
GO:0072594      4.38413104884357e-46    77.4392712550607        1.03051691924434
35      204     establishment of protein localization to organelle
GO:0000956      2.7940988881495e-45     86.3944852941176        0.853712545844578
33      169     nuclear-transcribed mRNA catabolic process
GO:0006402      1.81051505713781e-44    80.9808620689655        0.899176527575946
33      178     mRNA catabolic process
GO:0071845      1.75932632861188e-42    55.4359197907585        1.43464120130095
36      284     cellular component disassembly at cellular level
GO:0006401      2.76505748599724e-42    68.1392441860465        1.03556847277005
33      205     RNA catabolic process
GO:0022411      2.97990060333806e-42    54.5405405405405        1.45484741540378
36      288     cellular component disassembly
GO:0019058      3.00185284970202e-42    62.7559547051933        1.16690886443845
34      231     viral infectious cycle
GO:0022415      2.08782623158343e-40    54.5913319718629        1.31340391668397
34      260     viral reproductive process
GO:0033365      8.01380570191847e-33    29.3138668589281        2.38938481765968
35      473     protein localization to organelle
GO:0006605      8.62989115072256e-33    29.2449946049634        2.39443637118538
35      474     protein targeting
GO:0016032      4.52561273743294e-32    29.1873578060628        2.27825064009411
34      451     viral reproduction
GO:0022613      1.2057844796455e-09     13.0824290002309        1.1365995432842 12
225     ribonucleoprotein complex biogenesis
GO:0071843      2.39667406935383e-09    12.2634505669098        1.20732129264411
12      239     cellular component biogenesis at cellular level
GO:0042254      3.57386137050076e-09    16.2601347493434        0.752681475330427
10      149     ribosome biogenesis
GO:0042273      2.87680213437773e-07    104.130434782609        0.0606186423084908
4       12      ribosomal large subunit biogenesis
GO:0006364      9.00074231039749e-07    15.614964073727 0.525361566673587       7
104     rRNA processing
GO:0016072      1.31627386519054e-06    14.6991762283024        0.555670887827832
7       110     rRNA metabolic process
GO:0030490      4.26634606660256e-06    154.007142857143        0.0353608746799529
3       7       maturation of SSU-rRNA
Tissue: Adipose_Subcutaneous=>Nerve_Tibial      Type:   asymmetric
SourceGene:     GGPS1(ENSG00000152904.7)
TargetGeneSet:  PRDM16  RPL11   PABPC4  RPS8    RPL5    CCDC18  RP11    RP4
FAM20B  ARL8A   SCN9A   C2orf88 CFLAR-AS1       EEF1B2  CTDSPL  RPL14   CEP97
IGSF11  KPNA1   SNX4    EIF4G1  EIF4A2  TIGD2   ARFIP1  TBC1D9B TRIM38  RPS10
RPL10A  FOXP4   PAQR8   L3MBTL3 MRPS12  SERAC1  BCAP29  RPS20   EEF1D   SCRIB   RPS6
GRHPR   NANS    TLR4    RPL7A   RPL13AP5        ACTR1A  RPLP2   RPL27A  CTD
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PTPRJ   EHD1    PPP2R5B RAB6A   RPS3    LETMD1  ERBB3   RPL41   MARS    RPL6    EFS
U6      TBC1D2B MIR1225 ROGDI   RPS15A  RPL26   RPL23A  CCL18   RPL17   FAM171A2
KPNA2   FOXK2   TWSG1   TCF3    RPL36   ELAVL1  UBA52   RPS16   HIPK4   TOMM40
PPM1N   RPL18   TTYH1   RPL28   ARFGAP3 FAM19A5 MOV10L1 GPC4
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      5.08858156509752e-37    101.576704545455        0.501349387585634
25      105     translational elongation
GO:0006415      1.13805039329915e-34    105.25  0.434502802574216       23      91
translational termination
GO:0000184      1.38536212841634e-33    80.2077192982456        0.568195972597052
24      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006614      4.54893549397025e-33    87.1951219512195        0.501349387585634
23      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      5.79164416485982e-33    86.1385542168675        0.506124143657878
23      106     cotranslational protein targeting to membrane
GO:0045047      5.79164416485982e-33    86.1385542168675        0.506124143657878
23      106     protein targeting to ER
GO:0072599      5.79164416485982e-33    86.1385542168675        0.506124143657878
23      106     establishment of protein localization to endoplasmic reticulum
GO:0006413      1.27574770764564e-32    63.775053686471 0.725762922981109       25
152     translational initiation
GO:0070972      8.71259019175334e-32    75.1947368421053        0.563421216524808
23      118     protein localization to endoplasmic reticulum
GO:0000956      2.1436292027501e-31     56.1789772727273        0.806933776209259
25      169     nuclear-transcribed mRNA catabolic process
GO:0006401      7.258606590239e-31      47.9768741067949        0.978824994810048
26      205     RNA catabolic process
GO:0006402      8.43308013765557e-31    52.8409090909091        0.849906580859456
25      178     mRNA catabolic process
GO:0072594      2.98468906509292e-29    45.0831640426613        0.974050238737804
25      204     establishment of protein localization to organelle
GO:0019080      3.8827124741542e-29     55.6796875      0.720988166908864       23
151     viral genome expression
GO:0019083      3.8827124741542e-29     55.6796875      0.720988166908864       23
151     viral transcription
GO:0006612      5.35128619543073e-29    54.8153846153846        0.730537679053353
23      153     protein targeting to membrane
GO:0043624      5.35128619543073e-29    54.8153846153846        0.730537679053353
23      153     cellular protein complex disassembly
GO:0043241      1.16992369186893e-28    52.7666666666667        0.754411459414573
23      158     protein complex disassembly
GO:0034623      1.20400417720169e-27    47.1225165562914        0.83080755657048
23      174     cellular macromolecular complex disassembly
GO:0032984      2.37796437734916e-27    45.5961538461538        0.8546813369317 23
179     macromolecular complex disassembly
GO:0019058      2.82782745493207e-26    36.5217391304348        1.1029686526884 24
231     viral infectious cycle
GO:0022415      5.10160442095071e-25    31.9683615819209        1.24143657878348
24      260     viral reproductive process
GO:0071845      4.34119211381525e-24    28.9682051282051        1.35603072451733
24      284     cellular component disassembly at cellular level
GO:0033365      5.78442278102426e-24    21.3886544258701        2.25845962217148
28      473     protein localization to organelle
GO:0022411      6.08552141405383e-24    28.5212121212121        1.37512974880631
24      288     cellular component disassembly
GO:0006605      6.13020669156525e-24    21.3391665755223        2.26323437824372
28      474     protein targeting
GO:0016032      2.51014901109774e-19    17.4301327088212        2.15341498858211
24      451     viral reproduction
GO:0042273      2.2890049584565e-07     110.569230769231        0.0572970728669296
4       12      ribosomal large subunit biogenesis
GO:0042254      5.19842752494549e-07    13.2459016393443        0.711438654764376
8       149     ribosome biogenesis
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GO:0006364      6.10181228854743e-07    16.6270369138676        0.49657463151339
7       104     rRNA processing
GO:0016072      8.93626842774286e-07    15.651894769809 0.525223167946855       7
110     rRNA metabolic process
GO:0022613      1.15438184485564e-06    9.8375  1.07432011625493        9       225
ribonucleoprotein complex biogenesis
GO:0071843      1.90358788834925e-06    9.2295652173913 1.14116670126635        9
239     cellular component biogenesis at cellular level
Tissue: Nerve_Tibial=>Adipose_Subcutaneous      Type:   asymmetric
SourceGene:     HIVEP1(ENSG00000095951.11)
TargetGeneSet:  RP3     RP1     RPS8    BTF3L4  WDR78   RP11    RP4     GNG5    RPL5
RWDD3   STXBP3  HSD3BP4 ATF6    PRRC2C  MRPL55  RPS7    CALM2   UBC     COA5
TXNDC9  MMADHC  MTX2    SENP2   HIGD1A  SEMA3G  PCNP    RPL24   YWHAQP6 RNF7
PDCD10  DNAJC19 RELL1   COPS4   LAMTOR3 AIMP1   OSTC    ANAPC10 CMBL    SUB1    CDK7
ANKRA2  CETN3   ERAP1   CTD     MATR3   CTB     NPM1    RPL26L1 U1      NOL7
GPLD1   EYS     IGF2R   MALSU1  CBX3    BET1    BUD31   SPDYE2  HIPK2   ASPH
HEATR7A CHMP5   ATP6V1G1        RPL12   SSNA1   COMMD3  RPS24   MARK2P9 SBF2
RPS13   TSG101  POLR2G  PPP6R3  UCP2    UBE4A   NTM     PFDN5   ACTR6   C12orf45
TRIAP1  STARD13 RFXAP   MRPS31  DGKH    EBPL    PPP2R3C FKBP3   NEK9    C14orf80
CYFIP1  SNAP23  TTBK2   RPS3AP6 PPIB    RAB11A  RPS17L  CHTF8   HSBP1   DERL2
RPL26   NCOR1   PRPSAP2 RPS7P1  ERN1    C17orf90        MYL12A  MYL12B  PSMG2
C18orf32        RPS19   MEGF8   RPL18   RPS5    UBE2V1  PFDN4   RPL12P4 PI4KA
GSTT2   RPS19BP1        GNL3L   RPS4X   PSMD10  DOCK11  SSR4
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006614      5.31853245541676e-18    32.8850475367329        0.682997716421009
16      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      6.23205818299822e-18    32.5173789173789        0.6895024565774 16
106     cotranslational protein targeting to membrane
GO:0045047      6.23205818299822e-18    32.5173789173789        0.6895024565774 16
106     protein targeting to ER
GO:0072599      6.23205818299822e-18    32.5173789173789        0.6895024565774 16
106     establishment of protein localization to endoplasmic reticulum
GO:0006415      1.81309748591631e-17    35.6787141905396        0.591931354231541
15      91      translational termination
GO:0070972      3.70104721246605e-17    28.667672197084 0.767559338454086       16
118     protein localization to endoplasmic reticulum
GO:0019080      8.92631084441153e-17    23.4339019189765        0.982215763614975
17      151     viral genome expression
GO:0019083      8.92631084441153e-17    23.4339019189765        0.982215763614975
17      151     viral transcription
GO:0006414      1.71210179137508e-16    30.0991561181435        0.682997716421009
15      105     translational elongation
GO:0072594      8.18501634781108e-16    18.0445670628183        1.32696699190367
18      204     establishment of protein localization to organelle
GO:0000184      1.18437393455805e-15    26.0217867575463        0.774064078610477
15      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006612      2.54076105251855e-15    21.2914093206064        0.995225243927756
16      153     protein targeting to membrane
GO:0022415      3.92873589992143e-15    14.8383955739972        1.69123244066155
19      260     viral reproductive process
GO:0019058      7.34008832451422e-15    15.7272053372869        1.50259497612622
18      231     viral infectious cycle
GO:0006413      4.82600731905916e-14    19.7080291970803        0.988720503771365
15      152     translational initiation
GO:0043624      5.32295636403822e-14    19.563841496973 0.995225243927756       15
153     cellular protein complex disassembly
GO:0043241      8.59927424657248e-14    18.8731521642914        1.02774894470971
15      158     protein complex disassembly
GO:0000956      2.33426310187263e-13    17.5115074798619        1.09930108643   15
169     nuclear-transcribed mRNA catabolic process
GO:0034623      3.58973326371703e-13    16.9548602818247        1.13182478721196
15      174     cellular macromolecular complex disassembly
GO:0006402      5.01601595084808e-13    16.5341306204861        1.15784374783752
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15      178     mRNA catabolic process
GO:0032984      5.4465081225471e-13     16.4321549861068        1.16434848799391
15      179     macromolecular complex disassembly
GO:0006401      3.9367873386225e-12     14.1575616255829        1.33347173206007
15      205     RNA catabolic process
GO:0016032      8.11184977974904e-12    8.73267699253778        2.93363781053214
20      451     viral reproduction
GO:0033365      1.58270085419441e-10    7.75791483113069        3.07674209397274
19      473     protein localization to organelle
GO:0006605      1.64045588855248e-10    7.74030769230769        3.08324683412913
19      474     protein targeting
GO:0071845      4.02602609314716e-10    9.94400263517011        1.84734620441492
15      284     cellular component disassembly at cellular level
GO:0022411      4.88941229822078e-10    9.79552093476144        1.87336516504048
15      288     cellular component disassembly
GO:0042254      4.32489332404076e-08    12.1771154504967        0.969206283302194
10      149     ribosome biogenesis
GO:0042274      8.38161833336861e-08    61.9878997407087        0.11708532281503
5       18      ribosomal small subunit biogenesis
GO:0022613      2.26870176916479e-07    8.75875464474721        1.46356653518788
11      225     ribonucleoprotein complex biogenesis
GO:0071843      4.15216692928138e-07    8.21279856267174        1.55463289737734
11      239     cellular component biogenesis at cellular level
GO:0006364      4.99793810148488e-06    11.8284156890627        0.676492976264618
7       104     rRNA processing
GO:0016072      7.25372287208501e-06    11.1346947885281        0.715521417202962
7       110     rRNA metabolic process
Tissue: Adipose_Subcutaneous=>Nerve_Tibial      Type:   asymmetric
SourceGene:     HR(ENSG00000168453.10)
TargetGeneSet:  IGSF21  C1QA    C1QC    C1QB    RPS6KA1 LAPTM5  CSF3R   BRD8
MRPS21  CTSS    CD84    ARHGAP30        PTPRC   TLR5    SP140L  GPX1    UBA7
STAB1   PDE6B   SH3TC1  DTHD1   TLR1    TLR6    NSUN7   DAPP1   FYB     GZMA
SEPT8   PCDHA1  CSF1R   CD74    DOCK2   RP11    F13A1   LY86    AIF1    HLA-DRA
HLA-DMB HLA-DMA HLA-DOA DEFA6   MKRNP2  FGD2    VNN1    VNN3    IPCEF1  AOAH    TFEC
TBXAS1  MKRN1   CTSB    MSR1    ADAM28  DOCK8   SYK     FGD3    COL27A1 GGTA1P  MRC1
ASCL2   MS4A6A  MS4A7   CARNS1  FOLR2   KCNE3   SLCO2B1 IL10RA  AMICA1  CD3G
SORL1   SLC37A2 KCNJ5   C11orf45        CD4     PTPN6   CLEC7A  BIN2    NCKAP1L LYZ
YEATS4  SELPLG  P2RX4   LCP1    ITGAM   DPEP2   IRF8    ADAP2   EVI2B   EVI2A   MPO
AANAT   TMC8    HMHA1   VAV1    EMR1    STXBP2  MYO1F   LRRC25  GMIP    NUDT19
CEACAM21        CD37    SIGLEC9 CD33    FPR3    ZNF766  LILRB5  LILRA4  LAIR1
LILRB4  RPL28   ITGB2   NFAM1   KLHDC7B CSF2RA  TLR7    TLR8    CXorf21 CYBB
GPR34   WAS     BTK
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0050778      5.83421819973224e-17    12.5164556962025        2.59442253131271
24      364     positive regulation of immune response
GO:0002253      1.37762253364924e-16    13.7969425502518        2.1311327935783 22
299     activation of immune response
GO:0002757      3.63045077197809e-15    14.798721340388 1.67497059027057        19
235     immune response-activating signal transduction
GO:0002764      9.77356183820755e-15    13.9457787481805        1.76762853781745
19      248     immune response-regulating signaling pathway
GO:0002429      5.35930412653596e-13    18.8089887640449        0.947962078748876
14      133     immune response-activating cell surface receptor signaling pathway
GO:0002768      1.61754876053476e-12    17.2041486603284        1.02636495744239
14      144     immune response-regulating cell surface receptor signaling pathway
GO:0050851      3.62165101025428e-12    18.6963636363636        0.876686734482043
13      123     antigen receptor-mediated signaling pathway
GO:0042110      9.66559309237516e-12    9.88258745358609        2.27368348211196
18      319     T cell activation
GO:0050867      1.26412827960321e-11    11.5960591133005        1.71060826240399
16      240     positive regulation of cell activation
GO:0050870      1.70490997099201e-11    14.2184212409647        1.21880838696284
14      171     positive regulation of T cell activation
```

GO:0046649	2.29891985491694e-11	8.1303421920126	3.08622240675386	20	433	lymphocyte activation
GO:0051251	3.05709522713005e-11	12.0579545454545	1.5324199017369	15	215	positive regulation of lymphocyte activation
GO:0050865	3.22243936891259e-11	9.13715837104072	2.44474430835236	18	343	regulation of cell activation
GO:0002696	9.57221723963338e-11	11.0482693911593	1.6607155214172	15	233	positive regulation of leukocyte activation
GO:0002694	1.04518405122587e-10	9.13203794369645	2.28793855096533	17	321	regulation of leukocyte activation
GO:0051249	1.49271123631121e-10	9.69891084420337	2.01709224275137	16	283	regulation of lymphocyte activation
GO:0002252	2.22586293386065e-10	8.04475703324808	2.75122828869974	18	386	immune effector process
GO:0050863	5.2475924152608e-10	10.7460239917494	1.575185108297	14	221	regulation of T cell activation
GO:0006954	2.59299777239302e-08	6.17588189182127	3.29292090512767	17	462	inflammatory response
GO:0002521	2.9071042411463e-08	7.6794631710362	2.15251539685835	14	302	leukocyte differentiation
GO:0050852	3.38874650811354e-08	15.168085106383	0.705625908241644	9	99	T cell receptor signaling pathway
GO:0001817	3.55661817144971e-08	6.93908562367865	2.5587848591793	15	359	regulation of cytokine production
GO:0031294	5.75323042297869e-08	17.9494108405342	0.534565082001246	8	75	lymphocyte costimulation
GO:0031295	5.75323042297869e-08	17.9494108405342	0.534565082001246	8	75	T cell costimulation
GO:0001816	1.24326396961947e-07	6.26555023923445	2.81537609853989	15	395	cytokine production
GO:0002250	1.60882790896458e-07	9.05434782608696	1.41125181648329	11	198	adaptive immune response
GO:0030098	2.17512041569067e-07	8.76914845685965	1.45401702304339	11	204	lymphocyte differentiation
GO:0002443	3.0535618324637e-07	8.45804347826087	1.50390976403017	11	211	leukocyte mediated immunity
GO:0002504	3.98933557411334e-07	43.0102040816327	0.156805757387032	5	22	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II
GO:0045619	5.07255268071156e-07	13.1932909196067	0.705625908241644	8	99	regulation of lymphocyte differentiation
GO:0045058	6.36646490171908e-07	38.4774436090226	0.171060826240399	5	24	T cell selection
GO:0042742	7.15487089420626e-07	10.3114119922631	1.00498235416234	9	141	defense response to bacterium
GO:0030097	9.43330894915396e-07	5.28865665584416	3.30004843955436	15	463	hemopoiesis
GO:0030217	1.66945045570303e-06	9.24945722970039	1.11189537056259	9	156	T cell differentiation
GO:0050853	1.72916770905549e-06	30.4506802721088	0.206698498373815	5	29	B cell receptor signaling pathway
GO:0048534	2.16492874544693e-06	4.92471590909091	3.52812954120822	15	495	hemopoietic or lymphoid organ development
GO:0042108	3.75664466245746e-06	16.6835246061078	0.420524531174313	6	59	positive regulation of cytokine biosynthetic process
GO:0071346	4.68617126705722e-06	11.9524664750958	0.669988236108228	7	94	cellular response to interferon-gamma
GO:0045621	5.03771779945367e-06	15.7864506627393	0.441907134454363	6	62	positive regulation of lymphocyte differentiation
GO:0045577	5.39412032474818e-06	44.5532245532246	0.121168085253616	4	17	regulation of B cell differentiation
GO:0002460	5.67703879311226e-06	7.89114299851559	1.29008373122967	9	181	adaptive immune response based on somatic recombination of immune

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receptors built from immunoglobulin superfamily domains
GO:0019886      6.92478501404327e-06    143.45  0.0427652065600996      3       6
antigen processing and presentation of exogenous peptide antigen via MHC class II
GO:0042116      6.94617424957758e-06    22.1320346320346        0.270846308213964
5       38      macrophage activation
GO:0050900      8.38207304992738e-06    6.57124237769399        1.71773579683067
10      241     leukocyte migration
GO:0002274      1.10692443349267e-05    10.3891666666667        0.76264618365511
7       107     myeloid leukocyte activation
GO:0034341      1.40863437765481e-05    9.98677884615385        0.791156321361843
7       111     response to interferon-gamma
GO:0030593      1.45280962225576e-05    18.7192569335426        0.313611514774064
5       44      neutrophil chemotaxis
GO:0019724      1.67707201985632e-05    9.70473130841122        0.812538924641893
7       114     B cell mediated immunity
GO:0002275      1.81314245547875e-05    17.8036336485814        0.327866583627431
5       46      myeloid cell activation involved in immune response
GO:0002495      1.91888241560716e-05    86.058  0.0570202754134662      3       8
antigen processing and presentation of peptide antigen via MHC class II
GO:0045059      1.91888241560716e-05    86.058  0.0570202754134662      3       8
positive thymic T cell selection
Tissue: Nerve_Tibial=>Adipose_Subcutaneous      Type:   asymmetric
SourceGene:     JAZF1-AS1(ENSG00000234336.1)
TargetGeneSet:  RPL11   TMEM50A KHDRBS1 RP4     RP11    NRBP1   UBC     RPL31   MCM6
RPL37A  AAMP    RPL32   RPL14   RPL24   BTLA    MBNL1   RPL35A  PPP2R2C RPL34
ADAMTS16        TBCA    MAT2B   STC2    CSNK2B  RPS10   RPL10A  RPL39P3 MRPS12  ECD
ARF5    LEP     BIN3    RPL30   RPS6    PSMB7   RPL35   RPL12   RPL7A   MRVI1-AS1
RNF121  RPS25   RPL41   RPL14P1 POLR1D  C14orf119       ANKDD1A RPL35AP32
RPS17L  RPL17   RPL19   CTIF    TLE6    TLE2    UBA52   ZNF14   XRCC1   PTGIR
SLC1A5  RPS9    RPL28   U2AF1   NHP2L1  SAMM50  RPL10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      2.19924758994353e-41    169.602272727273        0.3589370977787 25
91      translational termination
GO:0000184      3.45602585800618e-40    128.971904266389        0.469379281710608
26      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006414      1.29833321434107e-39    139.78515625    0.414158189744654       25
105     translational elongation
GO:0006614      1.29833321434107e-39    139.78515625    0.414158189744654       25
105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.69541091254078e-39    138.049768518519        0.418102553456508
25      106     cotranslational protein targeting to membrane
GO:0045047      1.69541091254078e-39    138.049768518519        0.418102553456508
25      106     protein targeting to ER
GO:0072599      1.69541091254078e-39    138.049768518519        0.418102553456508
25      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      3.38396096066161e-38    120.136088709677        0.465434917998754
25      118     protein localization to endoplasmic reticulum
GO:0006413      3.70068139013524e-37    94.973886328725 0.599543284201785       26
152     translational initiation
GO:0006612      4.44900001617343e-37    94.2194564389129        0.603487647913639
26      153     protein targeting to membrane
GO:0000956      7.15594190037722e-36    83.58357771261  0.666597467303301       26
169     nuclear-transcribed mRNA catabolic process
GO:0019080      2.8308522503373e-35     88.4672619047619        0.595598920489931
25      151     viral genome expression
GO:0019083      2.8308522503373e-35     88.4672619047619        0.595598920489931
25      151     viral transcription
GO:0006402      3.01470694724752e-35    78.5848896434635        0.702096740709986
26      178     mRNA catabolic process
GO:0043624      4.03244913386787e-35    87.07275390625  0.603487647913639       25
153     cellular protein complex disassembly
GO:0043241      9.55427181679984e-35    83.7699718045113        0.623209466472908
25      158     protein complex disassembly
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GO:0034623      1.24961935582655e-33    74.6906459731544        0.68631928586257
25      174     cellular macromolecular complex disassembly
GO:0072594      1.27699410546344e-33    66.9836897426604        0.804650197218186
26      204     establishment of protein localization to organelle
GO:0006401      1.45941791563992e-33    66.6047936565147        0.808594560930039
26      205     RNA catabolic process
GO:0032984      2.64709413072781e-33    72.2402597402597        0.706041104421839
25      179     macromolecular complex disassembly
GO:0019058      2.09619562885012e-30    53.807645631068 0.91114801743824        25
231     viral infectious cycle
GO:0022415      4.42228106329537e-29    47.0711436170213        1.025534565082  25
260     viral reproductive process
GO:0071845      4.23392337754159e-28    42.636944980695 1.12019929416649        25
284     cellular component disassembly at cellular level
GO:0022411      6.04763774659291e-28    41.9765922053232        1.13597674901391
25      288     cellular component disassembly
GO:0033365      2.18099658442602e-25    28.1461883408072        1.86568403570687
27      473     protein localization to organelle
GO:0006605      2.30795948470955e-25    28.0812080536913        1.86962839941873
27      474     protein targeting
GO:0016032      1.74358332784865e-24    27.5669070208729        1.77890803404609
26      451     viral reproduction
GO:0022613      1.56171695073804e-08    14.0316674913409        0.887481835167116
10      225     ribonucleoprotein complex biogenesis
GO:0071843      2.77218191947728e-08    13.1608287652142        0.94270292713307
10      239     cellular component biogenesis at cellular level
GO:0042254      1.14025121156735e-07    16.5036908380373        0.587710193066224
8       149     ribosome biogenesis
GO:0000028      1.153971806579e-06      266.5   0.0236661822711231      3       6
ribosomal small subunit assembly
GO:0042273      1.248183947148e-05      88.7962962962963        0.0473323645422462
3       12      ribosomal large subunit biogenesis
Tissue: Nerve_Tibial=>Adipose_Subcutaneous      Type:   asymmetric
SourceGene:     NANOS3(ENSG00000187556.5)
TargetGeneSet:  RPL22   SPEN    CDC42   RP11    RPS8    RPS15AP10       BTF3L4  RP4
RPL5    EEF1A1P11       SNX7    RPS27   PRRC2C  ARPC5   RPS7    UBC     DUSP11
ANKRD36BP2      TXNDC9  MMADHC  SENP2   EEF1B2  ASIC4   TRNT1   RPL32   UBE2E1
RPL15   RPL29   DNAH1   RPL10AP6        RP13    PCNP    RPL24   C3orf17 TPRG1-AS2
RPL35A  COPS4   EEF1A1P9        RPL34   OSTC    CCDC109B        RPS3A   CTD
EEF1A1P19       BTF3    RPS23   SKP1    CTB     RPS14   RPL15P3 GPLD1   MCFD2P1
RPS10   RPL10A  GLO1    EEF1A1  MRPS12  IGF2R   ANKRD61 EEF1A1P6        MALSU1
VPS41   RPS3AP26        BUD31   FAM3C   ARF5    RPL7    EIF3H   RPL8    RPS6
ELAVL2  UBAP2   CLTA    HNRNPK  ATP6V1G1        RPL12   EEF1A1P5        RPL7A
COMMD3  CCNY    VN1R53P CDH23   RPS24   RPS3AP5 RPL13AP5        SFR1    LHPP
RPL27A  RPS13   TSG101  RPS3    SETP17  PHB2    CMAS    H3F3C   MYF6    RPL6
RPLP0   TPT1    EBPL    EAPP    FKBP3   RPL32P29        CGRRF1  JKAMP   C14orf159
TTBK2   RSL24D1 RPS3AP6 RAB11A  RPL4    MORF4L1 SEC11A  RPS15A  RRN3P2  HSBP1
RPL26   RPL17P43        RPS7P1  SUPT6H  RPL23A  RPL19   STAT5A  RPL27   RPS7P11
RPS2P48 USP36   MYL12A  MYL12B  VAPA    PSMG2   RPL17   RPS15   PIP5K1C RPSAP58
RPS19   MEGF8   CEACAMP2        RPL18   RPL13A  ACPT    RPS9    RPS5    SNRPB2  RP1
RPL41P1 PFDN4   RPL12P4 PI4KA   EIF3L   RPL3    GS1     RP6     PDZD11  RPS23P8
RPS4X   RPSAP14 RPL10   VBP1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      3.84591570766492e-71    154.567796610169        0.857380112102969
46      105     translational elongation
GO:0006415      2.16196924424638e-70    180.731454859114        0.743062763822573
44      91      translational termination
GO:0006614      5.76736347202654e-69    146.640410958904        0.857380112102969
45      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      9.9720990216942e-69     144.226364248821        0.86554563698014
45      106     cotranslational protein targeting to membrane
GO:0045047      9.9720990216942e-69     144.226364248821        0.86554563698014
45      106     protein targeting to ER
```

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GO:0072599      9.9720990216942e-69     144.226364248821        0.86554563698014
45      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      3.53917697518047e-68    126.544367283951        0.963531935506193
46      118     protein localization to endoplasmic reticulum
GO:0000184      8.06624369212832e-64    113.036396396396        0.971697460383364
44      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006413      4.47527293437489e-62    85.7497379454927        1.24115978133001
46      152     translational initiation
GO:0006612      5.28819604002475e-60    81.1929223744292        1.24932530620718
45      153     protein targeting to membrane
GO:0019080      2.14721967205047e-58    79.0532962869411        1.23299425645284
44      151     viral genome expression
GO:0019083      2.14721967205047e-58    79.0532962869411        1.23299425645284
44      151     viral transcription
GO:0043624      4.19910718122264e-58    77.5918670964543        1.24932530620718
44      153     cellular protein complex disassembly
GO:0043241      2.14664627476667e-57    74.1626363205311        1.29015293059304
44      158     protein complex disassembly
GO:0000956      6.31798476616127e-56    67.584  1.37997370424192        44      169
nuclear-transcribed mRNA catabolic process
GO:0072594      2.16423941995547e-55    57.3180379746835        1.66576707494291
46      204     establishment of protein localization to organelle
GO:0034623      2.69901455226841e-55    64.9617463617464        1.42080132862778
44      174     cellular macromolecular complex disassembly
GO:0006402      8.3276990259618e-55     63.0048406615571        1.45346342813646
44      178     mRNA catabolic process
GO:0032984      1.09859669494889e-54    62.5337337337337        1.46162895301363
44      179     macromolecular complex disassembly
GO:0006401      8.30988327641433e-52    52.339096860836 1.67393259982008        44
205     RNA catabolic process
GO:0019058      5.51750453719069e-51    46.8857711003093        1.88623624662653
45      231     viral infectious cycle
GO:0022415      1.68418515003962e-48    40.4784963364129        2.12303646806449
45      260     viral reproductive process
GO:0071845      4.07200278512508e-45    34.9150900900901        2.3190090651166 44
284     cellular component disassembly at cellular level
GO:0022411      7.77280592205043e-45    34.3329641116526        2.35167116462529
44      288     cellular component disassembly
GO:0033365      4.26057834754705e-39    21.610427825167 3.86229326690194        47
473     protein localization to organelle
GO:0016032      1.01124457558609e-38    21.9714677640604        3.68265171960418
46      451     viral reproduction
GO:0006605      9.99924074929472e-38    20.7564252336449        3.87045879177912
46      474     protein targeting
GO:0042254      1.12936693832616e-12    15.4314592088103        1.2166632066985 15
149     ribosome biogenesis
GO:0022613      3.99845339492456e-11    10.6006191950464        1.8372430973635 16
225     ribonucleoprotein complex biogenesis
GO:0042274      5.97449731042717e-11    82.1081081081081        0.14697944778908
7       18      ribosomal small subunit biogenesis
GO:0071843      9.87685386521456e-11    9.92526158445441        1.9515604456439 16
239     cellular component biogenesis at cellular level
GO:0006364      7.90125225689655e-10    15.7411315445684        0.849214587225798
11      104     rRNA processing
GO:0016072      1.44970325921689e-09    14.7808930425753        0.898207736488824
11      110     rRNA metabolic process
GO:0042273      2.52226602828915e-08    90.5562579013907        0.0979862985260536
5       12      ribosomal large subunit biogenesis
GO:0034470      8.3984688957256e-08     8.51766358892011        1.63310497543423
12      200     ncRNA processing
GO:0034660      3.64835798864627e-06    5.83039601907526        2.32717458999377
12      285     ncRNA metabolic process
GO:0030490      1.81382042849368e-05    93.45   0.0571586741401979      3       7
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maturation of SSU-rRNA
Tissue: Nerve_Tibial=>Adipose_Subcutaneous      Type:   cluster
SourceGene:     NANOS3(ENSG00000187556.5)
TargetGeneSet:  RPL22   SPEN    CDC42   RP11    RPS8    RPS15AP10       BTF3L4  RP4
RPL5    EEF1A1P11       SNX7    RPS27   PRRC2C  ARPC5   RPS7    UBC     DUSP11
ANKRD36BP2      TXNDC9  MMADHC  SENP2   EEF1B2  ASIC4   TRNT1   RPL32   UBE2E1
RPL15   RPL29   DNAH1   RPL10AP6        RP13    PCNP    RPL24   C3orf17 TPRG1-AS2
RPL35A  COPS4   EEF1A1P9        RPL34   OSTC    CCDC109B        RPS3A   CTD
EEF1A1P19       BTF3    RPS23   SKP1    CTB     RPS14   RPL15P3 GPLD1   MCFD2P1
RPS10   RPL10A  GLO1    EEF1A1  MRPS12  IGF2R   ANKRD61 EEF1A1P6        MALSU1
VPS41   RPS3AP26        BUD31   FAM3C   ARF5    RPL7    EIF3H   RPL8    RPS6
ELAVL2  UBAP2   CLTA    HNRNPK  ATP6V1G1        RPL12   EEF1A1P5        RPL7A
COMMD3  CCNY    VN1R53P CDH23   RPS24   RPS3AP5 RPL13AP5        SFR1    LHPP
RPL27A  RPS13   TSG101  RPS3    SETP17  PHB2    CMAS    H3F3C   MYF6    RPL6
RPLP0   TPT1    EBPL    EAPP    FKBP3   RPL32P29        CGRRF1  JKAMP   C14orf159
TTBK2   RSL24D1 RPS3AP6 RAB11A  RPL4    MORF4L1 SEC11A  RPS15A  RRN3P2  HSBP1
RPL26   RPL17P43        RPS7P1  SUPT6H  RPL23A  RPL19   STAT5A  RPL27   RPS7P11
RPS2P48 USP36   MYL12A  MYL12B  VAPA    PSMG2   RPL17   RPS15   PIP5K1C RPSAP58
RPS19   MEGF8   CEACAMP2        RPL18   RPL13A  ACPT    RPS9    RPS5    SNRPB2  RP1
RPL41P1 PFDN4   RPL12P4 PI4KA   EIF3L   RPL3    GS1     RP6     PDZD11  RPS23P8
RPS4X   RPSAP14 RPL10   VBP1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      3.84591570766492e-71    154.567796610169        0.857380112102969
46      105     translational elongation
GO:0006415      2.16196924424638e-70    180.731454859114        0.743062763822573
44      91      translational termination
GO:0006614      5.76736347202654e-69    146.640410958904        0.857380112102969
45      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      9.9720990216942e-69     144.226364248821        0.86554563698014
45      106     cotranslational protein targeting to membrane
GO:0045047      9.9720990216942e-69     144.226364248821        0.86554563698014
45      106     protein targeting to ER
GO:0072599      9.9720990216942e-69     144.226364248821        0.86554563698014
45      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      3.53917697518047e-68    126.544367283951        0.963531935506193
46      118     protein localization to endoplasmic reticulum
GO:0000184      8.06624369212832e-64    113.036396396396        0.971697460383364
44      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006413      4.47527293437489e-62    85.7497379454927        1.24115978133001
46      152     translational initiation
GO:0006612      5.28819604002475e-60    81.1929223744292        1.24932530620718
45      153     protein targeting to membrane
GO:0019080      2.14721967205047e-58    79.0532962869411        1.23299425645284
44      151     viral genome expression
GO:0019083      2.14721967205047e-58    79.0532962869411        1.23299425645284
44      151     viral transcription
GO:0043624      4.19910718122264e-58    77.5918670964543        1.24932530620718
44      153     cellular protein complex disassembly
GO:0043241      2.14664627476667e-57    74.1626363205311        1.29015293059304
44      158     protein complex disassembly
GO:0000956      6.31798476616127e-56    67.584  1.37997370424192        44      169
nuclear-transcribed mRNA catabolic process
GO:0072594      2.16423941995547e-55    57.3180379746835        1.66576707494291
46      204     establishment of protein localization to organelle
GO:0034623      2.69901455226841e-55    64.9617463617464        1.42080132862778
44      174     cellular macromolecular complex disassembly
GO:0006402      8.3276990259618e-55     63.0048406615571        1.45346342813646
44      178     mRNA catabolic process
GO:0032984      1.09859669494889e-54    62.5337337337337        1.46162895301363
44      179     macromolecular complex disassembly
GO:0006401      8.30988327641433e-52    52.339096860836 1.67393259982008        44
205     RNA catabolic process
GO:0019058      5.51750453719069e-51    46.8857711003093        1.88623624662653
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45      231     viral infectious cycle
GO:0022415      1.68418515003962e-48    40.4784963364129        2.12303646806449
45      260     viral reproductive process
GO:0071845      4.07200278512508e-45    34.9150900900901        2.3190090651166 44
284     cellular component disassembly at cellular level
GO:0022411      7.77280592205043e-45    34.3329641116526        2.35167116462529
44      288     cellular component disassembly
GO:0033365      4.26057834754705e-39    21.610427825167 3.86229326690194        47
473     protein localization to organelle
GO:0016032      1.01124457558609e-38    21.9714677640604        3.68265171960418
46      451     viral reproduction
GO:0006605      9.99924074929472e-38    20.7564252336449        3.87045879177912
46      474     protein targeting
GO:0042254      1.12936693832616e-12    15.4314592088103        1.2166632066985 15
149     ribosome biogenesis
GO:0022613      3.99845339492456e-11    10.6006191950464        1.8372430973635 16
225     ribonucleoprotein complex biogenesis
GO:0042274      5.97449731042717e-11    82.1081081081081        0.14697944778908
7       18      ribosomal small subunit biogenesis
GO:0071843      9.87685386521456e-11    9.92526158445441        1.9515604456439 16
239     cellular component biogenesis at cellular level
GO:0006364      7.90125225689655e-10    15.7411315445684        0.849214587225798
11      104     rRNA processing
GO:0016072      1.44970325921689e-09    14.7808930425753        0.898207736488824
11      110     rRNA metabolic process
GO:0042273      2.52226602828915e-08    90.5562579013907        0.0979862985260536
5       12      ribosomal large subunit biogenesis
GO:0034470      8.3984688957256e-08     8.51766358892011        1.63310497543423
12      200     ncRNA processing
GO:0034660      3.64835798864627e-06    5.83039601907526        2.32717458999377
12      285     ncRNA metabolic process
GO:0030490      1.81382042849368e-05    93.45   0.0571586741401979      3       7
maturation of SSU-rRNA
Tissue: Nerve_Tibial=>Adipose_Subcutaneous      Type:   cluster
SourceGene:     NHSL2(ENSG00000204131.6)
TargetGeneSet:  AGRN    MRPL20  RPL22   SPEN    HSPG2   RPL11   SYF2    ARID1A  RP4
RPS8    BTF3L4  TM2D1   GNG5    CCBL2   RPL5    RP11    STXBP3  HBXIP   ATP5F1
RAP1A   SRGAP2P1        MRPS21  RPS27   C1orf43 CKS1B   DAP3    SSR2    PMF1
PRRC2C  GAS5    ZBTB37  CR2     C1orf132        NENF    TOMM20  ACP1    RPS7
C2orf28 COX7A2L PREPL   SPTBN1  UBC     CCDC104 C1D     GMCL1   SNRPG   TPRKB
DGUOK   DGUOK-AS1       DCTN1   VAMP5   ANKRD36 COA5    MITD1   RPL31   RANBP2
GPR17   MMADHC  ARL6IP6 SNORA70F        HAT1    UBE2E3  SENP2   NBEAL1  EEF1B2
RPL37A  USP37   MFF     GIGYF2  RPL32   TBC1D5  RPL15   EIF1B   RPL14   SS18L2  MAP4
LAMB2   NICN1   RAD54L2 RPL29   SPCS1   KCTD6   RPL10AP6        CTD     RP13
C3orf26 NIT2    PCNP    RPL24   ZBTB20  CNBP    RNF7    RNF13   PHC3    RPL22L1
DNAJC19 EIF4G1  PPP1R2  RPL35A  MRFAP1L1        CNO     C4orf52 OCIAD1  MTHFD2L
ENOPH1  COPS4   LAMTOR3 UBE2D3  CISD2   RPL34   RPS3A   ERCC4   NIPBL   EEF1A1P19
MRPS36  TAF9    BTF3    TBCA    COX7C   HSPD1P11        EPB41L4A-AS1    HINT1   SKP1
PCDHGB3 HDAC3   CTB     RPS14   CCNG1   NUDCD2  MAT2B   NPM1    MSX2    GNB2L1
LYRM4   TMEM14C RPL15P3 CSNK2B  C6orf48 CUTA    RPS10   RPL10A  GLO1    C6orf130
MRPL32  RPL39P3 EEF1A1  WDR11   CCNC    MRPS12  SF3B5   C6orf72 RP3     IGF2R
SFT2D1  PSMB1   RP1     LSM5    OGDH    STAG3L4 C7orf23 RPS3AP26        CUX1
DUS4L   FAM3C   NDUFA5  ARF5    MTPN    ZC3HAV1L        BRAF    TRPV6   RHEB    MLL3
HMBOX1  PPAPDC1B        GOLGA7  KAT6A   C8orf40 HOOK3   TCEA1   RPS20   SNHG6   RPL7
ZFAND1  RPL30   POLR2K  EIF3E   EIF3H   TATDN1  EEF1D   CPSF1   RPL8    SNAPC3  RPS6
CHMP5   TLN1    RGP1    CLTA    SEC61B  INVS    ATP6V1G1        PSMB7   RPL35
RPL12   EEF1A1P5        RPL7A   C10orf31        RAB18   ZFAND4  VPS26A  RPS24
RPS3AP5 RPL13AP5        DNMBP-AS1       NDUFB8  GBF1    SFR1    NHLRC2  IGF2
RPL27A  RPS13   TSG101  EIF3M   CKAP5   AHNAK   FAU     PPP6R3  LAMTOR1 SPCS2   RPS3
CCDC90B TMEM126B        SDHD    ZBTB16  UBE4A   ATP5L   RPS25   THYN1   WNK1    ERC1
C12orf57        PHB2    SCAF11  MLL4    PFDN5   PRR13   ITGA7   RPL41   CNPY2   NACA
LRP1    NAP1L1  EEA1    USP44   RPL18AP3        ISCU    ARPC3   VPS29   C12orf51
RPL6    RPLP0   ZNF891  RPSAP54 MRP63   POLR1D  RFXAP   DGKH    TPT1    ZC3H13  ESD
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MED4    MZT1    CCNB1IP1        OXA1L   PPP2R3C RPS29   RPL36A  DNAAF2  KLHDC2  CNIH
CGRRF1  JKAMP   C14orf142       DYNC1H1 SIVA1   RPS20P33        PGBD4   CDAN1   B2M
RSL24D1 GTF2A2  RPS3AP6 RPS27L  USP3    RPL4    MYO9A   RCN2    MORF4L1 RPS17L
C15orf40        SEC11A  MEF2A   MPG     RGS11   ARHGDIG TSC2    SRRM2   TCEB2
RPS15A  METTL9  SRCAP   NAE1    ZFHX3   CDYL2   MLYCD   ANKRD11 DERL2   GABARAP
RPL26   RPL17P43        RPS7P1  SDF2    SUPT6H  RPL23A  TAOK1   ZNHIT3  RPL17
RPL19   SMARCE1 RPL27   RPS7P11 MRPL10  HOXB-AS5        SUPT4H1 SUMO2   MYL12B
PSMG2   C18orf21        C18orf32        RPS15   OAZ1    NFIC    RPL36   NDUFA11
EIF3G   WDR83OS ASNA1   C19orf53        FAM32A  RPL18A  UBA52   RPSAP58 SDHAF1
EIF3K   RPS16   EID2B   FBL     RPS19   ZNF222  SNRPD2  RPL18   RPL13A  RPS11   RPS9
CCDC106 RPS5    SNRPB2  CHMP4B  EIF2S2  PHF20   IFT52   NCOA3   DPM1    PFDN4
RPL12P4 RPS21   U2AF1   THAP7   ASLP1   MYH9    MPST    EIF3L   RPL3    ST13
PACSIN2 ATXN10  UXT     WASF4P  WDR45   CACNA1F HUWE1   RPS23P8 RPS4X   APOOL
RPL39   RAP2C   SSR4    RPL10   MXRA5P1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006614      6.45106691204202e-89    105.339485827291        2.28150301017231
68      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.76910328103097e-88    102.560119811724        2.30323161026919
68      106     cotranslational protein targeting to membrane
GO:0045047      1.76910328103097e-88    102.560119811724        2.30323161026919
68      106     protein targeting to ER
GO:0072599      1.76910328103097e-88    102.560119811724        2.30323161026919
68      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      1.01327684636074e-83    77.8793495934959        2.56397481143173
68      118     protein localization to endoplasmic reticulum
GO:0006415      4.12166115428914e-83    119.690202517789        1.977302608816  62
91      translational termination
GO:0006414      6.02087294137304e-83    91.9984939759036        2.28150301017231
65      105     translational elongation
GO:0006413      1.28380404644126e-78    50.7024335721181        3.30274721472562
71      152     translational initiation
GO:0000184      5.7399879383646e-76     65.5453090909091        2.58570341152861
64      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006612      5.55466429894088e-75    47.116472303207 3.3244758148225 69      153
protein targeting to membrane
GO:0019080      1.6869994287557e-70     43.995825426945 3.28101861462875        66
151     viral genome expression
GO:0019083      1.6869994287557e-70     43.995825426945 3.28101861462875        66
151     viral transcription
GO:0072594      2.09893799234257e-67    30.7646895015316        4.43263441976334
71      204     establishment of protein localization to organelle
GO:0043624      3.50991874841927e-65    39.1749003984064        3.3244758148225 63
153     cellular protein complex disassembly
GO:0000956      6.23368157818651e-65    35.2233935742972        3.67213341637257
65      169     nuclear-transcribed mRNA catabolic process
GO:0043241      4.27394447510369e-64    37.0998532187041        3.4331188153069 63
158     protein complex disassembly
GO:0034623      6.13749421481952e-64    33.5956670719576        3.78077641685696
65      174     cellular macromolecular complex disassembly
GO:0006402      3.59616494836834e-63    32.3971994171376        3.86769081724448
65      178     mRNA catabolic process
GO:0032984      5.5496516129275e-63     32.1107235961389        3.88941941734136
65      179     macromolecular complex disassembly
GO:0019058      8.50117794730148e-59    23.6977405356876        5.01930662237907
68      231     viral infectious cycle
GO:0006401      1.62730505587054e-58    26.0988238668962        4.45436301986022
65      205     RNA catabolic process
GO:0022415      6.22967086396807e-55    20.0766429539295        5.64943602518857
68      260     viral reproductive process
GO:0071845      2.0982633911219e-48     16.590013020117 6.17092242751367        65
284     cellular component disassembly at cellular level
GO:0022411      5.47737384812519e-48    16.2877519044789        6.25783682790118
65      288     cellular component disassembly
```

```
GO:0016032      1.89508869020437e-45    11.4848548918366        9.79959864369248
75      451     viral reproduction
GO:0033365      5.82016907928885e-45    11.0517960332748        10.2776278458238
76      473     protein localization to organelle
GO:0006605      6.81526150444609e-45    11.0232253705502        10.2993564459207
76      474     protein targeting
GO:0071843      9.69179643666664e-16    7.33553615112802        5.19313542315411
31      239     cellular component biogenesis at cellular level
GO:0022613      1.01318606176089e-14    7.2375402792696 4.8889350217978 29      225
ribonucleoprotein complex biogenesis
GO:0042274      1.19067414683568e-14    73.2814710042433        0.391114801743824
11      18      ribosomal small subunit biogenesis
GO:0042254      1.44127100552919e-14    9.27691034482759        3.23756141443499
24      149     ribosome biogenesis
GO:0006364      8.80285104973583e-12    9.93549654305468        2.25977441007543
18      104     rRNA processing
GO:0016072      2.35033860474211e-11    9.28356345475911        2.3901460106567 18
110     rRNA metabolic process
GO:0034470      7.51183818045965e-08    4.9660829665699 4.34572001937582        19
200     ncRNA processing
GO:0042273      8.30654399015847e-08    45.8798701298701        0.260743201162549
6       12      ribosomal large subunit biogenesis
GO:0034660      1.12999254286839e-06    3.76632795532113        6.19265102761055
21      285     ncRNA metabolic process
GO:0000028      3.16981716572228e-06    91.1935483870968        0.130371600581275
4       6       ribosomal small subunit assembly
GO:0030490      7.26944534829214e-06    60.7913978494624        0.152100200678154
4       7       maturation of SSU-rRNA
GO:0042255      1.68315364685945e-05    20.7796410709032        0.347657601550066
5       16      ribosome assembly
Tissue: Adipose_Subcutaneous=>Nerve_Tibial      Type:   asymmetric
SourceGene:     PLN(ENSG00000198523.5)
TargetGeneSet:  RPL22   RPL11   RPS8    RPL5    GAS5    RPL31   RPL37A  RPL32
RPL14   RP11    RPS10   RPL10A  MRPS12  RPS20   RPL30   RPS6    RPL12   RPL7A
PCBD1   OR52V1P RPL27A  RPS3    RPS25   RPL41   RPL6    RPL7AP6 RPS15A  RPL26
RPL23A  ACACA   RPL17   RPL19   RSL24D1P11      RPL36   PTGER1  UBA52   HPN
RPL28   SNORD17 PTTG1IP RPL10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      8.26332302859534e-60    959.071428571429        0.226697114386548
29      91      translational termination
GO:0006414      1.09589056363541e-57    781.637218045113        0.26157359352294
29      105     translational elongation
GO:0006614      1.09589056363541e-57    781.637218045113        0.26157359352294
29      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.5079171340912e-57     771.432282003711        0.26406477060411
29      106     cotranslational protein targeting to membrane
GO:0045047      1.5079171340912e-57     771.432282003711        0.26406477060411
29      106     protein targeting to ER
GO:0072599      1.5079171340912e-57     771.432282003711        0.26406477060411
29      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      5.38909278232418e-56    666.860353130016        0.293958895578161
29      118     protein localization to endoplasmic reticulum
GO:0000184      7.12221505251468e-56    659.404761904762        0.296450072659332
29      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      3.25185068166945e-55    590.661157024793        0.376167739256799
30      151     viral genome expression
GO:0019083      3.25185068166945e-55    590.661157024793        0.376167739256799
30      151     viral transcription
GO:0006413      2.0175966932126e-52     481.379790940767        0.37865891633797
29      152     translational initiation
GO:0006612      2.4882763124305e-52     477.464285714286        0.381150093419141
29      153     protein targeting to membrane
GO:0043624      2.4882763124305e-52     477.464285714286        0.381150093419141
```

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29      153     cellular protein complex disassembly
GO:0043241      6.94257702394279e-52    458.797342192691        0.393605978824995
29      158     protein complex disassembly
GO:0000956      5.87884912504229e-51    422.423469387755        0.421008926717874
29      169     nuclear-transcribed mRNA catabolic process
GO:0034623      1.47658466677695e-50    407.714285714286        0.433464812123728
29      174     cellular macromolecular complex disassembly
GO:0006402      3.02176630964737e-50    396.657718120805        0.443429520448412
29      178     mRNA catabolic process
GO:0032984      3.60426562279457e-50    393.985714285714        0.445920697529583
29      179     macromolecular complex disassembly
GO:0019058      3.33891897263147e-49    353.582089552239        0.575461905750467
30      231     viral infectious cycle
GO:0072594      2.15021886130407e-48    337.110204081633        0.508200124558854
29      204     establishment of protein localization to organelle
GO:0006401      2.50332734036146e-48    335.171266233766        0.510691301640025
29      205     RNA catabolic process
GO:0022415      1.44074904466958e-47    308.369565217391        0.647706041104422
30      260     viral reproductive process
GO:0071845      2.34920545731904e-46    278.759842519685        0.707494291052522
30      284     cellular component disassembly at cellular level
GO:0022411      3.6505774531439e-46     274.360465116279        0.717458999377206
30      288     cellular component disassembly
GO:0016032      4.24588308651024e-40    166.199524940618        1.12352086360805
30      451     viral reproduction
GO:0033365      1.84034379124319e-39    157.697516930023        1.17832675939381
30      473     protein localization to organelle
GO:0006605      1.96387618168055e-39    157.331081081081        1.18081793647498
30      474     protein targeting
GO:0042254      2.5066330389749e-09     28.9240121580547        0.371185385094457
8       149     ribosome biogenesis
GO:0022613      2.99435719193124e-09    21.912037037037 0.560514843263442       9
225     ribonucleoprotein complex biogenesis
GO:0071843      5.0824334643201e-09     20.5579710144928        0.595391322399834
9       239     cellular component biogenesis at cellular level
GO:0042273      1.5826893613868e-08     225.109375      0.0298941249740502      4
12      ribosomal large subunit biogenesis
GO:0006364      1.96388879581855e-07    29.2183673469388        0.259082416441769
6       104     rRNA processing
GO:0016072      2.74257268012292e-07    27.5211538461538        0.274029478928794
6       110     rRNA metabolic process
GO:0034470      8.98402702968043e-06    14.660824742268 0.498235416234171       6
200     ncRNA processing
GO:0042274      1.12920216089308e-05    87.2727272727273        0.0448411874610754
3       18      ribosomal small subunit biogenesis
Tissue: Adipose_Subcutaneous=>Nerve_Tibial      Type:   asymmetric
SourceGene:     RABGAP1(ENSG00000011454.11)
TargetGeneSet:  FUCA1   KPNA7   TMEM234 RPS8    RPL5    RP11    RPS27   ADCK3
FAM179A RPLP0P6 IGKV4-1 HNRNPA3 SLC40A1 ZNF197  IMPDH2  RPL29   PRICKLE2-AS2    CNBP
KLF3    CWC27   COL4A3BP        EPB41L4A-AS1    CAMLG   RPL15P3 NKAPL   MICB
RPS10   RPL10A  TRIM73  CALU    EPHA1   EIF3E   RPL12   RPL7A   FUT7    FBXL15
EIF3M   C1QTNF4 MMP8    IL10RA  RPL18AP3        C12orf47        RPL6    RPLP0
ATP8A2  ABHD12B BMF     STRC    STRCP1  CHD2    NME3    IGFALS  RPS2    RPL13
RPL17P43        RPL19   GPX4    RPL36   FUT3    ZNF562  CTD     SLC1A6  HPN
RPL18   RPL13A  RPS5    DBNDD2  RPL12P4 NPEPL1  LINC00316       PIK3IP1 CELSR1
TRABD   IGBP1   TTC3P1  RPL10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      3.1405522127058e-27     81.0474060822898        0.421424122898069
19      105     translational elongation
GO:0006415      1.50229988544227e-26    88.2739726027397        0.365234239844993
18      91      translational termination
GO:0000184      4.05336502099694e-26    69.6325641025641        0.477614005951145
19      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
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GO:0006413      9.97556369848819e-26    56.8620414673046        0.610061587433396
20      152     translational initiation
GO:0006614      2.45585809260828e-25    73.9965517241379        0.421424122898069
18      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      2.95038613061024e-25    73.1505681818182        0.425437685973289
18      106     cotranslational protein targeting to membrane
GO:0045047      2.95038613061024e-25    73.1505681818182        0.425437685973289
18      106     protein targeting to ER
GO:0072599      2.95038613061024e-25    73.1505681818182        0.425437685973289
18      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      2.3215428004227e-24     64.3185 0.473600442875926       18      118
protein localization to endoplasmic reticulum
GO:0019080      4.8191242550693e-24     52.6338383838384        0.606048024358176
19      151     viral genome expression
GO:0019083      4.8191242550693e-24     52.6338383838384        0.606048024358176
19      151     viral transcription
GO:0000956      4.45463458394984e-23    46.2593162393162        0.678292159712131
19      169     nuclear-transcribed mRNA catabolic process
GO:0006402      1.2323725263997e-22     43.6132881793259        0.714414227389108
19      178     mRNA catabolic process
GO:0006612      3.14379795856105e-22    47.5266666666667        0.614075150508615
18      153     protein targeting to membrane
GO:0043624      3.14379795856105e-22    47.5266666666667        0.614075150508615
18      153     cellular protein complex disassembly
GO:0043241      5.72732878705262e-22    45.8132142857143        0.634142965884714
18      158     protein complex disassembly
GO:0006401      1.92495522665908e-21    37.2116073890267        0.82278043042004
19      205     RNA catabolic process
GO:0034623      3.42937945510513e-21    41.0682692307692        0.698359975088229
18      174     cellular macromolecular complex disassembly
GO:0032984      5.78563282670552e-21    39.7788819875776        0.718427790464328
18      179     macromolecular complex disassembly
GO:0019058      1.92132847039728e-20    32.5881712626996        0.927133070375753
19      231     viral infectious cycle
GO:0071845      3.57280565206865e-20    28.1678628389155        1.1398519133624 20
284     cellular component disassembly at cellular level
GO:0022411      4.72376399290811e-20    27.7395915161037        1.15590616566328
20      288     cellular component disassembly
GO:0072594      6.36775219951183e-20    34.3717741935484        0.81876686734482
18      204     establishment of protein localization to organelle
GO:0022415      1.83835167582575e-19    28.6081498031706        1.04352639955712
19      260     viral reproductive process
GO:0016032      3.13296268580322e-16    17.0497008181707        1.81011694692409
20      451     viral reproduction
GO:0033365      1.23904310938058e-14    14.9576979554953        1.89841533457892
19      473     protein localization to organelle
GO:0006605      1.28737847597981e-14    14.923753169907 1.90242889765414        19
474     protein targeting
Tissue: Nerve_Tibial=>Adipose_Subcutaneous      Type:   asymmetric
SourceGene:     RP11-340F14.5(ENSG00000261827.1)
TargetGeneSet:  C1orf174        MFAP2   RPL11   SYF2    TMEM222 RP4     TRAPPC3
C1orf109        RRAGC   CCDC24  USP1    GTF2B   RP11    GOLPH3L CTSO    UFC1    NENF
DDIT3   MPHOSPH10       RPL31   LIMS2   UBE2E3  RPL32   EIF1B   RPL14   SS18L2
RPL24   CDV3    ACPL2   RNF7    COMMD2  RPL22L1 SENP2   RPL35A  SLBP    CNO
LAMTOR3 SLC9B2  RPL34   CNGB1   DCTD    BTF3    EPB41L4A-AS1    CTD     HINT1
UBE2D2  CCNG1   NUDCD2  NPM1    BOD1    RNF130  GABBR1  LYPLA2P1        RPL39P3
RAB32   TNRC18  TMEM60  DMTF1   C7orf23 TRIM4   RB1CC1  RPS20   NSMAF   SNHG6
RPL30   RNF139  TOMM5   ALG2    SURF2   FAM107B VPS26A  RPL13AP5        FAM204A
RPS13   EIF3M   C11orf55        RASGRP2 BRMS1   ANKRD49 CWC15   RPS25   RPUSD4
PCBP2   GTSF1   PA2G4   NACA    CDK4    CCDC59  METAP2  ALKBH2  PPP1CC  SLC15A4
POLR1D  WBP4    TPT1    MED4    NGDN    RPS29   CGRRF1  TIMM9   MED6    PSEN1
IGHV3-49        RSL24D1 PYGO1   USP3    SEC11A  RGS11   ARHGDIG PDIA2   METTL9
LCMT1   AQP8    DNAJA2  CRNDE   CMTM3   NOB1    ZDHHC7  CTNS    TMEM220 C17orf79
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TMEM98  ZNHIT3  RPL17   RPL19   DNAJC7  PTRH2   MYO15B  SPIRE1  SLC39A6 KDSR
TMED1   URI1    RPS16   ZNF230  DMWD    TRPM4   RPS11   CCDC106 CHMP4B  EIF2S2
RNF114  RPS21   MIS18A  DSCR3   PSMG1   U2AF1   CCDC117 TOM1    ST13    PHF5A
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0070972      1.40030546437951e-19    27.043504350435 0.979862985260536       19
118     protein localization to endoplasmic reticulum
GO:0006614      4.15334989408457e-19    28.8924949290061        0.871911978409799
18      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      4.96926750983946e-19    28.5621657754011        0.880215902013701
18      106     cotranslational protein targeting to membrane
GO:0045047      4.96926750983946e-19    28.5621657754011        0.880215902013701
18      106     protein targeting to ER
GO:0072599      4.96926750983946e-19    28.5621657754011        0.880215902013701
18      106     establishment of protein localization to endoplasmic reticulum
GO:0006415      9.08105050190388e-19    31.7986092889006        0.755657047955159
17      91      translational termination
GO:0006413      9.23301399557737e-19    21.5136363636364        1.26219638779323
20      152     translational initiation
GO:0006414      1.17795622861272e-17    26.7134819064431        0.871911978409799
17      105     translational elongation
GO:0006612      2.22075526967663e-17    19.9307669572927        1.27050031139714
19      153     protein targeting to membrane
GO:0000184      1.06524052959813e-16    23.0242718446602        0.988166908864438
17      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0072594      3.31139938655963e-16    15.3771739130435        1.69400041519618
20      204     establishment of protein localization to organelle
GO:0019080      6.39840647836301e-15    17.4865236922185        1.25389246418933
17      151     viral genome expression
GO:0019083      6.39840647836301e-15    17.4865236922185        1.25389246418933
17      151     viral transcription
GO:0043624      7.99513633158207e-15    17.2269417475728        1.27050031139714
17      153     cellular protein complex disassembly
GO:0043241      1.37602109238743e-14    16.6102045032018        1.31201992941665
17      158     protein complex disassembly
GO:0000956      4.25718658347756e-14    15.39620592744  1.40336308905958        17
169     nuclear-transcribed mRNA catabolic process
GO:0034623      6.92373527797761e-14    14.9006245748562        1.44488270707909
17      174     cellular macromolecular complex disassembly
GO:0006402      1.01031256913254e-13    14.5263221371284        1.47809840149471
17      178     mRNA catabolic process
GO:0032984      1.10875682814447e-13    14.43563466379  1.48640232509861        17
179     macromolecular complex disassembly
GO:0006401      1.03190226806756e-12    12.416391241479 1.70230433880008        17
205     RNA catabolic process
GO:0019058      7.11829907585459e-12    10.8878050993558        1.91820635250156
17      231     viral infectious cycle
GO:0033365      4.25565290545712e-11    6.90890990542558        3.92775586464605
22      473     protein localization to organelle
GO:0022415      4.67072579848617e-11    9.5687402612969 2.15902013701474        17
260     viral reproductive process
GO:0071845      1.86212395100869e-10    8.69379295298353        2.35831430350841
17      284     cellular component disassembly at cellular level
GO:0022411      2.31415006818054e-10    8.56303514491456        2.39152999792402
17      288     cellular component disassembly
GO:0006605      1.97555401668506e-09    6.11321585903084        3.93605978824995
20      474     protein targeting
GO:0016032      3.25677854497197e-08    5.66417606303491        3.74506954536018
18      451     viral reproduction
GO:0042254      4.41946260253503e-07    9.28188358404186        1.23728461698152
10      149     ribosome biogenesis
GO:0022613      2.67646245926574e-06    6.65724942124668        1.86838281087814
11      225     ribonucleoprotein complex biogenesis
GO:0071843      4.78680650115741e-06    6.24227426364075        1.98463774133278
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11      239     cellular component biogenesis at cellular level
Tissue: Nerve_Tibial=>Adipose_Subcutaneous      Type:   asymmetric
SourceGene:     RP11-516A11.1(ENSG00000228328.2)
TargetGeneSet:  ARID1A  RPS8    C1orf68 RPL29   RPL34   RPS3A   AFF4    RP11
LY6G6E  FAM135A RPS6    TPT1    RPS3AP6 RPL4    IRF8    RPL13   RPL27   GLTSCR2
STK35   RPL39
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      1.14499153212428e-16    225.047038327526        0.100754273060688
9       91      translational termination
GO:0034623      3.71475798518804e-16    145.030487804878        0.192651027610546
10      174     cellular macromolecular complex disassembly
GO:0006414      4.36314244552865e-16    192.040178571429        0.11625493045464
9       105     translational elongation
GO:0006614      4.36314244552865e-16    192.040178571429        0.11625493045464
9       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      4.76587842681298e-16    190.047128129602        0.117362120268494
9       106     cotranslational protein targeting to membrane
GO:0045047      4.76587842681298e-16    190.047128129602        0.117362120268494
9       106     protein targeting to ER
GO:0072599      4.76587842681298e-16    190.047128129602        0.117362120268494
9       106     establishment of protein localization to endoplasmic reticulum
GO:0032984      4.95900343977751e-16    140.69033530572 0.198186976679815       10
179     macromolecular complex disassembly
GO:0070972      1.29076584023977e-15    168.982961992136        0.130648398034738
9       118     protein localization to endoplasmic reticulum
GO:0000184      1.39576090835934e-15    167.435064935065        0.131755587848592
9       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      1.25504809296364e-14    129.413480885312        0.167185661891911
9       151     viral genome expression
GO:0019083      1.25504809296364e-14    129.413480885312        0.167185661891911
9       151     viral transcription
GO:0006413      1.33345031607535e-14    128.4995004995  0.168292851705764       9
152     translational initiation
GO:0006612      1.4161677045545e-14     127.598214285714        0.169400041519618
9       153     protein targeting to membrane
GO:0043624      1.4161677045545e-14     127.598214285714        0.169400041519618
9       153     cellular protein complex disassembly
GO:0043241      1.9019830452476e-14     123.273250239693        0.174935990588887
9       158     protein complex disassembly
GO:0000956      3.52243611240938e-14    114.709821428571        0.187115078541277
9       169     nuclear-transcribed mRNA catabolic process
GO:0071845      5.29855399750741e-14    86.1374695863747        0.314441907134454
10      284     cellular component disassembly at cellular level
GO:0006402      5.65922752959147e-14    108.532544378698        0.197079786865961
9       178     mRNA catabolic process
GO:0022411      6.09830219220966e-14    84.8741007194245        0.318870666389869
10      288     cellular component disassembly
GO:0072594      1.95978694839734e-13    93.8901098901099        0.225866722026157
9       204     establishment of protein localization to organelle
GO:0006401      2.04887268316851e-13    93.4045189504373        0.226973911840011
9       205     RNA catabolic process
GO:0019058      6.05431774037828e-13    82.3146718146718        0.255760847000208
9       231     viral infectious cycle
GO:0022415      1.76390039952359e-12    72.6556630620376        0.287869351601965
9       260     viral reproductive process
GO:0016032      2.44498073565706e-10    40.7036199095023        0.499342606048024
9       451     viral reproduction
GO:0033365      3.73067412356996e-10    38.7127463054187        0.523700781952806
9       473     protein localization to organelle
GO:0006605      3.80117561337389e-10    38.6267281105991        0.52480797176666
9       474     protein targeting
Tissue: Nerve_Tibial=>Adipose_Subcutaneous      Type:   asymmetric
SourceGene:     RP4-792G4.2(ENSG00000230798.1)
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TargetGeneSet:  IGSF21  RPL11   RP4     TRAPPC3 RPS8    UQCRH   RPL5    RP11
HBXIP   MRPS21  CTSO    UFC1    CYB5R1  DDIT3   UBC     IGKV1D-39       RPL31
C2orf49 MMADHC  C2orf47 RPL37A  RPL32   UBE2E1  EIF1B   RPL24   CNBP    RNF7    CPB1
C3orf55 DNAJC19 RPL35A  C4orf52 ENOPH1  RPL34   CICP16  SGTB    TAF9    BTF3
COX7C   CTD     SNX2    HINT1   SKP1    CTB     RPS14   ATP6V0E1        CUTA
RPS10   RPL10A  RPL39P3 MRPS12  ABCB5   TMEM60  DMTF1   RPL19P12        SRPK2
RPS20   SNHG6   RPL30   EIF3H   EEF1D   RPL8    RPS6    NDUFB6  CHCHD2P9
SEC61B  PSMB7   RPL35   BAMBI   ZFAND4  RPS24   ART5    RPL27A  RPS13   EIF3M
MRPL16  LAMTOR1 CLNS1A  TMEM126A        C11orf93        ATP5L   RPS25   C12orf57
CSAD    PFDN5   CNPY2   NACA    C12orf51        MRP63   EIF4A1P7        TPT1    ESD
COMMD6  EAPP    RPS29   RPL36A  RPS3AP6 RPS27L  RPLP1   MORF4L1 C15orf40
RPS15A  METTL9  RPL26   RPS7P1  RPL23A  RPL17   RPL19   KRT10   RPL27   RPS15
RPL36   TMED1   UQCRFS1 RPS19   LYPD3   SNRPD2  RPL18   RPS11   KLK5    EIF2S2
RNF114  DPM1    RPS21   ST13    XRCC6   FUNDC1  UXT     RPS4X   RPL39
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      4.58020427852195e-59    146.366576819407        0.680091343159643
38      91      translational termination
GO:0006414      3.38213362304763e-58    122.266798418972        0.784720780568819
39      105     translational elongation
GO:0006614      3.38213362304763e-58    122.266798418972        0.784720780568819
39      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      5.32575348629716e-58    120.433484750162        0.792194311812331
39      106     cotranslational protein targeting to membrane
GO:0045047      5.32575348629716e-58    120.433484750162        0.792194311812331
39      106     protein targeting to ER
GO:0072599      5.32575348629716e-58    120.433484750162        0.792194311812331
39      106     establishment of protein localization to endoplasmic reticulum
GO:0006413      1.7805400085611e-56     82.3396694214876        1.13597674901391
42      152     translational initiation
GO:0070972      8.3862438871158e-56     102.053935057788        0.881876686734482
39      118     protein localization to endoplasmic reticulum
GO:0000184      1.21871333762456e-53    95.5830687830688        0.889350217977995
38      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006612      1.07136259207137e-50    70.5480549199085        1.14345028025742
39      153     protein targeting to membrane
GO:0019080      4.20629708041496e-49    68.3615676359039        1.1285032177704 38
151     viral genome expression
GO:0019083      4.20629708041496e-49    68.3615676359039        1.1285032177704 38
151     viral transcription
GO:0043624      7.39063490526272e-49    67.1632298136646        1.14345028025742
38      153     cellular protein complex disassembly
GO:0043241      2.91462560720417e-48    64.3421428571429        1.18081793647498
38      158     protein complex disassembly
GO:0000956      5.02992104891155e-47    58.8937840785169        1.26302678015362
38      169     nuclear-transcribed mRNA catabolic process
GO:0072594      5.23455908171374e-47    50.8572453371593        1.52460037367656
40      204     establishment of protein localization to organelle
GO:0034623      1.7113446454692e-46     56.7086134453781        1.30039443637119
38      174     cellular macromolecular complex disassembly
GO:0019058      2.47949418495197e-46    45.5831107619796        1.7263857172514 41
231     viral infectious cycle
GO:0006402      4.42817693186929e-46    55.0728571428571        1.33028856134524
38      178     mRNA catabolic process
GO:0032984      5.59474172456195e-46    54.6784194528875        1.33776209258875
38      179     macromolecular complex disassembly
GO:0022415      4.32279565024158e-44    39.4659578818238        1.94311812331327
41      260     viral reproductive process
GO:0006401      1.51876948980354e-43    46.0810949529512        1.53207390492007
38      205     RNA catabolic process
GO:0016032      4.45820144890594e-38    23.5405405405405        3.37056259082416
44      451     viral reproduction
GO:0071845      7.23985373208038e-38    31.108362369338 2.12248287315757        38
284     cellular component disassembly at cellular level
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GO:0022411      1.25473837791022e-37    30.6019428571429        2.15237699813162
38      288     cellular component disassembly
GO:0033365      3.4103874100032e-33     19.7053275290216        3.53498027818144
41      473     protein localization to organelle
GO:0006605      3.71587653115593e-33    19.6584054324222        3.54245380942495
41      474     protein targeting
GO:0042274      3.07610727149457e-13    114.664 0.134523562383226       8       18
ribosomal small subunit biogenesis
GO:0022613      1.00265578829395e-11    11.7611816101519        1.68154452979033
16      225     ribonucleoprotein complex biogenesis
GO:0071843      2.49966109415737e-11    11.0118931565607        1.7861739671995 16
239     cellular component biogenesis at cellular level
GO:0006364      3.02294246046408e-10    17.3761223811107        0.777247249325306
11      104     rRNA processing
GO:0016072      5.56765771310408e-10    16.3161512027491        0.822088436786382
11      110     rRNA metabolic process
GO:0042254      1.10251701938669e-09    12.9616788321168        1.11355615528337
12      149     ribosome biogenesis
GO:0030490      1.01492952635634e-07    183.846153846154        0.0523147187045879
4       7       maturation of SSU-rRNA
GO:0034660      2.00803015829786e-07    7.07906346749226        2.12995640440108
13      285     ncRNA metabolic process
GO:0034470      2.90059233058808e-07    8.49255441008018        1.49470624870251
11      200     ncRNA processing
GO:0042273      1.39457871039722e-06    68.9182692307692        0.0896823749221507
4       12      ribosomal large subunit biogenesis
GO:0022618      6.89193924097439e-06    11.2269351935194        0.709985468133693
7       95      ribonucleoprotein complex assembly
GO:0000028      7.98768948879993e-06    136.571428571429        0.0448411874610754
3       6       ribosomal small subunit assembly
GO:0000462      7.98768948879993e-06    136.571428571429        0.0448411874610754
3       6       maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA,
5.8S rRNA, LSU-rRNA)
GO:0071826      9.68333273999527e-06    10.6196103481316        0.747353124351256
7       100     ribonucleoprotein complex subunit organization
Tissue: Skin_Sun_Exposed_Lower_leg=>Adipose_Subcutaneous        Type:   asymmetric
SourceGene:     BACH1-IT1(ENSG00000248476.1)
TargetGeneSet:  ATAD3A  MRTO4   GMEB1   U6      ATXN7L2 WDR3    GPATCH4 COG2
C1orf124        PPM1G   PNO1    POLR1A  SNRNP200        POLR1B  IWS1    SACM1L
IFRD2   RRP9    STAG1   GFM1    LSG1    FAM193A NOP14   HNRNPD  NAA15   NSUN2
UTP15   HARS    TCOF1   MAPK9   RIOK1   BAG6    WDR46   XPO5    SYNCRIP PUS7    RP11
KAT6A   KIAA2026        BAG1    NOL6    TESK1   CIZ1    ZMYND19 RRP12   CHUK
PPRC1   NOLC1   EIF6    SEC23IP CARS    NUP98   SF1     KLC2    DDX10   NOP2
DDX23   MARS    UTP20   ANAPC7  DDX55   PUS1    EP400   TSC22D1 KTN1-AS1
ZNF598  TRAP1   USP7    FBRS    SRCAP   SETD1A  E2F4    ZC3H18  MYBBP1A DHX33   PEMT
UTP6    TADA2A  SEH1L   DNMT1   PDE4A   ILF3    TNPO2   CC2D1A  ZNF333  CCDC97
TOMM40  CD3EAP  DHX34   GRWD1   ZNF335  DDX27   SCAF4   RRP1B   RRP1    PWP2
DEPDC5  PPP6R2  TIMM8A
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0071843      5.95310092169323e-15    18.0618618618619        1.27347588402187
17      239     cellular component biogenesis at cellular level
GO:0022613      4.12246425166107e-14    17.7770805553377        1.19887897031347
16      225     ribonucleoprotein complex biogenesis
GO:0042254      9.14114553339902e-13    21.2653952205882        0.793924295896478
13      149     ribosome biogenesis
GO:0034660      1.59772681679339e-12    13.753427996831 1.51858002906373        16
285     ncRNA metabolic process
GO:0034470      3.9079936678959e-11     15.4103442513369        1.0656701958342 13
200     ncRNA processing
GO:0006364      1.76290035351077e-10    22.6738647189584        0.554148501833783
10      104     rRNA processing
GO:0016072      3.08801441221038e-10    21.3044776119403        0.586118607708809
10      110     rRNA metabolic process
```

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GO:0006473      5.21450453179506e-06    11.7793388429752        0.682028925333887
7       128     protein acetylation
GO:0043543      1.1323242897632e-05     10.3919708029197        0.767282541000623
7       144     protein acylation
Tissue: Skin_Sun_Exposed_Lower_leg=>Adipose_Subcutaneous        Type:   cluster
SourceGene:     BACH1-IT1(ENSG00000248476.1)
TargetGeneSet:  ATAD3A  MRTO4   GMEB1   U6      ATXN7L2 WDR3    GPATCH4 COG2
C1orf124        PPM1G   PNO1    POLR1A  SNRNP200        POLR1B  IWS1    SACM1L
IFRD2   RRP9    STAG1   GFM1    LSG1    FAM193A NOP14   HNRNPD  NAA15   NSUN2
UTP15   HARS    TCOF1   MAPK9   RIOK1   BAG6    WDR46   XPO5    SYNCRIP PUS7    RP11
KAT6A   KIAA2026        BAG1    NOL6    TESK1   CIZ1    ZMYND19 RRP12   CHUK
PPRC1   NOLC1   EIF6    SEC23IP CARS    NUP98   SF1     KLC2    DDX10   NOP2
DDX23   MARS    UTP20   ANAPC7  DDX55   PUS1    EP400   TSC22D1 KTN1-AS1
ZNF598  TRAP1   USP7    FBRS    SRCAP   SETD1A  E2F4    ZC3H18  MYBBP1A DHX33   PEMT
UTP6    TADA2A  SEH1L   DNMT1   PDE4A   ILF3    TNPO2   CC2D1A  ZNF333  CCDC97
TOMM40  CD3EAP  DHX34   GRWD1   ZNF335  DDX27   SCAF4   RRP1B   RRP1    PWP2
DEPDC5  PPP6R2  TIMM8A
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0071843      5.95310092169323e-15    18.0618618618619        1.27347588402187
17      239     cellular component biogenesis at cellular level
GO:0022613      4.12246425166107e-14    17.7770805553377        1.19887897031347
16      225     ribonucleoprotein complex biogenesis
GO:0042254      9.14114553339902e-13    21.2653952205882        0.793924295896478
13      149     ribosome biogenesis
GO:0034660      1.59772681679339e-12    13.753427996831 1.51858002906373        16
285     ncRNA metabolic process
GO:0034470      3.9079936678959e-11     15.4103442513369        1.0656701958342 13
200     ncRNA processing
GO:0006364      1.76290035351077e-10    22.6738647189584        0.554148501833783
10      104     rRNA processing
GO:0016072      3.08801441221038e-10    21.3044776119403        0.586118607708809
10      110     rRNA metabolic process
GO:0006473      5.21450453179506e-06    11.7793388429752        0.682028925333887
7       128     protein acetylation
GO:0043543      1.1323242897632e-05     10.3919708029197        0.767282541000623
7       144     protein acylation
Tissue: Skin_Sun_Exposed_Lower_leg=>Adipose_Subcutaneous        Type:   asymmetric
SourceGene:     CDSN(ENSG00000204539.3)
TargetGeneSet:  SLC35E2B        RP11    PLA2G2F RP4     RPL5    TSHB    RAB25
SPATA17 RHOQ    UBC     ASPRV1  TPRKB   PMS1    EEF1B2  RPL29   SPCS1   RPL24
ZBTB38  RPL35A  NUP54   RPL34   OSTC    FRG1    CTB     RPS14   GPLD1   HIST1H1B
RPL10A  DST     SENP6   MRPS12  AIG1    HOXA5   NT5C3   GRB10   PRKAR2B SSBP1   RPS6
HRCT1   DAPK1   RPL12   RPL7A   C9orf104        ITGB1   RPL13AP5        BLOC1S2
ZBED5   PEX16   POLR2G  RPS25   WNT5B   HNRNPA1 SNRPF   RPL18AP3        C12orf45
RPL6    RPLP0   ALG5    EXOC5   ZNF280D MYO1E   RPS3AP6 TIPIN   RPS2    LITAF
RPL13   CTD     RPL19   DUSP3   ANKRD40 NT5C    TMEM241 HNRNPA1P7       PIP5K1C
ZNF823  ZNF44   RNASEH2A        RPS19   PLA2G4C RPL18   TEAD2   RPS5    RPL12P4
MRPL39  RPL3    ATXN10  FOXO4
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0070972      4.01447120634584e-31    69.1597894736842        0.596083316033493
23      118     protein localization to endoplasmic reticulum
GO:0006414      1.63532109211547e-30    74.2948263642807        0.530413120199294
22      105     translational elongation
GO:0006614      1.63532109211547e-30    74.2948263642807        0.530413120199294
22      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      2.0566077911272e-30     73.4052287581699        0.535464673725002
22      106     cotranslational protein targeting to membrane
GO:0045047      2.0566077911272e-30     73.4052287581699        0.535464673725002
22      106     protein targeting to ER
GO:0072599      2.0566077911272e-30     73.4052287581699        0.535464673725002
22      106     establishment of protein localization to endoplasmic reticulum
GO:0006415      4.27946954834511e-30    82.5461538461538        0.459691370839388
21      91      translational termination
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GO:0006612      2.44265744126145e-28    50.416  0.772887689433257       23      153
protein targeting to membrane
GO:0000184      2.03494710616023e-27    58.8461538461538        0.6011348695592 21
119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      8.8461963931469e-27     47.6482748138015        0.762784582381842
22      151     viral genome expression
GO:0019083      8.8461963931469e-27     47.6482748138015        0.762784582381842
22      151     viral transcription
GO:0072594      2.41925650647136e-25    36.080773480663 1.03051691924434        23
204     establishment of protein localization to organelle
GO:0006413      4.75051194318713e-25    43.9205813270699        0.76783613590755
21      152     translational initiation
GO:0043624      5.48718732480764e-25    43.5847902097902        0.772887689433257
21      153     cellular protein complex disassembly
GO:0043241      1.11119910296306e-24    41.979365524986 0.798145457061795       21
158     protein complex disassembly
GO:0000956      4.83123073510223e-24    38.829261954262 0.853712545844578       21
169     nuclear-transcribed mRNA catabolic process
GO:0034623      9.1051683141697e-24     37.5471342383107        0.878970313473116
21      174     cellular macromolecular complex disassembly
GO:0006401      9.51942795376862e-24    33.4608378870674        1.03556847277005
22      205     RNA catabolic process
GO:0006402      1.49043956798558e-23    36.5802302792749        0.899176527575946
21      178     mRNA catabolic process
GO:0032984      1.68267352320826e-23    36.3461538461538        0.904228081101654
21      179     macromolecular complex disassembly
GO:0019058      1.3797664014186e-22     29.2445820433437        1.16690886443845
22      231     viral infectious cycle
GO:0022415      1.8967345325648e-21     25.6286043829296        1.31340391668397
22      260     viral reproductive process
GO:0071845      3.00383735976349e-19    21.6741006142147        1.43464120130095
21      284     cellular component disassembly at cellular level
GO:0022411      4.01641446014241e-19    21.3433448573898        1.45484741540378
21      288     cellular component disassembly
GO:0006605      3.61892328803731e-18    15.1597278911565        2.39443637118538
24      474     protein targeting
GO:0016032      1.80512837404464e-17    14.9929906542056        2.27825064009411
23      451     viral reproduction
GO:0033365      5.1442244587579e-17     14.2375111111111        2.38938481765968
23      473     protein localization to organelle
GO:0071843      2.39667406935383e-09    12.2634505669098        1.20732129264411
12      239     cellular component biogenesis at cellular level
GO:0022613      1.55708901662507e-08    11.7428399155864        1.1365995432842 11
225     ribonucleoprotein complex biogenesis
GO:0042254      5.72128400092112e-08    14.3015625      0.752681475330427       9
149     ribosome biogenesis
GO:0042274      1.73804767524059e-06    59.4782608695652        0.0909279634627361
4       18      ribosomal small subunit biogenesis
GO:0000028      2.44679800247836e-06    205.357142857143        0.0303093211542454
3       6       ribosomal small subunit assembly
GO:0006364      1.38417502241937e-05    13.0490405117271        0.525361566673587
6       104     rRNA processing
GO:0016072      1.90780185477206e-05    12.2910447761194        0.555670887827832
6       110     rRNA metabolic process
Tissue: Skin_Sun_Exposed_Lower_leg=>Adipose_Subcutaneous        Type:   asymmetric
SourceGene:     FLG(ENSG00000143631.9)
TargetGeneSet:  TNFRSF25        VPS13D  UBR4    SH3BGRL3        KHDRBS1 KPNA7
TMEM234 EIF2C3  MACF1   PPCS    RPS8    TXNDC12 EFCAB7  TCTEX1D1        RP4     RPL5
RP11    DPH5    ATP5F1  HIPK1   POGZ    RPS27   MTX1    PRRC2C  PIK3C2B LPGAT1
ZC3H11B HIST3H2A        YWHAQ   SOS1-IT1        CCDC104 AAK1    ANKRD36BP2
PDE11A  EEF1B2  ITPR1   SETD5   RPL15   GOLGA4  RPSA    RPL14   ZNF445  NICN1   RBM6
RPL29   SPCS1   ATXN7   PCNP    ALDH1L1-AS1     H1FX    IGSF10  RPL22L1 AFAP1
RELL1   OCIAD1  PPA2    CCDC109B        RPS3A   CTSO    WWC2    TAF9    BTF3
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ZFYVE16 CTD     AFF4    SKP1    CTB     SYNPO   UBLCP1  RPL15P3 RPL10A  GLO1
YIPF3   EEF1A1  VTA1    HIVEP2  ARID1B  MLLT4   NPM1P13 EEF1A1P6        NT5C3
RPS3AP26        BUD31   MUC3A   SH2B2   ARMC10  MLL3    CHMP7   HMBOX1  KAT6A
HOOK3   CPNE3   EIF3E   EBAG9   EIF3H   TATDN1  LY6E    RPL8    RPS6    TESK1   TLN1
CLTA    LINC00092       KLF4    EEF1A1P5        RPL7A   U6      RPS3AP5 TCTN3
C10orf12        SFR1    NHLRC2  RPL27A  ZBED5   EIF3M   PEX16   CELF1   TMEM179B
NAA40   PPP2R5B C11orf2 C11orf30        GUCY1A2 WNT5B   PHB2    H3F3C   ADCY6
SMARCC2 NACA    RPL18AP3        ATXN2   RPL6    RPLP0   MLXIP   RPSAP54 ALG5    DGKH
THSD1P1 EAPP    LGALS3  SIPA1L1 TTBK2   RPS3AP47        CCNDBP1 COPS2   RSL24D1
RAB11A  LRRC49  ZNF592  RPS2    LITAF   NDE1    ARL6IP1 EIF3C   DDX19B  RPL13
SGSM2   RPL26   STX8    NCOR1   RPL17P43        TAOK1   RPL19   SMARCE1 RAMP2
VPS25   AOC3    ANKRD40 CEP95   PRKCA   NT5C    FOXK2   MPPE1   PSMG2   C18orf21
RPL17   RPS15   PIP5K1C RPL36   ALKBH7  HNRNPA1P10      LPHN1   RPL18A  ZNF585A
MEGF8   ZNF221  PVR     OPA3    RPL18   RPL13A  ZNF551  RPS5    ZNF446  UBE2M   DTD1
RPL41P1 RPL12P4 CBR3-AS1        TFF3    UBE2G2  YDJC    ZNF70   LIMK2   EIF3L   RPL3
TCF20   IGBP1   RPS23P8 RPS4X   HK2P1   RP1-177G6.2     RPL10   SLC10A3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      4.19883651788368e-36    45.1099508599509        1.18434710400664
31      105     translational elongation
GO:0006413      5.16994216446099e-35    31.6502430692419        1.71448342675247
34      152     translational initiation
GO:0006415      6.61977574294832e-35    49.6574386133847        1.02643415680576
29      91      translational termination
GO:0006614      1.85699031974156e-34    42.7458646616541        1.18434710400664
30      105     SRP-dependent cotranslational protein targeting to membrane
GO:0070972      2.54104864908073e-34    38.3342911877395        1.33098055497889
31      118     protein localization to endoplasmic reticulum
GO:0006613      2.56679635719011e-34    42.1804511278196        1.19562660023528
30      106     cotranslational protein targeting to membrane
GO:0045047      2.56679635719011e-34    42.1804511278196        1.19562660023528
30      106     protein targeting to ER
GO:0072599      2.56679635719011e-34    42.1804511278196        1.19562660023528
30      106     establishment of protein localization to endoplasmic reticulum
GO:0000184      1.26820094811398e-32    35.9863140998564        1.34226005120753
30      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006612      1.69750253516887e-30    27.2693740685544        1.72576292298111
31      153     protein targeting to membrane
GO:0072594      2.13473847346771e-30    21.8883720930233        2.30101723064148
34      204     establishment of protein localization to organelle
GO:0034623      1.15351800509854e-28    23.2302924348379        1.96263234378244
31      174     cellular macromolecular complex disassembly
GO:0006402      2.40969659025114e-28    22.5917851989281        2.00775032869698
31      178     mRNA catabolic process
GO:0032984      2.88836305185148e-28    22.4375511875512        2.01902982492561
31      179     macromolecular complex disassembly
GO:0019080      7.81204076880227e-28    25.1293124541228        1.70320393052384
29      151     viral genome expression
GO:0019083      7.81204076880227e-28    25.1293124541228        1.70320393052384
29      151     viral transcription
GO:0000956      1.06184197692109e-27    22.9604587007086        1.90623486263926
30      169     nuclear-transcribed mRNA catabolic process
GO:0043624      1.1697180491529e-27     24.7205103514685        1.72576292298111
29      153     cellular protein complex disassembly
GO:0043241      3.12606670420876e-27    23.7539627444174        1.78216040412428
29      158     protein complex disassembly
GO:0006401      2.21540800047131e-26    19.0497213514455        2.31229672687011
31      205     RNA catabolic process
GO:0019058      2.41564116429031e-22    15.0913994384513        2.60556362881462
29      231     viral infectious cycle
GO:0071845      5.30241404916631e-22    13.0280572523656        3.20337692893225
31      284     cellular component disassembly at cellular level
GO:0022411      8.08549203688693e-22    12.8216307039264        3.24849491384679
31      288     cellular component disassembly
```

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GO:0022415      7.07728650055852e-21    13.1696388188926        2.93266901944502
29      260     viral reproductive process
GO:0033365      3.6363156943002e-20     8.98459431701472        5.33520171614421
36      473     protein localization to organelle
GO:0006605      3.90054463529613e-20    8.9634343652249 5.34648121237285        36
474     protein targeting
GO:0016032      5.5316886595421e-18     8.42307692307692        5.08705279911425
33      451     viral reproduction
GO:0071843      8.35096820201633e-08    6.36341698841699        2.69579959864369
15      239     cellular component biogenesis at cellular level
GO:0022613      1.60694009045159e-06    5.75433962264151        2.53788665144281
13      225     ribonucleoprotein complex biogenesis
GO:0042254      7.1899920759704e-06     6.65303051676306        1.68064493806657
10      149     ribosome biogenesis
Tissue: Skin_Sun_Exposed_Lower_leg=>Adipose_Subcutaneous        Type:   cluster
SourceGene:     FLG(ENSG00000143631.9)
TargetGeneSet:  TNFRSF25        VPS13D  UBR4    SH3BGRL3        KHDRBS1 KPNA7
TMEM234 EIF2C3  MACF1   PPCS    RPS8    TXNDC12 EFCAB7  TCTEX1D1        RP4     RPL5
RP11    DPH5    ATP5F1  HIPK1   POGZ    RPS27   MTX1    PRRC2C  PIK3C2B LPGAT1
ZC3H11B HIST3H2A        YWHAQ   SOS1-IT1        CCDC104 AAK1    ANKRD36BP2
PDE11A  EEF1B2  ITPR1   SETD5   RPL15   GOLGA4  RPSA    RPL14   ZNF445  NICN1   RBM6
RPL29   SPCS1   ATXN7   PCNP    ALDH1L1-AS1     H1FX    IGSF10  RPL22L1 AFAP1
RELL1   OCIAD1  PPA2    CCDC109B        RPS3A   CTSO    WWC2    TAF9    BTF3
ZFYVE16 CTD     AFF4    SKP1    CTB     SYNPO   UBLCP1  RPL15P3 RPL10A  GLO1
YIPF3   EEF1A1  VTA1    HIVEP2  ARID1B  MLLT4   NPM1P13 EEF1A1P6        NT5C3
RPS3AP26        BUD31   MUC3A   SH2B2   ARMC10  MLL3    CHMP7   HMBOX1  KAT6A
HOOK3   CPNE3   EIF3E   EBAG9   EIF3H   TATDN1  LY6E    RPL8    RPS6    TESK1   TLN1
CLTA    LINC00092       KLF4    EEF1A1P5        RPL7A   U6      RPS3AP5 TCTN3
C10orf12        SFR1    NHLRC2  RPL27A  ZBED5   EIF3M   PEX16   CELF1   TMEM179B
NAA40   PPP2R5B C11orf2 C11orf30        GUCY1A2 WNT5B   PHB2    H3F3C   ADCY6
SMARCC2 NACA    RPL18AP3        ATXN2   RPL6    RPLP0   MLXIP   RPSAP54 ALG5    DGKH
THSD1P1 EAPP    LGALS3  SIPA1L1 TTBK2   RPS3AP47        CCNDBP1 COPS2   RSL24D1
RAB11A  LRRC49  ZNF592  RPS2    LITAF   NDE1    ARL6IP1 EIF3C   DDX19B  RPL13
SGSM2   RPL26   STX8    NCOR1   RPL17P43        TAOK1   RPL19   SMARCE1 RAMP2
VPS25   AOC3    ANKRD40 CEP95   PRKCA   NT5C    FOXK2   MPPE1   PSMG2   C18orf21
RPL17   RPS15   PIP5K1C RPL36   ALKBH7  HNRNPA1P10      LPHN1   RPL18A  ZNF585A
MEGF8   ZNF221  PVR     OPA3    RPL18   RPL13A  ZNF551  RPS5    ZNF446  UBE2M   DTD1
RPL41P1 RPL12P4 CBR3-AS1        TFF3    UBE2G2  YDJC    ZNF70   LIMK2   EIF3L   RPL3
TCF20   IGBP1   RPS23P8 RPS4X   HK2P1   RP1-177G6.2     RPL10   SLC10A3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      4.19883651788368e-36    45.1099508599509        1.18434710400664
31      105     translational elongation
GO:0006413      5.16994216446099e-35    31.6502430692419        1.71448342675247
34      152     translational initiation
GO:0006415      6.61977574294832e-35    49.6574386133847        1.02643415680576
29      91      translational termination
GO:0006614      1.85699031974156e-34    42.7458646616541        1.18434710400664
30      105     SRP-dependent cotranslational protein targeting to membrane
GO:0070972      2.54104864908073e-34    38.3342911877395        1.33098055497889
31      118     protein localization to endoplasmic reticulum
GO:0006613      2.56679635719011e-34    42.1804511278196        1.19562660023528
30      106     cotranslational protein targeting to membrane
GO:0045047      2.56679635719011e-34    42.1804511278196        1.19562660023528
30      106     protein targeting to ER
GO:0072599      2.56679635719011e-34    42.1804511278196        1.19562660023528
30      106     establishment of protein localization to endoplasmic reticulum
GO:0000184      1.26820094811398e-32    35.9863140998564        1.34226005120753
30      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006612      1.69750253516887e-30    27.2693740685544        1.72576292298111
31      153     protein targeting to membrane
GO:0072594      2.13473847346771e-30    21.8883720930233        2.30101723064148
34      204     establishment of protein localization to organelle
GO:0034623      1.15351800509854e-28    23.2302924348379        1.96263234378244
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31      174     cellular macromolecular complex disassembly
GO:0006402      2.40969659025114e-28    22.5917851989281        2.00775032869698
31      178     mRNA catabolic process
GO:0032984      2.88836305185148e-28    22.4375511875512        2.01902982492561
31      179     macromolecular complex disassembly
GO:0019080      7.81204076880227e-28    25.1293124541228        1.70320393052384
29      151     viral genome expression
GO:0019083      7.81204076880227e-28    25.1293124541228        1.70320393052384
29      151     viral transcription
GO:0000956      1.06184197692109e-27    22.9604587007086        1.90623486263926
30      169     nuclear-transcribed mRNA catabolic process
GO:0043624      1.1697180491529e-27     24.7205103514685        1.72576292298111
29      153     cellular protein complex disassembly
GO:0043241      3.12606670420876e-27    23.7539627444174        1.78216040412428
29      158     protein complex disassembly
GO:0006401      2.21540800047131e-26    19.0497213514455        2.31229672687011
31      205     RNA catabolic process
GO:0019058      2.41564116429031e-22    15.0913994384513        2.60556362881462
29      231     viral infectious cycle
GO:0071845      5.30241404916631e-22    13.0280572523656        3.20337692893225
31      284     cellular component disassembly at cellular level
GO:0022411      8.08549203688693e-22    12.8216307039264        3.24849491384679
31      288     cellular component disassembly
GO:0022415      7.07728650055852e-21    13.1696388188926        2.93266901944502
29      260     viral reproductive process
GO:0033365      3.6363156943002e-20     8.98459431701472        5.33520171614421
36      473     protein localization to organelle
GO:0006605      3.90054463529613e-20    8.9634343652249 5.34648121237285        36
474     protein targeting
GO:0016032      5.5316886595421e-18     8.42307692307692        5.08705279911425
33      451     viral reproduction
GO:0071843      8.35096820201633e-08    6.36341698841699        2.69579959864369
15      239     cellular component biogenesis at cellular level
GO:0022613      1.60694009045159e-06    5.75433962264151        2.53788665144281
13      225     ribonucleoprotein complex biogenesis
GO:0042254      7.1899920759704e-06     6.65303051676306        1.68064493806657
10      149     ribosome biogenesis
Tissue: Adipose_Subcutaneous=>Skin_Sun_Exposed_Lower_leg        Type:   asymmetric
SourceGene:     HIST1H2BPS3(ENSG00000226908.1)
TargetGeneSet:  ARHGEF19-AS1    RPL11   ZCCHC17 RP11    PPIE    CCDC23  RPS8
UQCRH   BTF3L4  ZYG11A  HBXIP   MRPS21  PAQR6   DCAF6   OCLM    SNRPE   NFASC   SRP9
TOMM20  RPS7    UBC     COA5    TXNDC9  RPL31   ERCC3   BBS5    NIF3L1  NBEAL1
EEF1B2  CCDC51  RYK     CLDN18  EIF2S1  PARL    NCBP2   TMEM128 C4orf52 RPL34   OSTC
RPS3A   CDKN2AIP        CTD     TAF9    ZFYVE16 CAMLG   PDF     TMEM14C TMEM14B
EEF1A1  IL6     RPS3AP26        GIGYF1  MRPS33  PRAGMIN C8orf40 RPS20   PAF1    RPS6
CLTA    C10orf31        RPS24   C10orf95        FAM204A FAM45A  PRKRIR  CLNS1A
RPS25   KANSL2  PRKAG1  PFDN5   C12orf47        RPL6    EBPL    CCNB1IP1        SNX6
QRSL1P3 PSEN1   MOAP1   TMEM87A PLDN    RSL24D1 RPS3AP6 SEC11A  RSL1D1  RPS15A
LYRM1   HSBP1   MED11   RPAIN   MIR497HG        RPL26   RPS7P1  ZNHIT3  RPL19
RPL27   RPS7P11 MRPS23  CEP95   NUP85   C18orf21        RPL17   CTB     KXD1
ZNF91   MED29   ZNF350  ZNF530  SNHG11  LINC00266-1     C22orf39        SNRPD3
TFIP11
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      4.68879241829736e-26    56.9770687936191        0.574008719119784
20      105     translational elongation
GO:0006614      2.60000832159518e-24    52.603488372093 0.574008719119784       19
105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      3.15525435272982e-24    51.9952107279694        0.579475468825687
19      106     cotranslational protein targeting to membrane
GO:0045047      3.15525435272982e-24    51.9952107279694        0.579475468825687
19      106     protein targeting to ER
GO:0072599      3.15525435272982e-24    51.9952107279694        0.579475468825687
19      106     establishment of protein localization to endoplasmic reticulum
```

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GO:0070972      2.77648144031352e-23    45.6543771043771        0.645076465296519
19      118     protein localization to endoplasmic reticulum
GO:0072594      6.07173632209886e-23    30.0925390399075        1.11521694000415
22      204     establishment of protein localization to organelle
GO:0006415      4.66691310185766e-22    52.9786399302528        0.497474223237146
17      91      translational termination
GO:0000184      1.45095272374048e-21    41.6942054861224        0.650543215002422
18      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      3.74181197590497e-21    34.1616161616162        0.825479205591309
19      151     viral genome expression
GO:0019083      3.74181197590497e-21    34.1616161616162        0.825479205591309
19      151     viral transcription
GO:0006413      4.25934168104889e-21    33.902380952381 0.830945955297211       19
152     translational initiation
GO:0006612      4.84392698848335e-21    33.6470149253731        0.836412705003114
19      153     protein targeting to membrane
GO:0019058      5.97187770952481e-19    22.7504217206201        1.26281918206353
20      231     viral infectious cycle
GO:0000956      9.91995462944465e-19    27.7904679187927        0.923880700297557
18      169     nuclear-transcribed mRNA catabolic process
GO:0006402      2.55635940821192e-18    26.2106557377049        0.973081447650682
18      178     mRNA catabolic process
GO:0043624      4.85934692713925e-18    28.7016129032258        0.836412705003114
17      153     cellular protein complex disassembly
GO:0022415      6.24684969268092e-18    19.9604519774011        1.4213549235347 20
260     viral reproductive process
GO:0043241      8.4773155886639e-18     27.6741020361473        0.863746453532627
17      158     protein complex disassembly
GO:0033365      2.7549704860241e-17     13.5311601538773        2.58577261089198
24      473     protein localization to organelle
GO:0006605      2.89098685052357e-17    13.5001212121212        2.59123936059788
24      474     protein targeting
GO:0006401      3.28504505635192e-17    22.3836240904708        1.12068368971005
18      205     RNA catabolic process
GO:0034623      4.45450046257981e-17    24.8258680912266        0.951214448827071
17      174     cellular macromolecular complex disassembly
GO:0032984      7.23068465679501e-17    24.0511748307447        0.978548197356584
17      179     macromolecular complex disassembly
GO:0016032      1.71301873968885e-15    12.5443094916779        2.46550411736212
22      451     viral reproduction
GO:0071845      1.04758933789708e-14    15.6482189079256        1.55255691647637
18      284     cellular component disassembly at cellular level
GO:0022411      1.33611111028828e-14    15.4120218579235        1.57442391529998
18      288     cellular component disassembly
GO:0022613      2.38077437408928e-10    13.156089193825 1.23001868382811        13
225     ribonucleoprotein complex biogenesis
GO:0071843      5.01844496662537e-10    12.3289085545723        1.30655317971075
13      239     cellular component biogenesis at cellular level
GO:0042274      3.48044442213014e-08    74.6309771309771        0.0984014947062487
5       18      ribosomal small subunit biogenesis
GO:0000387      6.52911111474096e-07    37.2817047817048        0.169469240882984
5       31      spliceosomal snRNP assembly
GO:0022618      8.36310802637277e-07    15.7809343434343        0.519341222060757
7       95      ribonucleoprotein complex assembly
GO:0071826      1.18534517842131e-06    14.9272700119474        0.546674970590271
7       100     ribonucleoprotein complex subunit organization
GO:0042254      1.48704832286028e-06    11.3722904804715        0.814545706179503
8       149     ribosome biogenesis
GO:0034660      3.29909815018209e-06    7.42924901185771        1.55802366618227
10      285     ncRNA metabolic process
Tissue: Adipose_Subcutaneous=>Skin_Sun_Exposed_Lower_leg        Type:   cluster
SourceGene:     HIST1H2BPS3(ENSG00000226908.1)
TargetGeneSet:  ARHGEF19-AS1    RPL11   ZCCHC17 RP11    PPIE    CCDC23  RPS8
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UQCRH   BTF3L4  ZYG11A  HBXIP   MRPS21  PAQR6   DCAF6   OCLM    SNRPE   NFASC   SRP9
TOMM20  RPS7    UBC     COA5    TXNDC9  RPL31   ERCC3   BBS5    NIF3L1  NBEAL1
EEF1B2  CCDC51  RYK     CLDN18  EIF2S1  PARL    NCBP2   TMEM128 C4orf52 RPL34   OSTC
RPS3A   CDKN2AIP        CTD     TAF9    ZFYVE16 CAMLG   PDF     TMEM14C TMEM14B
EEF1A1  IL6     RPS3AP26        GIGYF1  MRPS33  PRAGMIN C8orf40 RPS20   PAF1    RPS6
CLTA    C10orf31        RPS24   C10orf95        FAM204A FAM45A  PRKRIR  CLNS1A
RPS25   KANSL2  PRKAG1  PFDN5   C12orf47        RPL6    EBPL    CCNB1IP1        SNX6
QRSL1P3 PSEN1   MOAP1   TMEM87A PLDN    RSL24D1 RPS3AP6 SEC11A  RSL1D1  RPS15A
LYRM1   HSBP1   MED11   RPAIN   MIR497HG        RPL26   RPS7P1  ZNHIT3  RPL19
RPL27   RPS7P11 MRPS23  CEP95   NUP85   C18orf21        RPL17   CTB     KXD1
ZNF91   MED29   ZNF350  ZNF530  SNHG11  LINC00266-1     C22orf39        SNRPD3
TFIP11
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      4.68879241829736e-26    56.9770687936191        0.574008719119784
20      105     translational elongation
GO:0006614      2.60000832159518e-24    52.603488372093 0.574008719119784       19
105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      3.15525435272982e-24    51.9952107279694        0.579475468825687
19      106     cotranslational protein targeting to membrane
GO:0045047      3.15525435272982e-24    51.9952107279694        0.579475468825687
19      106     protein targeting to ER
GO:0072599      3.15525435272982e-24    51.9952107279694        0.579475468825687
19      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      2.77648144031352e-23    45.6543771043771        0.645076465296519
19      118     protein localization to endoplasmic reticulum
GO:0072594      6.07173632209886e-23    30.0925390399075        1.11521694000415
22      204     establishment of protein localization to organelle
GO:0006415      4.66691310185766e-22    52.9786399302528        0.497474223237146
17      91      translational termination
GO:0000184      1.45095272374048e-21    41.6942054861224        0.650543215002422
18      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      3.74181197590497e-21    34.1616161616162        0.825479205591309
19      151     viral genome expression
GO:0019083      3.74181197590497e-21    34.1616161616162        0.825479205591309
19      151     viral transcription
GO:0006413      4.25934168104889e-21    33.902380952381 0.830945955297211       19
152     translational initiation
GO:0006612      4.84392698848335e-21    33.6470149253731        0.836412705003114
19      153     protein targeting to membrane
GO:0019058      5.97187770952481e-19    22.7504217206201        1.26281918206353
20      231     viral infectious cycle
GO:0000956      9.91995462944465e-19    27.7904679187927        0.923880700297557
18      169     nuclear-transcribed mRNA catabolic process
GO:0006402      2.55635940821192e-18    26.2106557377049        0.973081447650682
18      178     mRNA catabolic process
GO:0043624      4.85934692713925e-18    28.7016129032258        0.836412705003114
17      153     cellular protein complex disassembly
GO:0022415      6.24684969268092e-18    19.9604519774011        1.4213549235347 20
260     viral reproductive process
GO:0043241      8.4773155886639e-18     27.6741020361473        0.863746453532627
17      158     protein complex disassembly
GO:0033365      2.7549704860241e-17     13.5311601538773        2.58577261089198
24      473     protein localization to organelle
GO:0006605      2.89098685052357e-17    13.5001212121212        2.59123936059788
24      474     protein targeting
GO:0006401      3.28504505635192e-17    22.3836240904708        1.12068368971005
18      205     RNA catabolic process
GO:0034623      4.45450046257981e-17    24.8258680912266        0.951214448827071
17      174     cellular macromolecular complex disassembly
GO:0032984      7.23068465679501e-17    24.0511748307447        0.978548197356584
17      179     macromolecular complex disassembly
GO:0016032      1.71301873968885e-15    12.5443094916779        2.46550411736212
22      451     viral reproduction
```

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GO:0071845      1.04758933789708e-14    15.6482189079256        1.55255691647637
18      284     cellular component disassembly at cellular level
GO:0022411      1.33611111028828e-14    15.4120218579235        1.57442391529998
18      288     cellular component disassembly
GO:0022613      2.38077437408928e-10    13.156089193825 1.23001868382811        13
225     ribonucleoprotein complex biogenesis
GO:0071843      5.01844496662537e-10    12.3289085545723        1.30655317971075
13      239     cellular component biogenesis at cellular level
GO:0042274      3.48044442213014e-08    74.6309771309771        0.0984014947062487
5       18      ribosomal small subunit biogenesis
GO:0000387      6.52911111474096e-07    37.2817047817048        0.169469240882984
5       31      spliceosomal snRNP assembly
GO:0022618      8.36310802637277e-07    15.7809343434343        0.519341222060757
7       95      ribonucleoprotein complex assembly
GO:0071826      1.18534517842131e-06    14.9272700119474        0.546674970590271
7       100     ribonucleoprotein complex subunit organization
GO:0042254      1.48704832286028e-06    11.3722904804715        0.814545706179503
8       149     ribosome biogenesis
GO:0034660      3.29909815018209e-06    7.42924901185771        1.55802366618227
10      285     ncRNA metabolic process
Tissue: Skin_Sun_Exposed_Lower_leg=>Adipose_Subcutaneous        Type:   asymmetric
SourceGene:     ITIH2(ENSG00000151655.12)
TargetGeneSet:  C1QA    C1QC    C1QB    VAV3    CD53    PTPN22  FCGR2A  HSPA6
PTPRC   KLHL12  NLRP3   REL     PLEK    HK2     VAMP8   CYTIP   PFKFB4  STAB1   CD86
TDGF1P6 KLHL7   YEATS2-AS1      FGF12-AS3       TLR2    MARCH1  SLC1A3  CTD
SERF1B  CD14    CSF1R   HAVCR2  DOCK2   F13A1   TRIM31  AIF1    FGD2    RNASET2
IKZF1   IRF5    TBXAS1  TAS2R4  RP11    SLA     SYK     FGD3    FKBP15  MRC1
ALOX5   PIK3AP1 GPAM    KCNQ1   TPP1    LYVE1   MS4A6A  MS4A7   CCDC88B FOLR2
SLCO2B1 MYO7A   IL10RA  GRAMD1B SLC37A2 PTPN6   CD163   C3AR1   GPR19   BIN2
ARHGAP9 CHST11  SELPLG  DENR    ALOX5AP GPR183  RNASE6  RIN3    PLCB2   PSTPIP1 MEFV
ITGAM   NOD2    CYBA    ARRB2   TMC8    FASN    FAM59A  GNA15   DENND1C VAV1
CD209   MYO1F   LRRC25  QPCTL   CD37    CD33    LILRB2  LAIR1   LILRA2  LILRA1
LILRB4  SIGLEC1 RP4     HCK     TRPM2   NFAM1   TLR7    TLR8    CYBB    WAS
ATP7A   BTK     SASH3   ARHGAP4
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0002252      4.64929932941652e-15    11.5845250639771        2.53754065462598
22      386     immune effector process
GO:0050778      2.06860823077317e-12    10.1528985507246        2.39291398519134
19      364     positive regulation of immune response
GO:0051249      3.6928613151707e-12     11.5447272026219        1.86042488409107
17      283     regulation of lymphocyte activation
GO:0046649      4.75697541221251e-12    9.00274414850686        2.84651581205453
20      433     lymphocyte activation
GO:0050865      7.75040933824717e-12    10.0922277722278        2.25486125527645
18      343     regulation of cell activation
GO:0002253      8.89163514691197e-12    10.8773413347881        1.96560791640717
17      299     activation of immune response
GO:0006954      1.5444731655871e-11     8.39457013574661        3.03716005812747
20      462     inflammatory response
GO:0001817      1.6552165497323e-11     9.60772365464448        2.36004428759255
18      359     regulation of cytokine production
GO:0002694      2.73910289637392e-11    10.0743927125506        2.11023458584181
17      321     regulation of leukocyte activation
GO:0050867      4.4185339385878e-11     11.7758333333333        1.57774548474154
15      240     positive regulation of cell activation
GO:0001816      7.99175910680171e-11    8.66795273691825        2.59670611030379
18      395     cytokine production
GO:0051251      1.20452972452744e-10    12.1718567655549        1.41339699674763
14      215     positive regulation of lymphocyte activation
GO:0042110      2.4962930731786e-10     9.39332414254084        2.0970867068023 16
319     T cell activation
GO:0002696      3.4920026195469e-10     11.1572241952759        1.53172790810325
14      233     positive regulation of leukocyte activation
```

GO:0002764	7.91708438270233e-10	10.4309380605677	1.63033700089959	14	248	immune response-regulating signaling pathway
GO:0002521	1.09870989918801e-09	9.19141986062718	1.98532973496644	15	302	leukocyte differentiation
GO:0050863	2.03171116026336e-09	10.7835365853659	1.45284063386617	13	221	regulation of T cell activation
GO:0002757	4.28282767285198e-09	10.0934959349593	1.54487578714276	13	235	immune response-activating signal transduction
GO:0051240	5.83317267710938e-09	6.92559419271748	2.99114248148917	17	455	positive regulation of multicellular organismal process
GO:0030098	8.87693882294628e-09	10.6656626506024	1.34108366203031	12	204	lymphocyte differentiation
GO:0002443	1.29617309746004e-08	10.2854029182055	1.3871012386686	12	211	leukocyte mediated immunity
GO:0050870	1.52546464459416e-08	11.61875	1.12414365787835	11	171	positive regulation of T cell activation
GO:0046651	1.62096576720511e-08	11.5457704821059	1.1307175973981	11	172	lymphocyte proliferation
GO:0032943	1.82811992378325e-08	11.4024978089395	1.14386547643762	11	174	mononuclear cell proliferation
GO:0050853	2.892807956625e-08	42.0117244748412	0.190644246072936	6	29	B cell receptor signaling pathway
GO:0070661	2.91327375525076e-08	10.8629211918686	1.19645699259567	11	182	leukocyte proliferation
GO:0050670	3.460543752458e-08	12.486391571554	0.946647290844924	10	144	regulation of lymphocyte proliferation
GO:0032944	3.69694969388881e-08	12.3930283224401	0.953221230364681	10	145	regulation of mononuclear cell proliferation
GO:0070663	5.1061780141714e-08	11.946218487395	0.986090927963463	10	150	regulation of leukocyte proliferation
GO:0030097	5.1249018514987e-08	6.3020417410019	3.04373399764722	16	463	hemopoiesis
GO:0050864	5.61233553369622e-08	17.9914974019839	0.53248910110027	8	81	regulation of B cell activation
GO:0050871	5.83874944861847e-08	24.2173597678917	0.354992734066847	7	54	positive regulation of B cell activation
GO:0042113	6.162525095668e-08	11.6931303990128	1.00581274652273	10	153	B cell activation
GO:0002250	6.92817607085643e-08	9.92226890756302	1.30164002491177	11	198	adaptive immune response
GO:0002697	8.07845295290836e-08	9.76353383458647	1.32136184347104	11	201	regulation of immune effector process
GO:0048534	1.28303207528184e-07	5.8674982162205	3.25410006227943	16	495	hemopoietic or lymphoid organ development
GO:0002449	1.40755423977504e-07	10.6399400524541	1.09784789979932	10	167	lymphocyte mediated immunity
GO:0050671	2.13483859705324e-07	14.9090909090909	0.631098193896616	8	96	positive regulation of lymphocyte proliferation
GO:0032946	2.31428507863939e-07	14.7405398424383	0.637672133416373	8	97	positive regulation of mononuclear cell proliferation
GO:0070665	2.93235676301156e-07	14.2568715642179	0.657393951975642	8	100	positive regulation of leukocyte proliferation
GO:0002460	2.98387086649269e-07	9.75920192638459	1.18988305307591	10	181	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains
GO:0006897	3.90705675177078e-07	6.696738172201	2.26800913431596	13	345	endocytosis
GO:0001819	4.03628815686415e-07	9.42439348620804	1.22932669019445	10	187	positive regulation of cytokine production
GO:0002768	4.2789146125138e-07	11.0240310077519	0.946647290844924	9	144	immune response-regulating cell surface receptor signaling pathway
GO:0032695	5.58308299541622e-07	90.1036106750392	0.0723133347173206	4	11	negative regulation of interleukin-12 production

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GO:0050707      5.84989016993478e-07    16.7139037433155        0.493045463981731
7       75      regulation of cytokine secretion
GO:0051607      7.52046966491052e-07    12.48035030104  0.742855165732475       8
113     defense response to virus
GO:0030217      8.4110703672493e-07     10.1155671570954        1.025534565082  9
156     T cell differentiation
GO:0042098      1.04663228106465e-06    11.908881922675 0.775724863331257       8
118     T cell proliferation
GO:0050715      1.09788502461903e-06    20.9721543722521        0.341844855027334
6       52      positive regulation of cytokine secretion
GO:0045088      1.44739083782945e-06    8.12109038737446        1.41339699674763
10      215     regulation of innate immune response
GO:0050663      1.74569161787216e-06    14.0186588103255        0.578506677738565
7       88      cytokine secretion
GO:0031347      2.23262646552198e-06    5.67723577235772        2.64929762646184
13      403     regulation of defense response
GO:0042108      2.341651746052e-06      18.1933432266271        0.387862431665629
6       59      positive regulation of cytokine biosynthetic process
GO:0002429      2.58657289106293e-06    10.4687816091954        0.874333956127604
8       133     immune response-activating cell surface receptor signaling pathway
GO:0032621      2.72629797643103e-06    234.032608695652        0.0328696975987821
3       5       interleukin-18 production
GO:0032655      3.06646316422408e-06    26.5296296296296        0.230087883191475
5       35      regulation of interleukin-12 production
GO:0045621      3.14464618440672e-06    17.215088282504 0.407584250224898       6
62      positive regulation of lymphocyte differentiation
GO:0045619      3.86048517389463e-06    12.3330039525692        0.650820012455885
7       99      regulation of lymphocyte differentiation
GO:0032615      4.07494624917772e-06    24.8680555555556        0.243235762230987
5       37      interleukin-12 production
GO:0042129      4.41287739692783e-06    12.0689071566731        0.663967891495398
7       101     regulation of T cell proliferation
GO:0042102      4.55065181314951e-06    16.0629213483146        0.433880008303924
6       66      positive regulation of T cell proliferation
GO:0009615      5.01757228999279e-06    7.00868701911144        1.62376306137984
10      247     response to virus
GO:0007229      5.42439944753266e-06    15.5425878941646        0.447027887343436
6       68      integrin-mediated signaling pathway
GO:0009306      8.06844089082708e-06    8.88826335131754        1.01896062556224
8       155     protein secretion
GO:0071706      8.21678493874274e-06    14.377662250545 0.479897584942219       6
73      tumor necrosis factor superfamily cytokine production
GO:0019724      9.85028159520951e-06    10.5929269328802        0.749429105252232
7       114     B cell mediated immunity
GO:0050708      1.10439899371224e-05    10.3971017514595        0.762576984291744
7       116     regulation of protein secretion
GO:0050714      1.12052339363367e-05    13.5638550403545        0.506193343021244
6       77      positive regulation of protein secretion
GO:0032602      1.36149834757131e-05    18.9338624338624        0.308975157428552
5       47      chemokine production
GO:0006959      1.53663161154454e-05    9.85049407114625        0.802020621410283
7       122     humoral immune response
GO:0046631      1.6118246502793e-05     12.6670609107037        0.539063040620026
6       82      alpha-beta T cell activation
GO:0050851      1.62070283714701e-05    9.76489028213166        0.808594560930039
7       123     antigen receptor-mediated signaling pathway
Tissue: Skin_Sun_Exposed_Lower_leg=>Adipose_Subcutaneous        Type:   cluster
SourceGene:     ITIH2(ENSG00000151655.12)
TargetGeneSet:  C1QA    C1QC    C1QB    VAV3    CD53    PTPN22  FCGR2A  HSPA6
PTPRC   KLHL12  NLRP3   REL     PLEK    HK2     VAMP8   CYTIP   PFKFB4  STAB1   CD86
TDGF1P6 KLHL7   YEATS2-AS1      FGF12-AS3       TLR2    MARCH1  SLC1A3  CTD
SERF1B  CD14    CSF1R   HAVCR2  DOCK2   F13A1   TRIM31  AIF1    FGD2    RNASET2
IKZF1   IRF5    TBXAS1  TAS2R4  RP11    SLA     SYK     FGD3    FKBP15  MRC1
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ALOX5   PIK3AP1 GPAM    KCNQ1   TPP1    LYVE1   MS4A6A  MS4A7   CCDC88B FOLR2
SLCO2B1 MYO7A   IL10RA  GRAMD1B SLC37A2 PTPN6   CD163   C3AR1   GPR19   BIN2
ARHGAP9 CHST11  SELPLG  DENR    ALOX5AP GPR183  RNASE6  RIN3    PLCB2   PSTPIP1 MEFV
ITGAM   NOD2    CYBA    ARRB2   TMC8    FASN    FAM59A  GNA15   DENND1C VAV1
CD209   MYO1F   LRRC25  QPCTL   CD37    CD33    LILRB2  LAIR1   LILRA2  LILRA1
LILRB4  SIGLEC1 RP4     HCK     TRPM2   NFAM1   TLR7    TLR8    CYBB    WAS
ATP7A   BTK     SASH3   ARHGAP4
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0002252      4.64929932941652e-15    11.5845250639771        2.53754065462598
22      386     immune effector process
GO:0050778      2.06860823077317e-12    10.1528985507246        2.39291398519134
19      364     positive regulation of immune response
GO:0051249      3.6928613151707e-12     11.5447272026219        1.86042488409107
17      283     regulation of lymphocyte activation
GO:0046649      4.75697541221251e-12    9.00274414850686        2.84651581205453
20      433     lymphocyte activation
GO:0050865      7.75040933824717e-12    10.0922277722278        2.25486125527645
18      343     regulation of cell activation
GO:0002253      8.89163514691197e-12    10.8773413347881        1.96560791640717
17      299     activation of immune response
GO:0006954      1.5444731655871e-11     8.39457013574661        3.03716005812747
20      462     inflammatory response
GO:0001817      1.6552165497323e-11     9.60772365464448        2.36004428759255
18      359     regulation of cytokine production
GO:0002694      2.73910289637392e-11    10.0743927125506        2.11023458584181
17      321     regulation of leukocyte activation
GO:0050867      4.4185339385878e-11     11.7758333333333        1.57774548474154
15      240     positive regulation of cell activation
GO:0001816      7.99175910680171e-11    8.66795273691825        2.59670611030379
18      395     cytokine production
GO:0051251      1.20452972452744e-10    12.1718567655549        1.41339699674763
14      215     positive regulation of lymphocyte activation
GO:0042110      2.4962930731786e-10     9.39332414254084        2.0970867068023 16
319     T cell activation
GO:0002696      3.4920026195469e-10     11.1572241952759        1.53172790810325
14      233     positive regulation of leukocyte activation
GO:0002764      7.91708438270233e-10    10.4309380605677        1.63033700089959
14      248     immune response-regulating signaling pathway
GO:0002521      1.09870989918801e-09    9.19141986062718        1.98532973496644
15      302     leukocyte differentiation
GO:0050863      2.03171116026336e-09    10.7835365853659        1.45284063386617
13      221     regulation of T cell activation
GO:0002757      4.28282767285198e-09    10.0934959349593        1.54487578714276
13      235     immune response-activating signal transduction
GO:0051240      5.83317267710938e-09    6.92559419271748        2.99114248148917
17      455     positive regulation of multicellular organismal process
GO:0030098      8.87693882294628e-09    10.6656626506024        1.34108366203031
12      204     lymphocyte differentiation
GO:0002443      1.29617309746004e-08    10.2854029182055        1.3871012386686 12
211     leukocyte mediated immunity
GO:0050870      1.52546464459416e-08    11.61875        1.12414365787835        11
171     positive regulation of T cell activation
GO:0046651      1.62096576720511e-08    11.5457704821059        1.1307175973981 11
172     lymphocyte proliferation
GO:0032943      1.82811992378325e-08    11.4024978089395        1.14386547643762
11      174     mononuclear cell proliferation
GO:0050853      2.892807956625e-08      42.0117244748412        0.190644246072936
6       29      B cell receptor signaling pathway
GO:0070661      2.91327375525076e-08    10.8629211918686        1.19645699259567
11      182     leukocyte proliferation
GO:0050670      3.460543752458e-08      12.486391571554 0.946647290844924       10
144     regulation of lymphocyte proliferation
GO:0032944      3.69694969388881e-08    12.3930283224401        0.953221230364681
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10      145     regulation of mononuclear cell proliferation
GO:0070663      5.1061780141714e-08     11.946218487395 0.986090927963463       10
150     regulation of leukocyte proliferation
GO:0030097      5.1249018514987e-08     6.3020417410019 3.04373399764722        16
463     hemopoiesis
GO:0050864      5.61233553369622e-08    17.9914974019839        0.53248910110027
8       81      regulation of B cell activation
GO:0050871      5.83874944861847e-08    24.2173597678917        0.354992734066847
7       54      positive regulation of B cell activation
GO:0042113      6.162525095668e-08      11.6931303990128        1.00581274652273
10      153     B cell activation
GO:0002250      6.92817607085643e-08    9.92226890756302        1.30164002491177
11      198     adaptive immune response
GO:0002697      8.07845295290836e-08    9.76353383458647        1.32136184347104
11      201     regulation of immune effector process
GO:0048534      1.28303207528184e-07    5.8674982162205 3.25410006227943        16
495     hemopoietic or lymphoid organ development
GO:0002449      1.40755423977504e-07    10.6399400524541        1.09784789979932
10      167     lymphocyte mediated immunity
GO:0050671      2.13483859705324e-07    14.9090909090909        0.631098193896616
8       96      positive regulation of lymphocyte proliferation
GO:0032946      2.31428507863939e-07    14.7405398424383        0.637672133416373
8       97      positive regulation of mononuclear cell proliferation
GO:0070665      2.93235676301156e-07    14.2568715642179        0.657393951975642
8       100     positive regulation of leukocyte proliferation
GO:0002460      2.98387086649269e-07    9.75920192638459        1.18988305307591
10      181     adaptive immune response based on somatic recombination of immune
receptors built from immunoglobulin superfamily domains
GO:0006897      3.90705675177078e-07    6.696738172201  2.26800913431596        13
345     endocytosis
GO:0001819      4.03628815686415e-07    9.42439348620804        1.22932669019445
10      187     positive regulation of cytokine production
GO:0002768      4.2789146125138e-07     11.0240310077519        0.946647290844924
9       144     immune response-regulating cell surface receptor signaling pathway
GO:0032695      5.58308299541622e-07    90.1036106750392        0.0723133347173206
4       11      negative regulation of interleukin-12 production
GO:0050707      5.84989016993478e-07    16.7139037433155        0.493045463981731
7       75      regulation of cytokine secretion
GO:0051607      7.52046966491052e-07    12.48035030104  0.742855165732475       8
113     defense response to virus
GO:0030217      8.4110703672493e-07     10.1155671570954        1.025534565082  9
156     T cell differentiation
GO:0042098      1.04663228106465e-06    11.908881922675 0.775724863331257       8
118     T cell proliferation
GO:0050715      1.09788502461903e-06    20.9721543722521        0.341844855027334
6       52      positive regulation of cytokine secretion
GO:0045088      1.44739083782945e-06    8.12109038737446        1.41339699674763
10      215     regulation of innate immune response
GO:0050663      1.74569161787216e-06    14.0186588103255        0.578506677738565
7       88      cytokine secretion
GO:0031347      2.23262646552198e-06    5.67723577235772        2.64929762646184
13      403     regulation of defense response
GO:0042108      2.341651746052e-06      18.1933432266271        0.387862431665629
6       59      positive regulation of cytokine biosynthetic process
GO:0002429      2.58657289106293e-06    10.4687816091954        0.874333956127604
8       133     immune response-activating cell surface receptor signaling pathway
GO:0032621      2.72629797643103e-06    234.032608695652        0.0328696975987821
3       5       interleukin-18 production
GO:0032655      3.06646316422408e-06    26.5296296296296        0.230087883191475
5       35      regulation of interleukin-12 production
GO:0045621      3.14464618440672e-06    17.215088282504 0.407584250224898       6
62      positive regulation of lymphocyte differentiation
GO:0045619      3.86048517389463e-06    12.3330039525692        0.650820012455885
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7       99      regulation of lymphocyte differentiation
GO:0032615      4.07494624917772e-06    24.8680555555556        0.243235762230987
5       37      interleukin-12 production
GO:0042129      4.41287739692783e-06    12.0689071566731        0.663967891495398
7       101     regulation of T cell proliferation
GO:0042102      4.55065181314951e-06    16.0629213483146        0.433880008303924
6       66      positive regulation of T cell proliferation
GO:0009615      5.01757228999279e-06    7.00868701911144        1.62376306137984
10      247     response to virus
GO:0007229      5.42439944753266e-06    15.5425878941646        0.447027887343436
6       68      integrin-mediated signaling pathway
GO:0009306      8.06844089082708e-06    8.88826335131754        1.01896062556224
8       155     protein secretion
GO:0071706      8.21678493874274e-06    14.377662250545 0.479897584942219       6
73      tumor necrosis factor superfamily cytokine production
GO:0019724      9.85028159520951e-06    10.5929269328802        0.749429105252232
7       114     B cell mediated immunity
GO:0050708      1.10439899371224e-05    10.3971017514595        0.762576984291744
7       116     regulation of protein secretion
GO:0050714      1.12052339363367e-05    13.5638550403545        0.506193343021244
6       77      positive regulation of protein secretion
GO:0032602      1.36149834757131e-05    18.9338624338624        0.308975157428552
5       47      chemokine production
GO:0006959      1.53663161154454e-05    9.85049407114625        0.802020621410283
7       122     humoral immune response
GO:0046631      1.6118246502793e-05     12.6670609107037        0.539063040620026
6       82      alpha-beta T cell activation
GO:0050851      1.62070283714701e-05    9.76489028213166        0.808594560930039
7       123     antigen receptor-mediated signaling pathway
Tissue: Skin_Sun_Exposed_Lower_leg=>Adipose_Subcutaneous        Type:   asymmetric
SourceGene:     ITIH5(ENSG00000123243.10)
TargetGeneSet:  RPL5    RP11    ACBD6   FAM129A SNRPE   RPS7P3  RP4     LINC00184
UBC     ASPRV1  TPRKB   DGUOK   RPIA    CCDC115 EEF1B2  IMPDH2  GRM2    RPL24
ZBTB38  MTHFD2L RPL34   EPB41L4A-AS1    CTB     NPM1    ERGIC1  TDP2    C6orf130
DST     MRPS12  AASS    CCDC136 SSBP1   ACTR3B  ESYT2   PHYHIP  RPS20   SNHG6
RPL30   COL14A1 RPL8    RPS6    RPL12   SSNA1   SLC25A16        ZDHHC6  SFXN4
EIF3M   LAMTOR1 TAF1D   RPS25   JAM3    PA2G4   PMCH    RPS2P5  RPLP0   TPT1    TMX1
GATM    RPS3AP6 PARP16  RPS2    SETD6   NQO1    EIF4A1  RPL27   DUSP3   STRA13  FBL
RPS19   RPL18   CTD     SNRPB   MYL9    RPL3    AMELX   RBM3    RPS4X   FAM122B
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      1.37290287199807e-24    65.751724137931 0.457753788665144       18
105     translational elongation
GO:0006415      6.39401949771585e-24    71.4858989424207        0.396719950176458
17      91      translational termination
GO:0006413      3.40217872490138e-23    46.2824675324675        0.662653103591447
19      152     translational initiation
GO:0006614      8.74213990076292e-23    60.054347826087 0.457753788665144       17
105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.0380492635078e-22     59.3754274548119        0.462113348557193
17      106     cotranslational protein targeting to membrane
GO:0045047      1.0380492635078e-22     59.3754274548119        0.462113348557193
17      106     protein targeting to ER
GO:0072599      1.0380492635078e-22     59.3754274548119        0.462113348557193
17      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      7.16419495487119e-22    52.2770124838571        0.514428067261781
17      118     protein localization to endoplasmic reticulum
GO:0000184      8.33292697399427e-22    51.7608695652174        0.51878762715383
17      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0000956      1.09434307592245e-20    37.7139072847682        0.73676562175628
18      169     nuclear-transcribed mRNA catabolic process
GO:0006402      2.84717607678322e-20    35.57   0.776001660784721       18      178
mRNA catabolic process
GO:0019080      5.64566457535249e-20    39.3118105126541        0.658293543699398
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17      151     viral genome expression
GO:0019083      5.64566457535249e-20    39.3118105126541        0.658293543699398
17      151     viral transcription
GO:0006612      7.10786592667512e-20    38.7282608695652        0.667012663483496
17      153     protein targeting to membrane
GO:0043624      7.10786592667512e-20    38.7282608695652        0.667012663483496
17      153     cellular protein complex disassembly
GO:0043241      1.24656410413481e-19    37.3418131359852        0.68881046294374‌1
17      158     protein complex disassembly
GO:0006401      3.76521331109698e-19    30.3764705882353        0.893709777870044
18      205     RNA catabolic process
GO:0034623      6.66196464841807e-19    33.4986153420105        0.758563421216525
17      174     cellular macromolecular complex disassembly
GO:0032984      1.08712553227867e-18    32.4533011272142        0.78036122067677
17      179     macromolecular complex disassembly
GO:0072594      1.02653306617973e-17    28.0652173913043        0.889350217977995
17      204     establishment of protein localization to organelle
GO:0019058      8.49142697558317e-17    24.4776513612353        1.00705833506332
17      231     viral infectious cycle
GO:0022415      6.21639667524559e-16    21.5123456790123        1.13348557193274
17      260     viral reproductive process
GO:0071845      2.71358709098729e-15    19.5454323400098        1.23811500934191
17      284     cellular component disassembly at cellular level
GO:0022411      3.42367614275736e-15    19.2514840365795        1.25555324891011
17      288     cellular component disassembly
GO:0016032      5.06635616100943e-12    11.8822881186135        1.9661615113141 17
451     viral reproduction
GO:0033365      1.07906029551034e-11    11.2911899313501        2.06207182893917
17      473     protein localization to organelle
GO:0006605      1.11574457936033e-11    11.2656740557511        2.06643138883122
17      474     protein targeting
GO:0022613      3.08854168778118e-09    14.0109633357297        0.980900975711023
11      225     ribonucleoprotein complex biogenesis
GO:0071843      5.81107353804976e-09    13.1376518218623        1.04193481419971
11      239     cellular component biogenesis at cellular level
GO:0042254      2.53669368384116e-07    14.6970986460348        0.6495744239153 8
149     ribosome biogenesis
GO:0022618      3.45736164571389e-06    16.9118864577173        0.414158189744654
6       95      ribonucleoprotein complex assembly
GO:0071826      4.66249303664084e-06    16.006718924972 0.435955989204899       6
100     ribonucleoprotein complex subunit organization
Tissue: Skin_Sun_Exposed_Lower_leg=>Adipose_Subcutaneous        Type:   cluster
SourceGene:     MAP4(ENSG00000047849.17)
TargetGeneSet:  RP4     SYF2    KHDRBS1 KPNA7   RP11    GAPDHP33        C1orf43
LPIN1   UBC     EIF5B   SNORD89 GLI2    UGGT1   MZT2B   ZRANB3  MMADHC  SLC40A1
SETD5   CRELD1  RPL15   GORASP1 MAP4    ATXN7   NDUFB4  PLXND1  COPB2   EIF2S1
EIF4G1  THPO    NOA1    FAM175A HSD17B11        EPB41L4A-AS1    AFF4    CAMLG
PCDHGC4 RPS14   MAT2B   TRIM41  RPL15P3 DEK     VARS    HLA-C   CSNK2B  AGPAT1
RPS18   YIPF3   C6orf72 ZNF277  ING3    MLL3    GOLGA7  HOOK3   EIF3E   EIF3H
TATDN1  RPL8    SMARCA2 TLN1    CLTA    MCART1  XPA     SPTAN1  EEF1A1P5
RPL7A   EIF2S2P3        PYROXD2 MRPL43  GBF1    SFR1    RPL27A  CKAP5   CD6
DNAJC4  C11orf2 PHB2    ATF7IP  ZCRB1   ARID2   PFDN5   NACA    RPL18AP3        RPL6
TRAC    GOLGA3  POLR1D  TPT1    ITM2B   HNRNPA3P5       RPS19P3 TIMM9   NEK9
KIAA1737        FAN1    UBR1    CCNDBP1 COPS2   C15orf39        SEC11A  MPG     CTD
NTAN1   GTF3C1  FTO     C16orf48        VPS53   RPL26   OMG     RPL19   CNTNAP1 CLTC
SUMO2   RPL17   TPGS1   NFIC    ALKBH7  PGLS    GPI     FAM98C  B3GNT8  GLTSCR2
RPL13A  ZNF524  CCDC106 RPS5    RRBP1   SCAND1  UBE2G2  DSTNP1  THAP7   TTC28
EIF3L   LINC00106       CHST7   IGBP1   SLC16A2 GPR174  AIFM1   RPL10   MT
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006413      1.50348157356512e-19    23.9208754208754        1.15701335547713
20      152     translational initiation
GO:0000184      5.80761101464227e-16    23.5290229291469        0.905819666459069
16      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
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GO:0006414      1.97119866493078e-15    25.0017543859649        0.799252646875649
15      105     translational elongation
GO:0006614      1.97119866493078e-15    25.0017543859649        0.799252646875649
15      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      2.28190457074742e-15    24.7252747252747        0.806864576845893
15      106     cotranslational protein targeting to membrane
GO:0045047      2.28190457074742e-15    24.7252747252747        0.806864576845893
15      106     protein targeting to ER
GO:0072599      2.28190457074742e-15    24.7252747252747        0.806864576845893
15      106     establishment of protein localization to endoplasmic reticulum
GO:0006415      6.15016037404275e-15    27.0151515151515        0.692685627292229
14      91      translational termination
GO:0070972      1.18170755331578e-14    21.8262646908533        0.898207736488824
15      118     protein localization to endoplasmic reticulum
GO:0006612      3.34669986240972e-14    17.6474607858363        1.16462528544737
16      153     protein targeting to membrane
GO:0000956      1.61154252642039e-13    15.7841746627729        1.28641616497128
16      169     nuclear-transcribed mRNA catabolic process
GO:0034623      2.54588053133933e-13    15.2792889846485        1.3244758148225 16
174     cellular macromolecular complex disassembly
GO:0006402      3.6322098745073e-13     14.8978198056212        1.35492353470348
16      178     mRNA catabolic process
GO:0032984      3.9641293195755e-13     14.8053778880042        1.36253546467373
16      179     macromolecular complex disassembly
GO:0043624      5.82808726800872e-13    16.2505720823799        1.16462528544737
15      153     cellular protein complex disassembly
GO:0043241      9.36613399522253e-13    15.6768494663231        1.2026849352986 15
158     protein complex disassembly
GO:0072594      2.99965710984588e-12    12.8139429606157        1.55283371392983
16      204     establishment of protein localization to organelle
GO:0006401      3.23349530185963e-12    12.7452437239671        1.56044564390008
16      205     RNA catabolic process
GO:0019080      7.81198589296222e-12    15.1198296836983        1.14940142550689
14      151     viral genome expression
GO:0019083      7.81198589296222e-12    15.1198296836983        1.14940142550689
14      151     viral transcription
GO:0071845      4.51469032940714e-11    9.6354556803995 2.16178811154937        17
284     cellular component disassembly at cellular level
GO:0022411      5.62549538531179e-11    9.49053684085228        2.19223583143035
17      288     cellular component disassembly
GO:0019058      2.2105555614356e-10     10.3252923976608        1.75835582312643
15      231     viral infectious cycle
GO:0022415      1.14607266483423e-09    9.084425349087  1.97910179226351        15
260     viral reproductive process
GO:0033365      1.66579391655435e-08    5.97104634495939        3.60044287592554
18      473     protein localization to organelle
GO:0006605      1.02496465035478e-07    5.55346933013341        3.60805480589579
17      474     protein targeting
GO:0016032      2.93149084197562e-07    5.44133039863047        3.43298041658017
16      451     viral reproduction
Tissue: Skin_Sun_Exposed_Lower_leg=>Adipose_Subcutaneous        Type:   asymmetric
SourceGene:     RAB11FIP5(ENSG00000135631.11)
TargetGeneSet:  NBPF1   MAN1C1  KHDRBS1 EIF2C3  SLFNL1  PPCS    TMEM53  RP4     RP11
AGL     HIPK1   MRPS21  PPP1R12B        SLC8A1  ST3GAL5 PDE11A  EEF1B2  ERBB4
ITM2C   ITPR1   LAMB2   ADAMTS9-AS1     LRIG1   RPL24   RPL22L1 NAT8L   AFAP1
RPS3A   FRG1    CTB     RPL15P3 C6orf130        YIPF3   RP1     DST     RARS2   BVES
HIVEP2  C6orf72 EEF1A1P6        NT5C3   RPS3AP26        CCDC136 SSBP1   RPL7
TATDN1  SLC45A4 RPS6    TLN1    CLTA    RPL12   FNBP1   EEF1A1P5        RPL7A
NACC2   SVIL    PRKG1   RPS24   RPS3AP5 EXOSC1  SFR1    ZDHHC6  RP13    ZBED5
C11orf9 GUCY1A2 JAM3    ADCY6   NACA    SLC35E3 RPL18AP3        RPL6    TPT1
DHRS4L2 EAPP    LGALS3  CCNDBP1 LITAF   PAPD5   RPL13   KIF1C   RPL26   RPL17P43
ANKRD40 PRKCA   NT5C    CTD     CTIF    RPL17   RPS15   PIP5K1C HNRNPA1P10
ZNF823  LPHN1   RPL18A  UBA52   RPL13A  ZNF551  RPS5    SLC24A3 RPL41P1 RPL12P4
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EIF3L   RPL3    UXT     RPS4X   RPL39   RPL10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      3.34308530451034e-27    56.6785714285714        0.610338384886859
21      105     translational elongation
GO:0006415      8.11219692278849e-27    62.9225352112676        0.528959933568611
20      91      translational termination
GO:0006402      1.03365059022287e-26    36.9168831168831        1.03466888104629
24      178     mRNA catabolic process
GO:0000184      5.71302332623627e-26    48.5340136054422        0.691716836205107
21      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0000956      1.08166172969118e-25    36.7261396811139        0.982354162341706
23      169     nuclear-transcribed mRNA catabolic process
GO:0006614      1.84568990510762e-25    52.5073529411765        0.610338384886859
20      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      2.26526531193945e-25    51.8931686046512        0.616151131409591
20      106     cotranslational protein targeting to membrane
GO:0045047      2.26526531193945e-25    51.8931686046512        0.616151131409591
20      106     protein targeting to ER
GO:0072599      2.26526531193945e-25    51.8931686046512        0.616151131409591
20      106     establishment of protein localization to endoplasmic reticulum
GO:0006413      3.42392842556969e-25    38.8602977667494        0.883537471455263
22      152     translational initiation
GO:0006401      3.43348159778401e-25    31.3502762430939        1.19161303716006
24      205     RNA catabolic process
GO:0070972      2.26075563861961e-24    45.500637755102 0.685904089682375       20
118     protein localization to endoplasmic reticulum
GO:0019080      4.02539928104472e-22    33.9599236641221        0.877724724932531
20      151     viral genome expression
GO:0019083      4.02539928104472e-22    33.9599236641221        0.877724724932531
20      151     viral transcription
GO:0006612      5.28706381099446e-22    33.4445488721804        0.889350217977995
20      153     protein targeting to membrane
GO:0043624      5.28706381099446e-22    33.4445488721804        0.889350217977995
20      153     cellular protein complex disassembly
GO:0043241      1.02780258194451e-21    32.2214673913044        0.918413950591655
20      158     protein complex disassembly
GO:0034623      7.45176687104006e-21    28.8413149350649        1.01141789495537
20      174     cellular macromolecular complex disassembly
GO:0032984      1.32853705363753e-20    27.9245283018868        1.04048162756903
20      179     macromolecular complex disassembly
GO:0072594      1.87577859497437e-19    24.0879755434783        1.18580029063733
20      204     establishment of protein localization to organelle
GO:0019058      2.25399144564704e-18    20.9656398104265        1.34274444675109
20      231     viral infectious cycle
GO:0022415      2.33499315247846e-17    18.39453125     1.51131409591032        20
260     viral reproductive process
GO:0071845      1.31406163340573e-16    16.6938920454545        1.65082001245589
20      284     cellular component disassembly at cellular level
GO:0022411      1.72529628947621e-16    16.4400652985075        1.67407099854681
20      288     cellular component disassembly
GO:0033365      2.03779779665013e-13    10.2617994100295        2.74942910525223
21      473     protein localization to organelle
GO:0006605      2.12314580931642e-13    10.2384105960265        2.75524185177496
21      474     protein targeting
GO:0016032      8.60047376795442e-13    10.1044083526682        2.62154868175213
20      451     viral reproduction
GO:0071843      1.19950273911573e-06    8.34297179275345        1.38924641893295
10      239     cellular component biogenesis at cellular level
GO:0006364      2.34541989196471e-06    13.3739456419869        0.604525638364127
7       104     rRNA processing
GO:0042254      2.37935104935418e-06    10.6203807390817        0.866099231887067
8       149     ribosome biogenesis
GO:0016072      3.41632890821383e-06    12.5895851721094        0.639402117500519
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7       110     rRNA metabolic process
GO:0022613      6.12658158286129e-06    7.86166666666667        1.3078679676147 9
225     ribonucleoprotein complex biogenesis
Tissue: Skin_Sun_Exposed_Lower_leg=>Adipose_Subcutaneous        Type:   cluster
SourceGene:     RP11-275F13.1(ENSG00000261664.1)
TargetGeneSet:  MRPL20  LRRC47  CNKSR1  SNHG12  SNRNP40 SFPQ    GNL2    EBNA1BP2
DPH2    MAGOH   TMEM48  ZZZ3    WDR3    SF3B4   GPATCH4 PRCC    METTL13 DHX9
RBBP5   RRP15   COG2    HEATR1  TRMT61B WDR43   TTC27   GEMIN6  PNPT1   MPHOSPH10
POLR1A  PTCD3   ANAPC1  POLR1B  DDX18   MKI67IP SPPL2B  FASTKD2 RNF25   ACSL3   CLN5
TATDN2  HHATL-AS1       SACM1L  VPRBP   RRP9    PDE12   SHQ1    ZBTB11  QTRTD1
STAG1   ATR     EIF2B5  ECE2    PSMD2   LSG1    NCBP2-AS1       CTBP1-AS1
NOP14   GRPEL1  METTL19 BST1    HRH2    PDS5A   UTP3    SDAD1   NAA15   PLRG1
NSUN2   MTRR    SLC30A5 CTD     HSPA4   HSPA9   HARS    TCOF1   G3BP1   RIOK1
PAK1IP1 BRD2    WDR46   FTSJD2  RPL7L1  POLR1C  XPO5    MTO1    SYNCRIP AMD1
HDDC2   HBS1L   TCP1    EIF3B   DDX56   CCT6A   TBL2    EIF4H   SRRT    NAPEPLD PUS7
ZC3HC1  ABCF2   UBE3C   KIAA1967        ELP3    MAK16   TGS1    NSMAF   C8orf38 POP1
BOP1    MTAP    NOL6    IARS    C9orf102        TEX10   PRPF4   ZNF79   TRUB2
FUBP3   EXOSC2  SURF6   SURF2   C9orf69 SDCCAG3 FAM208B SEPHS1  PDSS1   BMS1
ZNF239  CSTF2T  SEC24C  NDST2   RRP12   WNT8B   C10orf2 NOLC1   PDCD11  EIF6
SEC23IP C10orf137       PHRF1   CARS    NUP98   CTR9    IMMP1L  API5    BTBD18
PRPF19  WDR74   SF1     NARS2   DDX10   ZNF202  NOP2    PPHLN1  DDX23   BCDIN3D RP3
PA2G4   RP11    CYP27B1 CAND1   CCT2    UTP20   POLR3B  SART3   ANAPC7  DDX55
DHX37   PUS1    DDX51   NOC4L   POLE    SACS    COG3    ZC3H13  IPO5    CARKD
SUPT16H PRMT5   SGPP1   DCAF4   TRIP11  NIPA2   UBE3A   SPATA5L1        CORO2B
IDH3A   AEN     TBL3    RNPS1   USP7    GSPT1   CD2BP2  RNF40   DNAJA2  CTCF
DDX19A  ADAT1   ZC3H18  CTU2    ZNF778  METTL16 MYBBP1A PELP1   DHX33   NEURL4  PFAS
UTP6    AATF    MED1    PSME3   KPNB1   MRPL27  SRSF1   FTSJ3   NOL11   TMEM104
CCDC137 AFG3L2  TIMM21  SH2D3A  DNMT1   ILF3    TNPO2   GATAD2A FBL     PSMC4
ZNF576  CD3EAP  DHX34   GRWD1   PPP6R1  U2AF2   TRIM28  PSMF1   TRMT6   SNX5
ACTR5   ZNF335  NCOA5   TP53RK  DDX27   WDR4    RRP1    PWP2    PES1    ANKRD54
POLDIP3 PQBP1   SMC1A   FAM123B UTP14A  DKC1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0034660      6.64716275994768e-35    16.1339413223762        4.20074735312435
46      285     ncRNA metabolic process
GO:0071843      3.44265036636425e-32    16.9027484143763        3.52273199086568
41      239     cellular component biogenesis at cellular level
GO:0022613      4.84449512488626e-32    17.563505702234 3.3163794893087 40      225
ribonucleoprotein complex biogenesis
GO:0034470      2.60824130366708e-30    18.1530605131065        2.94789287938551
37      200     ncRNA processing
GO:0042254      1.89943549524489e-28    21.3378665533362        2.1961801951422 32
149     ribosome biogenesis
GO:0016072      4.76998324008044e-23    22.1417396745932        1.62134108366203
25      110     rRNA metabolic process
GO:0006364      2.46624558935442e-22    22.4730158730159        1.53290429728046
24      104     rRNA processing
GO:0006399      3.79284321596101e-12    11.3477891156463        1.84243304961594
17      125     tRNA metabolic process
GO:0000375      3.38084290262527e-11    7.70293609671848        3.08054805895786
20      209     RNA splicing, via transesterification reactions
GO:0008033      8.60588814778553e-11    14.39546875     1.13493875856342        13
77      tRNA processing
GO:0000377      1.71320003984959e-10    7.43959320144887        3.00685073697322
19      204     RNA splicing, via transesterification reactions with bulged
adenosine as nucleophile
GO:0000398      1.71320003984959e-10    7.43959320144887        3.00685073697322
19      204     nuclear mRNA splicing, via spliceosome
GO:0006397      2.0163848756993e-10     5.16824131553669        5.88104629437409
26      399     mRNA processing
GO:0009451      2.44197917782365e-10    18.4059405940594        0.78119161303716
11      53      RNA modification
GO:0008380      2.42218096615917e-09    5.33325216120784        4.7608470002076 22
323     RNA splicing
```

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GO:0022618      1.45642237428395e-07    9.17574257425743        1.40024911770812
11      95      ribonucleoprotein complex assembly
GO:0043414      1.67088938757195e-07    7.95944804280484        1.73925679883745
12      118     macromolecule methylation
GO:0071826      2.47709169935886e-07    8.65719212370675        1.47394643969275
11      100     ribonucleoprotein complex subunit organization
GO:0032259      5.25396601047119e-07    7.08340649692713        1.93086983599751
12      131     methylation
GO:0001510      7.75989745425052e-07    42.7584134615385        0.19161303716058
5       13      RNA methylation
GO:0006400      4.86431283957643e-06    26.303624260355 0.265310359144696       5
18      tRNA modification
GO:0000966      1.24937860070488e-05    203.385714285714        0.0589578575877102
3       4       RNA 5'-end processing
Tissue: Skin_Sun_Exposed_Lower_leg=>Adipose_Subcutaneous        Type:   asymmetric
SourceGene:     RP11-485G7.4(ENSG00000263179.1)
TargetGeneSet:  SLC2A5  NMNAT1  ARID1A  MEAF6   RPS8    RPL5    RP11    KCNA2   RPS7
ASXL2   PPP1CB  RGPD5   RPL15   NICN1   RPL29   ATXN7   PCNP    RPL24   RYK
EIF2B5-IT1      RELL1   LRBA    ACSL1   AFF4    CTB     RPL15P3 NKAPL   WDR11
ABRACL  ARID1B  SLC29A4 EEF1A1P6        RPS3AP26        TRBV6-5 CTD     RP1     ASPH
EIF3E   EIF3H   VPS28   RPS6    NIPSNAP3A       RPL7A   RPS24   FAS     RBP4    SCD
CARS-AS1        C11orf2 RSF1    GUCY1A2 MCRS1   NACA    NAP1L1  RPL18AP3        RPL6
RPSAP54 STARD13 DGKH    SNX6    PYGL    CCNDBP1 RAB11A  PIAS1   FANCA   MIR762
RPL26   SUPT6H  RPL19   NMT1    MED13   BPTF    AANAT   FASN    MYL12B  C18orf32
C19orf80        HNRNPA1P10      UBA52   RPS5    ID1     PHF20   CHD6    RPL12P4 CTA
EIF3L   LMF2    KDM5C-IT1       BCORL1  RPL10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006413      9.66275195319599e-21    37.5276558384548        0.725762922981109
18      152     translational initiation
GO:0006415      1.25185366783809e-19    52.2880116959064        0.434502802574216
15      91      translational termination
GO:0000184      2.09983507836892e-19    41.8508884411064        0.568195972597052
16      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      3.15294642759193e-19    34.7611940298507        0.720988166908864
17      151     viral genome expression
GO:0019083      3.15294642759193e-19    34.7611940298507        0.720988166908864
17      151     viral transcription
GO:0006414      1.2094858532895e-18     44.1111111111111        0.501349387585634
15      105     translational elongation
GO:0006614      1.2094858532895e-18     44.1111111111111        0.501349387585634
15      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.40388819777656e-18    43.6233211233211        0.506124143657878
15      106     cotranslational protein targeting to membrane
GO:0045047      1.40388819777656e-18    43.6233211233211        0.506124143657878
15      106     protein targeting to ER
GO:0072599      1.40388819777656e-18    43.6233211233211        0.506124143657878
15      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      7.50797766173008e-18    38.5086299892125        0.563421216524808
15      118     protein localization to endoplasmic reticulum
GO:0019058      1.99765200688039e-17    23.4780447390224        1.1029686526884 18
231     viral infectious cycle
GO:0000956      6.66778953631612e-17    28.0754716981132        0.806933776209259
16      169     nuclear-transcribed mRNA catabolic process
GO:0034623      1.06767194586507e-16    27.1774540243611        0.83080755657048
16      174     cellular macromolecular complex disassembly
GO:0006402      1.53978141557745e-16    26.4989517819706        0.849906580859456
16      178     mRNA catabolic process
GO:0022415      1.64417781157647e-16    20.6222654350997        1.24143657878348
18      260     viral reproductive process
GO:0032984      1.68503184580419e-16    26.3345294594282        0.8546813369317 16
179     macromolecular complex disassembly
GO:0006612      4.06752141945652e-16    28.6714975845411        0.730537679053353
15      153     protein targeting to membrane
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GO:0043624      4.06752141945652e-16    28.6714975845411        0.730537679053353
15      153     cellular protein complex disassembly
GO:0043241      6.62512402719812e-16    27.6592851592852        0.754411459414573
15      158     protein complex disassembly
GO:0006401      1.47441449051459e-15    22.670260557053 0.978824994810048       16
205     RNA catabolic process
GO:0072594      3.04689059812065e-14    20.8597883597884        0.974050238737804
15      204     establishment of protein localization to organelle
GO:0016032      1.85494133300682e-13    12.2708333333333        2.15341498858211
19      451     viral reproduction
GO:0071845      2.43996182693504e-13    15.8986201070121        1.35603072451733
16      284     cellular component disassembly at cellular level
GO:0022411      3.02770833846076e-13    15.6603773584906        1.37512974880631
16      288     cellular component disassembly
GO:0033365      5.22368641413717e-10    9.19862928863383        2.25845962217148
16      473     protein localization to organelle
GO:0006605      5.38703733188493e-10    9.17788580374063        2.26323437824372
16      474     protein targeting
GO:0042274      1.38476537020871e-06    63.156043956044 0.0859456093003944      4
18      ribosomal small subunit biogenesis
GO:0016568      4.28761626116254e-06    6.49568965517241        2.00062279427029
11      419     chromatin modification
GO:0006338      4.90339324014159e-06    15.8316722037652        0.43927755864646
6       92      chromatin remodeling
GO:0042254      6.79928077522267e-06    11.3221263062244        0.711438654764376
7       149     ribosome biogenesis
GO:0006364      9.97651998625834e-06    13.8814382896016        0.49657463151339
6       104     rRNA processing
GO:0022613      1.12667152753571e-05    8.56085215683312        1.07432011625493
8       225     ribonucleoprotein complex biogenesis
GO:0016072      1.37700397185243e-05    13.0750915750916        0.52522316794685
6       110     rRNA metabolic process
GO:0071843      1.74514667624435e-05    8.03406429635938        1.14116670126635
8       239     cellular component biogenesis at cellular level
Tissue: Skin_Sun_Exposed_Lower_leg=>Adipose_Subcutaneous        Type:   asymmetric
SourceGene:     RP11-930O11.1(ENSG00000259719.1)
TargetGeneSet:  VPS13D  SPEN    UBR4    KPNA7   HIPK1   ASH1L   PRRC2C  LPGAT1  PXDN
RPS7    ASXL2   MZT2B   USP37   USP40   RPL15   RPL29   DNAH1   CD38    TLR2    TBCA
AFF4    RPS14   TNIP1   RP11    AGXT2L2 RPL15P3 GPLD1   TAPBP   BRD7P4  MRPS12
MYO1G   GS1     CACNA2D1        VPS13B  EIF3H   TATDN1  CTA     RPL8    VPS13A
RPS24   RPL27A  RPS13   PACS1   ARID2   NACA    SUGT1   VPS13C  SEC11A  ZNF205  SMG1
RPL13   VPS53   RPL26   RPS7P1  RPL17   STAT5B  RPL27   HOXB7   RPS15   PTPRS   RYR1
PLAUR   RPL18   ZNF587  RALGAPB RPL12P4 CRYBB2  EIF3L   EGFL6   HUWE1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006614      1.57744928897971e-19    51.8115942028985        0.443221922358314
15      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.83195288190393e-19    51.2386526516961        0.447443083523632
15      106     cotranslational protein targeting to membrane
GO:0045047      1.83195288190393e-19    51.2386526516961        0.447443083523632
15      106     protein targeting to ER
GO:0072599      1.83195288190393e-19    51.2386526516961        0.447443083523632
15      106     establishment of protein localization to endoplasmic reticulum
GO:0006415      9.63146860465796e-19    55.3694390715667        0.384125666043872
14      91      translational termination
GO:0070972      9.8589662000356e-19     45.2311101730688        0.498097017507439
15      118     protein localization to endoplasmic reticulum
GO:0000184      1.12470471296061e-18    44.7930602006689        0.502318178672756
15      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006413      1.35662886591628e-18    37.2653594771242        0.641616497128226
16      152     translational initiation
GO:0006612      1.51058855663393e-18    36.9907542579075        0.645837658293544
16      153     protein targeting to membrane
GO:0006414      7.92606098015508e-18    46.8052373158756        0.443221922358314
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14      105     translational elongation
GO:0072594      1.59606545339533e-16    26.8595744680851        0.861116877724725
16      204     establishment of protein localization to organelle
GO:0000956      2.46953791183705e-16    30.1439864483343        0.71337623693862
15      169     nuclear-transcribed mRNA catabolic process
GO:0034623      3.83904766757613e-16    29.1858080393765        0.734482042765207
15      174     cellular macromolecular complex disassembly
GO:0006402      5.41099421018376e-16    28.4615897572686        0.751366687426476
15      178     mRNA catabolic process
GO:0032984      5.8881056306774e-16     28.2860551431601        0.755587848591793
15      179     macromolecular complex disassembly
GO:0019080      1.48143871610431e-15    30.9895946575555        0.637395335962909
14      151     viral genome expression
GO:0019083      1.48143871610431e-15    30.9895946575555        0.637395335962909
14      151     viral transcription
GO:0043624      1.78510167785488e-15    30.5394152762896        0.645837658293544
14      153     cellular protein complex disassembly
GO:0043241      2.81324041445762e-15    29.4686761229314        0.66694346412013
14      158     protein complex disassembly
GO:0006401      4.50225390318053e-15    24.370709382151 0.865338038890042       15
205     RNA catabolic process
GO:0019058      2.65071596581026e-14    21.3979468599034        0.975088229188292
15      231     viral infectious cycle
GO:0022415      1.50858042305001e-13    18.8265306122449        1.09750190298249
15      260     viral reproductive process
GO:0033365      4.8279469174266e-13     12.8203424482494        1.99660923119507
18      473     protein localization to organelle
GO:0006605      5.00398053106689e-13    12.7913096695226        2.00083039236039
18      474     protein targeting
GO:0071845      5.46390082962498e-13    17.1177468886375        1.19880977095011
15      284     cellular component disassembly at cellular level
GO:0022411      6.69346400676617e-13    16.8621595795509        1.21569441561138
15      288     cellular component disassembly
GO:0016032      3.47090805340659e-11    11.4063856960409        1.90374368555809
16      451     viral reproduction
GO:0042274      8.41122338662158e-07    72.0601503759399        0.075980900975711
4       18      ribosomal small subunit biogenesis
Tissue: Adipose_Subcutaneous=>Skin_Sun_Exposed_Lower_leg        Type:   cluster
SourceGene:     RPL7P57(ENSG00000224401.2)
TargetGeneSet:  RP11    EIF1AX  RPL11   RP4     RPS8    UQCRH   PRPF38A BCAS2
PAQR6   SNRPE   SH3YL1  RPS7    UBC     SNRPG   COA5    RPL31   MRPS9   SSB
WDR75   EEF1B2  RPL37A  CRBN    THUMPD3 RPL32   CMC1    CCDC72  PRKAR2A-AS1
THOC7   CCDC58  RPL35A  RPL34   EEF1A1P19       RAD17   NSA2    RPS23   COX7C
LYRM7   SLU7    NPM1    TDP2    BRD2    RPL10A  RPL39P3 EEF1A1  C6orf203
MRPS12  ZDHHC14 LSM5    YAE1D1  SEC61G  RPS20   UQCRB   TATDN1  C9orf123        RPS6
NDUFB6  CHMP5   RBM18   TSC1    RPS24   RPL13AP5        C11orf58        EIF3M   FAU
CLNS1A  TMEM123 RPS25   NACA    RPL14P1 C12orf45        RPL6    CCNA1   EBPL
COMMD6  PLDN    RSL24D1 RPS3AP6 NEIL1   BTBD1   UNKL    RPAIN   RPL26   RPS7P1
RPL17   RPL19   RPL27   KPNA2   RPL38   RIOK3   C18orf8 LSM7    ALKBH6  ZNF829
RPS16   RPS19   SNRPD2  RPS21   EEF1B2P3        VBP1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      2.76353115943587e-40    107.608695652174        0.530413120199294
27      105     translational elongation
GO:0006614      2.87558700282201e-38    100.127659574468        0.530413120199294
26      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      3.79813892675077e-38    98.8691489361702        0.535464673725002
26      106     cotranslational protein targeting to membrane
GO:0045047      3.79813892675077e-38    98.8691489361702        0.535464673725002
26      106     protein targeting to ER
GO:0072599      3.79813892675077e-38    98.8691489361702        0.535464673725002
26      106     establishment of protein localization to endoplasmic reticulum
GO:0006415      4.79075044474379e-38    112.941919191919        0.459691370839388
25      91      translational termination
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GO:0070972      8.59890237110418e-37    85.9010175763182        0.596083316033493
26      118     protein localization to endoplasmic reticulum
GO:0006413      1.74243825363436e-35    66.9271304347826        0.76783613590755
27      152     translational initiation
GO:0000184      9.03601568062273e-35    79.1445035460993        0.6011348695592 25
119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0000956      3.75840299789116e-34    58.8444580526638        0.853712545844578
27      169     nuclear-transcribed mRNA catabolic process
GO:0006612      1.36114060192244e-33    62.0750544479812        0.772887689433257
26      153     protein targeting to membrane
GO:0006402      1.66768097955149e-33    55.3021883098186        0.899176527575946
27      178     mRNA catabolic process
GO:0019080      5.78130277058681e-32    58.912037037037 0.762784582381842       25
151     viral genome expression
GO:0019083      5.78130277058681e-32    58.912037037037 0.762784582381842       25
151     viral transcription
GO:0043624      8.21753702828212e-32    57.9833984375   0.772887689433257       25
153     cellular protein complex disassembly
GO:0006401      9.24943435355489e-32    46.8246213971666        1.03556847277005
27      205     RNA catabolic process
GO:0043241      1.93655810887696e-31    55.7839912280702        0.798145457061795
25      158     protein complex disassembly
GO:0034623      2.48953699439478e-30    49.7378355704698        0.878970313473116
25      174     cellular macromolecular complex disassembly
GO:0072594      3.69737420890115e-30    44.1310064546976        1.03051691924434
26      204     establishment of protein localization to organelle
GO:0032984      5.245265723562e-30      48.1060606060606        0.904228081101654
25      179     macromolecular complex disassembly
GO:0022415      2.4576661809878e-27     33.4373522458629        1.31340391668397
26      260     viral reproductive process
GO:0019058      3.92667099875934e-27    35.8313106796116        1.16690886443845
25      231     viral infectious cycle
GO:0071845      7.4883102216333e-25     28.392454954955 1.43464120130095        25
284     cellular component disassembly at cellular level
GO:0022411      1.06497711733202e-24    27.9527091254753        1.45484741540378
25      288     cellular component disassembly
GO:0033365      3.74358203733785e-23    19.481847690387 2.38938481765968        28
473     protein localization to organelle
GO:0006605      3.96627331353422e-23    19.4367713004484        2.39443637118538
28      474     protein targeting
GO:0022613      7.67232272328643e-23    30.1217038539554        1.1365995432842 22
225     ribonucleoprotein complex biogenesis
GO:0071843      2.94216983843665e-22    28.1505376344086        1.20732129264411
22      239     cellular component biogenesis at cellular level
GO:0016032      3.85638659378562e-21    18.1616020025031        2.27825064009411
26      451     viral reproduction
GO:0042254      2.28979588109197e-17    30.0646352723915        0.752681475330427
16      149     ribosome biogenesis
GO:0042274      1.20031454780352e-14    176.836923076923        0.0909279634627361
8       18      ribosomal small subunit biogenesis
GO:0034660      4.20576973391884e-14    15.9828091684435        1.43969275482666
17      285     ncRNA metabolic process
GO:0006364      1.28620598802652e-13    30.5473984319316        0.525361566673587
12      104     rRNA processing
GO:0016072      2.55627992648516e-13    28.6651053864169        0.555670887827832
12      110     rRNA metabolic process
GO:0034470      1.92582378338584e-11    16.4423351158645        1.01031070514151
13      200     ncRNA processing
GO:0022618      1.07038452366635e-09    23.3699127906977        0.479897584942219
9       95      ribonucleoprotein complex assembly
GO:0071826      1.69853349330779e-09    22.078125       0.505155352570756       9
100     ribonucleoprotein complex subunit organization
GO:0000387      4.39079463156449e-07    40.5882352941176        0.156598159296934
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5       31      spliceosomal snRNP assembly
GO:0008380      6.07126667275544e-07    7.99865591397849        1.63165178880354
11      323     RNA splicing
GO:0000462      2.44679800247836e-06    205.357142857143        0.0303093211542454
3       6       maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA,
5.8S rRNA, LSU-rRNA)
GO:0030490      4.26634606660256e-06    154.007142857143        0.0353608746799529
3       7       maturation of SSU-rRNA
GO:0006397      4.73643415142512e-06    6.39715663451945        2.01556985675732
11      399     mRNA processing
GO:0000375      1.0050210757565e-05     8.68090317642556        1.05577468687288
8       209     RNA splicing, via transesterification reactions
Tissue: Skin_Sun_Exposed_Lower_leg=>Adipose_Subcutaneous        Type:   asymmetric
SourceGene:     RPP30(ENSG00000148688.6)
TargetGeneSet:  ZBTB17  KDM1A   KHDRBS1 RP4     EIF2C3  LEPRE1  HECTD3  HSPB11
MRPL37  LEPROT  LRRC40  GNG5    COL24A1 RPL5    CCDC18  RP11    KCNJ9   SNRPE
B3GALNT2        PRORSD1P        ETAA1   FAM136A UBTFL6  MMADHC  MLK7-AS1
NIF3L1  EEF1B2  TNS1    KCNE4   RPS12P5 RPSA    RPL14   IMPDH2  QARS    NICN1
SPCS1   SNX4    COMMD2  EGFEM1P EXOC7   OSTC    CCDC109B        DCTD    WWC2    FRG1
AGGF1P1 CTD     CDK7    RASA1   CTB     NPM1    GPLD1   RPS18   YIPF3   EEF1A1
RARS2   MRPS12  EPM2A   CTA     NT5C3   SSBP1   GIMAP7  GIMAP6  CSMD1   CCDC25
C8orf34 DPY19L4 FAM84B  RPS6    DCTN3   HRCT1   SLC35D2 GGTA1P  PSMB7   GDI2
ITGB1   RPL13AP5        GSTO1   RNU4-5P LHPP    SNORA23 ZBED5   PEX16   NDUFS3
PPP2R5B CCDC82  MCAM    NTM     HDAC7   TUBA1C  HNRNPA1 GRIP1   SLC35E3 METAP2
SLC25A3 IKBIP   NUP37   ALKBH2  FBXO21  RPLP0   RFXAP   MRPS31  DGKH    EBPL    NEK3
LGALS3  MOK     CCNDBP1 PARP16  RAB11A  RPS17L  SEC11A  RPS2    LITAF   MYH10
MPRIP-AS1       RPS7P1  ALDOC   TMEM101 MAPT    ANKRD40 CEP95   MYOM1   TTC39C
HNRNPA1P7       HAUS1   PIP5K1C SLC25A23        RNASEH2A        AP1M1   PDCD5
ZNF585A RPS19   MEGF8   CACNG7  RPL28   RPS5    SLC24A3 EPB41L1 WFDC13  CSTF1   RPL3
EEF1B2P3        RGN     PORCN   YIPF6   RBM41   RP1-177G6.2     SLC10A3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0070972      7.73350920734173e-15    22.5427395525538        0.873711161857311
15      118     protein localization to endoplasmic reticulum
GO:0006414      3.26182500051036e-14    23.5781637717122        0.777454847415404
14      105     translational elongation
GO:0006614      3.26182500051036e-14    23.5781637717122        0.777454847415404
14      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      3.73551811974013e-14    23.3202431042543        0.78485917929555
14      106     cotranslational protein targeting to membrane
GO:0045047      3.73551811974013e-14    23.3202431042543        0.78485917929555
14      106     protein targeting to ER
GO:0072599      3.73551811974013e-14    23.3202431042543        0.78485917929555
14      106     establishment of protein localization to endoplasmic reticulum
GO:0006612      3.84040546543063e-13    16.7840264650284        1.13286277766245
15      153     protein targeting to membrane
GO:0006415      2.80259329975766e-12    22.8087941372418        0.67379420109335
12      91      translational termination
GO:0072594      2.53373654071825e-11    12.2110075914424        1.51048370354993
15      204     establishment of protein localization to organelle
GO:0000184      7.10394135326821e-11    16.8070831283817        0.881115493737458
12      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      8.19149411134448e-11    14.2366635831021        1.11805411390215
13      151     viral genome expression
GO:0019083      8.19149411134448e-11    14.2366635831021        1.11805411390215
13      151     viral transcription
GO:0006401      3.27041027786169e-10    11.154759894162 1.51788803543007        14
205     RNA catabolic process
GO:0006402      6.40545495569124e-10    11.8843971631206        1.31797107466611
13      178     mRNA catabolic process
GO:0006413      1.24446052195603e-09    12.8156390977444        1.1254584457823 12
152     translational initiation
GO:0043624      1.34214153559714e-09    12.7238521836506        1.13286277766245
12      153     cellular protein complex disassembly
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GO:0043241      1.94244085203402e-09    12.2837779379957        1.16988443706318
12      158     protein complex disassembly
GO:0000956      4.1906640972259e-09     11.414280925243 1.25133208774479        12
169     nuclear-transcribed mRNA catabolic process
GO:0034623      5.83519367848991e-09    11.058089668616 1.28835374714553        12
174     cellular macromolecular complex disassembly
GO:0032984      8.03950940262332e-09    10.723227229751 1.32537540654626        12
179     macromolecular complex disassembly
GO:0019058      1.52478347774591e-08    8.96144837009565        1.71040066431389
13      231     viral infectious cycle
GO:0071843      2.28720374097545e-08    8.63933345885897        1.76963531935506
13      239     cellular component biogenesis at cellular level
GO:0022415      6.17921402246615e-08    7.89305711086226        1.92512628883814
13      260     viral reproductive process
GO:0022613      1.020867276516e-07      8.38013343217198        1.66597467303301
12      225     ribonucleoprotein complex biogenesis
GO:0042254      1.49955979284037e-07    10.5354891344656        1.10324545014186
10      149     ribosome biogenesis
GO:0071845      1.72617995788958e-07    7.18179320091073        2.10283025396166
13      284     cellular component disassembly at cellular level
GO:0016032      1.98402473283091e-07    5.62192749778957        3.33935367794616
16      451     viral reproduction
GO:0022411      2.02832419521597e-07    7.07531914893617        2.13244758148225
13      288     cellular component disassembly
GO:0033365      2.0184801718855e-06     4.94327890639833        3.50224897930939
15      473     protein localization to organelle
GO:0006605      2.07177738734815e-06    4.9321540210287 3.50965331118954        15
474     protein targeting
GO:0042255      4.82828383184175e-06    46.3818770226537        0.118469310082347
4       16      ribosome assembly
GO:0000028      7.76702447065936e-06    137.894230769231        0.0444259912808802
3       6       ribosomal small subunit assembly
GO:0042274      8.02575663301537e-06    39.750346740638 0.133277973842641       4
18      ribosomal small subunit biogenesis
GO:0006364      1.17964469341278e-05    10.2813402061856        0.770050515535257
7       104     rRNA processing
GO:0016072      1.70406276135602e-05    9.67834951456311        0.814476506816137
7       110     rRNA metabolic process
Tissue: Skin_Sun_Exposed_Lower_leg=>Adipose_Subcutaneous        Type:   asymmetric
SourceGene:     RSPH9(ENSG00000172426.9)
TargetGeneSet:  TNFRSF25        RP1     RP4     COL24A1 PKN2    RPL5    RP11
ATP5F1  U2      ADAMTSL4        PIGM    KIAA1383        GPR113  UBC     TPRKB
MRPS9   RBM43   EEF1B2  QARS    GRM2    SPCS1   RPL10AP6        ATG3    GPR171
RPL22L1 C3orf43 RPL35A  NAAA    RPL37   NDUFAF2 PPWD1   BTF3    RPS23   NPM1
RPL10A  C6orf130        SENP6   RARS2   UFL1    GOPC    MRPS12  PKD1L1  ECD     POT1
SSBP1   ZNF596  CHCHD7  RPL7    C8orf59 RPL30   U6      ZNF250  RPS6    PSMB7   DPM2
RPS24   BLOC1S2 ZBED5   IMMP1L  EIF3M   PEX16   PPP2R5B RPS25   CBX3P4  UHRF1BP1L
NUP37   RPLP0   ALG5    TPT1    TMTC4   LGALS3  RSL24D1 UNC45A  UBE2I   LITAF
RPL23A  RPL19   VPS25   FECH    TEAD2   RPS9    DTD1    IFT52   CSTF1   MRPL39
REPS2   UXT     RPS4X
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0070972      3.37340022439387e-22    45.8903571428571        0.604248840910664
18      118     protein localization to endoplasmic reticulum
GO:0006612      1.22713074263775e-21    36.7187245590231        0.783475192028233
19      153     protein targeting to membrane
GO:0006414      1.85824725656262e-21    48.4276315789474        0.537679053352709
17      105     translational elongation
GO:0006614      1.85824725656262e-21    48.4276315789474        0.537679053352709
17      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      2.20489973980139e-21    47.8801498127341        0.542799806241783
17      106     cotranslational protein targeting to membrane
GO:0045047      2.20489973980139e-21    47.8801498127341        0.542799806241783
17      106     protein targeting to ER
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GO:0072599      2.20489973980139e-21    47.8801498127341        0.542799806241783
17      106     establishment of protein localization to endoplasmic reticulum
GO:0006415      7.68629683613963e-21    52.6050574712644        0.465988512905681
16      91      translational termination
GO:0000184      7.13699961349572e-19    38.2296618680951        0.609369593799737
16      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006413      1.30190114620767e-18    31.4638076673164        0.77835443913916
17      152     translational initiation
GO:0072594      8.44615921303806e-18    24.5236175115207        1.04463358937098
18      204     establishment of protein localization to organelle
GO:0019080      3.59854005924456e-17    29.1024265644955        0.773233686250086
16      151     viral genome expression
GO:0019083      3.59854005924456e-17    29.1024265644955        0.773233686250086
16      151     viral transcription
GO:0043624      4.45746211556904e-17    28.6735464384596        0.783475192028233
16      153     cellular protein complex disassembly
GO:0043241      7.51285448947764e-17    27.6542010684798        0.8090789564736 16
158     protein complex disassembly
GO:0000956      2.22931742046762e-16    25.6461573135001        0.865407238253408
16      169     nuclear-transcribed mRNA catabolic process
GO:0034623      3.56379789069896e-16    24.8258402444347        0.891011002698775
16      174     cellular macromolecular complex disassembly
GO:0006402      5.13289498287159e-16    24.2060451255854        0.911494014255069
16      178     mRNA catabolic process
GO:0032984      5.61524128513149e-16    24.0558493759255        0.916614767144142
16      179     macromolecular complex disassembly
GO:0006401      4.87147113841289e-15    20.7086298120781        1.04975434226005
16      205     RNA catabolic process
GO:0019058      3.1930834512106e-14     18.1709703287891        1.18289391737596
16      231     viral infectious cycle
GO:0022415      2.01364976172497e-13    15.9785189372527        1.33139575115909
16      260     viral reproductive process
GO:0071845      7.85415494261642e-13    14.5229027277406        1.45429382049685
16      284     cellular component disassembly at cellular level
GO:0022411      9.73321335290367e-13    14.3052738336714        1.47477683205315
16      288     cellular component disassembly
GO:0006605      1.7900267005612e-12     10.5701498501498        2.4272368694208 19
474     protein targeting
GO:0016032      8.18141692971715e-12    10.35103926097  2.30945955297211        18
451     viral reproduction
GO:0033365      1.8035401165751e-11     9.83500784929356        2.42211611653173
18      473     protein localization to organelle
GO:0071843      3.36134997539575e-08    10.8353522695628        1.22385994048855
11      239     cellular component biogenesis at cellular level
GO:0042254      6.45674587116319e-08    14.0805494505494        0.76299218047194
9       149     ribosome biogenesis
GO:0022613      2.06240591122515e-07    10.2921511627907        1.15216940004152
10      225     ribonucleoprotein complex biogenesis
Tissue: Whole_Blood=>Adipose_Subcutaneous       Type:   asymmetric




SourceGene:     A2ML1(ENSG00000166535.14)       alpha-2-macroglobulin-like 1




TargetGeneSet:  RPL22   RP11    RP1     RPL11   RP4     RPL5    UBC     FABP1   COA5
```

LYG2 RPL31 MTX2 EEF1B2 MYEOV2 PA2G4P4 VWA5B2 RPL35A RPL34 CTD
UQCRQ RPS14 COX7A2 RWDD1 MRPS12 RPS20 SNHG6 COPS5 RPS6 CBWD6
RPS24 RBM4 RPS25 KRT5 ARL6IP4 EXOSC8 TPT1 RPS3AP6 RPLP1 C15orf38
KRT10 KRT14 DNAJC7 RPL27 DSC1 C19orf80 CASP14 LGALS7B ROMO1 TH1L
RPS19BP1 RP6 ARSF RPL39 PSMA6P1

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0006414	3.57E-25	117.0500511	0.27610546	16	105	translational elongation
GO:0006413	2.25E-24	85.61763668	0.399695523	17	152	translational initiation
GO:0006415	3.98E-24	123.0291762	0.239291399	15	91	translational termination
GO:0006614	3.96E-23	103.7898551	0.27610546	15	105	SRP-dependent cotranslational protein targeting to membrane
GO:0006613	4.61E-23	102.6421405	0.278735036	15	106	cotranslational protein targeting to membrane
GO:0045047	4.61E-23	102.6421405	0.278735036	15	106	protein targeting to ER
GO:0072599	4.61E-23	102.6421405	0.278735036	15	106	establishment of protein localization to endoplasmic reticulum

GO:0019080	1.64E-22	76.91851852	0.397065947	16	151	viral genome expression
GO:0019083	1.64E-22	76.91851852	0.397065947	16	151	viral transcription
GO:0070972	2.52E-22	90.60785141	0.310289945	15	118	protein localization to endoplasmic reticulum
GO:0000184	2.88E-22	89.73035117	0.312919521	15	119	"nuclear-transcribed mRNA catabolic process, nonsense-mediated decay"
GO:0000956	1.06E-21	67.78371955	0.444398312	16	169	nuclear-transcribed mRNA catabolic process
GO:0006402	2.49E-21	63.97755331	0.468064494	16	178	mRNA catabolic process
GO:0006612	1.47E-20	67.46219282	0.402325099	15	153	protein targeting to membrane
GO:0043624	1.47E-20	67.46219282	0.402325099	15	153	cellular protein complex disassembly
GO:0072594	2.32E-20	55.02901354	0.536433465	16	204	establishment of protein localization to organelle

GO:0043241	2.42E-20	65.0805716	0.415472978	15	158	protein complex disassembly
GO:0006401	2.52E-20	54.73400673	0.539063041	16	205	RNA catabolic process
GO:0034623	1.07E-19	58.4659557	0.457546191	15	174	cellular macromolecular complex disassembly
GO:0032984	1.65E-19	56.6635737	0.47069407	15	179	macromolecular complex disassembly
GO:0019058	1.76E-19	48.02706131	0.607432012	16	231	viral infectious cycle
GO:0022415	1.19E-18	42.23248882	0.68368971	16	260	viral reproductive process
GO:0071845	1.80E-16	34.29125586	0.746799529	15	284	cellular component disassembly at cellular level
GO:0022411	2.21E-16	33.77926421	0.757317833	15	288	cellular component disassembly
GO:0016032	7.37E-15	23.36969697	1.185938689	16	451	viral reproduction

GO:0033365	1.55E-14	22.20966779	1.243789357	16	473	protein localization to organelle
GO:0006605	1.60E-14	22.15958714	1.246418933	16	474	protein targeting
GO:0042254	3.98E-09	26.99196217	0.391806795	8	149	ribosome biogenesis
GO:0022613	5.05E-09	20.39798851	0.591654557	9	225	ribonucleoprotein complex biogenesis
GO:0071843	8.55E-09	19.13748126	0.628468618	9	239	cellular component biogenesis at cellular level
GO:0006364	8.57E-09	33.32623878	0.273475884	7	104	rRNA processing
GO:0016072	1.27E-08	31.3717507	0.289253339	7	110	rRNA metabolic process
GO:0042274	1.21E-07	121	0.047332365	4	18	ribosomal small subunit biogenesis
GO:0000028	3.34E-07	411.7142857	0.015777455	3	6	ribosomal small subunit assembly

GO:0034470	7.68E-07	16.63713856	0.525915162	7	200	ncRNA processing
GO:0042273	3.63E-06	137.1809524	0.03155491	3	12	ribosomal large subunit biogenesis
GO:0034660	8.06E-06	11.48120214	0.749429105	7	285	ncRNA metabolic process
GO:0042255	9.18E-06	94.94505495	0.042073213	3	16	ribosome assembly

Tissue: Whole_Blood=>Adipose_Subcutaneous Type: asymmetric

SourceGene: ACA64(ENSG00000239005.1) "small nucleolar RNA, H/ACA box 78"

TargetGeneSet: RPL11 TAF12 RP11 C2orf28 CCDC115 RPL24 RPL34 RPS3A NDUFS4 MIP BTF3 CTB NIPAL4 CSNK2B RPS20 RPL30 RPS6 RPL35 NUP188 RPS24 SFR1 FAM53B FAU RPS25 DNAL1 RPS3AP6 RPS15A GABARAP CTD RPL26 RPL17 C19orf53 UBA52 CHMP4B LAMA5 HCFC1 AMELY

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0006415	1.50E-25	166.5208978	0.201508546	15	91	translational termination
GO:0006414	1.50E-24	140.4803922	0.232509861	15	105	translational elongation

GO:0006614	1.50E-24	140.4803922	0.232509861	15	105	SRP-dependent cotranslational protein targeting to membrane
GO:0006613	1.75E-24	138.9269554	0.234724241	15	106	cotranslational protein targeting to membrane
GO:0045047	1.75E-24	138.9269554	0.234724241	15	106	protein targeting to ER
GO:0072599	1.75E-24	138.9269554	0.234724241	15	106	establishment of protein localization to endoplasmic reticulum
GO:0070972	9.61E-24	122.6384923	0.261296796	15	118	protein localization to endoplasmic reticulum
GO:0000184	1.10E-23	121.4507919	0.263511176	15	119	"nuclear-transcribed mRNA catabolic process, nonsense-mediated decay"
GO:0019080	4.62E-22	92.66652249	0.334371324	15	151	viral genome expression
GO:0019083	4.62E-22	92.66652249	0.334371324	15	151	viral transcription
GO:0006413	5.12E-22	91.98368398	0.336585703	15	152	translational initiation
GO:0006612	5.67E-22	91.31074169	0.338800083	15	153	protein targeting to membrane
GO:0043624	5.67E-22	91.31074169	0.338800083	15	153	cellular protein complex disassembly

GO:0043241	9.34E-22	88.08720691	0.349871981	15	158	protein complex disassembly
GO:0000956	2.65E-21	81.73223835	0.374230157	15	169	nuclear-transcribed mRNA catabolic process
GO:0034623	4.16E-21	79.13429523	0.385302055	15	174	cellular macromolecular complex disassembly
GO:0006402	5.91E-21	77.1706965	0.394159574	15	178	mRNA catabolic process
GO:0032984	6.44E-21	76.69476327	0.396373953	15	179	macromolecular complex disassembly
GO:0022415	3.53E-20	58.0942623	0.575738703	16	260	viral reproductive process
GO:0072594	4.80E-20	66.43323996	0.451733444	15	204	establishment of protein localization to organelle
GO:0006401	5.18E-20	66.07894737	0.453947824	15	205	RNA catabolic process
GO:0016032	1.78E-19	41.52886836	0.998685212	18	451	viral reproduction
GO:0019058	3.20E-19	58.01879085	0.511521694	15	231	viral infectious cycle

GO:0071845	7.30E-18	46.41373278	0.628883814	15	284	cellular component disassembly at cellular level
GO:0022411	9.02E-18	45.72074984	0.637741333	15	288	cellular component disassembly
GO:0006605	1.60E-17	34.6249453	1.049615944	17	474	protein targeting
GO:0033365	5.02E-16	30.55142232	1.047401564	16	473	protein localization to organelle
GO:0042274	7.87E-06	99.33793103	0.039858833	3	18	ribosomal small subunit biogenesis
GO:0022613	8.61E-06	14.96311907	0.498235416	6	225	ribonucleoprotein complex biogenesis
GO:0071843	1.21E-05	14.05018158	0.529236731	6	239	cellular component biogenesis at cellular level
GO:0042254	1.75E-05	18.35776749	0.329942565	5	149	ribosome biogenesis

Tissue: Whole_Blood=>Adipose_Subcutaneous Type: asymmetric

SourceGene: ANKRD18EP(ENSG00000217165.1) "ankyrin repeat domain 18E, pseudogene"

TargetGeneSet: HSPG2 RPL11 SYNC RPS8 RPL5 RP11 PRX CENPO
PPP1CB UBC ANKAR EEF1B2 RPL15 MAP4 RPL29 MIR135A1 RELL1
AIMP1 RPL34 NDUFAF2 BTF3 NSA2 TBCA CTB SYNPO NPM1 JARID2-AS1
GPLD1 RPL10A FILIP1 MRPS12 SFT2D1 RPS20 RPL30 EIF3H RPS6 CLTA
ANP32B RPL35 RPL12 RPL7A RPS24 RPL27A EIF3M ZNF705E SNORD15B
RPS25 PS5 NAP1L1 CCDC59 RPL18AP3 RPL31P52 RPL21 RSL24D1
RPS3AP6 RPS15A RPL13 RPL26 RPL17 RPL19 NT5C C18orf1 RPS15 RPL36
RPL18 RPS9 ZNF154 ZNF671 SNRPB2 MORC2

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0006414	1.69E-46	185.9480519	0.406892257	28	105	translational elongation
GO:0006415	3.43E-46	208.4789871	0.352639956	27	91	translational termination
GO:0006614	2.99E-44	170.8925729	0.406892257	27	105	SRP-dependent cotranslational protein targeting to membrane
GO:0006613	4.00E-44	168.7175906	0.410767421	27	106	cotranslational protein targeting to membrane
GO:0045047	4.00E-44	168.7175906	0.410767421	27	106	protein targeting to ER

GO:0072599	4.00E-44	168.7175906	0.410767421	27	106	establishment of protein localization to endoplasmic reticulum
GO:0006413	1.51E-43	124.6275218	0.589024981	29	152	translational initiation
GO:0070972	1.06E-42	146.3463433	0.457269393	27	118	protein localization to endoplasmic reticulum
GO:0000184	1.37E-42	144.7455022	0.461144557	27	119	"nuclear-transcribed mRNA catabolic process, nonsense-mediated decay"
GO:0019080	1.64E-39	107.1515573	0.585149817	27	151	viral genome expression
GO:0019083	1.64E-39	107.1515573	0.585149817	27	151	viral transcription
GO:0006612	2.41E-39	105.4359606	0.592900145	27	153	protein targeting to membrane

GO:0043624	2.41E-39	105.4359606	0.592900145	27	153	cellular protein complex disassembly
GO:0043241	6.18E-39	101.3761516	0.612275967	27	158	protein complex disassembly
GO:0000956	4.38E-38	93.45094706	0.654902775	27	169	nuclear-transcribed mRNA catabolic process
GO:0034623	1.02E-37	90.24067558	0.674278597	27	174	cellular macromolecular complex disassembly
GO:0006402	1.96E-37	87.82553094	0.689779254	27	178	mRNA catabolic process
GO:0032984	2.31E-37	87.24160617	0.693654418	27	179	macromolecular complex disassembly
GO:0072594	9.77E-36	74.78784337	0.790533527	27	204	establishment of protein localization to organelle

GO:0006401	1.12E-35	74.36245641	0.794408691	27	205	RNA catabolic process
GO:0019058	3.31E-34	64.76622718	0.895162965	27	231	viral infectious cycle
GO:0022415	9.14E-33	56.58931478	1.007542731	27	260	viral reproductive process
GO:0071845	1.07E-31	51.21776466	1.100546675	27	284	cellular component disassembly at cellular level
GO:0022411	1.57E-31	50.41854935	1.116047332	27	288	cellular component disassembly
GO:0016032	3.29E-26	30.67802537	1.747699121	27	451	viral reproduction
GO:0033365	1.18E-25	29.11883408	1.832952737	27	473	protein localization to organelle

GO:0006605	1.25E-25	29.05160842	1.836827901	27	474	protein targeting
GO:0042254	3.49E-13	28.38354346	0.577399488	12	149	ribosome biogenesis
GO:0022613	2.34E-12	20.22586661	0.871911978	13	225	ribonucleoprotein complex biogenesis
GO:0071843	5.03E-12	18.95420868	0.926164279	13	239	cellular component biogenesis at cellular level
GO:0006364	5.85E-09	24.82465278	0.403017092	8	104	rRNA processing
GO:0042274	6.00E-09	108.4615385	0.069752958	5	18	ribosomal small subunit biogenesis
GO:0016072	9.14E-09	23.35457516	0.426268078	8	110	rRNA metabolic process

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GO:0034470	9.41E-07	12.32899306	0.77503287	8	200
ncRNA processing




GO:0034660	1.34E-06	9.795790934	1.104421839	9	285
ncRNA metabolic process




GO:0042273	1.18E-05	90.47798742	0.046501972	3	12
ribosomal large subunit biogenesis




Tissue: Whole_Blood=>Adipose_Subcutaneous	Type:	cluster
SourceGene:	ENSG00000229344.1
TargetGeneSet:	LDLRAD2	HSPG2	RPL11	ARID1A	KPNA7	ZMYM4	THRAP3	RPS8
RPS15AP10	RPL5	RP11	SNX7	RPRD2	SPRR2D	JTB	RPS27	UBAP2L	SSR2
RAB25	SHISA4	NENF	CICP13	NBAS	PPP1CB	UBC	TMEM131	EIF5B	RANBP2
UGGT1	PLEKHA3	UBE2E3	TRIP12	BRK1	UBE2E1	RPL15	RAD54L2	RPL29	KCTD6	PCNP
RPL24	RYK	GPR87	EIF4G1	PPP1R2	HTT	BOD1L	DANCR	CISD2	RPL34
NDUFC1	RPS3A	NIPBL	CTD	TAF9	BTF3	AP3S1	CTB	MTND5P11	SIL1
HDAC3	RPS14	GNB2L1	RP3	TMEM14C	RPL15P3	DEK	RSL24D1P1	PPP1R10
AGPAT1	RPS18	GLO1	MRPL32	MTRNR2L9	WDR11	RWDD1	MRPS12	RAB32
IGF2R	PSMB1	STARD3NL	CLDN3	SPDYE2	ATXN7L1	FAM3C	DRP2	HMBOX1
HOOK3	RPS20	ARFGEF1	RPL30	TG	NFIB	RPS6	CLTA	PCSK5	NIPSNAP3A
ZNF462	ATP6V1G1	RPL12	PTGES	RPL7A	SEC16A	CALML5	PRINS	KIAA0913
RPS24	MRPL43	GBF1	RPL27A	MTRNR2L8	CKAP5	BAD	ZNHIT2	CCDC90B
C11orf73	FDX1	UBE4A	DDX6	ERC1	A2M	SCAF11	MLL4	PFDN5	CBX5
MYF6	USP44	GTF3A	ESD	NUDT15	MED4	DNAJC3	CCNB1IP1	CHD8
CGRRF1	DHRS7	YLPM1	C14orf142	CCNK	HERC2P10	USP8	RPS27L
CALML4	C15orf40	SEC11A	MPG	SPSB3	TSC2	NTAN1	RPS15A	GTF3C1
LONP2	FBXL8	PIEZO1	RPL13	VPS53	WDR81	POLR2A	RPL26	RPL23A	TAF15
RPL19	CDK12	KRT14	RPL27	XYLT2	SUPT4H1	CLTC	TNRC6C	ROCK1P1	DSG1
RPS15	AP3D1	NFIC	ARRDC5	PTPRS	NDUFA11	ZNF121	EIF3G	ZNF791	C19orf43
BRD4	UPF1	KRTDAP	SBSN	ZNF526	ERF	ZNF428	RPL18	NUCB1	NUCB1-AS1
RPL13A	KLK7	CCDC106	ZNF587	RPS5	KIF3B	CHMP4B	SCAND1	TOP1	NCOA3
RPL12P4	FAM211B	TTC28	EIF3L	RPL3	TNRC6B	EP300	TMSB4X	DYNLT3	UXT
WDR45	HUWE1	RPS4X	COX7B	RPL39	HCFC1	MT
GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0006415	1.06365468144771e-40	56.5663129973475	1.10829700366757
33	91	translational termination
GO:0006614	6.07105534805468e-40	47.9008133306884	1.27880423500104
34	105	SRP-dependent cotranslational protein targeting to membrane
GO:0006613	8.85206189936669e-40	47.2321987480438	1.29098332295343
34	106	cotranslational protein targeting to membrane
GO:0045047	8.85206189936669e-40	47.2321987480438	1.29098332295343
34	106	protein targeting to ER
GO:0072599	8.85206189936669e-40	47.2321987480438	1.29098332295343
34	106	establishment of protein localization to endoplasmic reticulum
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GO:0070972      5.95242744048001e-38    40.4505365526492        1.43713237838212
34      118     protein localization to endoplasmic reticulum
GO:0000184      8.25326467032465e-38    39.9718309859155        1.44931146633451
34      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006413      9.25877719238335e-37    31.3869458128079        1.85122136876341
36      152     translational initiation
GO:0006414      1.27246393757952e-36    43.2328767123288        1.27880423500104
32      105     translational elongation
GO:0019080      2.22646549820877e-35    30.2986671557838        1.83904228081102
35      151     viral genome expression
GO:0019083      2.22646549820877e-35    30.2986671557838        1.83904228081102
35      151     viral transcription
GO:0006612      1.08039642679469e-33    28.4828973843058        1.8634004567158 34
153     protein targeting to membrane
GO:0000956      1.57734892540332e-33    26.1953530221234        2.05826586395405
35      169     nuclear-transcribed mRNA catabolic process
GO:0006402      1.09225596040921e-32    24.5310717651143        2.16787765552557
35      178     mRNA catabolic process
GO:0043624      3.03514988855692e-32    27.2211538461538        1.8634004567158 33
153     cellular protein complex disassembly
GO:0043241      9.48800926251924e-32    26.1230769230769        1.92429589647775
33      158     protein complex disassembly
GO:0022415      1.13073206866945e-31    18.1030485186775        3.16656286762162
39      260     viral reproductive process
GO:0034623      1.16901936490966e-31    24.1745472837022        2.11916130371601
34      174     cellular macromolecular complex disassembly
GO:0032984      3.23586360878366e-31    23.3326857697912        2.18005674347796
34      179     macromolecular complex disassembly
GO:0019058      4.06249468988904e-31    19.3205147222428        2.81336931700228
37      231     viral infectious cycle
GO:0072594      1.63214336505591e-30    20.7188719627345        2.48453394228773
35      204     establishment of protein localization to organelle
GO:0006401      1.949266726902e-30      20.5955360867751        2.49671303024012
35      205     RNA catabolic process
GO:0033365      7.42989514764804e-28    11.1135585360634        5.76070860148087
45      473     protein localization to organelle
GO:0016032      1.25639378342209e-26    10.9885190918473        5.49276866652827
43      451     viral reproduction
GO:0006605      9.55009675508157e-26    10.384871691991 5.77288768943326        43
474     protein targeting
GO:0071845      2.00161424269755e-25    13.9824546412601        3.458860978479  35
284     cellular component disassembly at cellular level
GO:0022411      3.24250576211197e-25    13.7574636279539        3.50757733028856
35      288     cellular component disassembly
GO:0042274      1.90753772942983e-06    32.0782726045884        0.219223583143035
5       18      ribosomal small subunit biogenesis
GO:0022613      3.78516319362095e-06    5.29051394837365        2.74029478928794
13      225     ribonucleoprotein complex biogenesis
GO:0071843      7.31058455181605e-06    4.95784244530105        2.91080202062141
13      239     cellular component biogenesis at cellular level
GO:0006417      1.27264762000865e-05    5.56449704142012        2.19223583143035
11      180     regulation of translation
GO:0042254      1.41161258095143e-05    6.12637600762763        1.81468410490623
10      149     ribosome biogenesis
Tissue: Whole_Blood=>Adipose_Subcutaneous       Type:   asymmetric
SourceGene:     ENSG00000252229.1
TargetGeneSet:  MTND1P23        DNAJC11 CLSTN1  DFFA    DDI2    PAQR7   ARID1A
KPNA7   ZMYM4-AS1       THRAP3  RPS8    JAK1    WLS     RPL5    RP11    RPRD2
RPS27   UBAP2L  FCGR2C  TKT     POU2F1  RPS7    KIDINS220       CALM2   UBC     AAK1
GMCL1   TET3    EIF5B   UGGT1   RHOQP2  MYO1C   MLK7-AS1        TRIP12  GIGYF2  BRK1
LAMB2   RAD54L2 RPL29   APPL1   KCTD6   CTD     RPL24   ZBTB20  ACTG1P1 PDCD10
DNAJC19 PSMD2   BOD1L   PDGFRA  RPL34   RPS3A   SREK1IP1        SERF1B  FNIP1   SKP1
UBE2B   CTB     MTND5P11        CSF1R   RPS14   DOCK2   TBC1D9B RPL15P3 MTRNR2L9
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WDR11   RP1     TBPL1   PHACTR2 SCAF8   IGF2R   TRA2A   RPS3AP26        ARPC1A  MTPN
CLN8    KIF13B  HOOK3   ASPH    ZFHX4   FABP5   EEF1D   VPS28   RPL8    RPS6
RNU2-5P NIPSNAP3A       FKBP15  RPL12   GLE1    RPL7A   MRC1    PRINS   ZNF37BP
RPS24   FAM53B  VENTX   RPL27A  MTRNR2L8        CKAP5   C11orf31        FABP5P7 DDB1
SLCO2B1 TMEM126B        BACE1   UBE4A   DDX6    APPL2   CD163   GUCY2C  PFDN5   CBX5
LRP1    OS9     GNS     RBMS1P1 EEA1    PLXNC1  RPL18AP3        PARP4-AS1
PHF11   RPL13AP25       HNRNPA3P5       MYCBP2-AS1      DNAJC3  RNASE6  CHD8
C14orf28        C14orf43        SIVA1   C14orf80        GOLGA8IP        HERC2P10
FMN1    USP8    PIAS1   MEF2A   LRRK1   MPG     NME3    ABCC1   RPS15A  SRCAP
ZNF629  NFATC3  VPS4A   TERF2   ATXN1L  GLG1    VPS53   METTL16 RPL26   SSH2
TAF15   CDK12   DHX8    NMT1    MED13   TNRC6C  TBC1D16 ROCK1P1 ANKRD12 RPL17
RPL36   NDUFA11 MYO1F   ZNF121  BRD4    CYP4F12 SUPT5H  POU2F2  CNFN    RPL18
RPL13A  RPS5    SIRPG   TSHZ2   RPL12P4 TRPM2   CTA     TTC28   APOBEC3C        RPL3
TNRC6B  EP300   TMSB4X  DYNLT3  WDR45   TTC3P1  PGAM4   XIAP    MT
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      2.00188708910009e-27    39.5168344324887        0.963462736142828
24      91      translational termination
GO:0006414      2.61881020490939e-27    34.7119140625   1.11168777247249        25
105     translational elongation
GO:0070972      6.27573902089993e-26    29.8324092741935        1.24932530620718
25      118     protein localization to endoplasmic reticulum
GO:0006614      8.92408816331945e-26    32.6546080964686        1.11168777247249
24      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.14365709279469e-25    32.2541123085649        1.12227527506747
24      106     cotranslational protein targeting to membrane
GO:0045047      1.14365709279469e-25    32.2541123085649        1.12227527506747
24      106     protein targeting to ER
GO:0072599      1.14365709279469e-25    32.2541123085649        1.12227527506747
24      106     establishment of protein localization to endoplasmic reticulum
GO:0019080      1.85168014270543e-24    23.2124724409449        1.5987128918414 26
151     viral genome expression
GO:0019083      1.85168014270543e-24    23.2124724409449        1.5987128918414 26
151     viral transcription
GO:0000184      2.28689541570279e-24    27.8149326805386        1.25991280880216
24      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006413      5.03204695328668e-23    21.7934916338583        1.60930039443637
25      152     translational initiation
GO:0000956      7.67853154865473e-22    19.1975911458333        1.78928793855097
25      169     nuclear-transcribed mRNA catabolic process
GO:0006612      1.27275227658944e-21    20.434829637642 1.61988789703135        24
153     protein targeting to membrane
GO:0043624      1.27275227658944e-21    20.434829637642 1.61988789703135        24
153     cellular protein complex disassembly
GO:0034623      1.61290482923462e-21    18.5468225671141        1.84222545152585
25      174     cellular macromolecular complex disassembly
GO:0043241      2.80985180226919e-21    19.6653939604304        1.67282541000623
24      158     protein complex disassembly
GO:0006402      2.87041207150359e-21    18.0568321078431        1.88457546190575
25      178     mRNA catabolic process
GO:0032984      3.30768958865989e-21    17.9383116883117        1.89516296450073
25      179     macromolecular complex disassembly
GO:0006401      6.19080285127836e-21    16.1480666871948        2.17043803197011
26      205     RNA catabolic process
GO:0019058      9.13479201410615e-21    14.8046218487395        2.44571309943949
27      231     viral infectious cycle
GO:0072594      8.76506838445195e-20    15.4056826117318        2.15985052937513
25      204     establishment of protein localization to organelle
GO:0022415      2.08452272859195e-19    12.9353157572042        2.75275067469379
27      260     viral reproductive process
GO:0071845      2.0795496701577e-18     11.707337409672 3.00685073697322        27
284     cellular component disassembly at cellular level
GO:0022411      2.98547399506604e-18    11.5246305418719        3.04920074735312
27      288     cellular component disassembly
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GO:0016032      5.64076217151945e-17    8.39613583138173        4.77496367033423
31      451     viral reproduction
GO:0033365      2.15625534068943e-16    7.96558118833914        5.00788872742371
31      473     protein localization to organelle
GO:0006605      1.37190566205482e-14    7.28048205871693        5.01847623001868
29      474     protein targeting
GO:0042274      9.55270984107701e-07    37.1231808731809        0.19057504670957
5       18      ribosomal small subunit biogenesis
Tissue: Whole_Blood=>Adipose_Subcutaneous       Type:   cluster
SourceGene:     ENSG00000252229.1
TargetGeneSet:  MTND1P23        DNAJC11 CLSTN1  DFFA    DDI2    PAQR7   ARID1A
KPNA7   ZMYM4-AS1       THRAP3  RPS8    JAK1    WLS     RPL5    RP11    RPRD2
RPS27   UBAP2L  FCGR2C  TKT     POU2F1  RPS7    KIDINS220       CALM2   UBC     AAK1
GMCL1   TET3    EIF5B   UGGT1   RHOQP2  MYO1C   MLK7-AS1        TRIP12  GIGYF2  BRK1
LAMB2   RAD54L2 RPL29   APPL1   KCTD6   CTD     RPL24   ZBTB20  ACTG1P1 PDCD10
DNAJC19 PSMD2   BOD1L   PDGFRA  RPL34   RPS3A   SREK1IP1        SERF1B  FNIP1   SKP1
UBE2B   CTB     MTND5P11        CSF1R   RPS14   DOCK2   TBC1D9B RPL15P3 MTRNR2L9
WDR11   RP1     TBPL1   PHACTR2 SCAF8   IGF2R   TRA2A   RPS3AP26        ARPC1A  MTPN
CLN8    KIF13B  HOOK3   ASPH    ZFHX4   FABP5   EEF1D   VPS28   RPL8    RPS6
RNU2-5P NIPSNAP3A       FKBP15  RPL12   GLE1    RPL7A   MRC1    PRINS   ZNF37BP
RPS24   FAM53B  VENTX   RPL27A  MTRNR2L8        CKAP5   C11orf31        FABP5P7 DDB1
SLCO2B1 TMEM126B        BACE1   UBE4A   DDX6    APPL2   CD163   GUCY2C  PFDN5   CBX5
LRP1    OS9     GNS     RBMS1P1 EEA1    PLXNC1  RPL18AP3        PARP4-AS1
PHF11   RPL13AP25       HNRNPA3P5       MYCBP2-AS1      DNAJC3  RNASE6  CHD8
C14orf28        C14orf43        SIVA1   C14orf80        GOLGA8IP        HERC2P10
FMN1    USP8    PIAS1   MEF2A   LRRK1   MPG     NME3    ABCC1   RPS15A  SRCAP
ZNF629  NFATC3  VPS4A   TERF2   ATXN1L  GLG1    VPS53   METTL16 RPL26   SSH2
TAF15   CDK12   DHX8    NMT1    MED13   TNRC6C  TBC1D16 ROCK1P1 ANKRD12 RPL17
RPL36   NDUFA11 MYO1F   ZNF121  BRD4    CYP4F12 SUPT5H  POU2F2  CNFN    RPL18
RPL13A  RPS5    SIRPG   TSHZ2   RPL12P4 TRPM2   CTA     TTC28   APOBEC3C        RPL3
TNRC6B  EP300   TMSB4X  DYNLT3  WDR45   TTC3P1  PGAM4   XIAP    MT
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      2.00188708910009e-27    39.5168344324887        0.963462736142828
24      91      translational termination
GO:0006414      2.61881020490939e-27    34.7119140625   1.11168777247249        25
105     translational elongation
GO:0070972      6.27573902089993e-26    29.8324092741935        1.24932530620718
25      118     protein localization to endoplasmic reticulum
GO:0006614      8.92408816331945e-26    32.6546080964686        1.11168777247249
24      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.14365709279469e-25    32.2541123085649        1.12227527506747
24      106     cotranslational protein targeting to membrane
GO:0045047      1.14365709279469e-25    32.2541123085649        1.12227527506747
24      106     protein targeting to ER
GO:0072599      1.14365709279469e-25    32.2541123085649        1.12227527506747
24      106     establishment of protein localization to endoplasmic reticulum
GO:0019080      1.85168014270543e-24    23.2124724409449        1.5987128918414 26
151     viral genome expression
GO:0019083      1.85168014270543e-24    23.2124724409449        1.5987128918414 26
151     viral transcription
GO:0000184      2.28689541570279e-24    27.8149326805386        1.25991280880216
24      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006413      5.03204695328668e-23    21.7934916338583        1.60930039443637
25      152     translational initiation
GO:0000956      7.67853154865473e-22    19.1975911458333        1.78928793855097
25      169     nuclear-transcribed mRNA catabolic process
GO:0006612      1.27275227658944e-21    20.434829637642 1.61988789703135        24
153     protein targeting to membrane
GO:0043624      1.27275227658944e-21    20.434829637642 1.61988789703135        24
153     cellular protein complex disassembly
GO:0034623      1.61290482923462e-21    18.5468225671141        1.84222545152585
25      174     cellular macromolecular complex disassembly
GO:0043241      2.80985180226919e-21    19.6653939604304        1.67282541000623
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24      158     protein complex disassembly
GO:0006402      2.87041207150359e-21    18.0568321078431        1.88457546190575
25      178     mRNA catabolic process
GO:0032984      3.30768958865989e-21    17.9383116883117        1.89516296450073
25      179     macromolecular complex disassembly
GO:0006401      6.19080285127836e-21    16.1480666871948        2.17043803197011
26      205     RNA catabolic process
GO:0019058      9.13479201410615e-21    14.8046218487395        2.44571309943949
27      231     viral infectious cycle
GO:0072594      8.76506838445195e-20    15.4056826117318        2.15985052937513
25      204     establishment of protein localization to organelle
GO:0022415      2.08452272859195e-19    12.9353157572042        2.75275067469379
27      260     viral reproductive process
GO:0071845      2.0795496701577e-18     11.707337409672 3.00685073697322        27
284     cellular component disassembly at cellular level
GO:0022411      2.98547399506604e-18    11.5246305418719        3.04920074735312
27      288     cellular component disassembly
GO:0016032      5.64076217151945e-17    8.39613583138173        4.77496367033423
31      451     viral reproduction
GO:0033365      2.15625534068943e-16    7.96558118833914        5.00788872742371
31      473     protein localization to organelle
GO:0006605      1.37190566205482e-14    7.28048205871693        5.01847623001868
29      474     protein targeting
GO:0042274      9.55270984107701e-07    37.1231808731809        0.19057504670957
5       18      ribosomal small subunit biogenesis
Tissue: Whole_Blood=>Adipose_Subcutaneous       Type:   asymmetric
SourceGene:     KIR3DL2(ENSG00000240403.1)
TargetGeneSet:  RPS8    RP11    RPL32   RPL29   RPL35A  C4orf52 PAIP2   CTB
RPS14   GUSBP2  SNORA20 RPL7    EIF3H   EEF1D   RPS6    CLTA    BLOC1S2 CKAP5
ARPC3   TPT1    CGRRF1  RPS3AP6 RPS27L  RPLP1   RPS17L  C16orf13        RPL13
SUPT6H  RPL23A  C18orf32        SCARNA18        RPS15   RPL18   DHDH    GYG2-AS1
RPS4X   RPL10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      2.44776479587428e-27    184.038523274478        0.21797799460245
16      105     translational elongation
GO:0006413      1.0044230277057e-26     138.382905982906        0.315549096948308
17      152     translational initiation
GO:0006415      4.15583656027707e-26    188.75  0.18891426198879        15      91
translational termination
GO:0006614      4.16102202144838e-25    159.233333333333        0.21797799460245
15      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      4.84215706330037e-25    157.472527472527        0.220053975503425
15      106     cotranslational protein targeting to membrane
GO:0045047      4.84215706330037e-25    157.472527472527        0.220053975503425
15      106     protein targeting to ER
GO:0072599      4.84215706330037e-25    157.472527472527        0.220053975503425
15      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      2.67004705690014e-24    139.009708737864        0.244965746315134
15      118     protein localization to endoplasmic reticulum
GO:0000184      3.05215497429842e-24    137.663461538462        0.24704172721611
15      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      1.28839226808516e-22    105.036764705882        0.313473116047332
15      151     viral genome expression
GO:0019083      1.28839226808516e-22    105.036764705882        0.313473116047332
15      151     viral transcription
GO:0006612      1.58172070029641e-22    103.5   0.317625077849284       15      153
protein targeting to membrane
GO:0043624      1.58172070029641e-22    103.5   0.317625077849284       15      153
cellular protein complex disassembly
GO:0043241      2.60941149443229e-22    99.8461538461538        0.328004982354162
15      158     protein complex disassembly
GO:0000956      7.41763287803991e-22    92.6428571428571        0.350840772264895
15      169     nuclear-transcribed mRNA catabolic process
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GO:0034623      1.16489622571921e-21    89.6981132075472        0.361220676769774
15      174     cellular macromolecular complex disassembly
GO:0006402      1.65528529282346e-21    87.4723926380368        0.369524600373677
15      178     mRNA catabolic process
GO:0032984      1.80490563505889e-21    86.9329268292683        0.371600581274652
15      179     macromolecular complex disassembly
GO:0072594      1.34993586502559e-20    75.3015873015873        0.423500103799045
15      204     establishment of protein localization to organelle
GO:0006401      1.45507429475967e-20    74.9    0.425576084700021       15      205
RNA catabolic process
GO:0019058      9.03282815920188e-20    65.7638888888889        0.479551588125389
15      231     viral infectious cycle
GO:0022415      5.45410010289999e-19    57.8612244897959        0.539755034253685
15      260     viral reproductive process
GO:0071845      2.07466875589035e-18    52.6096654275093        0.589578575877102
15      284     cellular component disassembly at cellular level
GO:0022411      2.56240539447568e-18    51.8241758241758        0.597882499481005
15      288     cellular component disassembly
GO:0016032      2.08323179173028e-15    32.0756880733945        0.936267386340046
15      451     viral reproduction
GO:0033365      4.20956060763729e-15    30.4868995633188        0.981938966161511
15      473     protein localization to organelle
GO:0006605      4.34277122235995e-15    30.4183006535948        0.984014947062487
15      474     protein targeting
GO:0042274      2.28326335864882e-10    221.661538461538        0.0373676562175628
5       18      ribosomal small subunit biogenesis
GO:0006364      1.44839609929631e-09    44.9430748543254        0.215902013701474
7       104     rRNA processing
GO:0016072      2.15150248907704e-09    42.3073026593499        0.228357899107328
7       110     rRNA metabolic process
GO:0022613      1.32899350087514e-08    23.8022622538752        0.467095702719535
8       225     ribonucleoprotein complex biogenesis
GO:0042254      1.79491152814987e-08    30.6041028781384        0.309321154245381
7       149     ribosome biogenesis
GO:0071843      2.12892620731648e-08    22.3376623376623        0.496159435333195
8       239     cellular component biogenesis at cellular level
GO:0034470      1.36107562520756e-07    22.4365848164001        0.415196180195142
7       200     ncRNA processing
GO:0000028      1.60796442683759e-07    534     0.0124558854058543      3       6
ribosomal small subunit assembly
GO:0034660      1.48766010544459e-06    15.4834219580857        0.591654556778078
7       285     ncRNA metabolic process
GO:0042255      4.43961160337844e-06    123.145299145299        0.0332156944156114
3       16      ribosome assembly
Tissue: Whole_Blood=>Adipose_Subcutaneous       Type:   asymmetric
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SourceGene: MRPL53P1(ENSG00000235299.1) MRPL53P1 mitochondrial ribosomal protein L53 pseudogene 1

TargetGeneSet: C1orf86 RPL22 ICMT RP11 LDLRAD2 HSPG2 RPL11 ARID1A
KPNA7 RP1 KDM4A RPS8 RP4 PTGES3P1 RPL5 JTB RPS27
UBAP2L MTX1 MIR555 MEF2D RPS7 PPP1CB CALM2 UBC AAK1 GMCL1
DGUOK-AS1 EIF5B RANBP2 UGGT1 MYO1C SENP2 EEF1B2 TRIP12 GIGYF2
TRAF3IP1 BRK1 UBE2E1 GORASP1 DALRD3 RAD54L2 RPL29 RPL24 ABTB1 RYK
ACTG1P1 PDCD10 DNAJC19 PSMD2 7SK PPP1R2 NOP14 MAN2B2 RPL34 NDUFC1
RPS3A FBXO8 NPR3 CTD NDUFAF2 CHCHD2P2 COX7C HINT1 UBE2B CTB
MTND5P11 PAIP2 RPS14 RPL15P3 NOL7 DEK GPLD1 ABT1 RPS10
MTRNR2L9 WDR11 MRPS12 MALSU1 MPLKIP CHCHD2 RPS3AP26 CUX1
SLC26A4 RPL7 MED30 EEF1D RPL8 RPS6 NDUFB6 CLTA NIPSNAP3A
RPL35 ZNF79 RPL12 NUP188 RPL7A NACC2 PRINS RPS24 RPS3AP5 MRPL43 SUFU
FAM53B NUP98 PRKCDBP RPL27A MTRNR2L8 PIGCP1 CKAP5 C11orf31 DDB1
BAD C11orf2 RNASEH2C CCDC85B TMEM126B TMEM126A SDHD
BACE1 UBE4A DDX6 RPS25 USP5 PFDN5 HOXC8 CBX5 OS9 GNS EEA1
RPL18AP3 CUX2 ACADS PARP4-AS1 TPT1 MYCBP2-AS1 DNAJC3
HMGB3P4 CHD8 C14orf21 C14orf28 CGRRF1 YLPM1 CCNK SIVA1
GOLGA8IP MGA SNAP23 DUT RPS3AP6 RPS27L PIAS1 RPLP1 MORF4L1
SEC11A MRPL46 MPG MRPL28 FAM173A SPSB3 MPV17L ABCC1 RPS15A SRCAP
NFATC3 HSBP1 RPL13 VPS53 METTL16 RNASEK POLR2A TP53 LSMD1 VAMP2
RPL26 TRIM16 NCOR1 SUPT6H RPL23A NUFIP2 RPL19 WIPF2 RPL27 DHX8
MED13 BPTF NT5C TNRC6C C18orf32 RPL17 ATP5D RPS15 UQCR11
FAM108A1 NFIC RPL36 NDUFA11 TRAPPC5 SLC35E1 PGLS C19orf60
RPSAP58 HSPB6 RPS19 POU2F2 ZNF428 SLC1A5 RPL18 RPL13A ZNF587 ZSCAN22 RPS5
GAPDHP2 HM13 KIF3B SCAND1 SOGA1 TOP1 NCOA3 TSHZ2 DGCR2 DGCR6L
FAM211B CTA HMGB1P10 NF2 PRR14L MPST APOBEC3C RPL3
EP300 DYNLT3 WASF4P WDR45 APOOL RPL39 BCORL1 MT

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term

GO:0006414	3.73E-49	59.03534304	1.365995433	40	105
translational elongation					
GO:0006415	1.46E-48	67.92201258	1.183862708	38	91
translational termination					

GO:0006614	2.16E-47	56.30292862	1.365995433	39	105	SRP-dependent cotranslational protein targeting to membrane
GO:0006613	3.38E-47	55.45867976	1.379004913	39	106	cotranslational protein targeting to membrane
GO:0045047	3.38E-47	55.45867976	1.379004913	39	106	protein targeting to ER

GO:0072599	3.38E-47	55.45867976	1.379004913	39	106	establishment of protein localization to endoplasmic reticulum
GO:0070972	1.03E-46	49.15107415	1.535118677	40	118	protein localization to endoplasmic reticulum
GO:0000184	3.34E-43	44.35522634	1.548128157	38	119	"nuclear-transcribed mRNA catabolic process, nonsense-mediated decay"

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GO:0019080      8.74E-42        34.45824203     1.964431527     40      151
viral genome expression
```

```
GO:0019083      8.74E-42        34.45824203     1.964431527     40      151
viral transcription
```

GO:0006413 translational initiation	1.17E-41	34.14816602	1.977441008	40	152
GO:0006612 protein targeting to membrane	1.57E-41	33.84357809	1.990450488	40	153
GO:0043624 cellular protein complex disassembly	1.68E-38	31.1666087	1.990450488	38	153

GO:0000956	3.73E-38	28.4557047	2.198602173	39	169
nuclear-transcribed mRNA catabolic process					
GO:0043241	6.45E-38	29.85744444	2.055497889	38	158
protein complex disassembly					
GO:0034623	1.28E-37	27.39209545	2.263649574	39	174
cellular macromolecular complex disassembly					

GO:0072594	1.76E-37	24.1267059	2.653933984	41	204	establishment of protein localization to organelle
GO:0006402	3.34E-37	26.59630148	2.315687496	39	178	mRNA catabolic process

GO:0032984	4.23E-37	26.40445829	2.328696976	39	179	macromolecular complex disassembly
GO:0006401	5.17E-36	23.09254709	2.666943464	40	205	RNA catabolic process
GO:0019058	3.75E-35	20.65853921	3.005189952	41	231	viral infectious cycle

GO:0022415	3.04E-34	18.53368104	3.382464881	42	260
viral reproductive process					
GO:0033365	1.09E-30	11.50588774	6.153484188	49	473
protein localization to organelle					

GO:0006605	1.21E-30	11.47798561	6.166493668	49	474
protein targeting					
GO:0016032	1.39E-30	11.79156328	5.867275621	48	451
viral reproduction					
GO:0071845	5.39E-29	14.97608547	3.694692409	39	284
cellular component disassembly at cellular level					

GO:0022411	9.29E-29	14.73130104	3.74673033	39	288
cellular component disassembly					
GO:0042274	3.87E-13	79.63128492	0.234170646	9	18
ribosomal small subunit biogenesis					
GO:0042254	9.43E-10	9.142222414	1.938412567	15	149
ribosome biogenesis					

GO:0022613	5.89E-09	6.717695682	2.92713307	17	225	ribonucleoprotein complex biogenesis
GO:0006364	1.01E-08	10.50222332	1.352985953	12	104	rRNA processing

GO:0071843	1.46E-08	6.287787788	3.109265795	17	239	cellular component biogenesis at cellular level
GO:0016072	1.92E-08	9.855055659	1.431042834	12	110	rRNA metabolic process
GO:0042273	2.60E-07	55.6440281	0.156113764	5	12	ribosomal large subunit biogenesis

GO:0030490	9.42E-07	103.3333333	0.091066362	4	7
maturation of SSU-rRNA					
GO:0034470	1.20E-05	5.104569632	2.601896063	12	200
ncRNA processing					

Tissue: Whole_Blood=>Adipose_Subcutaneous Type: cluster
SourceGene: MRPL53P1(ENSG00000235299.1)

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TargetGeneSet:  C1orf86 RPL22   ICMT    RP11    LDLRAD2 HSPG2   RPL11   ARID1A
KPNA7   RP1     KDM4A   RPS8    RP4     PTGES3P1        RPL5    JTB     RPS27
UBAP2L  MTX1    MIR555  MEF2D   RPS7    PPP1CB  CALM2   UBC     AAK1    GMCL1
DGUOK-AS1       EIF5B   RANBP2  UGGT1   MYO1C   SENP2   EEF1B2  TRIP12  GIGYF2
TRAF3IP1        BRK1    UBE2E1  GORASP1 DALRD3  RAD54L2 RPL29   RPL24   ABTB1   RYK
ACTG1P1 PDCD10  DNAJC19 PSMD2   7SK     PPP1R2  NOP14   MAN2B2  RPL34   NDUFC1
RPS3A   FBXO8   NPR3    CTD     NDUFAF2 CHCHD2P2        COX7C   HINT1   UBE2B   CTB
MTND5P11        PAIP2   RPS14   RPL15P3 NOL7    DEK     GPLD1   ABT1    RPS10
MTRNR2L9        WDR11   MRPS12  MALSU1  MPLKIP  CHCHD2  RPS3AP26        CUX1
SLC26A4 RPL7    MED30   EEF1D   RPL8    RPS6    NDUFB6  CLTA    NIPSNAP3A
RPL35   ZNF79   RPL12   NUP188  RPL7A   NACC2   PRINS   RPS24   RPS3AP5 MRPL43  SUFU
FAM53B  NUP98   PRKCDBP RPL27A  MTRNR2L8        PIGCP1  CKAP5   C11orf31        DDB1
BAD     C11orf2 RNASEH2C        CCDC85B TMEM126B        TMEM126A        SDHD
BACE1   UBE4A   DDX6    RPS25   USP5    PFDN5   HOXC8   CBX5    OS9     GNS     EEA1
RPL18AP3        CUX2    ACADS   PARP4-AS1       TPT1    MYCBP2-AS1      DNAJC3
HMGB3P4 CHD8    C14orf21        C14orf28        CGRRF1  YLPM1   CCNK    SIVA1
GOLGA8IP        MGA     SNAP23  DUT     RPS3AP6 RPS27L  PIAS1   RPLP1   MORF4L1
SEC11A  MRPL46  MPG     MRPL28  FAM173A SPSB3   MPV17L  ABCC1   RPS15A  SRCAP
NFATC3  HSBP1   RPL13   VPS53   METTL16 RNASEK  POLR2A  TP53    LSMD1   VAMP2
RPL26   TRIM16  NCOR1   SUPT6H  RPL23A  NUFIP2  RPL19   WIPF2   RPL27   DHX8
MED13   BPTF    NT5C    TNRC6C  C18orf32        RPL17   ATP5D   RPS15   UQCR11
FAM108A1        NFIC    RPL36   NDUFA11 TRAPPC5 SLC35E1 PGLS    C19orf60
RPSAP58 HSPB6   RPS19   POU2F2  ZNF428  SLC1A5  RPL18   RPL13A  ZNF587  ZSCAN22 RPS5
GAPDHP2 HM13    KIF3B   SCAND1  SOGA1   TOP1    NCOA3   TSHZ2   DGCR2   DGCR6L
FAM211B CTA     HMGB1P10        NF2     PRR14L  MPST    APOBEC3C        RPL3
EP300   DYNLT3  WASF4P  WDR45   APOOL   RPL39   BCORL1  MT
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      3.73063837383387e-49    59.035343035343 1.36599543284202        40
105     translational elongation
GO:0006415      1.46340793209755e-48    67.9220125786163        1.18386270846308
38      91      translational termination
GO:0006614      2.15619985871634e-47    56.3029286150092        1.36599543284202
39      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      3.37677545824514e-47    55.4586797555845        1.3790049131548 39
106     cotranslational protein targeting to membrane
GO:0045047      3.37677545824514e-47    55.4586797555845        1.3790049131548 39
106     protein targeting to ER
GO:0072599      3.37677545824514e-47    55.4586797555845        1.3790049131548 39
106     establishment of protein localization to endoplasmic reticulum
GO:0070972      1.03199852307688e-46    49.1510741510741        1.53511867690817
40      118     protein localization to endoplasmic reticulum
GO:0000184      3.34093162568094e-43    44.3552263374486        1.54812815722095
38      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      8.7395666550836e-42     34.4582420258096        1.96443152722995
40      151     viral genome expression
GO:0019083      8.7395666550836e-42     34.4582420258096        1.96443152722995
40      151     viral transcription
GO:0006413      1.17411846562303e-41    34.148166023166 1.97744100754273        40
152     translational initiation
GO:0006612      1.57369689042792e-41    33.8435780913657        1.99045048785551
40      153     protein targeting to membrane
GO:0043624      1.68164805971791e-38    31.1666086956522        1.99045048785551
38      153     cellular protein complex disassembly
GO:0000956      3.73184480804594e-38    28.4557046979866        2.19860217286001
39      169     nuclear-transcribed mRNA catabolic process
GO:0043241      6.45243751909214e-38    29.8574444444444        2.05549788941942
38      158     protein complex disassembly
GO:0034623      1.282854874419e-37      27.3920954511559        2.26364957442392
39      174     cellular macromolecular complex disassembly
GO:0072594      1.76295983175462e-37    24.1267058970828        2.65393398380735
41      204     establishment of protein localization to organelle
GO:0006402      3.34364130480759e-37    26.5963014823041        2.31568749567504
39      178     mRNA catabolic process
```

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GO:0032984      4.23162209693341e-37    26.4044582933845        2.32869697598782
39      179     macromolecular complex disassembly
GO:0006401      5.1722689110407e-36     23.0925470925471        2.66694346412013
40      205     RNA catabolic process
GO:0019058      3.75419660603351e-35    20.6585392051557        3.00518995225244
41      231     viral infectious cycle
GO:0022415      3.03706919772999e-34    18.5336810355662        3.38246488132309
42      260     viral reproductive process
GO:0033365      1.09468083270523e-30    11.5058877426361        6.15348418794547
49      473     protein localization to organelle
GO:0006605      1.20902238516489e-30    11.4779856115108        6.16649366825825
49      474     protein targeting
GO:0016032      1.39328519956244e-30    11.7915632754342        5.86727562106429
48      451     viral reproduction
GO:0071845      5.39156390596749e-29    14.9760854677441        3.69469240882984
39      284     cellular component disassembly at cellular level
GO:0022411      9.29068973029194e-29    14.7313010430986        3.74673033008096
39      288     cellular component disassembly
GO:0042274      3.8721725988671e-13     79.6312849162011        0.23417064563006
9       18      ribosomal small subunit biogenesis
GO:0042254      9.43006407331837e-10    9.14222241394185        1.93841256660439
15      149     ribosome biogenesis
GO:0022613      5.89204997575501e-09    6.71769568151147        2.92713307037575
17      225     ribonucleoprotein complex biogenesis
GO:0006364      1.00730880064885e-08    10.5022233201581        1.35298595252924
12      104     rRNA processing
GO:0071843      1.45642476614937e-08    6.28778778778779        3.10926579475469
17      239     cellular component biogenesis at cellular level
GO:0016072      1.91523072560317e-08    9.85505565862709        1.43104283440592
12      110     rRNA metabolic process
GO:0042273      2.5989566538941e-07     55.6440281030445        0.156113763753373
5       12      ribosomal large subunit biogenesis
GO:0030490      9.41895577688388e-07    103.333333333333        0.0910663621894679
4       7       maturation of SSU-rRNA
GO:0034470      1.2033717020449e-05     5.10456963249516        2.60189606255622
12      200     ncRNA processing
Tissue: Whole_Blood=>Adipose_Subcutaneous       Type:   cluster
SourceGene:     MTND1P23(ENSG00000225972.1)
TargetGeneSet:  MTND1P23        RPL22   DDI2    RP1     RPL11   ARID1A  PRDX3P2
KPNA7   ZMYM4   THRAP3  RPS8    RP11    RPL5    RPRD2   RPS27   UBAP2L  RAB25   TKT
RPS7    CALM2   UBC     COMMD1  AAK1    TMEM131 EIF5B   UGGT1   UBR3    TRIP12
EFHD1   GIGYF2  SNED1   BRK1    RPL15   RAD54L2 RPL29   KCTD6   CTD     TMF1    PCNP
RPL24   RYK     GPR87   PDCD10  HTT     BOD1L   ZBTB12B PDGFRA  CISD2   RPL34
RPS3A   RHOBTB3 SKP1    CTB     MTND5P11        CSF1R   RPS14   LYRM4   RP3
RPL15P3 AGPAT1  MTRNR2L9        WDR11   PHACTR2 PPP1R14C        IGF2R   STARD3NL
RPS3AP26        POLR2J3 SPDYE2  TRBV6-5 CLN8    KIAA1967        DRP2    HMBOX1
HOOK3   ASPH    ARFGEF1 UBR5    NFIB    RPS6    HMGB3P24        CBWD6   NIPSNAP3A
ATP6V1G1        GAPVD1  RPL12   SETX    EEF1A1P5        RPL7A   SEC16A  KIAA0913
RPS3AP5 KLLN    MRPL43  DUSP5   RPL27A  MTRNR2L8        CKAP5   BTBD18  CCDC90B ATM
FDX1    UBE4A   MLL     DDX6    RPL23AP64       CD163L1 SCAF11  MLL4    PFDN5   CBX5
LRP1    OS9     GNS     EEA1    USP44   RPL18AP3        RPSAP54 GTF3A   TNFSF13B
CCNB1IP1        CHD8    C14orf28        CGRRF1  YLPM1   C14orf142       SIVA1
C15orf33        USP8    RPS27L  UBL7    SIN3A   SEC11A  MPG     RPS15A
SLX1B-SULT1A4   LONP2   FBXL8   NFATC3  TERF2   RPL13   VPS53   WDR81   RPL26
RPL23A  NUFIP2  TAF15   RPL19   CDK12   RPL27   MED13   TNRC6C  ROCK1P1 ANKRD12 DSG1
RPL17   FAM108A1        NFIC    C3      ZNF121  BRD4    RPSAP58 POU2F2  ZNF526
IGFL2   RPL18   NUCB1-AS1       RPL13A  RPS5    RRBP1   NCOA3   TSHZ2   RPL12P4
ICOSLG  PI4KAP1 YDJC    FAM211B CTA     HMGB1P10        TTC28   EIF3L   RPL3
TNRC6B  EP300   TMSB4X  DYNLT3  USP9X   RPS4X   RLIM    TTC3P1  PGAM4   APOOL
DOCK11  RP13    RPL10   MT
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      4.43951750615861e-38    59.8696931483817        0.92567988374507
30      91      translational termination
```

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GO:0006614      1.29222701416958e-37    51.3897949673812        1.068092173552  31
105     SRP-dependent cotranslational protein targeting to membrane
GO:0070972      1.75738623577027e-37    46.0036400404449        1.20033215694416
32      118     protein localization to endoplasmic reticulum
GO:0006613      1.81205197266399e-37    50.7010344827586        1.07826447996678
31      106     cotranslational protein targeting to membrane
GO:0045047      1.81205197266399e-37    50.7010344827586        1.07826447996678
31      106     protein targeting to ER
GO:0072599      1.81205197266399e-37    50.7010344827586        1.07826447996678
31      106     establishment of protein localization to endoplasmic reticulum
GO:0006414      6.50307642326397e-36    48.6461538461538        1.068092173552  30
105     translational elongation
GO:0000184      4.50928103369268e-34    40.9536156727168        1.21050446335894
30      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006413      1.36605743496636e-33    32.8904347826087        1.54619057504671
32      152     translational initiation
GO:0019080      3.54962424906352e-32    31.5879310344828        1.53601826863193
31      151     viral genome expression
GO:0019083      3.54962424906352e-32    31.5879310344828        1.53601826863193
31      151     viral transcription
GO:0000956      5.19550891365289e-32    28.7746112345287        1.71911978409799
32      169     nuclear-transcribed mRNA catabolic process
GO:0006612      5.50462448728236e-32    31.065715093273 1.55636288146149        31
153     protein targeting to membrane
GO:0006402      3.01707628337748e-31    26.9836807623585        1.81067054183102
32      178     mRNA catabolic process
GO:0043624      1.6843388982562e-30     29.5622263914947        1.55636288146149
30      153     cellular protein complex disassembly
GO:0034623      3.82730617094672e-30    26.4643718350615        1.76998131617189
31      174     cellular macromolecular complex disassembly
GO:0043241      4.70981669600893e-30    28.3974358974359        1.6072244135354 30
158     protein complex disassembly
GO:0032984      9.63588371523563e-30    25.5612767940354        1.8208428482458 31
179     macromolecular complex disassembly
GO:0072594      2.88086400958539e-29    22.8626895854398        2.07515050861532
32      204     establishment of protein localization to organelle
GO:0006401      3.38706482064813e-29    22.7289268660467        2.0853228150301 32
205     RNA catabolic process
GO:0019058      3.32502076082512e-26    18.8458620689655        2.34980278181441
31      231     viral infectious cycle
GO:0033365      5.44317706017976e-26    11.9755671148907        4.81150093419141
40      473     protein localization to organelle
GO:0071845      8.04758984305396e-26    16.2070664709583        2.8889350217978 33
284     cellular component disassembly at cellular level
GO:0022411      1.2725239793414e-25     15.9482972136223        2.92962424745692
33      288     cellular component disassembly
GO:0022415      1.3202462778126e-24     16.4254253877428        2.64479966784306
31      260     viral reproductive process
GO:0006605      8.78506809219884e-23    10.6735801955482        4.82167324060619
37      474     protein targeting
GO:0016032      1.83222706237215e-18    9.22112690671371        4.58771019306622
32      451     viral reproduction
GO:0044257      1.48355496018936e-05    4.08650458069063        4.08926717874196
15      402     cellular protein catabolic process
GO:0022613      1.88883383604748e-05    5.32538482682793        2.28876894332572
11      225     ribonucleoprotein complex biogenesis
Tissue: Whole_Blood=>Adipose_Subcutaneous       Type:   cluster
```

SourceGene: ROCK1P1(ENSG00000263006.1) "Rho-associated, coiled-coil containing protein kinase 1 pseudogene 1"

TargetGeneSet: MTND1P23 RPL22 DNAJC11 DFFA HSPG2 RPL11 PAFAH2
ARID1A PRDX3P2 KPNA7 THRAP3 RP1 RPS8 RPS15AP10 RPL5 RP11
RNU1-5 RPRD2 RPS27 UBAP2L ARHGEF11 TMEM63A UBC COMMD1 GMCL1
DGUOK RETSAT EIF5B UGGT1 MYO1C EEF1B2 RPL15 RAD54L2 RPL29 PCNP
RPL24 BOD1L ZBTB12B RPL34 RPS3A MND1 SNORA47 HINT1 SKP1 CTB
MTND5P11 PCDHGC5 RPS14 SLC2A3P1 RPL15P3 RPS10 RPL10A USP49
MTRNR2L9 WDR11 KIAA1919 TATDN2P2 IGF2R CYP51A1 RPS3AP26
MLL3 HOOK3 RBM12B EIF3H EEF1D RPL8 RPS6 NIPSNAP3A GAPVD1
RPL7A RPS24 RPS3AP5 SFR1 FAM53B RPL27A MTRNR2L8 CKAP5 TMEM126B
BACE1 UBE4A DDX6 SCAF11 CCDC65 MLL4 PFDN5 PSG1 CBX5 LRP1
ARPC3 VPS29 RP3 SBNO1 TPT1 HMGB3P4 CHD8 ZNF410 KIAA1737
SIVA1 GOLGA8IP HERC2P10 CCNDBP1 MORF4L1 SEC11A CTD NTAN1
RPS15A NFATC3 RPL13 VPS53 RPL26 SUPT6H RPL23A RPL19 WIPF2 RAMP2
RPL27 DHX8 ROCK1P1 RPL17 RPS15 FAM108A1 NFIC ZBTB7A ZNF121
MAST1 BRD4 GLT25D1 SUPT5H MIR642A RPL18 RPL13A RPS5 SCAND1 EPB41L1
SOGA1 TSHZ2 SCAF4 DGCR6L CTA RPL3 EP300 RP4 TMSB4X DYNLT3
HUWE1 RPS4X APOOL XIAP HCFC1 RPL10 AMELY MT

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0006414	3.66E-48	83.88823529	0.871911978	35	105	translational elongation

GO:0006415	8.20E-47	93.343044	0.755657048	33	91	translational termination
GO:0006614	2.99E-46	79.40386505	0.871911978	34	105	SRP-dependent cotranslational protein targeting to membrane
GO:0006613	4.38E-46	78.29554264	0.880215902	34	106	cotranslational protein targeting to membrane
GO:0045047	4.38E-46	78.29554264	0.880215902	34	106	protein targeting to ER

GO:0072599	4.38E-46	78.29554264	0.880215902	34	106
establishment of protein localization to endoplasmic reticulum					
GO:0070972	3.08E-44	67.05398671	0.979862985	34	118
protein localization to endoplasmic reticulum					
GO:0000184	2.78E-42	62.82878909	0.988166909	33	119
"nuclear-transcribed mRNA catabolic process, nonsense-mediated decay"					

GO:0019080 viral genome expression	7.90E-42	50.45892495	1.253892464	35	151
GO:0019083 viral transcription	7.90E-42	50.45892495	1.253892464	35	151
GO:0006413 translational initiation	1.02E-41	50.02413273	1.262196388	35	152
GO:0006612 protein targeting to membrane	6.40E-40	47.21594684	1.270500311	34	153

GO:0000956	2.57E-38	41.57312661	1.403363089	34	169
nuclear-transcribed mRNA catabolic process					
GO:0043624	2.96E-38	44.91982759	1.270500311	33	153
cellular protein complex disassembly					
GO:0034623	7.50E-38	40.07425249	1.444882707	34	174
cellular macromolecular complex disassembly					
GO:0043241	9.44E-38	43.10786207	1.312019929	33	158
protein complex disassembly					

GO:0006402	1.72E-37	38.9500969	1.478098401	34	178	mRNA catabolic process
GO:0032984	2.12E-37	38.678749	1.486402325	34	179	macromolecular complex disassembly
GO:0072594	2.41E-35	32.93255814	1.694000415	34	204	establishment of protein localization to organelle
GO:0006401	2.87E-35	32.7376581	1.702304339	34	205	RNA catabolic process

GO:0019058	6.89E-35	29.69537815	1.918206353	35	231
viral infectious cycle					
GO:0022415	1.88E-34	26.99043367	2.159020137	36	260
viral reproductive process					
GO:0071845	1.18E-31	23.28703047	2.358314304	35	284
cellular component disassembly at cellular level					
GO:0022411	1.95E-31	22.91234597	2.391529998	35	288
cellular component disassembly					

GO:0016032	3.36E-28	15.61696096	3.745069545	38	451
viral reproduction					
GO:0033365	1.96E-27	14.80370059	3.927755865	38	473
protein localization to organelle					
GO:0006605	3.09E-26	14.17325136	3.936059788	37	474
protein targeting					
GO:0042274	2.85E-07	47.88628763	0.149470625	5	18
ribosomal small subunit biogenesis					

GO:0022613	3.63E-07	7.364632238	1.868382811	12	225	ribonucleoprotein complex biogenesis
GO:0071843	6.93E-07	6.903573177	1.984637741	12	239	cellular component biogenesis at cellular level
GO:0006364	2.37E-06	10.59151786	0.863608055	8	104	rRNA processing
GO:0016072	3.61E-06	9.964285714	0.913431596	8	110	rRNA metabolic process

GO:0042254 4.09E-06 8.218725869 1.237284617 9 149
ribosome biogenesis

GO:0030490 1.91E-05 91.83974359 0.058127465 3 7
maturation of SSU-rRNA

Tissue: Whole_Blood=>Adipose_Subcutaneous Type: cluster
SourceGene: RP11-156P1.1(ENSG00000263142.1)
TargetGeneSet: MTND1P23 RPL22 CLSTN1 DFFA HSPG2 RPL11 ARID1A
WASF2 PHACTR4 TAF12 PUM1 KPNA7 THRAP3 MFI2 RPS8 RP4 CCBL2 RPL5
RP11 ATP5F1 RPRD2 ZNF687 SPRR1B RPS27 ASH1L MIR555 SSR2 TKT GAS5
ELK4 RPS7 PPP1CB UBC COMMD1 GMCL1 DGUOK COA5 EIF5B RANBP2
UGGT1 SENP2 EEF1B2 TRIP12 GIGYF2 SNED1 BRK1 RPL15 DALRD3 LAMB2
RAD54L2 RPL29 KCTD6 RPL24 PHC3 DNAJC19 EIF4G1 RPL35A ZFYVE28 AFAP1
BOD1L RPL34 NDUFC1 ANAPC10 RPS3A RPL6P12 NDUFS4 CTD NDUFAF2 MRPS36 BTF3
TBCA COX7C APC HINT1 SKP1 CTB MTND5P11 RPS14 SLC2A3P1
GNB2L1 RPL15P3 GFOD1 NOL7 PRRC2A AGPAT1 RPS18 TAPBP SYNGAP1 RPS10
RPL10A MRPL32 MTRNR2L9 COX7A2 WDR11 MRPS12 PHACTR2 IGF2R PSMB1
FOXK1 ADCY1 CHCHD2 RPS3AP26 TRRAP MRPS33 MLL3 KIAA1967 DRP2
KAT6A HOOK3 RPS20 PAG1 KIAA1429 RPL30 EIF3H EEF1D RPL8 NFIB
RPS6 TLN1 CLTA NIPSNAP3A TMEM245 RC3H2 RPL35 RPL12 LRRC8A SETX
GTF3C4 RPL7A SEC16A COMMD3 KIAA0913 RPS24 MRPL43 FAM53B RPL27A
MTRNR2L8 CKAP5 C11orf31 PPP6R3 CCDC90B C11orf73 UBE4A
ATP5L DDX6 RPS25 H2AFJ MLL4 PFDN5 CBX5 LRP1 EEA1 RPL18AP3
SBNO1 GOLGA3 TPT1 ESD MED4-AS1 DNAJC3 CCNB1IP1 CHD8
YLPM1 GOLGA8IP HERC2 USP8 RPS3AP6 RPS27L PIAS1 CALML4 SIN3A
C15orf40 SEC11A MRPL46 CIB1 MPG HBQ1 NME3 SPSB3 NDUFB10 ECI1
RPS15A SRCAP ZNF629 FBXL8 NFATC3 ATXN1L ZNF778 RPL13 VPS53 WDR81
POLR2A RPL26 KIAA0100 RPL23A TAF15 RPL17 RPL19 MED1 CDK12
WIPF2 RPL27 CLTC MED13 NT5C TNRC6C NPLOC4 ANAPC11 ROCK1P1 ANKRD12 DSG4
ZNF407 ATP5D RPS15 NFIC PTPRS RPL36 TRAPPC5 ZNF121 PIN1 C19orf43

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BRD4    SLC35E1 UBA52   GATAD2A RPSAP58 POU2F2  ZNF428  IGFL2   ARHGAP35
RPL18   RPL13A  ZNF264  RPS5    KIF3B   SCAND1  NCOA3   TSHZ2   RPL12P4 SON
C22orf29        MIR1306 DGCR6L  HMGB1P10        TTC28   UQCR10  RP3     MPST
EIF3L   RPL3    TNRC6B  EP300   ZC3H7B  ZBED4   TMSB4X  DYNLT3  UXT     HUWE1
UBQLN2  NHSL2   RPS4X   COX7B   RPL39   MCTS1   XIAP    HCFC1   RPL10   MT
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      5.89933309633214e-57    64.6297948260482        1.57670749429105
46      105     translational elongation
GO:0006614      5.89933309633214e-57    64.6297948260482        1.57670749429105
46      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006415      6.53477919546686e-57    76.7713688353216        1.36647982838558
44      91      translational termination
GO:0006613      1.03006189095429e-56    63.5481481481482        1.59172375614144
46      106     cotranslational protein targeting to membrane
GO:0045047      1.03006189095429e-56    63.5481481481482        1.59172375614144
46      106     protein targeting to ER
GO:0072599      1.03006189095429e-56    63.5481481481482        1.59172375614144
46      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      4.96891286863683e-54    52.9119558154646        1.77191889834614
46      118     protein localization to endoplasmic reticulum
GO:0000184      4.10039540896099e-52    50.0628535512256        1.78693516019653
45      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006413      3.57260818519646e-51    38.5889849795175        2.28247180125943
48      152     translational initiation
GO:0019080      3.5160917247145e-48     36.1979392926761        2.26745553940904
46      151     viral genome expression
GO:0019083      3.5160917247145e-48     36.1979392926761        2.26745553940904
46      151     viral transcription
GO:0006612      7.04185746667432e-48    35.5163141498606        2.29748806310982
46      153     protein targeting to membrane
GO:0043624      2.46605133196567e-46    34.2199612403101        2.29748806310982
45      153     cellular protein complex disassembly
GO:0000956      1.25329217738777e-45    30.8613131745353        2.53774825271607
46      169     nuclear-transcribed mRNA catabolic process
GO:0043241      1.27470216854243e-45    32.6942272072443        2.37256937236177
45      158     protein complex disassembly
GO:0034623      5.60180436364997e-45    29.6452850877193        2.61282956196803
46      174     cellular macromolecular complex disassembly
GO:0006402      1.78824078307116e-44    28.7387914230019        2.67289460936959
46      178     mRNA catabolic process
GO:0032984      2.37853567125793e-44    28.5206876841226        2.68791087121998
46      179     macromolecular complex disassembly
GO:0072594      6.88679885481271e-43    24.7890221056576        3.06331741747976
47      204     establishment of protein localization to organelle
GO:0006401      2.15182360495151e-41    23.812939056236 3.07833367933015        46
205     RNA catabolic process
GO:0019058      7.45876356362686e-39    20.4284495021337        3.46875648744032
46      231     viral infectious cycle
GO:0022415      1.1977323386528e-37     18.1990334161834        3.90422808110165
47      260     viral reproductive process
GO:0071845      5.09744630689954e-37    16.8464547186842        4.26461836551104
48      284     cellular component disassembly at cellular level
GO:0022411      1.01277834122005e-36    16.5609467455621        4.3246834129126 48
288     cellular component disassembly
GO:0033365      1.24346992248694e-32    10.9230273657701        7.10269185523493
54      473     protein localization to organelle
GO:0016032      1.33541202097787e-31    10.9276220855168        6.77233409452633
52      451     viral reproduction
GO:0006605      1.50289697290595e-31    10.6032240310527        7.11770811708532
53      474     protein targeting
GO:0042274      4.32260026440763e-09    43.1    0.270292713307038       7       18
ribosomal small subunit biogenesis
GO:0042254      3.81992070276261e-07    6.60589677047289        2.23742301570826
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13      149     ribosome biogenesis
GO:0022613      1.55064279758008e-06    4.95898161244696        3.37865891633797
15      225     ribonucleoprotein complex biogenesis
GO:0071843      3.27945978912267e-06    4.64440417256011        3.58888658224344
15      239     cellular component biogenesis at cellular level
GO:0006364      3.61499274462288e-06    7.26693390893206        1.56169123244066
10      104     rRNA processing
GO:0016072      6.00643764925281e-06    6.8280193236715 1.65178880354301        10
110     rRNA metabolic process
GO:0022904      1.37605177398398e-05    7.03597480106101        1.44156113763753
9       96      respiratory electron transport chain
GO:0006417      1.76133241900498e-05    4.90104529616725        2.70292713307038
12      180     regulation of translation
Tissue: Whole_Blood=>Adipose_Subcutaneous       Type:   asymmetric
SourceGene:     RP11-160E2.11(ENSG00000262292.1)
TargetGeneSet:  MTND1P23        DNAJC11 DFFA    MFN2    C1orf144        HSPG2
RPL11   ARID1A  PHACTR4 PRDX3P2 KPNA7   TXLNA   ZBTB8OS MACF1   RPS8    RPS15AP10
RP4     RPL5    RP11    RPRD2   RPS27   ASH1L   SSR2    ARHGEF11        TMEM63A NBAS
PPP1CB  DHX57   UBC     GMCL1   DGUOK   DCTN1   SUCLG1  TMEM131 COA5    EIF5B
RANBP2  UGGT1   USP37   TRIP12  GIGYF2  HDLBP   BRK1    RPL15   RAD54L2 RPL29
FAM208A PCNP    RPL24   DNAJC19 PSMD2   EIF4G1  HTT     AFAP1   BOD1L   RPL34
NDUFC1  RPS3A   NIPBL   CTD     MRPS36  ERAP1   HINT1   SKP1    UBE2B   CTB
MTND5P11        KDM3B   PAIP2   RPS14   SLC2A3P1        RPL15P3 PRRC2A  AGPAT1
SYNGAP1 RPL10A  USP49   MTRNR2L9        WDR11   KIAA1919        RWDD1   MRPS12
TATDN2P2        IGF2R   ANKRD61 MPLKIP  CHCHD2  RPS3AP26        TRRAP   HIPK2   MLL3
DRP2    HMBOX1  KIF13B  KAT6A   HOOK3   PRKDC   RPS20   ARFGEF1 RPL30   EIF3H
MED30   EEF1D   RPL8    RPS6    CLTA    NIPSNAP3A       NUP188  SETX    RPL7A
NACC2   SEC16A  BMS1    RPS24   SFR1    EIF6    NSMCE4A FAM53B  PHRF1   RPL27A
MTRNR2L8        CKAP5   INCENP  ZBTB3   UBE4A   DDX6    USP5    H2AFJ   SCAF11  MLL4
PFDN5   CBX5    USP44   SART3   RP3     SBNO1   EP400   GOLGA3  TPT1    ESD     MED4
MYCBP2-AS1      DNAJC3  CHD8    C14orf21        FNTB    YLPM1   KIAA1737
GOLGA8IP        HERC2   HERC2P10        MGA     CCNDBP1 DUT     RPS27L  MYO9A
C15orf40        SEC11A  LRRK1   C16orf13        FAM173A NME3    SPSB3   TCEB2
RPS15A  GTF3C1  SRCAP   CNOT1   ZNF778  RPL13   VPS53   WDR81   METTL16 ZZEF1
POLR2A  RPL26   TOM1L2  KIAA0100        SUPT6H  RPL23A  TAOK1   RPL17   RPL19
CDK12   RPL27   DHX8    KPNB1   CLTC    DCAF7   NT5C    TNRC6C  TBC1D16 NPLOC4
ANAPC11 RPS15   FAM108A1        AP3D1   NFIC    PTPRS   RPL36   TUBB4A  TRAPPC5
RAB11B  ZNF121  PIN1    TNPO2   C19orf43        NACC1   BRD4    SLC35E1 UPF1
GATAD2A SUPT5H  POU2F2  MEGF8   ZNF428  ARHGAP35        RPL18   RPS5    RRBP1
KIF3B   SCAND1  SOGA1   TOP1    NCOA3   PRPF6   BTG3    SCAF4   URB1    MCM3AP
PI4KA   ZNF70   TTC28   NF2     PRR14L  DEPDC5  MPST    RPL3    EP300   DYNLT3
HUWE1   RPS4X   TTC3P1  RPL39   XIAP    HCFC1   RPL10   MT
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      7.93120786946066e-42    52.4815088757396        1.28461698152377
35      91      translational termination
GO:0006614      7.42072388663324e-41    44.0310559006211        1.48225036329666
36      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.1109152407343e-40     43.3989795918367        1.49636703342329
36      106     cotranslational protein targeting to membrane
GO:0045047      1.1109152407343e-40     43.3989795918367        1.49636703342329
36      106     protein targeting to ER
GO:0072599      1.1109152407343e-40     43.3989795918367        1.49636703342329
36      106     establishment of protein localization to endoplasmic reticulum
GO:0006414      3.20522472751164e-39    41.9437869822485        1.48225036329666
35      105     translational elongation
GO:0070972      9.97086882210217e-39    37.0165505226481        1.66576707494291
36      118     protein localization to endoplasmic reticulum
GO:0000184      1.41326910528304e-38    36.5679862306368        1.67988374506955
36      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      2.66846485142243e-37    28.6326900522444        2.13161718912186
38      151     viral genome expression
GO:0019083      2.66846485142243e-37    28.6326900522444        2.13161718912186
38      151     viral transcription
```

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GO:0006413      3.51775361986536e-37    28.3795180722892        2.14573385924849
38      152     translational initiation
GO:0000956      2.83416296036044e-35    24.6669732364573        2.38571725140129
38      169     nuclear-transcribed mRNA catabolic process
GO:0006402      2.35136427778691e-34    23.0665232358003        2.512767282541  38
178     mRNA catabolic process
GO:0006612      3.42251206224134e-34    25.8791208791209        2.15985052937513
36      153     protein targeting to membrane
GO:0043624      8.74469948793941e-33    24.7976632233477        2.15985052937513
35      153     cellular protein complex disassembly
GO:0043241      2.94057867862393e-32    23.7812094097272        2.2304338800083 35
158     protein complex disassembly
GO:0034623      4.941537903453e-32      21.9083850931677        2.45630060203446
36      174     cellular macromolecular complex disassembly
GO:0072594      5.56051456808098e-32    19.4178400348381        2.87980070583351
38      204     establishment of protein localization to organelle
GO:0006401      6.74841506781684e-32    19.3001947911406        2.89391737596014
38      205     RNA catabolic process
GO:0032984      1.4544615601827e-31     21.1348651348651        2.52688395266764
36      179     macromolecular complex disassembly
GO:0022415      1.85677402419733e-31    16.1119421800151        3.67033423292506
41      260     viral reproductive process
GO:0019058      4.23274920995736e-31    17.3025568181818        3.26095079925265
39      231     viral infectious cycle
GO:0033365      6.87570972132975e-27    9.712433838701  6.67718496989828        47
473     protein localization to organelle
GO:0016032      8.45429329251521e-27    9.95049226441632        6.36661822711231
46      451     viral reproduction
GO:0071845      1.90694595434763e-26    13.0286511901264        4.00913431596429
38      284     cellular component disassembly at cellular level
GO:0022411      3.2183712458171e-26     12.8165301204819        4.06560099647083
38      288     cellular component disassembly
GO:0006605      7.27531125689954e-26    9.40012421625458        6.69130164002491
46      474     protein targeting
GO:0016568      5.05915899457672e-07    3.9930389653184 5.91488478306   21      419
chromatin modification
GO:0022613      7.10503497627726e-07    5.30498866213152        3.17625077849284
15      225     ribonucleoprotein complex biogenesis
GO:0071843      1.52047873261881e-06    4.96846655328798        3.37388416026573
15      239     cellular component biogenesis at cellular level
GO:0042274      3.93836789527174e-06    27.5106300734441        0.254100062279427
5       18      ribosomal small subunit biogenesis
GO:0042254      8.55041496082584e-06    5.82710069835549        2.10338384886859
11      149     ribosome biogenesis
Tissue: Whole_Blood=>Adipose_Subcutaneous       Type:   cluster
SourceGene:     RP11-160E2.11(ENSG00000262292.1)
TargetGeneSet:  MTND1P23        DNAJC11 DFFA    MFN2    C1orf144        HSPG2
RPL11   ARID1A  PHACTR4 PRDX3P2 KPNA7   TXLNA   ZBTB8OS MACF1   RPS8    RPS15AP10
RP4     RPL5    RP11    RPRD2   RPS27   ASH1L   SSR2    ARHGEF11        TMEM63A NBAS
PPP1CB  DHX57   UBC     GMCL1   DGUOK   DCTN1   SUCLG1  TMEM131 COA5    EIF5B
RANBP2  UGGT1   USP37   TRIP12  GIGYF2  HDLBP   BRK1    RPL15   RAD54L2 RPL29
FAM208A PCNP    RPL24   DNAJC19 PSMD2   EIF4G1  HTT     AFAP1   BOD1L   RPL34
NDUFC1  RPS3A   NIPBL   CTD     MRPS36  ERAP1   HINT1   SKP1    UBE2B   CTB
MTND5P11        KDM3B   PAIP2   RPS14   SLC2A3P1        RPL15P3 PRRC2A  AGPAT1
SYNGAP1 RPL10A  USP49   MTRNR2L9        WDR11   KIAA1919        RWDD1   MRPS12
TATDN2P2        IGF2R   ANKRD61 MPLKIP  CHCHD2  RPS3AP26        TRRAP   HIPK2   MLL3
DRP2    HMBOX1  KIF13B  KAT6A   HOOK3   PRKDC   RPS20   ARFGEF1 RPL30   EIF3H
MED30   EEF1D   RPL8    RPS6    CLTA    NIPSNAP3A       NUP188  SETX    RPL7A
NACC2   SEC16A  BMS1    RPS24   SFR1    EIF6    NSMCE4A FAM53B  PHRF1   RPL27A
MTRNR2L8        CKAP5   INCENP  ZBTB3   UBE4A   DDX6    USP5    H2AFJ   SCAF11  MLL4
PFDN5   CBX5    USP44   SART3   RP3     SBNO1   EP400   GOLGA3  TPT1    ESD     MED4
MYCBP2-AS1      DNAJC3  CHD8    C14orf21        FNTB    YLPM1   KIAA1737
GOLGA8IP        HERC2   HERC2P10        MGA     CCNDBP1 DUT     RPS27L  MYO9A
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POLR2A  RPL26   TOM1L2  KIAA0100        SUPT6H  RPL23A  TAOK1   RPL17   RPL19
CDK12   RPL27   DHX8    KPNB1   CLTC    DCAF7   NT5C    TNRC6C  TBC1D16 NPLOC4
ANAPC11 RPS15   FAM108A1        AP3D1   NFIC    PTPRS   RPL36   TUBB4A  TRAPPC5
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GATAD2A SUPT5H  POU2F2  MEGF8   ZNF428  ARHGAP35        RPL18   RPS5    RRBP1
KIF3B   SCAND1  SOGA1   TOP1    NCOA3   PRPF6   BTG3    SCAF4   URB1    MCM3AP
PI4KA   ZNF70   TTC28   NF2     PRR14L  DEPDC5  MPST    RPL3    EP300   DYNLT3
HUWE1   RPS4X   TTC3P1  RPL39   XIAP    HCFC1   RPL10   MT
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      7.93120786946066e-42    52.4815088757396        1.28461698152377
35      91      translational termination
GO:0006614      7.42072388663324e-41    44.0310559006211        1.48225036329666
36      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.1109152407343e-40     43.3989795918367        1.49636703342329
36      106     cotranslational protein targeting to membrane
GO:0045047      1.1109152407343e-40     43.3989795918367        1.49636703342329
36      106     protein targeting to ER
GO:0072599      1.1109152407343e-40     43.3989795918367        1.49636703342329
36      106     establishment of protein localization to endoplasmic reticulum
GO:0006414      3.20522472751164e-39    41.9437869822485        1.48225036329666
35      105     translational elongation
GO:0070972      9.97086882210217e-39    37.0165505226481        1.66576707494291
36      118     protein localization to endoplasmic reticulum
GO:0000184      1.41326910528304e-38    36.5679862306368        1.67988374506955
36      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      2.66846485142243e-37    28.6326900522444        2.13161718912186
38      151     viral genome expression
GO:0019083      2.66846485142243e-37    28.6326900522444        2.13161718912186
38      151     viral transcription
GO:0006413      3.51775361986536e-37    28.3795180722892        2.14573385924849
38      152     translational initiation
GO:0000956      2.83416296036044e-35    24.6669732364573        2.38571725140129
38      169     nuclear-transcribed mRNA catabolic process
GO:0006402      2.35136427778691e-34    23.0665232358003        2.512767282541  38
178     mRNA catabolic process
GO:0006612      3.42251206224134e-34    25.8791208791209        2.15985052937513
36      153     protein targeting to membrane
GO:0043624      8.74469948793941e-33    24.7976632233477        2.15985052937513
35      153     cellular protein complex disassembly
GO:0043241      2.94057867862393e-32    23.7812094097272        2.2304338800083 35
158     protein complex disassembly
GO:0034623      4.941537903453e-32      21.9083850931677        2.45630060203446
36      174     cellular macromolecular complex disassembly
GO:0072594      5.56051456808098e-32    19.4178400348381        2.87980070583351
38      204     establishment of protein localization to organelle
GO:0006401      6.74841506781684e-32    19.3001947911406        2.89391737596014
38      205     RNA catabolic process
GO:0032984      1.4544615601827e-31     21.1348651348651        2.52688395266764
36      179     macromolecular complex disassembly
GO:0022415      1.85677402419733e-31    16.1119421800151        3.67033423292506
41      260     viral reproductive process
GO:0019058      4.23274920995736e-31    17.3025568181818        3.26095079925265
39      231     viral infectious cycle
GO:0033365      6.87570972132975e-27    9.712433838701  6.67718496989828        47
473     protein localization to organelle
GO:0016032      8.45429329251521e-27    9.95049226441632        6.36661822711231
46      451     viral reproduction
GO:0071845      1.90694595434763e-26    13.0286511901264        4.00913431596429
38      284     cellular component disassembly at cellular level
GO:0022411      3.2183712458171e-26     12.8165301204819        4.06560099647083
38      288     cellular component disassembly
```

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GO:0006605      7.27531125689954e-26    9.40012421625458        6.69130164002491
46      474     protein targeting
GO:0016568      5.05915899457672e-07    3.9930389653184 5.91488478306   21      419
chromatin modification
GO:0022613      7.10503497627726e-07    5.30498866213152        3.17625077849284
15      225     ribonucleoprotein complex biogenesis
GO:0071843      1.52047873261881e-06    4.96846655328798        3.37388416026573
15      239     cellular component biogenesis at cellular level
GO:0042274      3.93836789527174e-06    27.5106300734441        0.254100062279427
5       18      ribosomal small subunit biogenesis
GO:0042254      8.55041496082584e-06    5.82710069835549        2.10338384886859
11      149     ribosome biogenesis
Tissue: Whole_Blood=>Adipose_Subcutaneous       Type:   asymmetric
SourceGene:     RP11-676J12.7(ENSG00000262003.1)
TargetGeneSet:  RPL22   MST1P9  KHDRBS1 RP4     RP11    GAS5    RPS7    UBC
RPL31   EEF1B2  RPL32   RPL15   CCDC12  RPL24   RPL34   BTF3    CTD     UBE2D2
RPS14   RPS18   SLC26A4 RPL30   EIF3H   RPS6    ANP32B  RPL35   RPL7A   RPS24
KRT17   NAP1L1  TPT1    HMGN1P24        MED6    RPS3AP6 SEC11A  CHMP1A  RPL26
RPS7P1  RPL17   RPL27   FASN    FAM32A  RPS11   CCDC106 RPL3    PGAM1P7 RPS4X
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      7.28762727938273e-39    253.238554216867        0.268839526676355
22      105     translational elongation
GO:0006614      7.28762727938273e-39    253.238554216867        0.268839526676355
22      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      9.18709778112143e-39    250.206349206349        0.271399903120891
22      106     cotranslational protein targeting to membrane
GO:0045047      9.18709778112143e-39    250.206349206349        0.271399903120891
22      106     protein targeting to ER
GO:0072599      9.18709778112143e-39    250.206349206349        0.271399903120891
22      106     establishment of protein localization to endoplasmic reticulum
GO:0006415      6.00536191284438e-38    268.95  0.232994256452841       21      91
translational termination
GO:0070972      1.23979948816468e-37    218.747222222222        0.302124420455332
22      118     protein localization to endoplasmic reticulum
GO:0000184      3.05396912720757e-35    191.732142857143        0.304684796899869
21      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006413      5.14374647620722e-35    161.152820512821        0.38917721956958
22      152     translational initiation
GO:0006612      6.00155745904302e-35    159.911450381679        0.391737596014117
22      153     protein targeting to membrane
GO:0019080      6.65844791257209e-33    144.213461538462        0.386616843125043
21      151     viral genome expression
GO:0019083      6.65844791257209e-33    144.213461538462        0.386616843125043
21      151     viral transcription
GO:0043624      8.93583699021507e-33    142.008522727273        0.391737596014117
21      153     cellular protein complex disassembly
GO:0043241      1.83147031627765e-32    136.777828467153        0.4045394782368 21
158     protein complex disassembly
GO:0072594      4.82396830690036e-32    114.69010989011 0.522316794685489       22
204     establishment of protein localization to organelle
GO:0000956      8.17637173766711e-32    126.514358108108        0.432703619126704
21      169     nuclear-transcribed mRNA catabolic process
GO:0034623      1.55961763645306e-31    122.337009803922        0.445505501349388
21      174     cellular macromolecular complex disassembly
GO:0006402      2.57767079133985e-31    119.186703821656        0.455747007127534
21      178     mRNA catabolic process
GO:0032984      2.91715038613628e-31    118.424050632911        0.458307383572071
21      179     macromolecular complex disassembly
GO:0006401      5.74692238821335e-30    101.504755434783        0.524877171130026
21      205     RNA catabolic process
GO:0019058      7.75910438986615e-29    88.775  0.59144695868798        21      231
viral infectious cycle
GO:0022415      1.00353320410872e-27    77.8438807531381        0.665697875579545
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21      260     viral reproductive process
GO:0071845      6.71095433016046e-27    70.6204847908745        0.727146910248426
21      284     cellular component disassembly at cellular level
GO:0022411      9.06057056968201e-27    69.5428370786517        0.737388416026573
21      288     cellular component disassembly
GO:0033365      7.84288111884257e-24    45.4081300813008        1.21105805826586
22      473     protein localization to organelle
GO:0006605      8.2161911069685e-24     45.3044247787611        1.2136184347104 22
474     protein targeting
GO:0016032      1.23042816851143e-22    42.6837209302326        1.15472977648606
21      451     viral reproduction
GO:0022613      7.98120775456516e-08    18.0479898299698        0.57608470002076
8       225     ribonucleoprotein complex biogenesis
GO:0042254      8.54563461789605e-08    23.4516431924883        0.38149609023597
7       149     ribosome biogenesis
GO:0042274      1.08453084725298e-07    124.675324675325        0.0460867760016608
4       18      ribosomal small subunit biogenesis
GO:0071843      1.27078117795642e-07    16.9374533512465        0.611929970244274
8       239     cellular component biogenesis at cellular level
GO:0006364      6.3609947487871e-06     22.5931186868687        0.266279150231818
5       104     rRNA processing
GO:0016072      8.37237154329821e-06    21.2931547619048        0.281641408899038
5       110     rRNA metabolic process
Tissue: Whole_Blood=>Adipose_Subcutaneous       Type:   asymmetric




SourceGene:     SKA2(ENSG00000182628.7) spindle and kinetochore associated complex
subunit 2




TargetGeneSet:  VPS13D  UBR4    KIAA0090        HSPG2   RPL11   PRDX3P2 KPNA7   SZT2
RPS8    RPL5    RP11    ASH1L   MIR555  GON4L   LPGAT1  SOS1    COX7A2L USP34   TET3
VAMP5   RANBP2  UGGT1   TRIP12  GPC1    RPL32   RPL15   RPL29   PCNP    SNORA7B
DNAJC19 HTT     BOD1L   COPS4   RPL34   NDUFC1  MTRR    NIPBL   BDP1    SKP1
RPS14   RPL15P3 LINC00243       CUL9    XPO5    MLL3    NOM1    KAT6A   PRKDC
TTC35   EIF3H   CTA     RANBP6  RPS6    CLTA    TNC     NUP188  SETX    RPL7A
QSOX2   PHYH    KIAA0913        PDZD8   EIF6    LRRC56  RPL27A  PIGCP1  KDM2A   GAL
CCDC90B ATM     UBE4A   MLL4    PFDN5   XPOT    RP1     MLXIP   SBNO1   TPT1
ZC3H13  COMMD6  COL4A2-AS1      TEP1    CHD8    NIN     HERC2   MGA     RPS27L
CALML4  CIB1    NDUFB10 CIITA   RPS15A  SMG1    SRCAP   CNOT1   AARS    ZNF23
CHST4   RPL13   ZZEF1   RPL26   C17orf48        SLC47A1 SUPT6H  RPL23A  RPL17
RPL19   AOC2    CTD     ZNF236  RPS15   BRD4    ZNF587  LBP     RALGAPB SYNJ1   SON
```

UBE2G2 MCM3AP MPST EP300 ZBED4 ZNF81 KDM5C HUWE1 RPS4X RPL39 RP4 RPL10

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0006415	5.08E-26	48.65454545	0.686388485	21	91	translational termination
GO:0000184	6.21E-25	37.13591658	0.897584942	22	119	"nuclear-transcribed mRNA catabolic process, nonsense-mediated decay"
GO:0006414	1.35E-24	40.50568182	0.791986714	21	105	translational elongation
GO:0006614	1.35E-24	40.50568182	0.791986714	21	105	SRP-dependent cotranslational protein targeting to membrane

GO:0006613	1.68E-24	40.0263369	0.799529444	21	106
cotranslational protein targeting to membrane					
GO:0045047	1.68E-24	40.0263369	0.799529444	21	106
protein targeting to ER					
GO:0072599	1.68E-24	40.0263369	0.799529444	21	106
establishment of protein localization to endoplasmic reticulum					
GO:0000956	2.84E-24	27.64527383	1.274721473	24	169
nuclear-transcribed mRNA catabolic process					

GO:0006402	1.03E-23	26.0131398	1.342606048	24	178	mRNA catabolic process
GO:0070972	1.87E-23	35.04510309	0.890042212	21	118	protein localization to endoplasmic reticulum
GO:0019080	1.54E-22	27.86117794	1.138952322	22	151	viral genome expression
GO:0019083	1.54E-22	27.86117794	1.138952322	22	151	viral transcription
GO:0006413	1.79E-22	27.644916	1.146495052	22	152	translational initiation

GO:0043624	2.08E-22	27.43195578	1.154037783	22	153	cellular protein complex disassembly
GO:0006401	3.26E-22	22.09060773	1.546259774	24	205	RNA catabolic process
GO:0043241	4.32E-22	26.41413117	1.191751436	22	158	protein complex disassembly
GO:0034623	3.81E-21	23.60707804	1.312435126	22	174	cellular macromolecular complex disassembly

GO:0006612	5.61E-21	25.68956612	1.154037783	21	153
protein targeting to membrane					
GO:0032984	7.19E-21	22.84720697	1.350148779	22	179
macromolecular complex disassembly					
GO:0072594	1.31E-19	19.67411898	1.538717044	22	204
establishment of protein localization to organelle					
GO:0019058	1.98E-18	17.09981851	1.74237077	22	231
viral infectious cycle					
GO:0006605	8.86E-18	10.77030394	3.575254308	28	474
protein targeting					

GO:0022415	2.54E-17	14.98541486	1.961109958	22	260
viral reproductive process					
GO:0033365	8.96E-17	10.25899595	3.567711577	27	473
protein localization to organelle					
GO:0071845	1.67E-16	13.58954111	2.142135492	22	284
cellular component disassembly at cellular level					
GO:0022411	2.24E-16	13.3813845	2.172306415	22	288
cellular component disassembly					

GO:0016032	2.94E-15	9.722222222	3.401771504	25	451
viral reproduction					
GO:0042254	1.83E-06	9.129857143	1.12386686	9	149
ribosome biogenesis					
GO:0016570	4.35E-06	6.327020408	1.968652688	11	261
histone modification					
GO:0016569	5.40E-06	6.176100128	2.013909072	11	267
covalent chromatin modification					
GO:0022613	7.61E-06	6.637068358	1.697114387	10	225
ribonucleoprotein complex biogenesis					

GO:0042274	8.64E-06	38.9877551	0.135769151	4	18	ribosomal small subunit biogenesis
GO:0071843	1.29E-05	6.22513343	1.802712615	10	239	cellular component biogenesis at cellular level
GO:0006364	1.33E-05	10.0783303	0.784443983	7	104	rRNA processing
GO:0016568	1.59E-05	4.64819376	3.160404124	13	419	chromatin modification

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GO:0016072      1.92E-05        9.487245384     0.829700367     7       110     rRNA
metabolic process
```

```
Tissue: Whole_Blood=>Adipose_Subcutaneous       Type:   cluster
SourceGene:     SKA2(ENSG00000182628.7)
TargetGeneSet:  VPS13D  UBR4    KIAA0090        HSPG2   RPL11   PRDX3P2 KPNA7   SZT2
RPS8    RPL5    RP11    ASH1L   MIR555  GON4L   LPGAT1  SOS1    COX7A2L USP34   TET3
VAMP5   RANBP2  UGGT1   TRIP12  GPC1    RPL32   RPL15   RPL29   PCNP    SNORA7B
DNAJC19 HTT     BOD1L   COPS4   RPL34   NDUFC1  MTRR    NIPBL   BDP1    SKP1
RPS14   RPL15P3 LINC00243       CUL9    XPO5    MLL3    NOM1    KAT6A   PRKDC
TTC35   EIF3H   CTA     RANBP6  RPS6    CLTA    TNC     NUP188  SETX    RPL7A
QSOX2   PHYH    KIAA0913        PDZD8   EIF6    LRRC56  RPL27A  PIGCP1  KDM2A   GAL
CCDC90B ATM     UBE4A   MLL4    PFDN5   XPOT    RP1     MLXIP   SBNO1   TPT1
ZC3H13  COMMD6  COL4A2-AS1      TEP1    CHD8    NIN     HERC2   MGA     RPS27L
CALML4  CIB1    NDUFB10 CIITA   RPS15A  SMG1    SRCAP   CNOT1   AARS    ZNF23
CHST4   RPL13   ZZEF1   RPL26   C17orf48        SLC47A1 SUPT6H  RPL23A  RPL17
RPL19   AOC2    CTD     ZNF236  RPS15   BRD4    ZNF587  LBP     RALGAPB SYNJ1   SON
UBE2G2  MCM3AP  MPST    EP300   ZBED4   ZNF81   KDM5C   HUWE1   RPS4X   RPL39   RP4
RPL10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      5.08265285222481e-26    48.6545454545455        0.686388485225936
21      91      translational termination
GO:0000184      6.20707647381988e-25    37.1359165777936        0.897584942218532
22      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006414      1.35355223956287e-24    40.5056818181818        0.791986713722234
21      105     translational elongation
GO:0006614      1.35355223956287e-24    40.5056818181818        0.791986713722234
21      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.67808866830512e-24    40.0263368983957        0.799529444329112
21      106     cotranslational protein targeting to membrane
GO:0045047      1.67808866830512e-24    40.0263368983957        0.799529444329112
21      106     protein targeting to ER
GO:0072599      1.67808866830512e-24    40.0263368983957        0.799529444329112
21      106     establishment of protein localization to endoplasmic reticulum
GO:0000956      2.84276513215265e-24    27.6452738336714        1.27472147256245
24      169     nuclear-transcribed mRNA catabolic process
GO:0006402      1.02718916831435e-23    26.0131398013751        1.34260604802436
24      178     mRNA catabolic process
GO:0070972      1.8718659352694e-23     35.0451030927835        0.890042211611653
21      118     protein localization to endoplasmic reticulum
GO:0019080      1.54188313293787e-22    27.8611779381627        1.13895232163864
22      151     viral genome expression
GO:0019083      1.54188313293787e-22    27.8611779381627        1.13895232163864
22      151     viral transcription
GO:0006413      1.79234540152662e-22    27.6449160035367        1.14649505224552
22      152     translational initiation
GO:0043624      2.08118992313669e-22    27.4319557778363        1.1540377828524 22
153     cellular protein complex disassembly
GO:0006401      3.26019612331964e-22    22.0906077348066        1.54625977441008
24      205     RNA catabolic process
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GO:0043241	4.32304443474305e-22	26.4141311697093	1.19175143588679
22	158	protein complex disassembly
GO:0034623	3.80972730832128e-21	23.6070780399274	1.31243512559684
22	174	cellular macromolecular complex disassembly
GO:0006612	5.61471104620423e-21	25.6895661157025	1.1540377828524 21
153	protein targeting to membrane
GO:0032984	7.18547446031269e-21	22.8472069697635	1.35014877863124
22	179	macromolecular complex disassembly
GO:0072594	1.30764677196797e-19	19.6741189844638	1.5387170438032 22
204	establishment of protein localization to organelle
GO:0019058	1.982088327887e-18	17.0998185117967	1.74237077018891
22	231	viral infectious cycle
GO:0006605	8.86029571348654e-18	10.7703039362232	3.57525430766037
28	474	protein targeting
GO:0022415	2.5398257890994e-17	14.9854148555974	1.96110995778839
22	260	viral reproductive process
GO:0033365	8.96421478629371e-17	10.2589959531882	3.56771157705349
27	473	protein localization to organelle
GO:0071845	1.66613343238302e-16	13.5895411073089	2.14213549235347
22	284	cellular component disassembly at cellular level
GO:0022411	2.24033549592335e-16	13.3813844957221	2.17230641478098
22	288	cellular component disassembly
GO:0016032	2.94083958466102e-15	9.72222222222222	3.40177150370217
25	451	viral reproduction
GO:0042254	1.83429122788905e-06	9.12985714285714	1.12386686042488
9	149	ribosome biogenesis
GO:0016570	4.34628421000627e-06	6.32702040816327	1.96865268839527
11	261	histone modification
GO:0016569	5.40119841554895e-06	6.17610012755102	2.01390907203654
11	267	covalent chromatin modification
GO:0022613	7.6149980667054e-06	6.63706835799859	1.69711438654764
10	225	ribonucleoprotein complex biogenesis
GO:0042274	8.6384978716643e-06	38.9877551020408	0.135769150923812
4	18	ribosomal small subunit biogenesis
GO:0071843	1.2912402130024e-05	6.2251334303736 1.80271261504394	10
239	cellular component biogenesis at cellular level
GO:0006364	1.33223485277612e-05	10.0783303011926	0.784443983115355
7	104	rRNA processing
GO:0016568	1.58957143921517e-05	4.64819376026273	3.16040412428206
13	419	chromatin modification
GO:0016072	1.92310225544999e-05	9.48724538359033	0.829700366756626
7	110	rRNA metabolic process
Tissue: Whole_Blood=>Adipose_Subcutaneous	Type:	asymmetric




SourceGene:	SPRR2E(ENSG00000203785.4)	small proline-rich protein 2E
```

TargetGeneSet: RPL22 RP11 RPL11 RP4 RPS8 RPL5 LCE2C S100A13
CICP13 B3GALNT2 PREPL UBC LONRF2 RPL31 R3HDM1 EEF1B2 SP100
CHL1-AS2 RPL32 UBE2E1 GORASP1 RHOA RNF123 FAM208A RPL24 EIF4G1 LPP
RPL35A UBE2D3 RPL34 FRG1 CTD BTF3 DTWD2 HINT1 UBE2B PAIP2
RPS14 SLU7 GRM4 RPL39P3 ASCC3 TNRC18 DAGLB RP9 CUX1 GTF2E2
RPS20 RPL30 PLEC RPS6 FOXD4L5 CALML5 RPS24 KLLN GBF1 NSMCE4A FAU
CCND1 RPS25 ING4 USP5 CLEC2B KRT5 PFDN5 RPL41 RPS7P10 TPT1
COMMD6 NGDN KLHDC2 CGRRF1 SNW1 HERC2 CCNDBP1 RPS3AP6 RPS17L SEC11A TSC2
GTF3C1 YPEL3 IST1 TERF2IP MYBBP1A RPL26 RPL23A ZNHIT3 RPL17 RPL19
KRT10 RPL27 RPS26P8 PNPO RPTOR DSG1 WDR7 PIP5K1C C19orf43
CASP14 DMWD CCDC106 CHMP4B TH1L PPIL2 TTC28 RPL3 PHF16 RPS4X
RPL39 RP1 FLNA

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0006415	7.73E-39	91.36789773	0.585634212	27	91	translational termination
GO:0006414	8.37E-39	79.89370629	0.675731783	28	105	translational elongation
GO:0006614	8.37E-39	79.89370629	0.675731783	28	105	SRP-dependent cotranslational protein targeting to membrane

GO:0006613	1.13E-38	78.86390533	0.682167324	28	106	cotranslational protein targeting to membrane
GO:0045047	1.13E-38	78.86390533	0.682167324	28	106	protein targeting to ER
GO:0072599	1.13E-38	78.86390533	0.682167324	28	106	establishment of protein localization to endoplasmic reticulum
GO:0070972	3.35E-37	68.29128205	0.759393814	28	118	protein localization to endoplasmic reticulum
GO:0000184	4.36E-37	67.53609467	0.765829354	28	119	"nuclear-transcribed mRNA catabolic process, nonsense-mediated decay"

GO:0019080	1.26E-35	52.8744877	0.97176666	29	151
viral genome expression					
GO:0019083	1.26E-35	52.8744877	0.97176666	29	151
viral transcription					
GO:0006413	1.55E-35	52.44092988	0.978202201	29	152
translational initiation					
GO:0006612	9.70E-34	49.04910769	0.984637741	28	153
protein targeting to membrane					
GO:0000956	1.91E-32	43.43436989	1.087606394	28	169
nuclear-transcribed mRNA catabolic process					

GO:0043624	4.66E-32	46.20779221	0.984637741	27	153	cellular protein complex disassembly
GO:0006402	8.90E-32	40.80246154	1.145526261	28	178	mRNA catabolic process
GO:0043241	1.18E-31	44.42852186	1.016815445	27	158	protein complex disassembly
GO:0034623	1.86E-30	39.54823748	1.119784098	27	174	cellular macromolecular complex disassembly
GO:0032984	4.17E-30	38.23385167	1.151961802	27	179	macromolecular complex disassembly
GO:0072594	4.88E-30	34.71118881	1.312850322	28	204	

establishment of protein localization to organelle

GO:0006401 5.62E-30 34.51264668 1.319285863 28 205 RNA catabolic process

GO:0019058 5.71E-30 31.75464109 1.486609923 29 231 viral infectious cycle

GO:0022415 1.92E-28 27.71124188 1.673240606 29 260 viral reproductive process

GO:0071845 2.58E-27 25.06047794 1.827693585 29 284 cellular component disassembly at cellular level

GO:0022411 3.89E-27 24.66644546 1.853435748 29 288 cellular component disassembly

GO:0033365	1.47E-24	16.55492361	3.044010795	32	473	protein localization to organelle
GO:0006605	2.55E-23	15.70541761	3.050446336	31	474	protein targeting
GO:0016032	9.34E-23	15.76405384	2.902428898	30	451	viral reproduction
GO:0042274	1.05E-09	82.44827586	0.115839734	6	18	ribosomal small subunit biogenesis
GO:0006364	1.18E-09	18.28249167	0.669296242	10	104	rRNA processing

```
GO:0022613      1.93E-09        10.84304245     1.447996678     13      225
ribonucleoprotein complex biogenesis
```

```
GO:0016072      2.06E-09        17.17831325     0.707909487     10      110     rRNA
metabolic process
```

```
GO:0042254      2.85E-09        13.82290562     0.958895578     11      149
ribosome biogenesis
```

```
GO:0071843      4.02E-09        10.16128319     1.53809425      13      239
cellular component biogenesis at cellular level
```

```
GO:0000028      2.39E-08        322.6067416     0.038613245     4       6
ribosomal small subunit assembly
```

GO:0034470 ncRNA processing	6.13E-07	8.984147115	1.287108159	10	200
GO:0042273 ribosomal large subunit biogenesis	7.65E-07	80.61797753	0.07722649	4	12
GO:0042255 ribosome assembly	2.76E-06	53.73033708	0.102968653	4	16
GO:0030490 maturation of SSU-rRNA	8.86E-06	119.6166667	0.045048786	3	7
GO:0034660 ncRNA metabolic process	1.45E-05	6.169989047	1.834129126	10	285

```
Tissue: Whole_Blood=>Adipose_Subcutaneous       Type:   cluster
SourceGene:     SPRR2E(ENSG00000203785.4)
TargetGeneSet:  RPL22   RP11    RPL11   RP4     RPS8    RPL5    LCE2C   S100A13
CICP13  B3GALNT2        PREPL   UBC     LONRF2  RPL31   R3HDM1  EEF1B2  SP100
CHL1-AS2        RPL32   UBE2E1  GORASP1 RHOA    RNF123  FAM208A RPL24   EIF4G1  LPP
RPL35A  UBE2D3  RPL34   FRG1    CTD     BTF3    DTWD2   HINT1   UBE2B   PAIP2
RPS14   SLU7    GRM4    RPL39P3 ASCC3   TNRC18  DAGLB   RP9     CUX1    GTF2E2
RPS20   RPL30   PLEC    RPS6    FOXD4L5 CALML5  RPS24   KLLN    GBF1    NSMCE4A FAU
CCND1   RPS25   ING4    USP5    CLEC2B  KRT5    PFDN5   RPL41   RPS7P10 TPT1
COMMD6  NGDN    KLHDC2  CGRRF1  SNW1    HERC2   CCNDBP1 RPS3AP6 RPS17L  SEC11A  TSC2
GTF3C1  YPEL3   IST1    TERF2IP MYBBP1A RPL26   RPL23A  ZNHIT3  RPL17   RPL19
KRT10   RPL27   RPS26P8 PNPO    RPTOR   DSG1    WDR7    PIP5K1C C19orf43
CASP14  DMWD    CCDC106 CHMP4B  TH1L    PPIL2   TTC28   RPL3    PHF16   RPS4X
RPL39   RP1     FLNA
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      7.72884393684555e-39    91.3678977272727        0.585634212165248
27      91      translational termination
GO:0006414      8.37337098585874e-39    79.8937062937063        0.675731783267594
28      105     translational elongation
GO:0006614      8.37337098585874e-39    79.8937062937063        0.675731783267594
28      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.13294458388643e-38    78.8639053254438        0.682167324060619
28      106     cotranslational protein targeting to membrane
GO:0045047      1.13294458388643e-38    78.8639053254438        0.682167324060619
28      106     protein targeting to ER
GO:0072599      1.13294458388643e-38    78.8639053254438        0.682167324060619
28      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      3.34821915675842e-37    68.2912820512821        0.759393813576915
28      118     protein localization to endoplasmic reticulum
GO:0000184      4.35928217000196e-37    67.5360946745562        0.76582935436994
28      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      1.26227486656478e-35    52.874487704918 0.97176665974673        29
151     viral genome expression
GO:0019083      1.26227486656478e-35    52.874487704918 0.97176665974673        29
151     viral transcription
GO:0006413      1.55314173234673e-35    52.4409298780488        0.978202200539755
29      152     translational initiation
GO:0006612      9.70480562031126e-34    49.0491076923077        0.98463774133278
28      153     protein targeting to membrane
GO:0000956      1.90901476025287e-32    43.4343698854337        1.08760639402118
28      169     nuclear-transcribed mRNA catabolic process
GO:0043624      4.65639857893906e-32    46.2077922077922        0.98463774133278
27      153     cellular protein complex disassembly
GO:0006402      8.90346234957301e-32    40.8024615384615        1.1455262611584 28
178     mRNA catabolic process
GO:0043241      1.17784356769807e-31    44.4285218598196        1.0168154452979 27
158     protein complex disassembly
GO:0034623      1.86496318324784e-30    39.5482374768089        1.1197840979863 27
174     cellular macromolecular complex disassembly
GO:0032984      4.17269589186328e-30    38.2338516746412        1.15196180195142
27      179     macromolecular complex disassembly
GO:0072594      4.87501965816886e-30    34.7111888111888        1.31285032177704
28      204     establishment of protein localization to organelle
GO:0006401      5.62137155944716e-30    34.5126466753585        1.31928586257006
28      205     RNA catabolic process
GO:0019058      5.71349547817322e-30    31.7546410891089        1.48660992318871
29      231     viral infectious cycle
GO:0022415      1.92259800752942e-28    27.7112418831169        1.67324060618642
29      260     viral reproductive process
GO:0071845      2.58264470548763e-27    25.0604779411765        1.82769358521902
29      284     cellular component disassembly at cellular level
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GO:0022411      3.88927150912513e-27    24.6664454633205        1.85343574839111
29      288     cellular component disassembly
GO:0033365      1.46869717982695e-24    16.5549236087878        3.04401079510068
32      473     protein localization to organelle
GO:0006605      2.55084263704195e-23    15.7054176072235        3.05044633589371
31      474     protein targeting
GO:0016032      9.34258344922867e-23    15.7640538400633        2.90242889765414
30      451     viral reproduction
GO:0042274      1.05243575360753e-09    82.448275862069 0.115839734274445       6
18      ribosomal small subunit biogenesis
GO:0006364      1.18066354692682e-09    18.2824916688029        0.669296242474569
10      104     rRNA processing
GO:0022613      1.93229251667979e-09    10.8430424528302        1.44799667843056
13      225     ribonucleoprotein complex biogenesis
GO:0016072      2.05563449216074e-09    17.178313253012 0.707909487232717       10
110     rRNA metabolic process
GO:0042254      2.85318349956482e-09    13.8229056203606        0.958895578160681
11      149     ribosome biogenesis
GO:0071843      4.02171194587049e-09    10.1612831858407        1.5380942495329 13
239     cellular component biogenesis at cellular level
GO:0000028      2.38750166526337e-08    322.606741573034        0.0386132447581482
4       6       ribosomal small subunit assembly
GO:0034470      6.13445314774594e-07    8.98414711477489        1.28710815860494
10      200     ncRNA processing
GO:0042273      7.64878389605521e-07    80.6179775280899        0.0772264895162964
4       12      ribosomal large subunit biogenesis
GO:0042255      2.75732673726494e-06    53.7303370786517        0.102968652688395
4       16      ribosome assembly
GO:0030490      8.86430808154284e-06    119.616666666667        0.0450487855511729
3       7       maturation of SSU-rRNA
GO:0034660      1.45155741712303e-05    6.16998904709748        1.83412912601204
10      285     ncRNA metabolic process
Tissue: Artery_Tibial=>Adipose_Subcutaneous     Type:   asymmetric
SourceGene:     C11orf31(ENSG00000211450.4)
TargetGeneSet:  SDHB    RPL11   USP1    RPL5    RP11    SARS    ATP5F1  PSMB4   DAP3
MRPL55  TOMM20  FOSL2   UBC     FAM136A MMADHC  RPL15   NICN1   NICN1-AS1
RPL29   EIF2S1  PDCD10  PARL    OCIAD1  COPS4   RPS3A   NDUFS4  MRPS36  BTF3    TBCA
SNX2    HINT1   CTB     RPS14   TTC1    NUDCD2  NPM1    NOL7    C6orf136
RPS10   RP1     RWDD1   C6orf72 BTF3P10 PMPCB   MLL5    HMBOX1  DCTN6   RPS20P22
RPS20   SNHG6   RPL30   POLR2K  EIF3H   NDUFB9  CLTA    ARHGAP12        VDAC2
RPS24   RPP30   HBG2    RPL27A  C11orf2 RPS25   WNK1    C12orf57        PHB2
PFDN5   RBMS2   SLC25A3 ARL6IP4 POLR1D  ESD     JKAMP   ATPBD4  TGM6    PSMA4
SEC11A  RPL23A  RPL17   RPL19   RPL27   MSI2    NT5C    PSMG2   ABCA7   EEF2
RPL36   EIF3K   EID2B   RPL18   RPL13A  A1BG    RPS5    MANBAL  PFDN4   POLR2F
SLC25A6 RBM3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      3.08424583132542e-29    63.110843373494 0.595806518580029       22
105     translational elongation
GO:0006614      3.08424583132542e-29    63.110843373494 0.595806518580029       22
105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      3.87646818659544e-29    62.3551587301587        0.601480866376029
22      106     cotranslational protein targeting to membrane
GO:0045047      3.87646818659544e-29    62.3551587301587        0.601480866376029
22      106     protein targeting to ER
GO:0072599      3.87646818659544e-29    62.3551587301587        0.601480866376029
22      106     establishment of protein localization to endoplasmic reticulum
GO:0006415      6.93494022351022e-29    70.3229508196721        0.516365649436025
21      91      translational termination
GO:0006413      9.992261528195e-29      46.0377155172414        0.862500864992042
24      152     translational initiation
GO:0070972      5.04596411503333e-28    54.5149305555556        0.669573039928033
22      118     protein localization to endoplasmic reticulum
GO:0019080      3.82882451442477e-27    43.3716896186441        0.856826517196042
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23      151     viral genome expression
GO:0019083      3.82882451442477e-27    43.3716896186441        0.856826517196042
23      151     viral transcription
GO:0072594      4.65097648153165e-27    34.7691855336666        1.15756695038406
25      204     establishment of protein localization to organelle
GO:0000184      3.24271177524783e-26    50.132318501171 0.675247387724033       21
119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006612      2.19839305005828e-25    39.8519083969466        0.868175212788042
22      153     protein targeting to membrane
GO:0019058      3.33679887462828e-24    28.3098450774613        1.31077434087606
24      231     viral infectious cycle
GO:0043624      8.56702202828602e-24    37.1307749627422        0.868175212788042
21      153     cellular protein complex disassembly
GO:0043241      1.72967910578967e-23    35.7630728730406        0.896546951768044
21      158     protein complex disassembly
GO:0022415      5.86835954597837e-23    24.7802454704851        1.47533042696007
24      260     viral reproductive process
GO:0000956      7.47061096541792e-23    33.0794195835179        0.958964777524047
21      169     nuclear-transcribed mRNA catabolic process
GO:0034623      1.40371466395077e-22    31.9871423979428        0.987336516504048
21      174     cellular macromolecular complex disassembly
GO:0006402      2.29223431219755e-22    31.1634123420695        1.01003390768805
21      178     mRNA catabolic process
GO:0032984      2.58632388693747e-22    30.9639966798091        1.01570825548405
21      179     macromolecular complex disassembly
GO:0006401      4.71128993918159e-21    26.5400035637919        1.16324129818006
21      205     RNA catabolic process
GO:0016032      1.15092522315007e-19    15.2329411764706        2.55913085599612
26      451     viral reproduction
GO:0071845      4.33331843302748e-18    18.4645016518108        1.61151477406408
21      284     cellular component disassembly at cellular level
GO:0033365      5.3770560060619e-18     13.6287985588972        2.68396650750813
25      473     protein localization to organelle
GO:0006605      5.65427916447554e-18    13.597468057672 2.68964085530413        25
474     protein targeting
GO:0022411      5.7800394069971e-18     18.1827224166513        1.63421216524808
21      288     cellular component disassembly
Tissue: Artery_Tibial=>Adipose_Subcutaneous     Type:   asymmetric
SourceGene:     CHCHD2(ENSG00000106153.12)
TargetGeneSet:  PARK7   RPL11   RP4     NDUFS5  SNRPE   ACP1    TPRKB   RPL31   MTX2
RPL32   RNF7    RPL35A  NDUFS4  MRPS36  TAF9    BTF3    TBCA    RPS23   COX7C
CETN3   CTD     HINT1   RPS14   CTB     C6orf130        RHAG    RWDD1   RP11
SEC61G  ECD     POP7    NDUFA5  RPS20   SNHG6   UQCRB   RPL30   NDUFB9  DCTN3
SEC61B  RPL35   COMMD3  VDAC2   C11orf10        ATP5L   RPS25   PHB2    PFDN5
DIABLO  ARL6IP4 MZT1    CGRRF1  RPS17L  SEC11A  NDUFAB1 SPAG7   RPS7P1  RPL17
FBXO47  RPL19   RPL27   ATP5H   ARL16   RPL36   CHST8   COX6B1  EIF3K   SNRPD2
ATP5J   RPL18AP2        POLR2F  RBM3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006614      7.03976132543265e-25    68.8195669607057        0.443221922358314
18      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      8.45565769191813e-25    68.0327695560254        0.447443083523632
18      106     cotranslational protein targeting to membrane
GO:0045047      8.45565769191813e-25    68.0327695560254        0.447443083523632
18      106     protein targeting to ER
GO:0072599      8.45565769191813e-25    68.0327695560254        0.447443083523632
18      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      6.63760362954319e-24    59.8186046511628        0.498097017507439
18      118     protein localization to endoplasmic reticulum
GO:0006612      8.92627169749687e-22    44.2015503875969        0.645837658293544
18      153     protein targeting to membrane
GO:0072594      5.29130411215114e-21    34.7355212355212        0.861116877724725
19      204     establishment of protein localization to organelle
GO:0006415      1.62079772068301e-20    61.4159038901602        0.384125666043872
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15      91      translational termination
GO:0006414      1.57744928897971e-19    51.8115942028985        0.443221922358314
15      105     translational elongation
GO:0000184      1.12470471296061e-18    44.7930602006689        0.502318178672756
15      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      1.21742447933262e-18    37.5440329218107        0.637395335962909
16      151     viral genome expression
GO:0019083      1.21742447933262e-18    37.5440329218107        0.637395335962909
16      151     viral transcription
GO:0006413      1.35662886591628e-18    37.2653594771242        0.641616497128226
16      152     translational initiation
GO:0043624      5.43998896255014e-17    33.6767485822306        0.645837658293544
15      153     cellular protein complex disassembly
GO:0043241      8.88382813665698e-17    32.4878382487078        0.66694346412013
15      158     protein complex disassembly
GO:0000956      2.46953791183705e-16    30.1439864483343        0.71337623693862
15      169     nuclear-transcribed mRNA catabolic process
GO:0034623      3.83904766757613e-16    29.1858080393765        0.734482042765207
15      174     cellular macromolecular complex disassembly
GO:0006402      5.41099421018376e-16    28.4615897572686        0.751366687426476
15      178     mRNA catabolic process
GO:0032984      5.8881056306774e-16     28.2860551431601        0.755587848591793
15      179     macromolecular complex disassembly
GO:0019058      1.15687302256038e-15    23.4418604651163        0.975088229188292
16      231     viral infectious cycle
GO:0006401      4.50225390318053e-15    24.370709382151 0.865338038890042       15
205     RNA catabolic process
GO:0022415      7.47946083592459e-15    20.6134790528233        1.09750190298249
16      260     viral reproductive process
GO:0033365      3.54667723281708e-14    13.8863016572268        1.99660923119507
19      473     protein localization to organelle
GO:0006605      3.6842870520675e-14     13.8547880690738        2.00083039236039
19      474     protein targeting
GO:0022904      1.96361923406354e-13    37.0247058823529        0.405231471870459
11      96      respiratory electron transport chain
GO:0071845      5.46390082962498e-13    17.1177468886375        1.19880977095011
15      284     cellular component disassembly at cellular level
GO:0022411      6.69346400676617e-13    16.8621595795509        1.21569441561138
15      288     cellular component disassembly
GO:0016032      2.84394503268349e-12    12.424172601592 1.90374368555809        17
451     viral reproduction
GO:0022900      8.10682903244319e-12    25.5182113821138        0.565635596152515
11      134     electron transport chain
GO:0045333      1.53232386652478e-11    23.9464122137405        0.599404885475054
11      142     cellular respiration
GO:0015980      4.68549160853122e-09    11.7011414735386        1.2958964777524 12
307     energy derivation by oxidation of organic compounds
GO:0042773      4.12663652303786e-08    38.1791574279379        0.198394574769912
6       47      ATP synthesis coupled electron transport
GO:0042775      4.12663652303786e-08    38.1791574279379        0.198394574769912
6       47      mitochondrial ATP synthesis coupled electron transport
GO:0006119      1.50061983272357e-07    30.0797202797203        0.244827347588402
6       58      oxidative phosphorylation
GO:0006091      1.82777171040905e-07    8.22645211930926        1.8066569787558 12
428     generation of precursor metabolites and energy
GO:0006120      3.8658007803264e-07     41.3565668202765        0.151961801951422
5       36      mitochondrial electron transport, NADH to ubiquinone
GO:0000028      1.4185070319737e-06     248.051724137931        0.0253269669919037
3       6       ribosomal small subunit assembly
GO:0022618      2.85536039820472e-06    17.529315628192 0.401010310705142       6
95      ribonucleoprotein complex assembly
GO:0071826      3.85292758948488e-06    16.5911025145068        0.422116116531728
6       100     ribonucleoprotein complex subunit organization
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GO:0022613      4.41542322260067e-06    9.85862098947918        0.949761262196388
8       225     ribonucleoprotein complex biogenesis
GO:0071843      6.88629834733271e-06    9.25198072367884        1.00885751851083
8       239     cellular component biogenesis at cellular level
GO:0042776      1.98613510017866e-05    74.3793103448276        0.0548750951491246
3       13      mitochondrial ATP synthesis coupled proton transport
Tissue: Artery_Tibial=>Adipose_Subcutaneous     Type:   cluster
SourceGene:     ENSG00000233280.1
TargetGeneSet:  RP1     RPL22   VPS13D  DDI2    HSPG2   SYF2    PPP1R8  RP4     MFI2
PTPRF   RPS8    RPS15AP10       BTF3L4  GNG5    CCBL2   RPL5    BCAS2   MRPS21
LCE2C   ASH1L   SSR2    F11R    TKT     PRRC2C  ABL2    RP11    CEP350  RABIF
C1orf31 ACP1    RPS7    EIF2AK1 PRKD3   COX7A2L RHOQ    UBC     REL     USP34   TET3
RANBP2  MMADHC  ACVR1C  MLK7-AS1        MTX2    COQ10B  NBEAL1  EFHD1   GIGYF2
SETD5   RPL32   NR2C2   UBE2E1  RPL15   HIGD1A  RAD54L2 CTD     EBLN2   CRYBG3  PCNP
RPL24   RNF7    COMMD2  PDCD10  PHC3    DNAJC19 RPL35A  RELL1   OCIAD1  COPS4
HSP90AB3P       AIMP1   RPL34   OSMR    NDUFAF2 MRPS36  TAF9    BTF3    TBCA
CETN3   ERAP1   HINT1   AFF4    SKP1    UBE2B   CAMLG   CTB     UBE2D2  CD14
PCDHGB3 ADRA1B  SLC2A3P1        PHACTR1 NOL7    HLA-H   PGBD1   RNF5    RPS10
RPL10A  WDR11   ASF1A   RP3     IGF2R   ADCY1   BAIAP2L1        TRRAP   TRIP6   CUX1
BCAP29  MLL3    DCTN6   HOOK3   FNTA    POLR2K  UBR5    MED30   TRAPPC9 EIF2C2
HEATR7A C9orf82 TLN1    CLTA    CBWD3   ATP6V1G1        PSMB7   SETX    RPL7A
COMMD3  RPS24   GVINP2  RPL27A  SBF2    TSG101  PPP6R3  NUMA1   CWC15   UBE4A
RPS25   C12orf57        H2AFJ   SCAF11  MLL4    PFDN5   COPZ1   SMARCC2 BAZ2A
STAT6   LRP1    RBMS1P1 HELB    RAP1B   KITLG   SSH1    MLXIP   DGKH    ESD     MZT1
DCUN1D2-AS2     CCNB1IP1        PPP2R3C QRSL1P3 TRAPPC6B        CGRRF1  DNAL1
DYNC1H1 CYFIP1  GANC    RPS3AP6 DENND4A RAB11A  MORF4L1 KIAA1199        SEC11A  SELS
TSC2    SRRM2   RPS15A  SRCAP   CNOT1   CFDP1   MON1B   HSBP1   VPS53   MINK1
CCDC144B        RPL23A  MYO18A  TAOK1   RPL19   CDK12   RPL27   NSFP1   SUPT4H1
PRKCA   PGS1    RP13    MYL12A  PSMG2   C18orf32        CD209   BRD4    ZNF573
SIPA1L3 EIF3K   EID2B   CYP2A6  DEDD2   MEGF8   SNRPD2  RPL18   NUCB1   RPS9
ZNF587  RPS5    RPL12P4 SON     PI4KA   RPL9P7  USP9X   UXT     KDM5C   HUWE1
GNL3L   RBM41   RPL39   HCFC1   RPL10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006614      3.60452441375796e-28    31.2839294463498        1.33693170022836
27      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      4.78547717282206e-28    30.8857534467468        1.34966438308768
27      106     cotranslational protein targeting to membrane
GO:0045047      4.78547717282206e-28    30.8857534467468        1.34966438308768
27      106     protein targeting to ER
GO:0072599      4.78547717282206e-28    30.8857534467468        1.34966438308768
27      106     establishment of protein localization to endoplasmic reticulum
GO:0006415      6.14875651840199e-27    33.8312368972746        1.15867414019791
25      91      translational termination
GO:0070972      1.13952422292122e-26    26.7902288794009        1.50245657739949
27      118     protein localization to endoplasmic reticulum
GO:0006414      3.22049758618174e-25    27.8832547169811        1.33693170022836
25      105     translational elongation
GO:0000184      9.40671726302102e-24    23.707011909541 1.51518926025881        25
119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      1.3272647340486e-23     19.614803780563 1.92263511175697        27
151     viral genome expression
GO:0019083      1.3272647340486e-23     19.614803780563 1.92263511175697        27
151     viral transcription
GO:0006413      1.59690271830262e-23    19.4565095541401        1.93536779461629
27      152     translational initiation
GO:0006612      1.9186088076088e-23     19.3007279344859        1.94810047747561
27      153     protein targeting to membrane
GO:0072594      2.34653730682892e-22    15.0661013824885        2.59746730330081
29      204     establishment of protein localization to organelle
GO:0019058      6.19337934755397e-22    13.632486916069 2.94124974050239        30
231     viral infectious cycle
GO:0022415      1.61670274422966e-21    12.4205268715929        3.3104975434226 31
260     viral reproductive process
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GO:0006401      4.01545056268925e-21    14.2879907286687        2.61019998616013
28      205     RNA catabolic process
GO:0000956      5.13191516470086e-21    16.253164556962 2.15182340322469        26
169     nuclear-transcribed mRNA catabolic process
GO:0043624      6.6319908939653e-21     17.3680719339623        1.94810047747561
25      153     cellular protein complex disassembly
GO:0034623      1.10404650952067e-20    15.6985118029422        2.21548681752128
26      174     cellular macromolecular complex disassembly
GO:0043241      1.50542847107781e-20    16.709225894926 2.0117638917722 25      158
protein complex disassembly
GO:0006402      2.00110659828975e-20    15.2810626249167        2.26641754895855
26      178     mRNA catabolic process
GO:0032984      2.31627685820607e-20    15.1801108629106        2.27915023181787
26      179     macromolecular complex disassembly
GO:0016032      5.33743806455075e-19    8.11904916965158        5.74243996955228
36      451     viral reproduction
GO:0071845      2.72366671185017e-18    10.2807843137255        3.61608193204622
29      284     cellular component disassembly at cellular level
GO:0022411      4.00080715567273e-18    10.1191181965376        3.6670126634835 29
288     cellular component disassembly
GO:0033365      1.94130986388419e-17    7.41649045386289        6.02255899245727
35      473     protein localization to organelle
GO:0006605      1.5298532013436e-16     7.123   6.03529167531659        34      474
protein targeting
GO:0016570      1.24741135191901e-06    5.05881079520854        3.32323022628192
15      261     histone modification
GO:0016569      1.65689785694498e-06    4.93624964778811        3.39962632343782
15      267     covalent chromatin modification
GO:0016568      1.68963740738602e-06    3.99201515151515        5.33499411805411
19      419     chromatin modification
GO:0071843      1.18315312369579e-05    4.72320550639135        3.04311120337693
13      239     cellular component biogenesis at cellular level
GO:0006511      1.70610103794359e-05    3.80925013683634        4.63469656079164
16      364     ubiquitin-dependent protein catabolic process
Tissue: Artery_Tibial=>Adipose_Subcutaneous     Type:   asymmetric
SourceGene:     HIST1H2BI(ENSG00000168242.3)
TargetGeneSet:  STK40   RP4     RP11    HIPK1   MRPS21  BATF3   OR7E62P RPL31
RPL32   RPL35A  RPL34   UBE2QL1 JARID2-AS1      FOXP4   RP1     MRPS12  YWHAZP6
VPS13A  RPL12   ATP5L   RPL41   MLXIP   RILPL1  ANKRD20A19P     RPS15A  RPL26
C17orf51        RPL17   VPS25   RPL27   ANKRD40 PIP5K1C ZNF823
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      1.78325549682361e-16    118.065843621399        0.157428551657325
10      91      translational termination
GO:0006414      7.89882819762901e-16    100.568421052632        0.181648328835375
10      105     translational elongation
GO:0006614      7.89882819762901e-16    100.568421052632        0.181648328835375
10      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      8.7133434798242e-16     99.5138888888889        0.183378312919521
10      106     cotranslational protein targeting to membrane
GO:0045047      8.7133434798242e-16     99.5138888888889        0.183378312919521
10      106     protein targeting to ER
GO:0072599      8.7133434798242e-16     99.5138888888889        0.183378312919521
10      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      2.63560516523313e-15    88.3827160493827        0.204138121929278
10      118     protein localization to endoplasmic reticulum
GO:0000184      2.87467034349544e-15    87.565749235474 0.205868106013425       10
119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      3.28262315323143e-14    67.5413711583924        0.26122759670611
10      151     viral genome expression
GO:0019083      3.28262315323143e-14    67.5413711583924        0.26122759670611
10      151     viral transcription
GO:0006413      3.51044963663819e-14    67.0610328638498        0.262957580790257
10      152     translational initiation
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GO:0006612      3.75236081255074e-14    66.5874125874126        0.264687564874403
10      153     protein targeting to membrane
GO:0043624      3.75236081255074e-14    66.5874125874126        0.264687564874403
10      153     cellular protein complex disassembly
GO:0043241      5.20125158025491e-14    64.3153153153153        0.273337485295135
10      158     protein complex disassembly
GO:0000956      1.02855993134244e-13    59.8197064989518        0.292367310220746
10      169     nuclear-transcribed mRNA catabolic process
GO:0034623      1.38113512859077e-13    57.9756097560976        0.301017230641478
10      174     cellular macromolecular complex disassembly
GO:0006402      1.73742476558946e-13    56.5793650793651        0.307937166978064
10      178     mRNA catabolic process
GO:0032984      1.83847693355907e-13    56.2406311637081        0.30966715106221
10      179     macromolecular complex disassembly
GO:0072594      6.85030496520499e-13    48.9072164948454        0.352916753165871
10      204     establishment of protein localization to organelle
GO:0006401      7.19472842217583e-13    48.6529914529915        0.354646737250017
10      205     RNA catabolic process
GO:0019058      2.37606065091673e-12    42.8506787330317        0.399626323437824
10      231     viral infectious cycle
GO:0022415      7.71088005492001e-12    37.8026666666667        0.449795861878071
10      260     viral reproductive process
GO:0071845      1.849551847592e-11      34.4330900243309        0.491315479897585
10      284     cellular component disassembly at cellular level
GO:0022411      2.12382569663949e-11    33.9280575539568        0.498235416234171
10      288     cellular component disassembly
GO:0016032      1.70492184763235e-09    21.1413454270597        0.780222821950038
10      451     viral reproduction
GO:0033365      2.69983390067445e-09    20.1051115910727        0.818282471801259
10      473     protein localization to organelle
GO:0006605      2.75534740067316e-09    20.0603448275862        0.820012455885406
10      474     protein targeting
Tissue: Artery_Tibial=>Adipose_Subcutaneous     Type:   asymmetric
SourceGene:     MRPL13(ENSG00000172172.3)
TargetGeneSet:  RP4     NDUFS5  C1orf210        ACP1    RP11    CRYBG3  RPL7AP11
PDCD10  MRPS36  CTD     RP1     RPL24P4 COX7A2  NDUFA4  SEC61G  ECD     UQCRB
COX6C   SEC61B  RPL13AP5        NDUFS3  C11orf10        OR7E2P  ATP5L   HYLS1   IL26
VPS29   RPS7P10 CGRRF1  RDH11   ERH     SLIRP   C14orf2 TMEM85  RPS17L  POLR3K
NPRL3   NDUFAB1 TXNDC17 RPS7P1  RPL27   ATP5G1  ATP5H   ARL16   NDUFA7  PIN1
COX6B1  POLR2I  ZNF569  SNRPD2  TMSB4XP6        ATP5J   SNX12   COX7B   TCEAL3  RP3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      4.60628960515308e-19    77.3734939759036        0.279011833091136
13      96      respiratory electron transport chain
GO:0022900      4.20164127634141e-17    52.9335993160445        0.389454017023043
13      134     electron transport chain
GO:0045333      9.1083609869236e-17     49.6230954290297        0.412705003113971
13      142     cellular respiration
GO:0015980      2.04719997843038e-12    21.5218156228008        0.892256591239361
13      307     energy derivation by oxidation of organic compounds
GO:0006091      1.31534330343842e-10    15.1160781055256        1.24392775586465
13      428     generation of precursor metabolites and energy
GO:0042773      4.08341038300971e-09    58.4065040650407        0.136599543284202
6       47      ATP synthesis coupled electron transport
GO:0042775      4.08341038300971e-09    58.4065040650407        0.136599543284202
6       47      mitochondrial ATP synthesis coupled electron transport
GO:0006119      1.50343407811389e-08    46.0160256410256        0.168569649159228
6       58      oxidative phosphorylation
GO:0042776      4.32334705153945e-08    168.421052631579        0.0377828523977579
4       13      mitochondrial ATP synthesis coupled proton transport
GO:0006120      5.71898886355174e-08    62.6765475152572        0.104629437409176
5       36      mitochondrial electron transport, NADH to ubiquinone
GO:0015985      1.83089273168167e-07    108.233082706767        0.0523147187045879
4       18      energy coupled proton transport, down electrochemical gradient
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GO:0015986      1.83089273168167e-07    108.233082706767        0.0523147187045879
4       18      ATP synthesis coupled proton transport
GO:0006754      1.18765230172136e-05    33.6    0.142412289806934       4       49
ATP biosynthetic process
Tissue: Artery_Tibial=>Adipose_Subcutaneous     Type:   asymmetric
SourceGene:     NDUFA11(ENSG00000174886.7)
TargetGeneSet:  MINOS1  RP4     MRPL9   MIR555  SNRPE   RP11    ACP1    MORN2
SOS1-IT1        C1D     TPRKB   RPL31   HOXD-AS2        KCTD18  KRBOX1  PCNP
PDCD10  DNAJC19 RPL35A  LAMTOR3 RPL34   NDUFAF2 ISCA1P1 TAF9    COX7C   CTD     RP1
CENPQ   RPL39P3 NDUFA4  LSM5    SEC61G  SRI     ECD     NDUFA5  DCTN6   UQCRB
RPL30   COX6C   POLR2K  SEC61B  RPL35   COMMD3  RAB18   C11orf10        FAU
TMEM126A        ATP5L   RPS25   CCDC59  SNRPF   C12orf45        C14orf28        ERH
SLIRP   RPLP1   MORF4L1 SEC11A  NDUFAB1 RPL27   ICT1    PFDN4   ATP5J   EEF1B2P3
NDUFB11 TBL1Y
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006614      1.42433965812439e-15    47.3349875930521        0.370562590824164
12      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.60214729655642e-15    46.8281505728314        0.374091758355823
12      106     cotranslational protein targeting to membrane
GO:0045047      1.60214729655642e-15    46.8281505728314        0.374091758355823
12      106     protein targeting to ER
GO:0072599      1.60214729655642e-15    46.8281505728314        0.374091758355823
12      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      6.02682002649471e-15    41.4920174165457        0.416441768735728
12      118     protein localization to endoplasmic reticulum
GO:0006612      1.42762418440875e-13    31.1162029459902        0.539962632343782
12      153     protein targeting to membrane
GO:0072594      1.79133086949973e-13    25.4501240011022        0.719950176458377
13      204     establishment of protein localization to organelle
GO:0006415      6.10276563851381e-13    43.1165311653117        0.321154245380943
10      91      translational termination
GO:0022904      4.15506443813974e-11    35.2536945812808        0.338800083039236
9       96      respiratory electron transport chain
GO:0006414      9.4051309650409e-11     31.9285714285714        0.370562590824164
9       105     translational elongation
GO:0019080      1.01777498621358e-10    24.665282823041 0.532904297280465       10
151     viral genome expression
GO:0019083      1.01777498621358e-10    24.665282823041 0.532904297280465       10
151     viral transcription
GO:0043624      1.15959009805225e-10    24.3169026095855        0.539962632343782
10      153     cellular protein complex disassembly
GO:0043241      1.59415400058667e-10    23.4871456822676        0.557608470002076
10      158     protein complex disassembly
GO:0000184      2.91777662601654e-10    27.8376623376623        0.419970936267386
9       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0000956      3.09584731097889e-10    21.8453750575242        0.596429312850322
10      169     nuclear-transcribed mRNA catabolic process
GO:0034623      4.12293794258691e-10    21.1719214753123        0.614075150508615
10      174     cellular macromolecular complex disassembly
GO:0006402      5.15243812730897e-10    20.6620209059233        0.62819182063525
10      178     mRNA catabolic process
GO:0032984      5.44313297866754e-10    20.5383172174917        0.631720988166909
10      179     macromolecular complex disassembly
GO:0022900      8.45924531024241e-10    24.4714285714286        0.472908449242267
9       134     electron transport chain
GO:0045333      1.41805383370691e-09    22.9865735767991        0.501141789495537
9       142     cellular respiration
GO:0006401      2.04070786799352e-09    17.7673545966229        0.723479343990035
10      205     RNA catabolic process
GO:0006413      2.59291329191954e-09    21.3641358641359        0.536433464812124
9       152     translational initiation
GO:0033365      6.42348114808723e-09    10.3672768878719        1.66929624247457
13      473     protein localization to organelle
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GO:0019058      6.4563142589381e-09     15.6483831806644        0.815237699813162
10      231     viral infectious cycle
GO:0006605      6.58809317519468e-09    10.3440461239868        1.67282541000623
13      474     protein targeting
GO:0022415      1.99720989599994e-08    13.8048780487805        0.917583558231264
10      260     viral reproductive process
GO:0071845      4.60418442504915e-08    12.5743279330604        1.00228357899107
10      284     cellular component disassembly at cellular level
GO:0022411      5.25208351095055e-08    12.3898929636778        1.01640024911771
10      288     cellular component disassembly
GO:0015980      9.56108317800119e-08    11.5816703621582        1.08345443221922
10      307     energy derivation by oxidation of organic compounds
GO:0016032      3.73676437074146e-07    8.725   1.59165455677808        11      451
viral reproduction
GO:0006091      2.01425804648476e-06    8.15847823550006        1.51048370354993
10      428     generation of precursor metabolites and energy
Tissue: Artery_Tibial=>Adipose_Subcutaneous     Type:   asymmetric
SourceGene:     NDUFB3(ENSG00000119013.4)
TargetGeneSet:  RP11    RP1     NDUFS5  TPI1P1  RP4     PFN1P1  MIR4426 MRPS36P1
RPL7AP11        RBBP4P1 CTD     RPL24P4 COX7A2  NDUFA4  SEC61G  ECD     UQCRB
COX6C   ST13P5  NDUFS3  C11orf10        ATP5L   RPS7P10 MRPL52  C14orf2 POLR3K
NPRL3   NDUFAB1 PFN1    TXNDC17 ATP5G1  SNRPEP4 COX6B1  TMSB4XP6        ATP5J
EEF1B2P3        COX7B   RP3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      7.80090279040335e-19    154.679411764706        0.152792194311812
11      96      respiratory electron transport chain
GO:0022900      3.5316252424918e-17     106.609078590786        0.213272437893571
11      134     electron transport chain
GO:0045333      6.80627528109078e-17    100.04262086514 0.226005120752889       11
142     cellular respiration
GO:0015980      3.58734576149402e-13    43.7646396396396        0.488616704726317
11      307     energy derivation by oxidation of organic compounds
GO:0006091      1.32945171280711e-11    30.7995603517186        0.681198532973497
11      428     generation of precursor metabolites and energy
GO:0042773      9.41480564335991e-09    95.1455026455026        0.0748045117984915
5       47      ATP synthesis coupled electron transport
GO:0042775      9.41480564335991e-09    95.1455026455026        0.0748045117984915
5       47      mitochondrial ATP synthesis coupled electron transport
GO:0006119      2.78034991876831e-08    75.3406708595388        0.0923119507300533
5       58      oxidative phosphorylation
GO:0006120      2.77656681191249e-07    94.7105263157895        0.0572970728669296
4       36      mitochondrial electron transport, NADH to ubiquinone
GO:0042776      9.96830635216091e-07    216.27  0.0206906096463913      3       13
mitochondrial ATP synthesis coupled proton transport
GO:0015985      2.82937347018751e-06    144.13  0.0286485364334648      3       18
energy coupled proton transport, down electrochemical gradient
GO:0015986      2.82937347018751e-06    144.13  0.0286485364334648      3       18
ATP synthesis coupled proton transport
Tissue: Artery_Tibial=>Adipose_Subcutaneous     Type:   asymmetric
SourceGene:     NDUFB7(ENSG00000099795.1)
TargetGeneSet:  PARK7   RPL11   ZBTB8OS RP4     NDUFS5  RPL5    ATP5F1  SIKE1
MIR4426 SNRPE   CHML    ACP1    RPS7    CALM2   UBC     C1D     SNRPG   FAM136A
TPRKB   TXNDC9  RPL31   MZT2B   MTX2    MOB4    RPL32   LSM3    UBE2E1  DLEC1   RP11
PCNP    SNX4    COMMD2  PDCD10  DNAJC19 RPL35A  COMMD8  UGT2B17 RPL34   AP1AR
ANAPC10 NDUFS4  MRPS36  TAF9    BTF3    TBCA    COX7C   CETN3   CTD     HINT1
UBE2D2  RPS14   RPL26L1 NOL7    HMGN4   RPL39P3 COX7A2  RWDD1   MRPS12  NDUFA4
GPR141  SEC61G  ECD     ACN9    NDUFA5  SSBP1   DCTN6   RPS20   SNHG6   UQCRB
RPL30   COX6C   POLR2K  NDUFB9  SEC61B  RPL35   COMMD3  ARHGAP12        RPL13AP5
FAU     TMEM126B        ATP5L   RPS25   PHB2    PFDN5   C12orf73        VPS29
ARL6IP4 RPS7P10 EIF4A1P7        HMGB1   MZT1    MRPL52  CGRRF1  ERH     SLIRP
C14orf2 ATPBD4  RPLP1   RPS17L  HOMER2  SEC11A  C16orf13        TCEB2   NDUFAB1
SPAG7   TXNDC17 RPS7P1  RPL17   RPL27   ATP5G1  ATP5H   STRA13  ZNF519  RPS15
RPL36   PIN1    POLR2I  RPS16   MEGF8   SNRPD2  RPL18   PFDN4   ATP5J   SNRPD3
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POLR2F  EEF1B2P3        RBM3    COX7B   TCEAL4  TCEAL3  CXorf69
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006614      1.28353323524086e-33    60.2025316455696        0.755657047955159
26      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.69178424414832e-33    59.4458333333333        0.762853781745208
26      106     cotranslational protein targeting to membrane
GO:0045047      1.69178424414832e-33    59.4458333333333        0.762853781745208
26      106     protein targeting to ER
GO:0072599      1.69178424414832e-33    59.4458333333333        0.762853781745208
26      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      3.73538629239976e-32    51.6485507246377        0.849214587225798
26      118     protein localization to endoplasmic reticulum
GO:0019080      9.68825446215926e-31    40.2200460829493        1.08670680229742
27      151     viral genome expression
GO:0019083      9.68825446215926e-31    40.2200460829493        1.08670680229742
27      151     viral transcription
GO:0006415      5.54551082225793e-30    59.6254538852578        0.654902774894471
23      91      translational termination
GO:0006612      5.49561410491831e-29    37.3228346456693        1.10110026987752
26      153     protein targeting to membrane
GO:0072594      1.6657132242262e-28     29.6641746411483        1.46813369317002
28      204     establishment of protein localization to organelle
GO:0006414      2.14506421732264e-28    49.3970189701897        0.755657047955159
23      105     translational elongation
GO:0000184      4.91311555762776e-27    42.1518775720165        0.856411321015847
23      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019058      1.5065378015306e-25     24.3099694423224        1.66244550550135
27      231     viral infectious cycle
GO:0000956      8.3796949490573e-25     29.3834482758621        1.2162480105183 24
169     nuclear-transcribed mRNA catabolic process
GO:0006413      1.92604936992911e-24    31.2962005933582        1.09390353608747
23      152     translational initiation
GO:0043624      2.2545261378898e-24     31.0532763532764        1.10110026987752
23      153     cellular protein complex disassembly
GO:0006402      3.03706954557625e-24    27.6487012987013        1.28101861462875
24      178     mRNA catabolic process
GO:0022415      3.78675213310944e-24    21.2406220389053        1.87115078541277
27      260     viral reproductive process
GO:0043241      4.87136289438155e-24    29.8926383173297        1.13708393882776
23      158     protein complex disassembly
GO:0034623      4.82812957457821e-23    26.6951189600196        1.25223167946855
23      174     cellular macromolecular complex disassembly
GO:0032984      9.42424685329472e-23    25.8304051915163        1.28821534841879
23      179     macromolecular complex disassembly
GO:0006401      9.72753108292477e-23    23.4795580110497        1.47533042696007
24      205     RNA catabolic process
GO:0071845      2.36747278556812e-19    16.2542307692308        2.04387239637395
24      284     cellular component disassembly at cellular level
GO:0022411      3.28741623876774e-19    16.0034090909091        2.07265933153415
24      288     cellular component disassembly
GO:0016032      6.07495664728637e-19    12.127410725395 3.24572693931216        28
451     viral reproduction
GO:0033365      2.13944444062467e-18    11.5096392667061        3.40405508269324
28      473     protein localization to organelle
GO:0006605      2.26187252998951e-18    11.4830068444654        3.41125181648329
28      474     protein targeting
GO:0022904      2.05207720126966e-16    29.6837286724927        0.690886443844717
15      96      respiratory electron transport chain
GO:0022900      3.43762193935482e-14    20.1510716646209        0.964362327866584
15      134     electron transport chain
GO:0045333      8.21109615471839e-14    18.8710961691586        1.02193619818698
15      142     cellular respiration
GO:0022613      6.72834175581413e-11    11.3459069020867        1.61926510276105
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15      225     ribonucleoprotein complex biogenesis
GO:0071843      1.57751916069337e-10    10.6262540128411        1.72001937582174
15      239     cellular component biogenesis at cellular level
GO:0015980      5.73780055812087e-10    8.78225554514214        2.20939727354508
16      307     energy derivation by oxidation of organic compounds
GO:0042274      2.07863538610071e-09    73.1377551020408        0.129541208220884
6       18      ribosomal small subunit biogenesis
GO:0042776      2.15422177732748e-08    90.5239898989899        0.0935575392706387
5       13      mitochondrial ATP synthesis coupled proton transport
GO:0042773      4.0483575735676e-08     25.8115979381443        0.338246488132309
7       47      ATP synthesis coupled electron transport
GO:0042775      4.0483575735676e-08     25.8115979381443        0.338246488132309
7       47      mitochondrial ATP synthesis coupled electron transport
GO:0006364      5.6838232291922e-08     14.2125207756233        0.74846031416511
9       104     rRNA processing
GO:0006091      6.45780521719966e-08    6.14960282436011        3.08020206214103
16      428     generation of precursor metabolites and energy
GO:0016072      9.26968797246056e-08    13.3625846795206        0.791640716905404
9       110     rRNA metabolic process
GO:0042254      1.1436294305676e-07     10.8740241849074        1.07231333471732
10      149     ribosome biogenesis
GO:0034660      1.2797969306365e-07     7.39233193277311        2.051069130164  13
285     ncRNA metabolic process
GO:0015985      1.39369542087303e-07    55.6876456876457        0.129541208220884
5       18      energy coupled proton transport, down electrochemical gradient
GO:0015986      1.39369542087303e-07    55.6876456876457        0.129541208220884
5       18      ATP synthesis coupled proton transport
GO:0006119      1.81414863204859e-07    20.2288255508389        0.41741055982285
7       58      oxidative phosphorylation
GO:0006120      1.96388879581855e-07    29.2183673469388        0.259082416441769
6       36      mitochondrial electron transport, NADH to ubiquinone
GO:0022618      3.97268581095797e-07    13.6590038314176        0.683689710054667
8       95      ribonucleoprotein complex assembly
GO:0071826      5.90465807038686e-07    12.9121376811594        0.719673379004913
8       100     ribonucleoprotein complex subunit organization
GO:0000387      2.56590481848436e-06    27.8185703185703        0.223098747491523
5       31      spliceosomal snRNP assembly
GO:0000028      7.12935624986512e-06    142.019801980198        0.0431804027402948
3       6       ribosomal small subunit assembly
GO:0015992      7.6944232837172e-06     14.5785714285714        0.474984430143243
6       66      proton transport
GO:0006818      9.16205574648414e-06    14.1063199473338        0.489377897723341
6       68      hydrogen transport
GO:0006839      9.78099672067121e-06    10.6015517058136        0.74846031416511
7       104     mitochondrial transport
GO:0034470      1.37541921510622e-05    7.02143841278589        1.43934675800983
9       200     ncRNA processing
GO:0000377      1.61104282598361e-05    6.87546558704453        1.46813369317002
9       204     RNA splicing, via transesterification reactions with bulged
adenosine as nucleophile
GO:0000398      1.61104282598361e-05    6.87546558704453        1.46813369317002
9       204     nuclear mRNA splicing, via spliceosome
GO:0000375      1.95323648034354e-05    6.70121052631579        1.50411736212027
9       209     RNA splicing, via transesterification reactions
Tissue: Adipose_Subcutaneous=>Artery_Tibial     Type:   asymmetric
SourceGene:     NDUFS5(ENSG00000168653.6)
TargetGeneSet:  AURKAIP1        MRPL20  PARK7   MECR    NDUFS5  PPCS    ERI3
UQCRH   HBXIP   ATP5F1  SDHC    TMCO1   SNRPE   C1orf31 SLC4A1AP        COMMD1  MDH1
SNRPG   PRADC1  TPRKB   BOLA3   FAM138B TSN     ATP5G3  MTX2    NDUFB3  AP1S3
MYEOV2  ARPC4   LSM3    CMC1    CCDC72  SPCS1   ATG3    RNF7    MRPL47  NDUFB5
MRPL1   LAMTOR3 SETP20  LARP7   EXOSC9  NDUFC1  SCOC    LSM6    PDCD6   NDUFS6
C5orf44 ANKRD32 CAST    GIN1    MAN2A1  HINT1   UQCRQ   PDF     ATOX1   CTB
EEF1E1  HLA-F-AS1       PFDN6   HNRNPC  MEA1    COX7A2  COQ3    RTN4IP1 SF3B5   LSM5
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MPLKIP  SEC61G  CHCHD2  STAG3L4 PMS2P1  RP11    LSM1    TCEB1   MRPS35  DECR1
MRPL13  CTA     CTD     C9orf123        ACER2   NDUFB6  DCTN3   SEC61B  ATP6V1G1
COQ4    TMEM141 PRPF18  ECHS1   POLR2L  MRPL23  DENND5A SBF2    IMMP1L  NDUFS3
TIMM10  C11orf10        FIBP    BCRP1   MRPL11  NDUFS8  MRPL21  MRPL48  CLNS1A
TMEM126A        SDHD    ATP5L   MRPL51  COPS7A  MAGOHB  TFCP2   NDUFA12 SNRPF
NUP37   TRIAP1  POP5    DENR    EFHA1   MED4    MRPL52  SCFD1   C14orf126
ARHGAP5-AS1     C14orf166       ACTR10  COX16   SLIRP   NDUFB1  CINP    C14orf2
ATPBD4  GTF2A2  RAB11A  COX5A   MRPS11  IGF1R   MRPL28  NDUFAB1 COX4NB  PSMB6
TXNDC17 SMCR8   STAT5B  VPS25   ATP5G1  MRPL27  NACA2   ICT1    RNF213  C17orf89
SNRPD1  IER3IP1 UQCR11  TIMM13  MRPL54  C19orf70        PIN1    MRPL4   NDUFB7
C19orf42        NDUFA13 POP4    COX6B1  TBCB    HSPBP1  SLC27A5 ITPA    COMMD7
ATP5E   ATP5J   SNRPD3  TXN2    PDZD11  COX7B   NDUFA1  NAA10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      3.18715826637257e-32    46.8118377785897        0.969898276935852
27      96      respiratory electron transport chain
GO:0022900      2.10603152505072e-29    31.7854173329069        1.35381634488963
28      134     electron transport chain
GO:0045333      1.20422694257494e-28    29.5382099316087        1.43464120130095
28      142     cellular respiration
GO:0015980      2.98979089463873e-20    12.5063948840927        3.10165386478444
29      307     energy derivation by oxidation of organic compounds
GO:0042773      1.57166228753119e-17    45.8696051423324        0.474846031416511
14      47      ATP synthesis coupled electron transport
GO:0042775      1.57166228753119e-17    45.8696051423324        0.474846031416511
14      47      mitochondrial ATP synthesis coupled electron transport
GO:0006091      2.86164959095461e-17    9.03677872119217        4.32412981800567
30      428     generation of precursor metabolites and energy
GO:0006119      4.24587644473892e-16    34.3756887052342        0.585980208982077
14      58      oxidative phosphorylation
GO:0006120      7.27037195699802e-16    53.2873134328358        0.363711853850945
12      36      mitochondrial electron transport, NADH to ubiquinone
GO:0015985      1.61144132962743e-08    51.0464285714286        0.181855926925472
6       18      energy coupled proton transport, down electrochemical gradient
GO:0015986      1.61144132962743e-08    51.0464285714286        0.181855926925472
6       18      ATP synthesis coupled proton transport
GO:0000387      1.99629258587082e-08    29.9661270983213        0.313196318593869
7       31      spliceosomal snRNP assembly
GO:0042776      1.18505858352551e-07    63.3732269503546        0.131340391668397
5       13      mitochondrial ATP synthesis coupled proton transport
GO:0008380      1.68507574076243e-07    5.61182660987221        3.26330357760709
16      323     RNA splicing
GO:0006397      5.73525880711992e-07    4.80317788871302        4.03113971351464
17      399     mRNA processing
GO:0000375      1.37645706149734e-06    6.41321312220623        2.11154937374576
12      209     RNA splicing, via transesterification reactions
GO:0015992      4.40188110241071e-06    12.1597366174857        0.666805065393398
7       66      proton transport
GO:0008334      4.43650775997925e-06    25.3280141843972        0.252577676285378
5       25      histone mRNA metabolic process
GO:0006818      5.38804658805275e-06    11.7594055902819        0.687011279496229
7       68      hydrogen transport
GO:0000291      5.44830224774408e-06    24.1202296521445        0.262680783336793
5       26      nuclear-transcribed mRNA catabolic process, exonucleolytic
GO:0043928      5.44830224774408e-06    24.1202296521445        0.262680783336793
5       26      exonucleolytic nuclear-transcribed mRNA catabolic process involved
in deadenylation-dependent decay
GO:0000377      7.03630480951238e-06    5.95785837651123        2.06103383848869
11      204     RNA splicing, via transesterification reactions with bulged
adenosine as nucleophile
GO:0000398      7.03630480951238e-06    5.95785837651123        2.06103383848869
11      204     nuclear mRNA splicing, via spliceosome
GO:0006754      9.38036671582839e-06    14.2146179401993        0.495052245519341
6       49      ATP biosynthetic process
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GO:0006839      1.01830676064649e-05    8.58031400966184        1.05072313334717
8       104     mitochondrial transport
Tissue: Artery_Tibial=>Adipose_Subcutaneous     Type:   asymmetric
SourceGene:     PIN1(ENSG00000127445.7)
TargetGeneSet:  RPL22   VPS13D  RPL11   SYF2    PRDX3P2 KHDRBS1 RP4     RPS8    RPL5
RP11    SNX7    ATP5F1  SNRPE   ZNF672  ACP1    YWHAQ   TTC32   COX7A2L UBC
PPP3R1  RPL31   MMADHC  MTX2    KCTD18  RPL15   GORASP1 HIGD1A  GRM2    PCNP
ITGB5-AS1       PDCD10  PARL    RPL35A  OCIAD1  HSD17B11        RPL34   ANAPC10
RPS3A   C4orf46 NDUFS4  MRPS36  TAF9    FCHO2   BTF3    TBCA    RPS23   CTD     SNX2
UBE2D2  NDFIP1  RPS14   TDP2    RPS10   RPL10A  C6orf130        RWDD1   MRPS12
C6orf72 BTF3P10 NDUFA5  SSBP1   DCTN6   RPL30   VPS13B  POLR2K  EIF3H   CLTA
SLC35D2 RPL35   RAB18   VN1R53P AGAP6   VDAC2   RPS24   SFR1    RPL27A  C11orf58
FAU     RPS25   PFDN5   YEATS4  C12orf45        MLXIP   POLR1D  DGKH    TPT1
RSL24D1 RPS3AP6 RAB11A  MORF4L1 SEC11A  SRRM2   VPS53   MINK1   GABARAP RPL19
RAPGEFL1        RPL27   RNF213  FOXK2   PSMG2   RNF138  RPL17   ABCA7   RPS15
RPL36   BRD4    RPL18   ZNF667  SLC4A11 PFDN4   PI4KA   MORC2   POLR2F  KDM5C
HUWE1   RPL10   VAMP7
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      1.82968058331037e-37    79.2902960526316        0.648605632828178
27      91      translational termination
GO:0006614      2.2625275620165e-37     69.1927272727273        0.748391114801744
28      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      3.05920692959468e-37    68.3008547008547        0.755518649228427
28      106     cotranslational protein targeting to membrane
GO:0045047      3.05920692959468e-37    68.3008547008547        0.755518649228427
28      106     protein targeting to ER
GO:0072599      3.05920692959468e-37    68.3008547008547        0.755518649228427
28      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      8.96793570318084e-36    59.1442962962963        0.841049062348626
28      118     protein localization to endoplasmic reticulum
GO:0006414      1.52646240815652e-35    64.9949392712551        0.748391114801744
27      105     translational elongation
GO:0019080      3.81709586088656e-34    45.6971643774922        1.07625769842917
29      151     viral genome expression
GO:0019083      3.81709586088656e-34    45.6971643774922        1.07625769842917
29      151     viral transcription
GO:0000184      6.66852194647906e-34    55.0503432494279        0.84817659677531
27      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006413      2.08450014353447e-32    42.8249462365591        1.08338523285586
28      152     translational initiation
GO:0006612      2.53852081156221e-32    42.47936        1.09051276728254        28
153     protein targeting to membrane
GO:0043624      1.05713437487409e-30    40.0996240601504        1.09051276728254
27      153     cellular protein complex disassembly
GO:0043241      2.665009726269e-30      38.5555443953395        1.12615043941596
27      158     protein complex disassembly
GO:0072594      3.94930482849469e-30    31.7387644787645        1.45401702304339
29      204     establishment of protein localization to organelle
GO:0000956      1.82349348747595e-29    35.5413269088213        1.20455331810947
27      169     nuclear-transcribed mRNA catabolic process
GO:0034623      4.17424947541628e-29    34.3203544575725        1.24019099024289
27      174     cellular macromolecular complex disassembly
GO:0006402      7.94469852801563e-29    33.4017950505403        1.26870112794962
27      178     mRNA catabolic process
GO:0032984      9.30795624462891e-29    33.1797091412742        1.27582866237631
27      179     macromolecular complex disassembly
GO:0019058      1.63632534474771e-28    27.4440727856569        1.64646045256384
29      231     viral infectious cycle
GO:0006401      4.17105803182987e-27    28.2813424009462        1.46114455747007
27      205     RNA catabolic process
GO:0022415      5.39847106719936e-27    23.9495144495144        1.85315895093765
29      260     viral reproductive process
GO:0071845      3.08334812511755e-23    19.4786504198239        2.02421977717805
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27      284     cellular component disassembly at cellular level
GO:0022411      4.48730900500021e-23    19.1746823956443        2.05272991488478
27      288     cellular component disassembly
GO:0006605      8.29034726793334e-22    13.5143905191874        3.37845131824787
31      474     protein targeting
GO:0016032      2.66158111989196e-21    13.5948329157583        3.21451802643416
30      451     viral reproduction
GO:0033365      1.32816501122266e-19    12.2722181641101        3.37132378382119
29      473     protein localization to organelle
GO:0042274      1.32769017726668e-07    56.2598116169545        0.128295619680299
5       18      ribosomal small subunit biogenesis
GO:0022613      5.79743579126563e-07    7.89689150751727        1.60369524600374
11      225     ribonucleoprotein complex biogenesis
GO:0071843      1.05259489543742e-06    7.40465293668955        1.7034807279773 11
239     cellular component biogenesis at cellular level
GO:0042254      1.13787450749353e-06    9.71671732522796        1.06200262957581
9       149     ribosome biogenesis
GO:0006364      9.17638429143643e-06    10.7127362542955        0.741263580375061
7       104     rRNA processing
GO:0030490      1.20555222457629e-05    107.58  0.0498927409867829      3       7
maturation of SSU-rRNA
GO:0016072      1.32749181066227e-05    10.0844457928803        0.78402878693516
7       110     rRNA metabolic process
Tissue: Artery_Tibial=>Adipose_Subcutaneous     Type:   asymmetric
SourceGene:     PPP1R35(ENSG00000160813.2)
TargetGeneSet:  IL28RA  RAB42   CTSS    C1orf85 SLAMF9  CD84    NUF2    ASPM    NEK2
ZNF692  GCC2    BUB1    HJURP   FANCD2  SGOL1   HEMK1   RP11    SKIL    NCEH1   PARL
CTBP1   CENPE   MAD2L1  NEK1    HEXB    KCNN2   KIF20A  GM2A    RGL2    TREML4
PLA2G7  IMPG1   NDUFAF4 HSF2    BLVRA   CHMP7   DNAJC5B SCRIB   MELK    FBP1
IKBKAP  DAB2IP  ZNF248  CEP55   CTBP2   MKI67   DDB2    RBM14   MPP2    TCTN2
SLC7A8  DLGAP5  NPC2    BUB1B   CASC5   NUSAP1  CCNB2   APH1B   PRC1    ADCY9
GLIS2   ASPHD1  ORAI3   ORC6    ELMO3   DPEP2   CDT1    AURKB   EVI2B   CCT6B
TOP2A   KIF18B  QRICH2  BIRC5   RP13    PSTPIP2 SKA1    MUM1    ACP5    ASF1B   TPX2
MYBL2   UBE2C   C21orf59        SOWAHD
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0000087      8.11545192707253e-18    16.610650887574 1.91820635250156        22
360     M phase of mitotic cell cycle
GO:0000280      7.48784246976667e-17    16.0087386018237        1.86492284270985
21      350     nuclear division
GO:0007067      7.48784246976667e-17    16.0087386018237        1.86492284270985
21      350     mitosis
GO:0048285      2.30635355685262e-16    15.0698424068768        1.97148986229327
21      370     organelle fission
GO:0051301      9.84499542895747e-16    12.9711627906977        2.40841464258529
22      452     cell division
GO:0007059      1.65357408919032e-14    25.1287477954145        0.745969137083939
14      140     chromosome segregation
GO:0000236      2.29063332390665e-11    28.4557213930348        0.452909833229534
10      85      mitotic prometaphase
GO:0007017      1.98673818066692e-10    9.7383136930904 2.0940419348142 16      393
microtubule-based process
GO:0010564      4.26290201811313e-10    9.21064338083862        2.20593730537679
16      414     regulation of cell cycle process
GO:0000226      1.53348202076876e-09    11.2020263671875        1.433326413397  13
269     microtubule cytoskeleton organization
GO:0007346      6.32103781543842e-08    8.93449643140365        1.61449034668881
12      303     regulation of mitotic cell cycle
GO:0031577      8.45574181198128e-08    33.6572769953052        0.223790741125182
6       42      spindle checkpoint
GO:0071156      1.41374166330406e-07    9.30237154150198        1.40668465850114
11      264     regulation of cell cycle arrest
GO:0007051      2.14855989955282e-07    19.5904109589041        0.426268078333679
7       80      spindle organization
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GO:0000819      3.14610820744488e-07    26.3221065523576        0.277074250916892
6       52      sister chromatid segregation
GO:0007088      4.15025086482453e-07    17.6456790123457        0.468894886167047
7       88      regulation of mitosis
GO:0051783      4.15025086482453e-07    17.6456790123457        0.468894886167047
7       88      regulation of nuclear division
GO:0045786      4.67338759798248e-07    6.68300412735849        2.32848937789772
13      437     negative regulation of cell cycle
GO:0007050      5.30062805352234e-07    7.2486102133161 1.9661615113141 12      369
cell cycle arrest
GO:0000075      5.91210608297621e-07    9.09804426145136        1.28946093695938
10      242     cell cycle checkpoint
GO:0071173      9.28542025236463e-07    34.3510536398467        0.181163933291814
5       34      spindle assembly checkpoint
GO:0034453      1.07880770747736e-06    33.2037037037037        0.186492284270985
5       35      microtubule anchoring
GO:0008608      1.68232414067792e-06    60.5310853530032        0.0905819666459069
4       17      attachment of spindle microtubules to kinetochore
GO:0051313      2.71771295428337e-06    52.4529680365297        0.101238668604249
4       19      attachment of spindle microtubules to chromosome
GO:0030071      3.09433502478164e-06    26.1988304093567        0.229119092104353
5       43      regulation of mitotic metaphase/anaphase transition
GO:0007091      3.89494661238576e-06    24.8854166666667        0.239775794062695
5       45      mitotic metaphase/anaphase transition
GO:0000070      5.9790036781241e-06     22.6167929292929        0.261089197979379
5       49      mitotic sister chromatid segregation
GO:0000910      1.05418242064569e-05    13.7189500640205        0.500864992042073
6       94      cytokinesis
GO:0000086      1.1323242897632e-05     10.3919708029197        0.767282541000623
7       144     G2/M transition of mitotic cell cycle
Tissue: Artery_Tibial=>Adipose_Subcutaneous     Type:   asymmetric
SourceGene:     RP11-122C5.1(ENSG00000249911.1)
TargetGeneSet:  RP11    RPL32   RPL15   RPL34   NKD2    BTF3    CTB     RPS14
C6orf130        ARF5    RPL30   RPS6    ANP32B  HIF1AN  UBXN1   RPS25   PFDN5
RPL41   RPL31P52        TPT1    RPL36A  SEC11A  RPS15A  CTD     RPL26   RPL17
RPL19   MSI2    NFIC    RPL36   CCDC106 RPS4X   APOOL   RPL10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006614      1.14896144109454e-27    198.209161624892        0.210712061449035
16      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.35206783370638e-27    195.993162393162        0.212718842986645
16      106     cotranslational protein targeting to membrane
GO:0045047      1.35206783370638e-27    195.993162393162        0.212718842986645
16      106     protein targeting to ER
GO:0072599      1.35206783370638e-27    195.993162393162        0.212718842986645
16      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      8.45158216386469e-27    172.790346907994        0.236800221437963
16      118     protein localization to endoplasmic reticulum
GO:0006415      2.08823149905626e-26    202.246240601504        0.182617119922497
15      91      translational termination
GO:0006414      2.09274983470356e-25    170.619047619048        0.210712061449035
15      105     translational elongation
GO:0006612      6.73796736003385e-25    128.332397529478        0.307037575254308
16      153     protein targeting to membrane
GO:0000184      1.53646023528533e-24    147.506868131868        0.238807002975573
15      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      6.49938859362646e-23    112.547268907563        0.303024012179088
15      151     viral genome expression
GO:0019083      6.49938859362646e-23    112.547268907563        0.303024012179088
15      151     viral transcription
GO:0006413      7.20438898109483e-23    111.717935349322        0.305030793716698
15      152     translational initiation
GO:0072594      7.92730701992663e-23    93.1849427168576        0.40938343367241
16      204     establishment of protein localization to organelle
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GO:0043624      7.98015086234435e-23    110.900621118012        0.307037575254308
15      153     cellular protein complex disassembly
GO:0043241      1.31694056865968e-22    106.985514485514        0.317071482942357
15      158     protein complex disassembly
GO:0000956      3.74629653040939e-22    99.2671614100186        0.339146079856065
15      169     nuclear-transcribed mRNA catabolic process
GO:0034623      5.88527129669815e-22    96.1118598382749        0.349179987544115
15      174     cellular macromolecular complex disassembly
GO:0006402      8.36500265154566e-22    93.7269938650307        0.357207113694554
15      178     mRNA catabolic process
GO:0032984      9.12170926387528e-22    93.1489547038328        0.359213895232164
15      179     macromolecular complex disassembly
GO:0006401      7.3662835824345e-21     80.2556390977444        0.41139021521002
15      205     RNA catabolic process
GO:0019058      4.58067706336739e-20    70.4662698412698        0.463566535187876
15      231     viral infectious cycle
GO:0022415      2.77114154915799e-19    61.9985422740525        0.521763199778562
15      260     viral reproductive process
GO:0071845      1.0557766715806e-18     56.3714816781731        0.569925956681198
15      284     cellular component disassembly at cellular level
GO:0022411      1.30432507449168e-18    55.5298273155416        0.577953082831638
15      288     cellular component disassembly
GO:0033365      6.20173941789631e-17    37.6098299949503        0.949207667289461
16      473     protein localization to organelle
GO:0006605      6.41279420733435e-17    37.5250251931475        0.951214448827071
16      474     protein targeting
GO:0016032      1.07194567004352e-15    34.3692660550459        0.905058473462044
15      451     viral reproduction
GO:0000028      1.44739365195045e-07    554.576923076923        0.0120406892256591
3       6       ribosomal small subunit assembly
GO:0042255      3.99834937900122e-06    127.890532544379        0.0321085046017577
3       16      ribosome assembly
GO:0042274      5.81045750171972e-06    110.823076923077        0.0361220676769774
3       18      ribosomal small subunit biogenesis
Tissue: Adipose_Subcutaneous=>Artery_Tibial     Type:   asymmetric
SourceGene:     RP11-40H20.1(ENSG00000214973.3)
TargetGeneSet:  ATPIF1  PPCS    C1orf50 BTBD19  UQCRH   TMEM167B        RP11
TRIB2   TPRKB   MRPS9   NDUFB3  DZIP1L  IGSF10  NDUFB5  FGFRL1  THEGL   NDUFC1
NDUFS6  ISCA1P1 COX7C   HINT1   COX7A2  SLC22A2 STAG3L1 PMS2P1  FAM160B2
RPL10AP2        DECR1   C9orf123        NUDT2   FAM27E1 PSMB7   ATP5C1  NDUFB8
USMG5   NAV2    NDUFS3  EML3    NEAT1   C11orf51        CCDC90B ATP5L   NDUFA9
MRPL51  FAM90A1 C12orf39        NDUFA12 RPS7P10 ZBTB25  COX16   SLIRP   NDUFB1
C14orf2 CTD     MYEF2   GTF2A2  POLR3K  PKD1P6  PSMB10  C17orf89        NPC1
UQCR11  PIN1    ATP5J   RPL12P9 ATP5O   POLR2F  COX7B   NDUFA1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      2.86037904656724e-28    118.07967032967 0.305584388623625       18
96      respiratory electron transport chain
GO:0022900      1.78822752289842e-25    79.1878078817734        0.426544875787143
18      134     electron transport chain
GO:0045333      5.36833090300841e-25    74.0374423963134        0.452010241505778
18      142     cellular respiration
GO:0015980      7.78780791892873e-19    31.3999011369254        0.977233409452633
18      307     energy derivation by oxidation of organic compounds
GO:0006091      1.22161031685955e-17    24.0807751516798        1.36239706594699
19      428     generation of precursor metabolites and energy
GO:0006119      1.90989284439664e-17    96.0109422492401        0.184623901460107
11      58      oxidative phosphorylation
GO:0042773      1.77864292754985e-16    107.867867867868        0.149609023596983
10      47      ATP synthesis coupled electron transport
GO:0042775      1.77864292754985e-16    107.867867867868        0.149609023596983
10      47      mitochondrial ATP synthesis coupled electron transport
GO:0006120      1.2898541533863e-15     129.531531531532        0.114594145733859
9       36      mitochondrial electron transport, NADH to ubiquinone
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GO:0042776      6.2905206281311e-08     152.338624338624        0.0413812192927825
4       13      mitochondrial ATP synthesis coupled proton transport
GO:0015985      2.66101931278596e-07    97.8979591836735        0.0572970728669296
4       18      energy coupled proton transport, down electrochemical gradient
GO:0015986      2.66101931278596e-07    97.8979591836735        0.0572970728669296
4       18      ATP synthesis coupled proton transport
GO:0006200      3.81956829649728e-06    24.9738675958188        0.238737803612207
5       75      ATP catabolic process
GO:0006754      1.71434037712978e-05    30.3915343915344        0.155975365026642
4       49      ATP biosynthetic process
Tissue: Adipose_Subcutaneous=>Artery_Tibial     Type:   cluster
SourceGene:     RPS7P10(ENSG00000226525.3)
TargetGeneSet:  AURKAIP1        MRPL20  FAM213B PARK7   CELA2B  PLEKHM2 RP11    UBR4
MINOS1  SDHDP1  RP1     ATPIF1  7SK     PSMB2   RP3     C1orf122        PPCS
UQCRH   HBXIP   ATP5F1  S100A6  CRTC2   LAMTOR2 SDHC    TMCO1   PFN1P1  MIR4426
SNRPE   MORF4L1P1       C1orf31 SCCPDH  ITGB1BP1        OST4    C2orf28 FTH1P3
CALM2   MDH1    SNRPG   TPRKB   BOLA3   SUCLG1  COX5B   TXNDC9  TSPO    SCRN3
ATP5G3  MTX2    NIF3L1  NDUFB3  MYEOV2  PPP1R7  LSM3    SPCS1   PDHB    ATG3
NDUFB4  MRPS22  RNF7    UBE2V1P2        MRPL47  MCCC1   NCBP2   CPZ     COMMD8
MRPL1   ENOPH1  MRPS18C PPA2    NUDT6   NDUFC1  SCOC    LSM6    C4orf27 PDCD6
NDUFS6  RBBP4P1 MOCS2   C5orf43 ISCA1P1 COX7C   CTD     CETN3   HINT1   FNIP1
UQCRQ   PDF     ARHGAP26        ATOX1   PPP1R2P3        RPL26L1 HIGD2A  NHP2    LSM2
PFDN6   HNRNPC  COX6A1P2        RPL24P4 MEA1    C6orf108        COX7A2  COQ3
FOXO3   MRPS12  SF3B5   MRPL18  NDUFA4  ANKMY2  LSM5    SEPT7   YAE1D1  PPIA
SEC61G  MDH2    TP53TG1 CDK6    ACN9    COPS6   PMS2P1  LRRN4   BPGM    JHDM1D
NDUFB2  SSBP1   DEFA3   CCDC25  LSM1    RPL10AP2        MRPS35  DECR1   COX6C
MRPL13  NDUFB9  C9orf46 SNRPEP2 C9orf123        PLIN2   NDUFB6  YBX1P10 RPS10P3
SEC61B  ATP5C1  CDC123  YWHAZP3 KIAA0913        SRP9P1  NDUFB8  USMG5   TCF7L2  UROS
ECHS1   POLR2L  MRPL23  ST13P5  IMMP1L  NDUFS3  C11orf10        CFL1    MRPL11
PPP1CA  MRPL21  C11orf51        CLNS1A  CCDC90B TMEM126A        SDHD    ATP5L   MLL
DCPS    DYRK4   COPS7A  COX14   MYL6    NDUFA12 SNRPF   CCDC53  NUP37   C12orf45
MED13L  COX6A1  TRIAP1  POP5    DENR    ULK1    FAM207BP        RPS7P10 N4BP2L2-IT1
DGKH    MED4    COX7CP1 MRPL52  MYH6    RPS29   COX16   SLIRP   NDUFB1  SLC25A29
C14orf2 TMEM85  GTF2A2  RAB11A  COX5A   WDR61   RPS17L  MRPS11  U6      MRPL28
MAPK8IP3        NDUFB10 NPIPP1  PKD1P6  NDUFAB1 ATXN2L  NUTF2   PSMB10  HSBP1
PSMB6   TXNDC17 LSMD1   C17orf75        PSMB3   G6PC3   GPATCH8 PLEKHM1 ATP5G1  PHB
RAD51C  ICT1    C17orf89        ANAPC11 EPG5    ATP5A1  IER3IP1 UQCR11  C19orf70
INSR    C19orf79        NDUFA7  PIN1    ZNF791  WDR83OS NDUFB7  AKAP8L  NDUFA13 POP4
COX6B1  PSENEN  TBCB    CYP2G1P NDUFA3  TBC1D20 SNRPB2  NAA20   ROMO1   ATP5E
PPIAP22 ATP5J   ATP5O   SNRPD3  MTMR3   SLC5A1  POLR2F  GTPBP1  NDUFA6  TTLL1   RP6
GS1     EEF1B2P3        GAPDHP1 RPS2P55 RP13    PDZD11  ITGB1BP2        COX7B
PSMD10  NXT2    NDUFA1  FTH1P8  CETN2   PSMA6P1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      2.28900664353924e-48    57.2154963680387        1.44156113763753
40      96      respiratory electron transport chain
GO:0045333      1.95163034183628e-46    36.6865636427982        2.13230918275552
44      142     cellular respiration
GO:0022900      1.89851180194962e-41    33.9944704892415        2.01217908795239
40      134     electron transport chain
GO:0015980      2.28260667625191e-35    15.3252153252153        4.60999238807003
48      307     energy derivation by oxidation of organic compounds
GO:0006091      1.25140480086024e-30    10.9748756455343        6.42696007196734
50      428     generation of precursor metabolites and energy
GO:0042773      9.56750064780683e-25    53.4198157548411        0.705764306968376
20      47      ATP synthesis coupled electron transport
GO:0042775      9.56750064780683e-25    53.4198157548411        0.705764306968376
20      47      mitochondrial ATP synthesis coupled electron transport
GO:0006119      3.92800276161135e-24    41.1110038610039        0.870943187322677
21      58      oxidative phosphorylation
GO:0006120      5.28408124888484e-24    71.4371859296482        0.540585426614075
18      36      mitochondrial electron transport, NADH to ubiquinone
GO:0015985      1.42221004526642e-12    68.3894230769231        0.270292713307038
9       18      energy coupled proton transport, down electrochemical gradient
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GO:0015986      1.42221004526642e-12    68.3894230769231        0.270292713307038
9       18      ATP synthesis coupled proton transport
GO:0042776      2.74228857669388e-12    108.93014354067 0.195211404055083       8
13      mitochondrial ATP synthesis coupled proton transport
GO:0006754      4.01334088685586e-08    15.3540865384615        0.735796830669158
9       49      ATP biosynthetic process
GO:0015992      4.80013218877625e-08    12.2308488612836        0.991073282125804
10      66      proton transport
GO:0006818      6.44429769370182e-08    11.8074296185241        1.02110580582659
10      68      hydrogen transport
GO:0000375      1.04999803973142e-07    5.79114788750548        3.13839872673171
16      209     RNA splicing, via transesterification reactions
GO:0009206      2.50301770650288e-07    12.0330882352941        0.900975711023459
9       60      purine ribonucleoside triphosphate biosynthetic process
GO:0009145      2.89832274965178e-07    11.800850591716 0.91599197287385        9
61      purine nucleoside triphosphate biosynthetic process
GO:0000387      3.02533742730919e-07    19.7361111111111        0.46550411736212
7       31      spliceosomal snRNP assembly
GO:0006839      4.46196502600813e-07    8.11937571771584        1.56169123244066
11      104     mitochondrial transport
GO:0000377      4.47596051955915e-07    5.51823039446802        3.06331741747976
15      204     RNA splicing, via transesterification reactions with bulged
adenosine as nucleophile
GO:0000398      4.47596051955915e-07    5.51823039446802        3.06331741747976
15      204     nuclear mRNA splicing, via spliceosome
GO:0009201      5.0720347144576e-07     10.954842032967 0.976057020275413       9
65      ribonucleoside triphosphate biosynthetic process
GO:0009142      8.53672039585274e-07    10.2216346153846        1.03612206767698
9       69      nucleoside triphosphate biosynthetic process
GO:0008334      1.49277132324399e-06    21.2746320778249        0.375406546259774
6       25      histone mRNA metabolic process
GO:0006200      1.75012456482418e-06    9.28846153846154        1.12621963877932
9       75      ATP catabolic process
GO:0008380      1.86170795560085e-06    4.13085097619244        4.85025257767629
18      323     RNA splicing
GO:0000291      1.91640257732766e-06    20.2094786729858        0.390422808110165
6       26      nuclear-transcribed mRNA catabolic process, exonucleolytic
GO:0006099      1.91640257732766e-06    20.2094786729858        0.390422808110165
6       26      tricarboxylic acid cycle
GO:0043928      1.91640257732766e-06    20.2094786729858        0.390422808110165
6       26      exonucleolytic nuclear-transcribed mRNA catabolic process involved
in deadenylation-dependent decay
GO:0046034      2.04380086286044e-06    6.85631067961165        1.81696768389731
11      121     ATP metabolic process
GO:0046356      2.43322641419875e-06    19.2457684495599        0.405439069960556
6       27      acetyl-CoA catabolic process
GO:0009152      2.44415243484746e-06    8.88273411371237        1.1712684243305 9
78      purine ribonucleotide biosynthetic process
GO:0009060      2.69779069651442e-06    13.5228571428571        0.630682997716421
7       42      aerobic respiration
GO:0009109      6.99634120062945e-06    15.5391906671528        0.480520379212511
6       32      coenzyme catabolic process
GO:0009260      8.10155114180119e-06    7.56036324786325        1.35146356653519
9       90      ribonucleotide biosynthetic process
GO:0006397      9.4570397907309e-06     3.49848484848485        5.991488478306  19
399     mRNA processing
GO:0051187      1.97713738455066e-05    12.6202606635071        0.570617950314857
6       38      cofactor catabolic process
Tissue: Adipose_Subcutaneous=>Artery_Tibial     Type:   cluster
SourceGene:     SHFM1(ENSG00000127922.5)
TargetGeneSet:  AURKAIP1        MRPL20  PARK7   SLC45A1 CASZ1   PLEKHM2 RP11    UBR4
ATPIF1  7SK     PSMB2   INSL3   PPCS    TDPX2   UQCRH   MAGOH   MRPL37  HBXIP
ATP5F1  MRPS21  SCNM1   THEM4   S100A6  DENND4B LAMTOR2 PFDN2   UFC1    SDHC
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TMCO1   RP4     MIR4426 SNRPE   ACP1    PXDN    PTRHD1  C2orf28 COMMD1  SNRPG
TPRKB   KDM3A   COX5B   IL1R1   TSN     MTX2    NDUFB3  EEF1B2  MYEOV2  PPP1R7  LSM3
TRANK1  CCDC72  SPCS1   C3orf26 ATG3    NDUFB4  UMPS    MRPS22  RNF7    UBE2V1P2
MRPL47  MRPL1   MRPS18C RG9MTD2 LAMTOR3 NPNT    EXOSC9  NDUFC1  LSM6    C4orf27
PDCD6   NDUFS6  RBBP4P1 COX7C   CTD     CETN3   HINT1   UQCRQ   PDF     ATOX1
LSM11   CTB     BNIP1   EEF1E1  NOL7    HLA-F-AS1       LSM2    PFDN6   HNRNPC
TEAD3   COX6A1P2        RPL24P4 MEA1    COX7A2  C6orf203        MRPS12  SF3B5
PSMB1   PSMG3   LSM5    YAE1D1  MPLKIP  CHCHD2  BUD31   COPS6   PMS2P1  ZNHIT1
MKLN1   JHDM1D  MRPS33  SSBP1   RBPMS   CHCHD7  TCEB1   MRPS35  DECR1   VPS13B
MRPL13  NDUFB9  CTA     HEATR7A PLIN2   ACER2   NDUFB6  DCTN3   SEC61B  COQ4
SURF2   EDF1    ATP5C1  CDC123  RPP30   EXOSC1  NDUFB8  LZTS2   USMG5   ADRA2A
TCF7L2  UROS    BCCIP   BNIP3   ECHS1   POLR2L  MRPL23  PRKCDBP DENND5A ST13P5
IMMP1L  NDUFS3  TIMM10  C11orf10        TRMT112 MRPL11  GSTP1   MRPL21  CLNS1A
TMEM126A        CWC15   SDHD    ATP5L   ARHGAP32        ITFG2   NDUFA9  MRPL51
COPS7A  CLSTN3  NDUFA12 SNRPF   NUP37   C12orf45        MED13L  POP5    DENR    TRAC
SAP18   DGKH    MED4    MRPL52  ARHGAP5-AS1     RPS29   C14orf166       ACTR10
COX16   MED6    SLIRP   NDUFB1  GLRX5   C14orf2 TMEM85  ATPBD4  SRP14   NDUFAF1
GTF2A2  RPLP1   COMMD4  WDR61   KIF7    MRPL28  PKD1P6  NDUFAB1 LCMT1   PSMB10
TRAPPC2L        PSMB6   TXNDC17 FAM18B1 USP32P3 STAT5B  VPS25   CCDC56  RPL27
ATP5G1  MRPL27  RAD51C  USP32   ICT1    RNF213  C17orf89        ARL16   STRA13
FOXK2   SNRPD1  NPC1    TTC39C  IER3IP1 CTIF    UQCR11  DOT1L   PIP5K1C MRPL54
C19orf70        NDUFA11 C19orf79        NDUFA7  PIN1    ZNF791  WDR83OS NDUFB7
AKAP8L  C19orf42        NDUFA13 POP4    COX6B1  TBCB    EIF3K   TIMM50  NDUFA3
HSPBP1  TBC1D20 EBF4    SNRPB2  NAA20   ROMO1   SRC     C20orf43        ATP5E
ATP5J   ATP5O   SNRPD3  TXN2    POLR2F  C22orf32        RP6     EEF1B2P3        UXT
PDZD11  COX7B   NDUFA1  RP3     FTH1P8  PSMA6P1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      4.592840749001e-40      45.4400586134261        1.42163172098817
35      96      respiratory electron transport chain
GO:0022900      1.09760855787478e-35    29.1793166704884        1.98436094387932
36      134     electron transport chain
GO:0045333      2.94674400912896e-33    25.8210202057119        2.10283025396166
35      142     cellular respiration
GO:0015980      2.3719550345587e-23     10.8135383971542        4.54625977441008
37      307     energy derivation by oxidation of organic compounds
GO:0042773      1.78318070340241e-21    44.9936664320901        0.69600719673379
18      47      ATP synthesis coupled electron transport
GO:0042775      1.78318070340241e-21    44.9936664320901        0.69600719673379
18      47      mitochondrial ATP synthesis coupled electron transport
GO:0006119      4.41564138584492e-21    35.4716633793557        0.858902498097017
19      58      oxidative phosphorylation
GO:0006120      1.71055328476584e-20    57.4424242424242        0.533111895370563
16      36      mitochondrial electron transport, NADH to ubiquinone
GO:0006091      3.75656934907675e-20    7.93348512669849        6.33810808940558
39      428     generation of precursor metabolites and energy
GO:0042776      2.25337263936207e-10    80.20692431562  0.192512628883814       7
13      mitochondrial ATP synthesis coupled proton transport
GO:0015985      3.9237361525384e-09     43.733860342556 0.266555947685281       7
18      energy coupled proton transport, down electrochemical gradient
GO:0015986      3.9237361525384e-09     43.733860342556 0.266555947685281       7
18      ATP synthesis coupled proton transport
GO:0000377      6.18089095008291e-08    6.03868471953578        3.02096740709985
16      204     RNA splicing, via transesterification reactions with bulged
adenosine as nucleophile
GO:0000398      6.18089095008291e-08    6.03868471953578        3.02096740709985
16      204     nuclear mRNA splicing, via spliceosome
GO:0000375      8.65885874068974e-08    5.88014863662532        3.09501072590132
16      209     RNA splicing, via transesterification reactions
GO:0000387      2.75271548332563e-07    20.0263687600644        0.459068576569096
7       31      spliceosomal snRNP assembly
GO:0008380      3.38592482816071e-07    4.46570512820513        4.78319839457477
19      323     RNA splicing
GO:0006839      3.88301096441851e-07    8.24111446580857        1.54010103107051
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11      104     mitochondrial transport
GO:0006397      5.04419637022262e-07    3.98934945308002        5.90865684035707
21      399     mRNA processing
GO:0000291      1.76742644042912e-06    20.5052884615385        0.385025257767629
6       26      nuclear-transcribed mRNA catabolic process, exonucleolytic
GO:0043928      1.76742644042912e-06    20.5052884615385        0.385025257767629
6       26      exonucleolytic nuclear-transcribed mRNA catabolic process involved
in deadenylation-dependent decay
GO:0015992      5.57481779288666e-06    9.49380649481085        0.977371808179365
8       66      proton transport
GO:0006818      6.99519943735294e-06    9.17605177993527        1.00698913569995
8       68      hydrogen transport
GO:0006754      7.1730428209445e-06     11.4291465378422        0.725624524254377
7       49      ATP biosynthetic process
GO:0006200      1.46104216620105e-05    8.21330241993914        1.11064978202201
8       75      ATP catabolic process
Tissue: Artery_Tibial=>Heart_Left_Ventricle     Type:   asymmetric
SourceGene:     ALG10B(ENSG00000175548.4)
TargetGeneSet:  CELA2B  CELA3B  CELA3A  AMY2A   CPB1    SPINK1  CLPS    SNHG5   CPA2
CPA1    PRSS1   PRSS3P1 GSDMD   PIGO    PNLIP   PNLIPRP1        PNLIPRP2        CFL1
GP2     CTRB2   CTRB1   DOHH    SYCN    RBPJL
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0007586      1.51426135092439e-12    87.3054074638233        0.158397342744447
8       109     digestion
GO:0044241      1.18997840725084e-06    200.25  0.0217977994602445      3       15
lipid digestion
GO:0022617      1.83105550247234e-05    72.7121212121212        0.0523147187045879
3       36      extracellular matrix disassembly
Tissue: Artery_Tibial=>Heart_Left_Ventricle     Type:   asymmetric
SourceGene:     ATCAY(ENSG00000167654.11)
TargetGeneSet:  SLC35E2 RPL11   DCDC2B  KIAA1522        RPL5    ANXA9   ASH1L
USP34   TGOLN2  ENO1P4  NGLY1   RPL14   RNF123  MGLL    RP11    FRYL    WWC2    CTD
SERF1B  GNB2L1  COQ3    TNRC18  MRPS24  RPS3AP26        RPS20   DCAF13  RPS24   TUB
PPP6R3  ERC1    MLL4    SMARCC2 COX17P1 ISCA2   C14orf1 CDC42BPB        VPS39
HERC1   RPL4    SEC11A  HDDC3   NDUFB10 TSC2    RPS15A  POLR2C  ZZEF1   RPL26
RPS7P1  TAOK1   RPL27   RPS7P11 MRPL27  SNRPD1  C18orf21        TNPO2   CIC
IQSEC2  COX7B   FUNDC2
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006614      5.3498284809783e-13     44.3095975232198        0.31970105875026
10      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      5.89440433861055e-13    43.8449754901961        0.322745830738357
10      106     cotranslational protein targeting to membrane
GO:0045047      5.89440433861055e-13    43.8449754901961        0.322745830738357
10      106     protein targeting to ER
GO:0072599      5.89440433861055e-13    43.8449754901961        0.322745830738357
10      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      1.75739236583815e-12    38.9406318082789        0.35928309459553
10      118     protein localization to endoplasmic reticulum
GO:0006415      6.14705621497614e-12    44.9216027874564        0.277074250916892
9       91      translational termination
GO:0019080      2.10359359521579e-11    29.7580308719232        0.459760570202754
10      151     viral genome expression
GO:0019083      2.10359359521579e-11    29.7580308719232        0.459760570202754
10      151     viral transcription
GO:0006414      2.28563692869326e-11    38.3330357142857        0.31970105875026
9       105     translational elongation
GO:0006612      2.39882978429815e-11    29.337721102427 0.46585011417895        10
153     protein targeting to membrane
GO:0000184      7.13438509531244e-11    33.4215584415584        0.362327866583627
9       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0034623      8.60882279304478e-11    25.543400286944 0.529790325929001       10
174     cellular macromolecular complex disassembly
GO:0032984      1.13906511263041e-10    24.7789766794292        0.54501418586949
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10      179     macromolecular complex disassembly
GO:0072594      4.11819688568161e-10    21.547907822923 0.621133485571933       10
204     establishment of protein localization to organelle
GO:0006413      6.43233951888559e-10    25.6495504495504        0.462805342190852
9       152     translational initiation
GO:0043624      6.81936805266407e-10    25.4696428571429        0.46585011417895
9       153     cellular protein complex disassembly
GO:0043241      9.07867156857262e-10    24.6063279002876        0.481073974119438
9       158     protein complex disassembly
GO:0019058      1.38261437436767e-09    18.8794250731967        0.703342329250571
10      231     viral infectious cycle
GO:0000956      1.64917272782406e-09    22.8969642857143        0.514566465988513
9       169     nuclear-transcribed mRNA catabolic process
GO:0006402      2.60802104409707e-09    21.6639053254438        0.541969413881392
9       178     mRNA catabolic process
GO:0022415      4.33241926972594e-09    16.6552941176471        0.791640716905404
10      260     viral reproductive process
GO:0006401      9.00427829797012e-09    18.6441690962099        0.62417825756003
9       205     RNA catabolic process
GO:0071845      1.00945754043179e-08    15.1706741090597        0.864715244619749
10      284     cellular component disassembly at cellular level
GO:0022411      1.15355570861207e-08    14.948159119763 0.87689433257214        10
288     cellular component disassembly
GO:0042273      3.63450224529092e-08    179.9875        0.0365372638571725      4
12      ribosomal large subunit biogenesis
GO:0033365      1.18742772274158e-07    10.0613275613276        1.44017715037022
11      473     protein localization to organelle
GO:0006605      1.21303468067644e-07    10.0388768898488        1.44322192235831
11      474     protein targeting
GO:0022613      3.33587853221997e-07    14.531490015361 0.685073697321985       8
225     ribonucleoprotein complex biogenesis
GO:0071843      5.27937993328423e-07    13.6373256373256        0.727700505155353
8       239     cellular component biogenesis at cellular level
GO:0006364      6.7936221870074e-07     23.0542427497315        0.316656286762162
6       104     rRNA processing
GO:0016032      7.598600501804e-07      9.31439242363612        1.37319216663207
10      451     viral reproduction
GO:0016072      9.46033587040975e-07    21.7150809716599        0.334924918690748
6       110     rRNA metabolic process
GO:0042254      5.55064422131899e-06    15.7497239602503        0.453671026226559
6       149     ribosome biogenesis
Tissue: Artery_Tibial=>Heart_Left_Ventricle     Type:   asymmetric
SourceGene:     ENSG00000230807.1
TargetGeneSet:  MRPL20  UBE4B   RP4     SPEN    EIF1AX  RP1     PUM1    AK2
AKR1A1  TAL1    ZCCHC11 RP11    ITGA10  MRPS21  PMF1    TMCO1   FAM5B   COG2
PQLC3   SOCS5   COX5B   UXS1    RANBP2  SCTR    CLASP1  ATP5G3  MYO1B   NDUFB3
KANSL1L RPL37A  CCDC72  RNF123  C3orf78 ABTB1   RPL35A  GAK     MXD4    LAMTOR3
PAPSS1  SMARCA5 CTSO    TMA16   TXNDC15 SOX9    SLC35A4 FBXO38  ARMC12  MRPL2
TDRD6   HMGN3   GTF3C6  C7orf26 NDUFA4  MRPS24  SEC61G  ECD     BRI3    ATP5J2  POP7
ZNF800  SLC13A4 NDUFB2  ZNF746  MCPH1   KAT6A   UBE2V2  MRPS35  C8orf59 NDUFB9  IL33
C9orf123        COL15A1 SLC31A1 RC3H2   RSU1    KIAA0913        C10orf11
EIF5AL1 USMG5   PPIAP19 AP2A2   C11orf10        FADS2   COX8A   VEGFB   PRDX5   FAU
PCNXL3  RELA    PPP6R3  PKNOX2  COX14   TENC1   NDUFA12 C12orf73        ULK1    DAD1
MRPL52  ADCY4   RPS29   FRMD6   PPM1A   ERH     ZFYVE1  NEK9    SLIRP   NDUFB1
VPS39   RPL4    IMP3    NPRL3   NDUFB10 FLYWCH2 SETD1A  COX4I1  ZC3H18  PSMB6
TXNDC17 CTC1    RPS7P1  GIT1    RASL10B RPL27   HDAC5   ITGA2B  PLEKHM1 NFE2L1
CALCOCO2        PPM1D   RPL38   ATP5H   LLGL2   C17orf89        MYL12B  GALNT1
CTDP1   C19orf35        SAFB    XAB2    MRPL4   CC2D1A  MAST3   MAU2    LPAR2
ATP13A1 COX6B1  PSENEN  BLVRB   TMEM91  PPP6R1  PLCG1   RPS21   CABIN1  TPST2
SNORD125        PLA2G6  TUBGCP6 SMS     EEF1B2P3        COX7B   NDUFA1  APLN
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      7.98769694576923e-15    22.5356125356125        0.87689433257214
15      96      respiratory electron transport chain
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GO:0022900      7.61119557949721e-14    16.5996493278784        1.22399833921528
16      134     electron transport chain
GO:0045333      2.9378183147757e-12     14.3266707046235        1.29707286692962
15      142     cellular respiration
GO:0015980      1.9929231767191e-08     6.64912904372556        2.80423500103799
16      307     energy derivation by oxidation of organic compounds
GO:0006120      3.02707805738153e-08    27.5944827586207        0.328835374714553
7       36      mitochondrial electron transport, NADH to ubiquinone
GO:0006415      1.40107317860821e-07    12.7040452111838        0.831222752750675
9       91      translational termination
GO:0042773      2.09804652824833e-07    19.9906 0.429312850321777       7       47
ATP synthesis coupled electron transport
GO:0042775      2.09804652824833e-07    19.9906 0.429312850321777       7       47
mitochondrial ATP synthesis coupled electron transport
GO:0006091      3.57086772064615e-07    5.00234846080609        3.90948723271746
17      428     generation of precursor metabolites and energy
GO:0006414      4.82418233945863e-07    10.8407012195122        0.959103176250778
9       105     translational elongation
GO:0006614      4.82418233945863e-07    10.8407012195122        0.959103176250778
9       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      5.23145762962558e-07    10.7281870756852        0.968237492215072
9       106     cotranslational protein targeting to membrane
GO:0045047      5.23145762962558e-07    10.7281870756852        0.968237492215072
9       106     protein targeting to ER
GO:0072599      5.23145762962558e-07    10.7281870756852        0.968237492215072
9       106     establishment of protein localization to endoplasmic reticulum
GO:0006119      9.22808339435138e-07    15.6668235294118        0.529790325929001
7       58      oxidative phosphorylation
GO:0070972      1.29897347402138e-06    9.53904676661445        1.07784928378659
9       118     protein localization to endoplasmic reticulum
GO:0043624      1.3627953712964e-06     8.12564484695632        1.39755034253685
10      153     cellular protein complex disassembly
GO:0043241      1.82632862887981e-06    7.8483606557377 1.44322192235831        10
158     protein complex disassembly
GO:0034623      4.35335253573461e-06    7.07467013194722        1.589370977787  10
174     cellular macromolecular complex disassembly
GO:0032984      5.60271956255934e-06    6.86293529925308        1.63504255760847
10      179     macromolecular complex disassembly
GO:0019080      9.94819710749006e-06    7.30522157334249        1.37928171060826
9       151     viral genome expression
GO:0019083      9.94819710749006e-06    7.30522157334249        1.37928171060826
9       151     viral transcription
GO:0006413      1.0493523203216e-05     7.25362442435613        1.38841602657256
9       152     translational initiation
GO:0006612      1.1064193692711e-05     7.20274390243902        1.39755034253685
9       153     protein targeting to membrane
GO:0000184      1.3130513094014e-05     8.25806451612903        1.08698359975088
8       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
Tissue: Artery_Tibial=>Heart_Left_Ventricle     Type:   cluster
SourceGene:     ENSG00000230807.1
TargetGeneSet:  MRPL20  UBE4B   RP4     SPEN    EIF1AX  RP1     PUM1    AK2
AKR1A1  TAL1    ZCCHC11 RP11    ITGA10  MRPS21  PMF1    TMCO1   FAM5B   COG2
PQLC3   SOCS5   COX5B   UXS1    RANBP2  SCTR    CLASP1  ATP5G3  MYO1B   NDUFB3
KANSL1L RPL37A  CCDC72  RNF123  C3orf78 ABTB1   RPL35A  GAK     MXD4    LAMTOR3
PAPSS1  SMARCA5 CTSO    TMA16   TXNDC15 SOX9    SLC35A4 FBXO38  ARMC12  MRPL2
TDRD6   HMGN3   GTF3C6  C7orf26 NDUFA4  MRPS24  SEC61G  ECD     BRI3    ATP5J2  POP7
ZNF800  SLC13A4 NDUFB2  ZNF746  MCPH1   KAT6A   UBE2V2  MRPS35  C8orf59 NDUFB9  IL33
C9orf123        COL15A1 SLC31A1 RC3H2   RSU1    KIAA0913        C10orf11
EIF5AL1 USMG5   PPIAP19 AP2A2   C11orf10        FADS2   COX8A   VEGFB   PRDX5   FAU
PCNXL3  RELA    PPP6R3  PKNOX2  COX14   TENC1   NDUFA12 C12orf73        ULK1    DAD1
MRPL52  ADCY4   RPS29   FRMD6   PPM1A   ERH     ZFYVE1  NEK9    SLIRP   NDUFB1
VPS39   RPL4    IMP3    NPRL3   NDUFB10 FLYWCH2 SETD1A  COX4I1  ZC3H18  PSMB6
TXNDC17 CTC1    RPS7P1  GIT1    RASL10B RPL27   HDAC5   ITGA2B  PLEKHM1 NFE2L1
```

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CALCOCO2        PPM1D   RPL38   ATP5H   LLGL2   C17orf89        MYL12B  GALNT1
CTDP1   C19orf35        SAFB    XAB2    MRPL4   CC2D1A  MAST3   MAU2    LPAR2
ATP13A1 COX6B1  PSENEN  BLVRB   TMEM91  PPP6R1  PLCG1   RPS21   CABIN1  TPST2
SNORD125        PLA2G6  TUBGCP6 SMS     EEF1B2P3        COX7B   NDUFA1  APLN
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      7.98769694576923e-15    22.5356125356125        0.87689433257214
15      96      respiratory electron transport chain
GO:0022900      7.61119557949721e-14    16.5996493278784        1.22399833921528
16      134     electron transport chain
GO:0045333      2.9378183147757e-12     14.3266707046235        1.29707286692962
15      142     cellular respiration
GO:0015980      1.9929231767191e-08     6.64912904372556        2.80423500103799
16      307     energy derivation by oxidation of organic compounds
GO:0006120      3.02707805738153e-08    27.5944827586207        0.328835374714553
7       36      mitochondrial electron transport, NADH to ubiquinone
GO:0006415      1.40107317860821e-07    12.7040452111838        0.831222752750675
9       91      translational termination
GO:0042773      2.09804652824833e-07    19.9906 0.429312850321777       7       47
ATP synthesis coupled electron transport
GO:0042775      2.09804652824833e-07    19.9906 0.429312850321777       7       47
mitochondrial ATP synthesis coupled electron transport
GO:0006091      3.57086772064615e-07    5.00234846080609        3.90948723271746
17      428     generation of precursor metabolites and energy
GO:0006414      4.82418233945863e-07    10.8407012195122        0.959103176250778
9       105     translational elongation
GO:0006614      4.82418233945863e-07    10.8407012195122        0.959103176250778
9       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      5.23145762962558e-07    10.7281870756852        0.968237492215072
9       106     cotranslational protein targeting to membrane
GO:0045047      5.23145762962558e-07    10.7281870756852        0.968237492215072
9       106     protein targeting to ER
GO:0072599      5.23145762962558e-07    10.7281870756852        0.968237492215072
9       106     establishment of protein localization to endoplasmic reticulum
GO:0006119      9.22808339435138e-07    15.6668235294118        0.529790325929001
7       58      oxidative phosphorylation
GO:0070972      1.29897347402138e-06    9.53904676661445        1.07784928378659
9       118     protein localization to endoplasmic reticulum
GO:0043624      1.3627953712964e-06     8.12564484695632        1.39755034253685
10      153     cellular protein complex disassembly
GO:0043241      1.82632862887981e-06    7.8483606557377 1.44322192235831        10
158     protein complex disassembly
GO:0034623      4.35335253573461e-06    7.07467013194722        1.589370977787  10
174     cellular macromolecular complex disassembly
GO:0032984      5.60271956255934e-06    6.86293529925308        1.63504255760847
10      179     macromolecular complex disassembly
GO:0019080      9.94819710749006e-06    7.30522157334249        1.37928171060826
9       151     viral genome expression
GO:0019083      9.94819710749006e-06    7.30522157334249        1.37928171060826
9       151     viral transcription
GO:0006413      1.0493523203216e-05     7.25362442435613        1.38841602657256
9       152     translational initiation
GO:0006612      1.1064193692711e-05     7.20274390243902        1.39755034253685
9       153     protein targeting to membrane
GO:0000184      1.3130513094014e-05     8.25806451612903        1.08698359975088
8       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
Tissue: Heart_Left_Ventricle=>Artery_Tibial     Type:   asymmetric
SourceGene:     ENSG00000239899.1
TargetGeneSet:  RPL22   SDHB    RP11    PPIH    MAGOH   PFN1P3  C1orf54 SNRPE   ARV1
RPS7    UBC     CCDC115 BTF3L4P2        HDLBP   SPCS1   CHMP2B  ATG3    MRPS18C BDH2
RPL34   LARP7   TBCA    MRPL22  UBLCP1  RPL26L1 SBDS    C7orf59 DCTN6   SEC61B
SH3PXD2A        POLR2G  SNRPF   TCP11L2 ARPC3   COMMD6  SRP54   C14orf166       ERH
COX16   SNURF   RPS7P1  ARL16   SNRPD1  MIR1181 SNRPB2  RP4     PSMD10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
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GO:0006612      1.27453364898476e-10    31.8526785714286        0.391737596014117
9       153     protein targeting to membrane
GO:0006614      1.92211993322925e-10    40.7166725915393        0.268839526676355
8       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      2.07530277581746e-10    40.2983814215341        0.271399903120891
8       106     cotranslational protein targeting to membrane
GO:0045047      2.07530277581746e-10    40.2983814215341        0.271399903120891
8       106     protein targeting to ER
GO:0072599      2.07530277581746e-10    40.2983814215341        0.271399903120891
8       106     establishment of protein localization to endoplasmic reticulum
GO:0070972      4.92673214021216e-10    35.8721003134796        0.302124420455332
8       118     protein localization to endoplasmic reticulum
GO:0000377      3.73574243788099e-08    20.0112596762843        0.522316794685489
8       204     RNA splicing, via transesterification reactions with bulged
adenosine as nucleophile
GO:0000398      3.73574243788099e-08    20.0112596762843        0.522316794685489
8       204     nuclear mRNA splicing, via spliceosome
GO:0072594      3.73574243788099e-08    20.0112596762843        0.522316794685489
8       204     establishment of protein localization to organelle
GO:0000375      4.50877038966395e-08    19.506604906502 0.535118676908172       8
209     RNA splicing, via transesterification reactions
GO:0006605      2.06029408872816e-07    11.1350574712644        1.2136184347104 10
474     protein targeting
GO:0000184      5.1838945958636e-07     24.495004282044 0.304684796899869       6
119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0000387      1.08899456367171e-06    64.5881032547699        0.079371669780638
4       31      spliceosomal snRNP assembly
GO:0008380      1.25349641021633e-06    12.3472359058566        0.827001591585357
8       323     RNA splicing
GO:0019080      2.09657457101439e-06    19.0464961067853        0.386616843125043
6       151     viral genome expression
GO:0019083      2.09657457101439e-06    19.0464961067853        0.386616843125043
6       151     viral transcription
GO:0033365      2.19659825432831e-06    9.66363916256158        1.21105805826586
9       473     protein localization to organelle
GO:0043624      2.26345082545556e-06    18.7847267939434        0.391737596014117
6       153     cellular protein complex disassembly
GO:0043241      2.72856670166277e-06    18.160441426146 0.4045394782368 6       158
protein complex disassembly
GO:0006415      3.29492299643312e-06    26.031976744186 0.232994256452841       5
91      translational termination
GO:0000956      4.02933468661639e-06    16.9218286166634        0.432703619126704
6       169     nuclear-transcribed mRNA catabolic process
GO:0022618      4.07494624917772e-06    24.8680555555556        0.243235762230987
5       95      ribonucleoprotein complex assembly
GO:0034623      4.76791874302665e-06    16.4124423963134        0.445505501349388
6       174     cellular macromolecular complex disassembly
GO:0071826      5.24624360037402e-06    23.5509868421053        0.256037644453671
5       100     ribonucleoprotein complex subunit organization
GO:0006402      5.43504343328772e-06    16.026256564141 0.455747007127534       6
178     mRNA catabolic process
GO:0032984      5.61316103833135e-06    15.932500466157 0.458307383572071       6
179     macromolecular complex disassembly
GO:0006397      6.02270326970651e-06    9.89364141458682        1.02159020137015
8       399     mRNA processing
GO:0006414      6.66670912870521e-06    22.365625       0.268839526676355       5
105     translational elongation
GO:0006401      1.22025309393652e-05    13.8255795104555        0.524877171130026
6       205     RNA catabolic process
Tissue: Heart_Left_Ventricle=>Artery_Tibial     Type:   asymmetric
SourceGene:     LINC00342(ENSG00000232931.1)
TargetGeneSet:  TTLL10  RPL11   ATPIF1  BEND5   HSD17B7 NTSR2   RPL31   RPL37A
RPL32   RPL10AP6        RP11    ATP5I   RPL37   RPS23   RPS18   RPL10A  RPL39P3
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TSPYL4  C7orf50 FTSJ2   RPL30   RPS24   PIK3AP1 RPL13AP5        RPS10P18
RPLP2   FAU     C11orf51        SNORD15A        RPS25   SAP18   RPS26P47
RNASE3  RPS29   BATF    HMGN2P5 IGSF6   SNORA70D        C17orf108       RPL27   SMG8
RPL38   ZNF77   B3GNT3  RPS11   CHMP2A  EEF1B2P3        RPS23P8
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0000184      7.42719078799523e-30    170.10297029703 0.271745899937721       18
119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006415      8.52135771726807e-30    205.952702702703        0.207805688187669
17      91      translational termination
GO:0006414      1.19774132786802e-28    173.018465909091        0.239775794062695
17      105     translational elongation
GO:0006614      1.19774132786802e-28    173.018465909091        0.239775794062695
17      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.42502169615293e-28    171.0625        0.242059373053768       17
106     cotranslational protein targeting to membrane
GO:0045047      1.42502169615293e-28    171.0625        0.242059373053768       17
106     protein targeting to ER
GO:0072599      1.42502169615293e-28    171.0625        0.242059373053768       17
106     establishment of protein localization to endoplasmic reticulum
GO:0070972      1.00710139228052e-27    150.612004950495        0.269462320946647
17      118     protein localization to endoplasmic reticulum
GO:0006401      2.26457001719109e-27    103.84331797235 0.468133693170023       19
205     RNA catabolic process
GO:0000956      5.91341668537133e-27    113.380132450331        0.385924849491385
18      169     nuclear-transcribed mRNA catabolic process
GO:0006402      1.56630778630558e-26    106.935 0.406477060411044       18      178
mRNA catabolic process
GO:0019080      8.4719982604753e-26     113.259328358209        0.344820427652066
17      151     viral genome expression
GO:0019083      8.4719982604753e-26     113.259328358209        0.344820427652066
17      151     viral transcription
GO:0006413      9.52877204336302e-26    112.4125        0.347104006643139       17
152     translational initiation
GO:0006612      1.07085505506166e-25    111.578125      0.349387585634212       17
153     protein targeting to membrane
GO:0043624      1.07085505506166e-25    111.578125      0.349387585634212       17
153     cellular protein complex disassembly
GO:0043241      1.89674334653211e-25    107.583776595745        0.360805480589579
17      158     protein complex disassembly
GO:0034623      1.04633766693221e-24    96.5115445859873        0.397342744446751
17      174     cellular macromolecular complex disassembly
GO:0032984      1.72447333136711e-24    93.5    0.408760639402117       17      179
macromolecular complex disassembly
GO:0072594      1.71120873279172e-23    80.8579545454545        0.46585011417895
17      204     establishment of protein localization to organelle
GO:0019058      1.4935510238952e-22     70.5221962616822        0.527506746937928
17      231     viral infectious cycle
GO:0022415      1.15837947159721e-21    61.9791666666667        0.593730537679053
17      260     viral reproductive process
GO:0071845      5.30437914201888e-21    56.3125 0.648536433464812       17      284
cellular component disassembly at cellular level
GO:0022411      6.74604316332267e-21    55.4656365313653        0.657670749429105
17      288     cellular component disassembly
GO:0016032      1.38385996314761e-17    34.2350230414747        1.02989412497405
17      451     viral reproduction
GO:0033365      3.0809023528745e-17     32.5320723684211        1.08013286277766
17      473     protein localization to organelle
GO:0006605      3.19206611551764e-17    32.4585612691466        1.08241644176874
17      474     protein targeting
GO:0022613      1.03848533290597e-05    14.4079147640791        0.513805272991488
6       225     ribonucleoprotein complex biogenesis
GO:0071843      1.46423493164358e-05    13.5288507391512        0.545775378866514
6       239     cellular component biogenesis at cellular level
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Tissue: Heart_Left_Ventricle=>Artery_Tibial     Type:   cluster
SourceGene:     MCM9(ENSG00000111877.12)
TargetGeneSet:  TPRG1L  RPL22   RP11    PSMB4   RP4     MIR4426 MRPS9   EEF1B2
XRCC5   RPL37A  RPL32   LSM3    SPCS1   SLC25A26        PLSCR4  KLHL7   EREG
RPL37   RPS23   COX7C   CTB     RPS14   MRPL22  PFDN6   C6orf203        ECD
UQCRB   RPL30   EIF3H   NDUFB9  RPS24   RPL13AP5        CUTC    SH3PXD2A
RPLP2   RPS13   ST13P5  FAU     MRPL11  ATP5L   RPS25   CLECL1  SLC25A3 RPS29
RPL36A  C14orf166       GCH1    SLIRP   RPL4    SEC11A  NAE1    TRAPPC2L
RPL26   GSDMA   PSMD3   TOP2A   RPL38   ICT1    CTD     POLR2I  EIF3K   RPS16   RPS5
CHMP2A  ATP5O   POLR2F  TOMM22  XRCC6   EEF1B2P3        PIN4    NDUFA1  MT
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006614      3.77581317469522e-28    76.4812834224599        0.465019721818559
20      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      4.6403266368115e-28     75.5866807610994        0.469448481073974
20      106     cotranslational protein targeting to membrane
GO:0045047      4.6403266368115e-28     75.5866807610994        0.469448481073974
20      106     protein targeting to ER
GO:0072599      4.6403266368115e-28     75.5866807610994        0.469448481073974
20      106     establishment of protein localization to endoplasmic reticulum
GO:0006415      1.4408454599776e-27     83.945987654321 0.403017092242751       19
91      translational termination
GO:0070972      4.70563162418768e-27    66.2755102040816        0.522593592138952
20      118     protein localization to endoplasmic reticulum
GO:0006612      2.2506420447113e-26     52.7404862579281        0.677600166078472
21      153     protein targeting to membrane
GO:0006414      2.79382704897336e-26    70.2116279069767        0.465019721818559
19      105     translational elongation
GO:0019058      1.31734390049684e-25    38.2407363977486        1.02304338800083
23      231     viral infectious cycle
GO:0019080      8.75518207734649e-25    49.4656488549618        0.668742647567642
20      151     viral genome expression
GO:0019083      8.75518207734649e-25    49.4656488549618        0.668742647567642
20      151     viral transcription
GO:0006413      1.0052200665236e-24     49.0874655647383        0.673171406823057
20      152     translational initiation
GO:0022415      2.10250796483243e-24    33.4928475867037        1.15147740640786
23      260     viral reproductive process
GO:0072594      1.18613646303371e-23    37.9062142584827        0.903466888104629
21      204     establishment of protein localization to organelle
GO:0000184      2.09800801047902e-23    55.3482565647869        0.527022351394367
18      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0043624      5.45992282597877e-23    44.9099502487562        0.677600166078472
19      153     cellular protein complex disassembly
GO:0043241      1.02976878829302e-22    43.2792965627498        0.699743962355546
19      158     protein complex disassembly
GO:0000956      3.86304711295922e-22    40.0745185185185        0.74846031416511
19      169     nuclear-transcribed mRNA catabolic process
GO:0034623      6.83337010906345e-22    38.7681720430108        0.770604110442184
19      174     cellular macromolecular complex disassembly
GO:0006402      1.0648771015588e-21     37.782250174703 0.788319147463843       19
178     mRNA catabolic process
GO:0032984      1.18776931445319e-21    37.5434722222222        0.792747906719258
19      179     macromolecular complex disassembly
GO:0016032      1.53748871462114e-21    21.0078849163356        1.9973704241921 25
451     viral reproduction
GO:0006401      1.64547942256295e-20    32.2364396654719        0.907895647360044
19      205     RNA catabolic process
GO:0071845      3.41452377745716e-19    24.3164600550964        1.25776762853782
20      284     cellular component disassembly at cellular level
GO:0022411      4.50722596817026e-19    23.9467435549525        1.27548266555948
20      288     cellular component disassembly
GO:0033365      4.69806337960388e-16    15.0563387528298        2.09480312781122
21      473     protein localization to organelle
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GO:0006605      4.9014825936731e-16     15.02202371785  2.09923188706664        21
474     protein targeting
GO:0042274      1.02171131577435e-06    68.4428571428571        0.0797176665974673
4       18      ribosomal small subunit biogenesis
GO:0022904      4.03401597916559e-06    16.4333333333333        0.425160888519826
6       96      respiratory electron transport chain
Tissue: Artery_Tibial=>Heart_Left_Ventricle     Type:   asymmetric
SourceGene:     RP11-330O11.2(ENSG00000237135.1)
TargetGeneSet:  LRRC47  RP11    KPNA7   MTMR9LP PKP1    NDUFB3  GRIP2   QRICH1
C3orf18 PSMC1P1 ZDHHC23 FGF12   NDUFS6  PAK1IP1 NUDT3   COX7A2  CYCS    MRPS24
PKD1L1  ATP5J2  HEMGN   GLE1    USMG5   NUMA1   SCARNA11        TMBIM6  PYGL    NPC2
TECPR2  CHTF18  NDUFB10 PARN    ELAC2   EFTUD2  ATP5G1  RNMT    SNRPD1  CYP2T2P
TRAPPC6A        ERCC1   NDUFA3  MKKS    CSTF1   ATP5J   C22orf32        LMF2
ZMYM3   NDUFA1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      1.39504059708167e-12    54.8965517241379        0.239152999792402
9       96      respiratory electron transport chain
GO:0022900      2.9432682968323e-11     38.1066666666667        0.333817728876894
9       134     electron transport chain
GO:0045333      4.97110600141933e-11    35.7944862155388        0.353747145526261
9       142     cellular respiration
GO:0015980      2.5219447117279e-09     18.2828282828283        0.764791363919452
10      307     energy derivation by oxidation of organic compounds
GO:0006120      2.56186638236061e-08    74.8387096774194        0.0896823749221507
5       36      mitochondrial electron transport, NADH to ubiquinone
GO:0006091      5.96347794793088e-08    12.8790945896209        1.06622379074113
10      428     generation of precursor metabolites and energy
GO:0042773      1.02206716530266e-07    55.1958525345622        0.11708532281503
5       47      ATP synthesis coupled electron transport
GO:0042775      1.02206716530266e-07    55.1958525345622        0.11708532281503
5       47      mitochondrial ATP synthesis coupled electron transport
GO:0006119      2.993531095236e-07      43.7066342057212        0.144488270707909
5       58      oxidative phosphorylation
GO:0042776      3.9917922038184e-06     130.954545454545        0.0323853020552211
3       13      mitochondrial ATP synthesis coupled proton transport
GO:0015985      1.12920216089308e-05    87.2727272727273        0.0448411874610754
3       18      energy coupled proton transport, down electrochemical gradient
GO:0015986      1.12920216089308e-05    87.2727272727273        0.0448411874610754
3       18      ATP synthesis coupled proton transport
GO:0090305      1.73993115539579e-05    30.4152542372881        0.156944156113764
4       63      nucleic acid phosphodiester bond hydrolysis
Tissue: Heart_Left_Ventricle=>Artery_Tibial     Type:   asymmetric
SourceGene:     RP11-385D13.1(ENSG00000251537.2)
TargetGeneSet:  RPL11   RP11    RP4     VPS72   PSMB4   IAH1    C2orf28 COX7A2L
BTF3L4P2        RPL32   CMC1    SPCS1   RPL24   NDUFB4  RPL35A  WDFY3-AS1
RPL34   CHCHD2P2        BTF3    RPS23   COX7C   CTB     RPS14   RPS10   MRPL2
PSMB1   NUDT1   DCTN6   RPS20   C8orf59 UQCRB   RPL30   VPS13B  TTC35   NSMCE2
RPS24   RPL27A  RPS13   TSPAN18 MRPL11  ATP5L   RPS25   PFDN5   ATP5G2  SLC25A3
MAPKBP1 C16orf13        RPS15A  TMEM219 RPL26   RPL17   CTD     RPS15   RPL36
C19orf53        EIF3K   SNRPD2  ATP5O   CXorf31 UXT     RPS4X
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006614      2.78776767256928e-33    132.583333333333        0.348764791363919
21      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      3.47026825666604e-33    131.014379084967        0.352086360805481
21      106     cotranslational protein targeting to membrane
GO:0045047      3.47026825666604e-33    131.014379084967        0.352086360805481
21      106     protein targeting to ER
GO:0072599      3.47026825666604e-33    131.014379084967        0.352086360805481
21      106     establishment of protein localization to endoplasmic reticulum
GO:0006415      1.4981523225137e-32     144.185110663984        0.302262819182064
20      91      translational termination
GO:0070972      4.06470290988334e-32    114.710194730813        0.391945194104214
21      118     protein localization to endoplasmic reticulum
```

GO:0006414	3.52471816938722e-31	120.319327731092	0.348764791363919	20	105	translational elongation
GO:0000184	5.34369164096264e-30	103.203463203463	0.395266763545775	20	119	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006413	1.21526158742964e-29	84.7362171331637	0.504878555117293	21	152	translational initiation
GO:0006612	1.40606205506072e-29	84.0883838383838	0.508200124558854	21	153	protein targeting to membrane
GO:0019080	8.58322204781122e-28	77.8189749182116	0.501556985675732	20	151	viral genome expression
GO:0019083	8.58322204781122e-28	77.8189749182116	0.501556985675732	20	151	viral transcription
GO:0043624	1.13276567279339e-27	76.6380236305048	0.508200124558854	20	153	cellular protein complex disassembly
GO:0043241	2.22867395160935e-27	73.8354037267081	0.52480797176666	20	158	protein complex disassembly
GO:0072594	7.82600038625716e-27	60.4371584699454	0.677600166078472	21	204	establishment of protein localization to organelle
GO:0000956	9.1346235840105e-27	68.3317353787153	0.561345235623832	20	169	nuclear-transcribed mRNA catabolic process
GO:0034623	1.6791184182238e-26	66.0899814471243	0.577953082831638	20	174	cellular macromolecular complex disassembly
GO:0006402	2.69629863716682e-26	64.3987341772152	0.591239360597883	20	178	mRNA catabolic process
GO:0032984	3.0297912127465e-26	63.989218328841	0.594560930039444	20	179	macromolecular complex disassembly
GO:0006401	5.02452753202794e-25	54.8957528957529	0.680921735520033	20	205	RNA catabolic process
GO:0019058	5.82542280477427e-24	48.0433310765064	0.767282541000623	20	231	viral infectious cycle
GO:0022415	6.47182437736391e-23	42.1517857142857	0.863608054805896	20	260	viral reproductive process
GO:0071845	3.8594136907233e-22	38.2548701298701	0.943325721403363	20	284	cellular component disassembly at cellular level
GO:0022411	5.11642205134461e-22	37.6732409381663	0.956611999169608	20	288	cellular component disassembly
GO:0016032	5.84405441841655e-21	27.5621301775148	1.49802781814407	22	451	viral reproduction
GO:0033365	4.14480729927265e-19	24.006145526057	1.57110234585842	21	473	protein localization to organelle
GO:0006605	4.3289800511741e-19	23.9514348785872	1.57442391529998	21	474	protein targeting
GO:0022613	4.53557893831128e-08	15.1570512820513	0.747353124351256	9	225	ribonucleoprotein complex biogenesis
GO:0071843	7.61773941984215e-08	14.2204013377926	0.793855096533112	9	239	cellular component biogenesis at cellular level
GO:0042274	3.168047146843e-07	93.4350649350649	0.0597882499481005	4	18	ribosomal small subunit biogenesis
GO:0042254	5.55893644049581e-07	17.1465132256956	0.49491384679261	7	149	ribosome biogenesis
GO:0022904	7.19167981058667e-07	22.7190476190476	0.318870666389869	6	96	respiratory electron transport chain
GO:0006364	1.15384517465125e-06	20.8527696793003	0.345443221922358	6	104	rRNA processing
GO:0016072	1.60448419455537e-06	19.6414835164835	0.365372638571725	6	110	rRNA metabolic process
GO:0022900	5.06430411526244e-06	15.9319196428571	0.445090305169192	6	134	electron transport chain
GO:0045333	7.07551797530415e-06	14.9863445378151	0.471662860701682	6	142	cellular respiration
GO:0042273	7.40932461213239e-06	106.622222222222	0.0398588332987337	3	12	ribosomal large subunit biogenesis

Tissue: Heart_Left_Ventricle=>Artery_Tibial	Type:	cluster

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SourceGene:     RP11-385D13.1(ENSG00000251537.2)
TargetGeneSet:  RPL11   RP11    RP4     VPS72   PSMB4   IAH1    C2orf28 COX7A2L
BTF3L4P2        RPL32   CMC1    SPCS1   RPL24   NDUFB4  RPL35A  WDFY3-AS1
RPL34   CHCHD2P2        BTF3    RPS23   COX7C   CTB     RPS14   RPS10   MRPL2
PSMB1   NUDT1   DCTN6   RPS20   C8orf59 UQCRB   RPL30   VPS13B  TTC35   NSMCE2
RPS24   RPL27A  RPS13   TSPAN18 MRPL11  ATP5L   RPS25   PFDN5   ATP5G2  SLC25A3
MAPKBP1 C16orf13        RPS15A  TMEM219 RPL26   RPL17   CTD     RPS15   RPL36
C19orf53        EIF3K   SNRPD2  ATP5O   CXorf31 UXT     RPS4X
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006614      2.78776767256928e-33    132.583333333333        0.348764791363919
21      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      3.47026825666604e-33    131.014379084967        0.352086360805481
21      106     cotranslational protein targeting to membrane
GO:0045047      3.47026825666604e-33    131.014379084967        0.352086360805481
21      106     protein targeting to ER
GO:0072599      3.47026825666604e-33    131.014379084967        0.352086360805481
21      106     establishment of protein localization to endoplasmic reticulum
GO:0006415      1.4981523225137e-32     144.185110663984        0.302262819182064
20      91      translational termination
GO:0070972      4.06470290988334e-32    114.710194730813        0.391945194104214
21      118     protein localization to endoplasmic reticulum
GO:0006414      3.52471816938722e-31    120.319327731092        0.348764791363919
20      105     translational elongation
GO:0000184      5.34369164096264e-30    103.203463203463        0.395266763545775
20      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006413      1.21526158742964e-29    84.7362171331637        0.504878555117293
21      152     translational initiation
GO:0006612      1.40606205506072e-29    84.0883838383838        0.508200124558854
21      153     protein targeting to membrane
GO:0019080      8.58322204781122e-28    77.8189749182116        0.501556985675732
20      151     viral genome expression
GO:0019083      8.58322204781122e-28    77.8189749182116        0.501556985675732
20      151     viral transcription
GO:0043624      1.13276567279339e-27    76.6380236305048        0.508200124558854
20      153     cellular protein complex disassembly
GO:0043241      2.22867395160935e-27    73.8354037267081        0.52480797176666
20      158     protein complex disassembly
GO:0072594      7.82600038625716e-27    60.4371584699454        0.677600166078472
21      204     establishment of protein localization to organelle
GO:0000956      9.1346235840105e-27     68.3317353787153        0.561345235623832
20      169     nuclear-transcribed mRNA catabolic process
GO:0034623      1.6791184182238e-26     66.0899814471243        0.577953082831638
20      174     cellular macromolecular complex disassembly
GO:0006402      2.69629863716682e-26    64.3987341772152        0.591239360597883
20      178     mRNA catabolic process
GO:0032984      3.0297912127465e-26     63.989218328841 0.594560930039444       20
179     macromolecular complex disassembly
GO:0006401      5.02452753202794e-25    54.8957528957529        0.680921735520033
20      205     RNA catabolic process
GO:0019058      5.82542280477427e-24    48.0433310765064        0.767282541000623
20      231     viral infectious cycle
GO:0022415      6.47182437736391e-23    42.1517857142857        0.863608054805896
20      260     viral reproductive process
GO:0071845      3.8594136907233e-22     38.2548701298701        0.943325721403363
20      284     cellular component disassembly at cellular level
GO:0022411      5.11642205134461e-22    37.6732409381663        0.956611999169608
20      288     cellular component disassembly
GO:0016032      5.84405441841655e-21    27.5621301775148        1.49802781814407
22      451     viral reproduction
GO:0033365      4.14480729927265e-19    24.006145526057 1.57110234585842        21
473     protein localization to organelle
GO:0006605      4.3289800511741e-19     23.9514348785872        1.57442391529998
21      474     protein targeting
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GO:0022613      4.53557893831128e-08    15.1570512820513        0.747353124351256
9       225     ribonucleoprotein complex biogenesis
GO:0071843      7.61773941984215e-08    14.2204013377926        0.793855096533112
9       239     cellular component biogenesis at cellular level
GO:0042274      3.168047146843e-07      93.4350649350649        0.0597882499481005
4       18      ribosomal small subunit biogenesis
GO:0042254      5.55893644049581e-07    17.1465132256956        0.49491384679261
7       149     ribosome biogenesis
GO:0022904      7.19167981058667e-07    22.7190476190476        0.318870666389869
6       96      respiratory electron transport chain
GO:0006364      1.15384517465125e-06    20.8527696793003        0.345443221922358
6       104     rRNA processing
GO:0016072      1.60448419455537e-06    19.6414835164835        0.365372638571725
6       110     rRNA metabolic process
GO:0022900      5.06430411526244e-06    15.9319196428571        0.445090305169192
6       134     electron transport chain
GO:0045333      7.07551797530415e-06    14.9863445378151        0.471662860701682
6       142     cellular respiration
GO:0042273      7.40932461213239e-06    106.622222222222        0.0398588332987337
3       12      ribosomal large subunit biogenesis
Tissue: Heart_Left_Ventricle=>Artery_Tibial     Type:   cluster
SourceGene:     RP11-6O2.3(ENSG00000261616.1)
TargetGeneSet:  MEGF6   ATPIF1  SNORA16A        SNRNP40 TCHH    EIF5B   PAX8
FMNL2   EEF1B2  RPL37A  RPL32   LSM3    KIF9    RP11    CCDC72  MRPS18C LARP7
RPL37   RPS23   CTB     MRPL2   C6orf203        C7orf50 TOMM7   CPVL    TRGV10  ECD
ATP5J2  PMS2P1  SSBP1   BRF2    NDUFB9  LINC00032       FXN     RPL35   MRC1
RPL13AP5        IMMP1L  MS4A7   CTD     FAU     BARX2   PSMC1P9 SAP18   RPL13AP25
STK24-AS1       RPS29   SLIRP   NDUFB1  IGHV3-7 HMGN2P5 MEFV    UBE2MP1 MTHFSD
TRAPPC2L        RPL38   PPP4R1  SERPINB7        C19orf70        COX6B1  NDUFA3
PSMF1   RPS21   SNRPD3  POLR2F  TOMM22  RRP7A   PARVG   RP6     EEF1B2P3
RGAG1   NDUFA1  RP13
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      3.98314419680397e-12    35.0134638922889        0.385094457130994
10      105     translational elongation
GO:0000956      2.01102768541235e-11    23.6045810729355        0.619818697667981
11      169     nuclear-transcribed mRNA catabolic process
GO:0006402      3.53363687110955e-11    22.3183632734531        0.652826793993495
11      178     mRNA catabolic process
GO:0006415      3.66938032653629e-11    35.7106430155211        0.333748529513528
9       91      translational termination
GO:0006614      1.35366372521252e-10    30.4730113636364        0.385094457130994
9       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.4751918093616e-10     30.156747891284 0.388762023389385       9
106     cotranslational protein targeting to membrane
GO:0045047      1.4751918093616e-10     30.156747891284 0.388762023389385       9
106     protein targeting to ER
GO:0072599      1.4751918093616e-10     30.156747891284 0.388762023389385       9
106     establishment of protein localization to endoplasmic reticulum
GO:0019080      1.52571484891548e-10    23.5147616691407        0.553802505016954
10      151     viral genome expression
GO:0019083      1.52571484891548e-10    23.5147616691407        0.553802505016954
10      151     viral transcription
GO:0072594      1.53781885538094e-10    19.2764618800888        0.748183516711646
11      204     establishment of protein localization to organelle
GO:0006401      1.62064477386812e-10    19.1757486499755        0.751851082970037
11      205     RNA catabolic process
GO:0006413      1.62871361935406e-10    23.3475270226007        0.557470071275344
10      152     translational initiation
GO:0006612      1.73786559763246e-10    23.1826313221662        0.561137637533735
10      153     protein targeting to membrane
GO:0070972      3.8857989319948e-10     26.8142201834862        0.43277281849007
9       118     protein localization to endoplasmic reticulum
GO:0000184      4.19215804296945e-10    26.5685950413223        0.43644038474846
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9       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0043624      3.93107983477693e-09    20.2471590909091        0.561137637533735
9       153     cellular protein complex disassembly
GO:0043241      5.21875967628323e-09    19.5608602806589        0.579475468825687
9       158     protein complex disassembly
GO:0019058      9.58092578263479e-09    14.9184468062717        0.847207805688188
10      231     viral infectious cycle
GO:0034623      1.21573298519984e-08    17.6442148760331        0.638156528959934
9       174     cellular macromolecular complex disassembly
GO:0032984      1.5565729221242e-08     17.1192513368984        0.656494360251886
9       179     macromolecular complex disassembly
GO:0022415      2.95291480224285e-08    13.1609302325581        0.95356722718151
10      260     viral reproductive process
GO:0016032      5.65316012502317e-07    8.30833333333333        1.65407238253408
11      451     viral reproduction
GO:0071845      8.00505984618337e-07    10.5047107438017        1.04158881738288
9       284     cellular component disassembly at cellular level
GO:0045333      8.05893126774758e-07    16.0774557165862        0.52079440869144
7       142     cellular respiration
GO:0022411      8.99494055057545e-07    10.3511730205279        1.05625908241644
9       288     cellular component disassembly
GO:0033365      9.04296479496618e-07    7.90022675736961        1.73475884021867
11      473     protein localization to organelle
GO:0006605      9.23262607950261e-07    7.88259796359148        1.73842640647706
11      474     protein targeting
GO:0022904      1.30995586247285e-06    20.2950354609929        0.352086360805481
6       96      respiratory electron transport chain
GO:0006119      2.16324166921229e-06    28.1937893081761        0.212718842986645
5       58      oxidative phosphorylation
GO:0006120      8.7062961231538e-06     36.6479591836735        0.132032385302055
4       36      mitochondrial electron transport, NADH to ubiquinone
GO:0022900      9.12150819894347e-06    14.2320478723404        0.491453878624317
6       134     electron transport chain
Tissue: Heart_Left_Ventricle=>Artery_Tibial     Type:   asymmetric
SourceGene:     RP11-881M11.4(ENSG00000256196.1)
TargetGeneSet:  RP1     PPIH    RP11    RP4     HSD3BP5 MRPS21  PSMB4   S100A6  PMF1
ACBD6   DHX9    NENF    RPS7    ROCK2   GTF3C2  MCEE    EXOC6B  DGUOK   RNF181
RPL31   MAP4K4  SMARCAL1        HDLBP   THUMPD3 RPL32   TBC1D5  THRB-IT1
TMEM89  VPRBP   SPCS1   NDUFB4  ZBTB38  UBQLN4P1        UBE2V1P2        RPL35A
TMEM128 RPL34   EXOSC9  NDUFC1  FRG1    CDK7    COL4A3BP        CTD     MAN2A1  PDF
ATOX1   RPL26L1 HIVEP1  APOM    CSNK2B  TAF11   PEX6    MRPL2   C6orf72 ARID1B
C6orf70 PSMB1   CHCHD2  SBDS    NSUN5   TRRAP   C7orf59 PMS2P1  FIS1    SH2B2
ST7-AS1 ARF5    KAT6A   C8orf40 RPL10AP2        CHCHD7  C8orf59 RBM12B  DCTN3
SEC61B  STX17   AKAP2   KIF20B  FAM204A METTL10 TMEM80  RPL27A  RPS13   POLR2G
OTUB1   KLC2    GAL     ATP5L   DAZAP2  WIBG    SSH1    RPS7P10 MED4-AS1
FANCM   RPS29   TCF12   COMMD4  CPEB1   KIF22   DDX19B  ZNF18   C17orf108
PGAP3   RPL27   MRPS23  BRIP1   C17orf90        C18orf21        C19orf79        BRD4
ZNF226  SNRPD2  RPS11   C19orf48        ZNF611  NLRP9   TRAPPC2 ZNF530  ZNF552
ZNF256  MT1P3   MMP24   SNHG11  IFT52   SLC35C2 USP16   IGLV1-41        EBP     RBM3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006614      1.01827296410455e-13    25.518849752339 0.668465850114179       13
105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.15469488928884e-13    25.2426840887437        0.674832191543838
13      106     cotranslational protein targeting to membrane
GO:0045047      1.15469488928884e-13    25.2426840887437        0.674832191543838
13      106     protein targeting to ER
GO:0072599      1.15469488928884e-13    25.2426840887437        0.674832191543838
13      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      4.74744411074256e-13    22.3389993972272        0.751228288699744
13      118     protein localization to endoplasmic reticulum
GO:0019080      6.29003231242625e-13    18.632603406326 0.961317555878486       14
151     viral genome expression
GO:0019083      6.29003231242625e-13    18.632603406326 0.961317555878486       14
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151     viral transcription
GO:0000184      1.15281512984895e-11    19.9794392523364        0.757594630129403
12      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006415      1.175221973048e-11      24.2390432098765        0.579337070098955
11      91      translational termination
GO:0006612      1.36550618939728e-11    16.7131103074141        0.974050238737804
13      153     protein targeting to membrane
GO:0072594      3.82294072612714e-11    13.385020242915 1.2987336516504 14      204
establishment of protein localization to organelle
GO:0000956      4.82346741374753e-11    14.9820675105485        1.07591170161235
13      169     nuclear-transcribed mRNA catabolic process
GO:0006414      5.7552382341731e-11     20.6087470449173        0.668465850114179
11      105     translational elongation
GO:0006402      9.26646282702262e-11    14.1558879938627        1.13320877447927
13      178     mRNA catabolic process
GO:0019058      2.00447753500612e-10    11.697270471464 1.47062487025119        14
231     viral infectious cycle
GO:0043624      2.25052217805629e-10    15.1255319148936        0.974050238737804
12      153     cellular protein complex disassembly
GO:0043241      3.27283440030383e-10    14.602397260274 1.0058819458861 12      158
protein complex disassembly
GO:0006401      5.37465029970302e-10    12.1420754219409        1.30509999308006
13      205     RNA catabolic process
GO:0022415      9.47557506538276e-10    10.2971648947259        1.6552487717113 14
260     viral reproductive process
GO:0034623      9.98440746345093e-10    13.1453703703704        1.10774340876064
12      174     cellular macromolecular complex disassembly
GO:0032984      1.38225142147504e-09    12.7473053892216        1.13957511590893
12      179     macromolecular complex disassembly
GO:0016032      3.06268020579448e-09    7.2726574500768 2.87121998477614        17
451     viral reproduction
GO:0006413      3.13538362690941e-09    13.6938972068996        0.967683897308145
11      152     translational initiation
GO:0071845      2.3556966040621e-07     7.76856617647059        1.80804096602311
12      284     cellular component disassembly at cellular level
GO:0022411      2.73821998260101e-07    7.65380434782609        1.83350633174175
12      288     cellular component disassembly
GO:0033365      1.62631130964055e-06    5.43545053348975        3.01127949622863
14      473     protein localization to organelle
GO:0006605      1.66720723715982e-06    5.42324414715719        3.01764583765829
14      474     protein targeting
Tissue: Heart_Left_Ventricle=>Artery_Tibial     Type:   cluster
SourceGene:     RP4-631H13.6(ENSG00000230953.1)
TargetGeneSet:  RPL22   RPL11   TRAPPC3 MED8    RP11    RP4     CTSS    RPS27   DPM3
RPS7    UBC     MITD1   RAMP1   RPL29   KCTD6   RPL35A  TACC3   GRPEL1  RPL34
RPS3A   ZCCHC9  UBE2D2  CTB     HMMR    PRELID1 PRL     C2      RPS10   RPL10A  RPF2
RPS3AP26        C7orf59 FNTA    FBXL6   RPS6    TUSC1   SWI5    RPS3AP5 KAZALD1
FBXL15  C10orf137       RPL27A  RPS13   FAU     CCDC85B TMEM126A        EMG1    RPL6
LINC00417       POMP    ERH     FMN1    RPS3AP6 NUBP2   RPS15A  NSMCE1  BCL7C   CTU2
RPL26   RPL23A  RPL17   KRT13   GOSR2   CTD     RPL36   RYR1    RPS16   RPL18
ZNF133  RANBP1  UXT
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      3.68277265270592e-36    127.479102167183        0.384125666043872
23      91      translational termination
GO:0006414      1.48312179992786e-34    105.611039794608        0.443221922358314
23      105     translational elongation
GO:0006614      1.48312179992786e-34    105.611039794608        0.443221922358314
23      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.88930212116187e-34    104.331325301205        0.447443083523632
23      106     cotranslational protein targeting to membrane
GO:0045047      1.88930212116187e-34    104.331325301205        0.447443083523632
23      106     protein targeting to ER
GO:0072599      1.88930212116187e-34    104.331325301205        0.447443083523632
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23      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      2.86047310536738e-33    91.0761772853186        0.498097017507439
23      118     protein localization to endoplasmic reticulum
GO:0000184      3.53679202202736e-33    90.1211622807018        0.502318178672756
23      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      1.2975108437028e-30     67.4395559210526        0.637395335962909
23      151     viral genome expression
GO:0019083      1.2975108437028e-30     67.4395559210526        0.637395335962909
23      151     viral transcription
GO:0006413      1.52496023742732e-30    66.9120767033864        0.641616497128226
23      152     translational initiation
GO:0006612      1.79019432167935e-30    66.3927125506073        0.645837658293544
23      153     protein targeting to membrane
GO:0043624      1.79019432167935e-30    66.3927125506073        0.645837658293544
23      153     cellular protein complex disassembly
GO:0043241      3.92432840569913e-30    63.911306042885 0.66694346412013        23
158     protein complex disassembly
GO:0000956      2.01266739516958e-29    59.0504686373468        0.71337623693862
23      169     nuclear-transcribed mRNA catabolic process
GO:0072594      3.72057301998404e-29    51.2072072072072        0.861116877724725
24      204     establishment of protein localization to organelle
GO:0034623      4.07350845599307e-29    57.0751132798885        0.734482042765207
23      174     cellular macromolecular complex disassembly
GO:0006402      7.04843933636908e-29    55.5865874363328        0.751366687426476
23      178     mRNA catabolic process
GO:0032984      8.06702076175517e-29    55.226383265857 0.755587848591793       23
179     macromolecular complex disassembly
GO:0006401      2.07564556529311e-27    47.2504337767496        0.865338038890042
23      205     RNA catabolic process
GO:0019058      3.51439709011963e-26    41.268471659919 0.975088229188292       23
231     viral infectious cycle
GO:0071845      1.2870944248384e-25     35.2515592515593        1.19880977095011
24      284     cellular component disassembly at cellular level
GO:0022411      1.80817577907636e-25    34.7076167076167        1.21569441561138
24      288     cellular component disassembly
GO:0022415      5.64206211747876e-25    36.1446813235621        1.09750190298249
23      260     viral reproductive process
GO:0033365      5.24664523475711e-23    23.1714924896133        1.99660923119507
26      473     protein localization to organelle
GO:0006605      5.53778955384153e-23    23.118112244898 2.00083039236039        26
474     protein targeting
GO:0016032      8.15064581497228e-21    21.2109627191594        1.90374368555809
24      451     viral reproduction
GO:0006364      2.58623905985937e-07    19.1009927453226        0.439000761192997
7       104     rRNA processing
GO:0016072      3.79862200443738e-07    17.9807623157138        0.464327728184901
7       110     rRNA metabolic process
GO:0042274      8.41122338662158e-07    72.0601503759399        0.075980900975711
4       18      ribosomal small subunit biogenesis
GO:0034470      1.83839607117553e-06    11.1619496855346        0.844232233063456
8       200     ncRNA processing
GO:0042254      2.94517320801079e-06    13.0067814293166        0.628953013632275
7       149     ribosome biogenesis
GO:0022613      4.41542322260067e-06    9.85862098947918        0.949761262196388
8       225     ribonucleoprotein complex biogenesis
GO:0071843      6.88629834733271e-06    9.25198072367884        1.00885751851083
8       239     cellular component biogenesis at cellular level
GO:0042273      1.53240389507124e-05    82.6494252873563        0.0506539339838073
3       12      ribosomal large subunit biogenesis
Tissue: Heart_Left_Ventricle=>Artery_Tibial     Type:   cluster
SourceGene:     SGK3(ENSG00000104205.7)
TargetGeneSet:  SSU72   RPL22   RPL11   TRNAU1AP        SERINC2 RP1     RP11
MAGOH   RP4     MRPS21  RPS27   SNRPE   ARF1    RPL35P1 FTH1P3  UBC     DGUOK
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RPL31 MZT2B ARPC4 RPL32 RPL14 RPL10AP6 SENP7 RPL24 RPL35A
RPL34 BTF3 TBCA RPS23 ATG12 CTD RPS14 RDBP RPS18 RPS10
TAF11 RPL10A MRPS12 RPA3 TOMM7 C7orf59 RPS20 C8orf59 RPL30 SEC61B
RPL13AP5 BUB3 RPL27A C11orf58 RPS13 C11orf10 FAU
MRPL11 RPS25 C12orf57 PFDN5 CCDC59 RPL18AP3 GPN3 SRSF9
ARL6IP4 KIAA1704 RPL13AP25 COMMD6 PPP2R3C RPS29 RPL36A ERH
RPL7AP6 DYNC1H1 RSL24D1 RPLP1 IST1 RPS7P1 RPL17 RPL19 RPL27 ACBD4
RPL38 RPS15 RPL36 FBXL12 WDR83OS RPL18A UBA52 SNRPA RPS19 SNRPD2
RPL18 RPS11 RPS9 RPS5 SLC27A5 MT1P3 RPS21 UXT RRAGB RPS23P8 PIN4
XIST FAM127B

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0006415	1.57455419803483e-63	239.29674796748	0.491177081170853	37	91	translational termination
GO:0006414	5.78022036667412e-63	202.846268656716	0.566742785966369	38	105	translational elongation
GO:0006614	5.78022036667412e-63	202.846268656716	0.566742785966369	38	105	SRP-dependent cotranslational protein targeting to membrane
GO:0006613	8.98587057611901e-63	199.849264705882	0.572140336308906	38	106	cotranslational protein targeting to membrane
GO:0045047	8.98587057611901e-63	199.849264705882	0.572140336308906	38	106	protein targeting to ER
GO:0072599	8.98587057611901e-63	199.849264705882	0.572140336308906	38	106	establishment of protein localization to endoplasmic reticulum
GO:0070972	1.23164253147627e-60	169.729375	0.636910940419348	38	118	protein localization to endoplasmic reticulum
GO:0000184	1.80453127497669e-60	167.622222222222	0.642308490761885	38	119	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080	5.40186848028664e-58	127.330357142857	0.815030101723064	39	151	viral genome expression
GO:0019083	5.40186848028664e-58	127.330357142857	0.815030101723064	39	151	viral transcription
GO:0006612	1.17324426745036e-55	117.78347826087	0.825825202408138	38	153	protein targeting to membrane
GO:0000956	8.25130701679587e-54	103.281679389313	0.912186007888727	38	169	nuclear-transcribed mRNA catabolic process
GO:0006413	1.0166946493539e-53	111.886744432662	0.820427652065601	37	152	translational initiation
GO:0043624	1.33724293941541e-53	110.914423885618	0.825825202408138	37	153	cellular protein complex disassembly
GO:0043241	5.10614434635478e-53	106.293892360411	0.852812954120822	37	158	protein complex disassembly
GO:0006402	7.39965128898052e-53	96.5810714285714	0.960763960971559	38	178	mRNA catabolic process
GO:0072594	2.62428925183606e-52	86.1090909090909	1.10110026987752	39	204	establishment of protein localization to organelle
GO:0034623	2.73344903640097e-51	93.7746127826242	0.939173759601412	37	174	cellular macromolecular complex disassembly
GO:0032984	8.70764332879594e-51	90.4409137753349	0.966161511314096	37	179	macromolecular complex disassembly
GO:0006401	2.68274690096029e-50	80.8125748502994	1.10649782022005	38	205	RNA catabolic process
GO:0019058	5.04178657435553e-50	73.859375	1.24683412912601	39	231	viral infectious cycle
GO:0022415	7.01197806148395e-48	64.0361990950226	1.40336308905958	39	260	viral reproductive process
GO:0071845	7.98676431043288e-43	51.6107435568283	1.53290429728046	37	284	cellular component disassembly at cellular level
GO:0022411	1.37307247233716e-42	50.7738800893985	1.55449449865061	37	288	cellular component disassembly
GO:0016032	9.51183752138724e-40	35.7587399154821	2.43429520448412	40	451	viral reproduction
GO:0033365	2.16702394685727e-37	32.1175115207373	2.55304131201993	39	473	protein localization to organelle

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GO:0006605      2.35489516309937e-37    32.0413793103448        2.55843886236247
39      474     protein targeting
GO:0022613      5.11558695623592e-14    17.489118691156 1.21444882707079        16
225     ribonucleoprotein complex biogenesis
GO:0071843      1.31113260928741e-13    16.3749457543758        1.29001453186631
16      239     cellular component biogenesis at cellular level
GO:0042254      4.15417956967026e-10    16.9354315379624        0.804235001037991
11      149     ribosome biogenesis
GO:0042274      3.26261657760861e-08    75.6585879873551        0.0971559061656633
5       18      ribosomal small subunit biogenesis
GO:0006364      8.47438320281285e-08    16.9964285714286        0.561345235623832
8       104     rRNA processing
GO:0016072      1.31346588354507e-07    15.9899159663866        0.593730537679053
8       110     rRNA metabolic process
GO:0022618      7.66284453746082e-07    16.0043213828425        0.512767282541001
7       95      ribonucleoprotein complex assembly
GO:0071826      1.08642122355679e-06    15.1385733757383        0.539755034253685
7       100     ribonucleoprotein complex subunit organization
GO:0034660      2.93190961612754e-06    7.53903743315508        1.538301847623  10
285     ncRNA metabolic process
GO:0034470      1.19737078681023e-05    8.44107142857143        1.07951006850737
8       200     ncRNA processing
Tissue: Heart_Left_Ventricle=>Artery_Tibial     Type:   asymmetric
SourceGene:     SRPX2(ENSG00000102359.5)
TargetGeneSet:  CHCHD2P6        SPEN    SDHDP1  SRSF4   MECR    SLC2A1  CRTC2   SDHC
RP4     SLC41A1 RP11    ODC1    ITSN2   OST4    MORN2   COX5B   NDUFB3  LSM3
SETD2   LAMB2   DZIP3   NDUFB4  UBA5    OCIAD1  NDUFC1  C4orf27 CCDC111 PDCD6
NIPBL   UQCRQ   SAP30L  FBXW11  NHP2    HNRNPC  FOXP4   HMGN3   GTF2H5  RPA3
NDUFA4  GNG11   ATP5J2  PMS2P1  UBE2V2  DECR1   COX6C   PLIN2   NDUFB6  YBX1P10 DLG5
NDUFB8  PDZD8   RPLP2   C11orf84        MARK2   MRPL11  C11orf51        INPPL1
CLNS1A  DCUN1D5 MLL     PRDM10  SNRPF   MRPS31  SNRPGP14        C14orf2 MNS1
ZNF609  LARP6   AXIN1   CREBBP  NDUFAB1 C1QBP   ARHGAP44        ATP5G1  PPP1R9B ICT1
SPIRE1  SNRPD1  UQCR11  GNA11   NDUFA11 NDUFA7  DNM2    NDUFB7  NDUFA13 COX6B1
CAPNS1  COX7A1  SAMD4B  ARHGAP35        NDUFA3  CDS2    ITCH    SYS1    PCIF1
ATP5E   MRPL40  TCF20   SYAP1   RPS2P55 PDZD11  COX7B   RPL39   NDUFA1  FAM127A
CETN2   MECP2
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      5.39257369326029e-31    67.1895317930893        0.597882499481005
23      96      respiratory electron transport chain
GO:0022900      2.31735939610556e-27    44.0701895925777        0.834544322192236
23      134     electron transport chain
GO:0045333      9.56187231160494e-27    41.0844098833563        0.884367863815653
23      142     cellular respiration
GO:0015980      1.91663543718354e-21    19.2021276595745        1.91197840979863
25      307     energy derivation by oxidation of organic compounds
GO:0006091      4.36092091650197e-19    14.1065764925373        2.66555947685281
26      428     generation of precursor metabolites and energy
GO:0006120      1.53887312940392e-16    79.8460759493671        0.224205937305377
11      36      mitochondrial electron transport, NADH to ubiquinone
GO:0042773      4.2209206802955e-15     55.4061181434599        0.292713307037575
11      47      ATP synthesis coupled electron transport
GO:0042775      4.2209206802955e-15     55.4061181434599        0.292713307037575
11      47      mitochondrial ATP synthesis coupled electron transport
GO:0006119      5.22075051791067e-14    42.4061405871263        0.361220676769774
11      58      oxidative phosphorylation
Tissue: Heart_Left_Ventricle=>Artery_Tibial     Type:   asymmetric
SourceGene:     TMEM209(ENSG00000146842.11)
TargetGeneSet:  MTND1P23        DVL1    MRPL20  PANK4   CTNNBIP1        SNORA59A
ZBTB17  KHDRBS1 RP11    PSMB2   STK40   RP1     PPIH    PRPF38A RP4     LRRC39
MAGI3   PEX11B  MRPS21  SMG5    EDEM3   IVNS1ABP        MIR4426 NUCKS1  INTS7   NENF
TATDN3  NUP133  TOMM20  PXDN    EIF3FP3 STAMBP  DGUOK   RPL31   MAP4K4  CCDC115
PLEKHB2 FMNL2   UBE2V1  WIPF1   SMARCAL1        RPL37A  RNF25   TTLL4   INHA
HDLBP   THUMPD3 RPL32   GOLGA4  ZNF662  KRBOX1  KIF9    PHF7    SPCS1   RPL10AP6
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RPL24   CD200R1 RPL7AP11        FAM86HP ZBTB38  UBQLN4P1        RPL35A  ZNF718
ABCA11P MYL5    TMEM128 DCAF16  SLC30A9 MTHFD2L LARP7   PLK4    OTUD4   WWC2    FRG1
FAM105B RPL37   FBXO4   CTD     RPS23   PPIP5K2 P4HA2   SEC24A  CTB     PDF
RPS14   UBLCP1  BRD2    TAF11   RPL10A  FTSJD2  MRPL2   GSTA4   RPL39P3 HMGN3
RARS2   RSPH4A  TAB2    PHF10   C6orf70 FAM120B TOMM7   PMS2P4  STAG3L4 EIF4H
GTF2IP1 ECD     PMS2P1  ST7-AS1 IMPDH1  TMEM209 SSBP1   SLC4A2  KIAA1967
C8orf40 RPL10AP2        CHCHD7  C8orf44 HNRNPA1P4       C8orf59 RPL30   UTP23
NDUFB9  ERMP1   DCTN3   FAM205A C9orf103        RPS10P3 BICD2   INVS    CDC26
RPL35   SCAI    STXBP1  PPP1R26 CDNF    C1DP1   FGFBP3  RPL13AP5        C10orf12
ACADSB  METTL10 SIRT3   RPLP2   AP2A2   SWAP70  PLEKHA7 PEX16   C11orf10        FAU
PITPNM1 C11orf51        C2CD3   C11orf1 USP28   DPAGT1  PRKAG1  DAZAP2  PRR13
ATP5G2  WIBG    RPL41   RPL14P1 XPOT    C12orf34        DIABLO  RFC3    CLN5
STK24-AS1       A2LD1   FANCM   RPS29   EXD2    ERH     GSTZ1   RPL3P4  HMGN2P5
TMEM85  ATPBD4  TYRO3   TP53BP1 GALK2   TCF12   COMMD4  PEAK1   UBE2I   ADCY9   PARN
MPV17L  KIF22   FUS     NUDT21  NAE1    TMEM170A        CYB5D2  UPF3AP1 DRG2
LLGL1   FOXO3B  C17orf108       RPS7P1  CCT6B   RPL17   RPL19   PGAP3   SMARCE1
DHX58   VPS25   RPL27   MRPL10  ANKRD40 BRIP1   RPL38   SLC25A19        ELAC1
CIRBP   PNPLA6  NDUFA7  HOOK2   PIK3R2  UBA52   GAPDHS  COX6B1  ALKBH6  EIF3K
HNRNPL  RPS16   SNRPA   RPS19   ZNF155  ZNF226  TRAPPC6A        SNRPD2  RPS11
AKT1S1  C19orf48        PPP2R1A NLRP9   ZSCAN22 ZNF446  CHMP2A  DTD1    CDK5RAP1
MT1P3   MMP24   C20orf4 SNHG11  IFT52   SLC35C2 RPS21   C21orf119       GCFC1-AS1
U2AF1   CRKL    EWSR1   PICK1   CTA     RANGAP1 TCF20   EBP     RBM3    SUV39H1
RRAGB   RPS23P8 CXorf56 FAM122C IDH3G
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0000184      4.4475426789295e-27     25.6325791855204        1.63047539962632
28      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006415      1.24960699750726e-24    29.2043232115286        1.24683412912601
24      91      translational termination
GO:0006614      2.1188291150343e-24     25.6015173410405        1.43865476437617
25      105     SRP-dependent cotranslational protein targeting to membrane
GO:0070972      2.12773192742727e-24    23.2675682507583        1.61677392567988
26      118     protein localization to endoplasmic reticulum
GO:0006613      2.74069048104523e-24    25.2836651680582        1.45235623832261
25      106     cotranslational protein targeting to membrane
GO:0045047      2.74069048104523e-24    25.2836651680582        1.45235623832261
25      106     protein targeting to ER
GO:0072599      2.74069048104523e-24    25.2836651680582        1.45235623832261
25      106     establishment of protein localization to endoplasmic reticulum
GO:0006414      5.33902265678678e-23    24.1328224776501        1.43865476437617
24      105     translational elongation
GO:0000956      1.36403264097387e-22    16.4846057571965        2.31554909694831
28      169     nuclear-transcribed mRNA catabolic process
GO:0006402      5.96612376275673e-22    15.4856470588235        2.43886236246627
28      178     mRNA catabolic process
GO:0072594      1.98155304673631e-21    13.8042941673711        2.7951006850737 29
204     establishment of protein localization to organelle
GO:0006413      2.10436781491553e-21    16.9482281284607        2.08262403985883
26      152     translational initiation
GO:0006612      2.5058898393247e-21     16.8135872550815        2.09632551380527
26      153     protein targeting to membrane
GO:0019080      2.9833039674986e-20     16.2021745114231        2.06892256591239
25      151     viral genome expression
GO:0019083      2.9833039674986e-20     16.2021745114231        2.06892256591239
25      151     viral transcription
GO:0006401      3.10642150925915e-20    13.0983050847458        2.80880215902014
28      205     RNA catabolic process
GO:0043624      6.58223766990509e-19    15.1018444266239        2.09632551380527
24      153     cellular protein complex disassembly
GO:0034623      1.05790892337272e-18    13.6788610001164        2.38405646668051
25      174     cellular macromolecular complex disassembly
GO:0043241      1.43125680767102e-18    14.5331960885229        2.16483288353747
24      158     protein complex disassembly
GO:0032984      2.13673782115282e-18    13.2300502965243        2.4525638364127 25
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179     macromolecular complex disassembly
GO:0019058      1.03035553385597e-15    9.85394803299848        3.16504048162757
25      231     viral infectious cycle
GO:0022415      1.64760724398278e-14    8.62009592916   3.56238322607432        25
260     viral reproductive process
GO:0006605      6.2895206258191e-14     6.02344218502971        6.49449865061241
32      474     protein targeting
GO:0071845      1.25384141502437e-13    7.8079317963711 3.89121860078887        25
284     cellular component disassembly at cellular level
GO:0022411      1.72368501580996e-13    7.68698213147542        3.94602449657463
25      288     cellular component disassembly
GO:0016032      6.12524478137023e-13    5.86698337292161        6.1793647498443 30
451     viral reproduction
GO:0033365      2.07562715114111e-12    5.56675266043212        6.48079717666598
30      473     protein localization to organelle
Tissue: Heart_Left_Ventricle=>Artery_Tibial     Type:   cluster
SourceGene:     TMEM209(ENSG00000146842.11)
TargetGeneSet:  MTND1P23        DVL1    MRPL20  PANK4   CTNNBIP1        SNORA59A
ZBTB17  KHDRBS1 RP11    PSMB2   STK40   RP1     PPIH    PRPF38A RP4     LRRC39
MAGI3   PEX11B  MRPS21  SMG5    EDEM3   IVNS1ABP        MIR4426 NUCKS1  INTS7   NENF
TATDN3  NUP133  TOMM20  PXDN    EIF3FP3 STAMBP  DGUOK   RPL31   MAP4K4  CCDC115
PLEKHB2 FMNL2   UBE2V1  WIPF1   SMARCAL1        RPL37A  RNF25   TTLL4   INHA
HDLBP   THUMPD3 RPL32   GOLGA4  ZNF662  KRBOX1  KIF9    PHF7    SPCS1   RPL10AP6
RPL24   CD200R1 RPL7AP11        FAM86HP ZBTB38  UBQLN4P1        RPL35A  ZNF718
ABCA11P MYL5    TMEM128 DCAF16  SLC30A9 MTHFD2L LARP7   PLK4    OTUD4   WWC2    FRG1
FAM105B RPL37   FBXO4   CTD     RPS23   PPIP5K2 P4HA2   SEC24A  CTB     PDF
RPS14   UBLCP1  BRD2    TAF11   RPL10A  FTSJD2  MRPL2   GSTA4   RPL39P3 HMGN3
RARS2   RSPH4A  TAB2    PHF10   C6orf70 FAM120B TOMM7   PMS2P4  STAG3L4 EIF4H
GTF2IP1 ECD     PMS2P1  ST7-AS1 IMPDH1  TMEM209 SSBP1   SLC4A2  KIAA1967
C8orf40 RPL10AP2        CHCHD7  C8orf44 HNRNPA1P4       C8orf59 RPL30   UTP23
NDUFB9  ERMP1   DCTN3   FAM205A C9orf103        RPS10P3 BICD2   INVS    CDC26
RPL35   SCAI    STXBP1  PPP1R26 CDNF    C1DP1   FGFBP3  RPL13AP5        C10orf12
ACADSB  METTL10 SIRT3   RPLP2   AP2A2   SWAP70  PLEKHA7 PEX16   C11orf10        FAU
PITPNM1 C11orf51        C2CD3   C11orf1 USP28   DPAGT1  PRKAG1  DAZAP2  PRR13
ATP5G2  WIBG    RPL41   RPL14P1 XPOT    C12orf34        DIABLO  RFC3    CLN5
STK24-AS1       A2LD1   FANCM   RPS29   EXD2    ERH     GSTZ1   RPL3P4  HMGN2P5
TMEM85  ATPBD4  TYRO3   TP53BP1 GALK2   TCF12   COMMD4  PEAK1   UBE2I   ADCY9   PARN
MPV17L  KIF22   FUS     NUDT21  NAE1    TMEM170A        CYB5D2  UPF3AP1 DRG2
LLGL1   FOXO3B  C17orf108       RPS7P1  CCT6B   RPL17   RPL19   PGAP3   SMARCE1
DHX58   VPS25   RPL27   MRPL10  ANKRD40 BRIP1   RPL38   SLC25A19        ELAC1
CIRBP   PNPLA6  NDUFA7  HOOK2   PIK3R2  UBA52   GAPDHS  COX6B1  ALKBH6  EIF3K
HNRNPL  RPS16   SNRPA   RPS19   ZNF155  ZNF226  TRAPPC6A        SNRPD2  RPS11
AKT1S1  C19orf48        PPP2R1A NLRP9   ZSCAN22 ZNF446  CHMP2A  DTD1    CDK5RAP1
MT1P3   MMP24   C20orf4 SNHG11  IFT52   SLC35C2 RPS21   C21orf119       GCFC1-AS1
U2AF1   CRKL    EWSR1   PICK1   CTA     RANGAP1 TCF20   EBP     RBM3    SUV39H1
RRAGB   RPS23P8 CXorf56 FAM122C IDH3G
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0000184      4.4475426789295e-27     25.6325791855204        1.63047539962632
28      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006415      1.24960699750726e-24    29.2043232115286        1.24683412912601
24      91      translational termination
GO:0006614      2.1188291150343e-24     25.6015173410405        1.43865476437617
25      105     SRP-dependent cotranslational protein targeting to membrane
GO:0070972      2.12773192742727e-24    23.2675682507583        1.61677392567988
26      118     protein localization to endoplasmic reticulum
GO:0006613      2.74069048104523e-24    25.2836651680582        1.45235623832261
25      106     cotranslational protein targeting to membrane
GO:0045047      2.74069048104523e-24    25.2836651680582        1.45235623832261
25      106     protein targeting to ER
GO:0072599      2.74069048104523e-24    25.2836651680582        1.45235623832261
25      106     establishment of protein localization to endoplasmic reticulum
GO:0006414      5.33902265678678e-23    24.1328224776501        1.43865476437617
24      105     translational elongation
```

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GO:0000956      1.36403264097387e-22    16.4846057571965        2.31554909694831
28      169     nuclear-transcribed mRNA catabolic process
GO:0006402      5.96612376275673e-22    15.4856470588235        2.43886236246627
28      178     mRNA catabolic process
GO:0072594      1.98155304673631e-21    13.8042941673711        2.7951006850737 29
204     establishment of protein localization to organelle
GO:0006413      2.10436781491553e-21    16.9482281284607        2.08262403985883
26      152     translational initiation
GO:0006612      2.5058898393247e-21     16.8135872550815        2.09632551380527
26      153     protein targeting to membrane
GO:0019080      2.9833039674986e-20     16.2021745114231        2.06892256591239
25      151     viral genome expression
GO:0019083      2.9833039674986e-20     16.2021745114231        2.06892256591239
25      151     viral transcription
GO:0006401      3.10642150925915e-20    13.0983050847458        2.80880215902014
28      205     RNA catabolic process
GO:0043624      6.58223766990509e-19    15.1018444266239        2.09632551380527
24      153     cellular protein complex disassembly
GO:0034623      1.05790892337272e-18    13.6788610001164        2.38405646668051
25      174     cellular macromolecular complex disassembly
GO:0043241      1.43125680767102e-18    14.5331960885229        2.16483288353747
24      158     protein complex disassembly
GO:0032984      2.13673782115282e-18    13.2300502965243        2.4525638364127 25
179     macromolecular complex disassembly
GO:0019058      1.03035553385597e-15    9.85394803299848        3.16504048162757
25      231     viral infectious cycle
GO:0022415      1.64760724398278e-14    8.62009592916   3.56238322607432        25
260     viral reproductive process
GO:0006605      6.2895206258191e-14     6.02344218502971        6.49449865061241
32      474     protein targeting
GO:0071845      1.25384141502437e-13    7.8079317963711 3.89121860078887        25
284     cellular component disassembly at cellular level
GO:0022411      1.72368501580996e-13    7.68698213147542        3.94602449657463
25      288     cellular component disassembly
GO:0016032      6.12524478137023e-13    5.86698337292161        6.1793647498443 30
451     viral reproduction
GO:0033365      2.07562715114111e-12    5.56675266043212        6.48079717666598
30      473     protein localization to organelle
Tissue: Heart_Left_Ventricle=>Artery_Tibial     Type:   asymmetric
SourceGene:     TNFSF8(ENSG00000106952.3)
TargetGeneSet:  SSR2    DNM3    EIF3FP3 IGKV2-28        GRIP2   BAP1    ACTR8   PARL
LGALS13 MED10   RPS14   C6orf47 TOX     EXOSC2  RPL7A   RPL13AP5        SF3B2
NFRKB   KRT80   ATP5G2  RPLP0   LINC00402       CTD     RP11    RPL4    ARNT2
CMTM4   MRPL10  MBD1    GTF2F1  ELOF1   TNPO2   KXD1    CD22    PAK4    RPS16   FBL
SNRPA   TOMM40  RPS9    RPS5    U2AF1   PES1    TSR2    CD24P4
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0042254      5.80270567036366e-11    35.2978021978022        0.360874679952944
9       149     ribosome biogenesis
GO:0022613      8.95478012879855e-11    26.4204651162791        0.544944986506124
10      225     ribonucleoprotein complex biogenesis
GO:0006614      1.18585378692479e-10    43.7388316151203        0.254307660369525
8       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.28051824785142e-10    43.2894935752079        0.25672963808733
8       106     cotranslational protein targeting to membrane
GO:0045047      1.28051824785142e-10    43.2894935752079        0.25672963808733
8       106     protein targeting to ER
GO:0072599      1.28051824785142e-10    43.2894935752079        0.25672963808733
8       106     establishment of protein localization to endoplasmic reticulum
GO:0071843      1.62090198429492e-10    24.7807860262009        0.578852674555394
10      239     cellular component biogenesis at cellular level
GO:0070972      3.04443730394314e-10    38.5346801346801        0.28579337070099
8       118     protein localization to endoplasmic reticulum
GO:0072594      9.59066382228669e-10    25.2443786982249        0.494083454432219
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9       204     establishment of protein localization to organelle
GO:0006415      1.80959242668293e-09    42.6547619047619        0.220399972320255
7       91      translational termination
GO:0019080      2.18633765244899e-09    29.5736855736856        0.365718635388554
8       151     viral genome expression
GO:0019083      2.18633765244899e-09    29.5736855736856        0.365718635388554
8       151     viral transcription
GO:0006612      2.42699389846001e-09    29.1616858237548        0.370562590824164
8       153     protein targeting to membrane
GO:0006414      4.96878665174025e-09    36.5255102040816        0.254307660369525
7       105     translational elongation
GO:0000956      5.33051794798591e-09    26.2341844950541        0.409314234309044
8       169     nuclear-transcribed mRNA catabolic process
GO:0006402      8.02117185783308e-09    24.8296296296296        0.431112033769289
8       178     mRNA catabolic process
GO:0000184      1.1940679007949e-08     31.9285714285714        0.288215348418795
7       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006401      2.42382829928545e-08    21.3859748072946        0.496505432150024
8       205     RNA catabolic process
GO:0019058      6.12718217428007e-08    18.8579970104634        0.559476852812954
8       231     viral infectious cycle
GO:0006413      6.51431909511458e-08    24.6051724137931        0.368140613106359
7       152     translational initiation
GO:0043624      6.81501319057261e-08    24.4349315068493        0.370562590824164
7       153     cellular protein complex disassembly
GO:0043241      8.50084415069431e-08    23.6175496688742        0.382672479413189
7       158     protein complex disassembly
GO:0033365      1.12931857761601e-07    12.0544276457883        1.14559546052176
10      473     protein localization to organelle
GO:0022415      1.52404299006734e-07    16.6537330981775        0.629714206629299
8       260     viral reproductive process
GO:0034623      1.64550189728571e-07    21.3308383233533        0.421424122898069
7       174     cellular macromolecular complex disassembly
GO:0006364      1.64612882806908e-07    30.2280084447572        0.25188568265172
6       104     rRNA processing
GO:0032984      1.99626642814782e-07    20.703488372093 0.433534011487094       7
179     macromolecular complex disassembly
GO:0016072      2.29963934403525e-07    28.4721485411141        0.26641754895855
6       110     rRNA metabolic process
GO:0006605      1.3448823802972e-06     10.3853598014888        1.14801743823957
9       474     protein targeting
GO:0071845      4.41264252702976e-06    12.7608303249097        0.687841671856619
7       284     cellular component disassembly at cellular level
GO:0022411      4.83831668235229e-06    12.5756227758007        0.697529582727839
7       288     cellular component disassembly
GO:0034470      7.57338935750658e-06    15.1674369001066        0.484395543560999
6       200     ncRNA processing
GO:0016032      9.48070968541251e-06    9.34570688069559        1.09231195073005
8       451     viral reproduction
Tissue: Artery_Tibial=>Muscle_Skeletal  Type:   asymmetric




SourceGene:     ANGPTL1(ENSG00000116194.7)      angiopoietin-like 1
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TargetGeneSet: GPR153 PHF13 TMEM201 NMNAT1 RP11 PTAFR ZMYM1 GPX6
FAM159A MYSM1 SH3GLB1 SELE DNM3OS SYT14 SDCCAG8 KCNK3 SUPT7L MAP4K4
NFE2L2 SLC11A1 COL6A3 TIMP4 TMEM43 ABHD14A-ACY1 PTPRG DBR1 TM4SF1
SNORA63 ATP13A4 IL8 G3BP2 NFKB1 GAB1 ZNF827 CLCN3 NLN PIK3R1
ZNF225 HBEGF FGF18 COL23A1 JARID2 FKBP5 PIM1 ENPP4 COQ3 GJA1
PDGFA MAFK KBTBD2 POR LAMB1 PODXL EPHB6 GIMAP6 CTD RNF122
C8orf4 GEM NIPAL2 U6 HAS2 DENND3 GADD45G AIF1L LCN6 GATA3 RIN2
CSTF2T EGR2 KIAA1274 PANK1 CHST15 DAGLA NAA40 RELT FZD4
SLC2A3 MFAP5 TSPAN31 IGF1 TDG GPR133 MRPS31 FOS POMT2 CSPG4
NARFL TMEM204 NPIP EEF2K PALB2 CX3CL1 ZNRF1 TAF1C RP4 RAP1GAP2
CCL2 C1QTNF1 CCDC57 SLC16A3 RNF125 IZUMO4 CYP4F22 HIF3A PPP1R15A
UBOX5 RBM38 JAM2 DGCR2 GGT5 DNAL4 RPA4 CSTF2

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:2000147	5.93E-08	10.11642857	1.284893779	11	211	positive regulation of cell motility
GO:0040017	7.90E-08	9.817614424	1.321431043	11	217	positive regulation of locomotion
GO:0051272	8.67E-08	9.721840659	1.333610131	11	219	positive regulation of cellular component movement

GO:0030335	5.00E-07	9.219055057	1.260535603	10	207
positive regulation of cell migration					
GO:0070555	3.47E-06	16.87765539	0.41408899	6	68
response to interleukin-1					
GO:0071347	6.72E-06	22.12542478	0.267939935	5	44
cellular response to interleukin-1					
GO:0050900	1.56E-05	6.939054998	1.467580098	9	241
leukocyte migration					

GO:0043491 1.66E-05 12.58889215 0.541969414 6 89
protein kinase B signaling cascade

GO:0051897 1.87E-05 17.59773789 0.328835375 5 54
positive regulation of protein kinase B signaling cascade

Tissue: Muscle_Skeletal=>Artery_Tibial Type: asymmetric

SourceGene: DNAH11(ENSG00000105877.12)

TargetGeneSet: MECR NFASC MDH1 MXD1 SLC25A12 NDUFB3 EPHA6 RP11
TIMMDC1 HCLS1 TM4SF1-AS1 ZAR1 CCNI PRDM8 WDFY3-AS2 PCDH10 CTD
SKP2 F2R FNIP1 UQCRQ GRIA1 RANBP17 SH3PXD2B HLA-F-AS1
LAMA4 NDUFA4 C9orf123 TLR4 H2AFY2 KIAA1274 POU6F1 MTIF3
LACC1 TRAV9-2 KIF7 LSMD1 MMP28 SLC14A1 NDUFA7 GMIP C20orf118
ARFGEF2 ATP5J LANCL3 PDZD11 COX7B PCDH11X

GOBPID Pvalue OddsRatio ExpCount Count Size Term

GO:0045333 1.34E-09 31.57987839 0.343920836 8 142
cellular respiration

GO:0022904 2.64E-09 40.24438202 0.232509861 7 96
respiratory electron transport chain

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GO:0022900      2.73E-08        28.12795276     0.324545014     7       134
electron transport chain



GO:0015980      5.41E-07        13.98934721     0.743547159     8       307
energy derivation by oxidation of organic compounds



GO:0006091      6.46E-06        9.87372134      1.036606463     8       428
generation of precursor metabolites and energy



Tissue: Artery_Tibial=>Muscle_Skeletal  Type:   asymmetric





SourceGene:     ENSG00000260884.1       AC009120.5 (novel lincRNA)






TargetGeneSet:  MTND1P23        RPL22   CELA2A  WDTC1   MFI2    KDM4A   RP4
RPS27   C1orf192        PRRC2C  OBSCN   UBC     IGKV1-5 RPL31   ORMDL1  EEF1B2
GIGYF2  RAD54L2 RPL29   RPL24   COPG1   RP11    RPL35A  BOD1L   LGALS13 RPL34
H3F3AP6 RPS3A   RPL37   CHCHD2P2        BTF3    NSA2    MAN2A1  CTD     CTB
MTND5P11        GFOD1-AS1       RPS18   RPL10A  UBR2    MTRNR2L9        MRPS12
FOXK1   FBXL18  HIP1    RPS3AP26        TRIM56  PRSS3P2 RPS20   RPL30   EIF3E
FAM91A1 NFIB    PCSK5   FAM35B  POLR3A  HIF1AN  FBXL15  OR52E8  RPL27A  MTRNR2L8
RPS13   MS4A1   RPL37P2 C11orf73        MMP1    RPS25   SNX19   MLL4    SPRYD3
PFDN5   VPS29   C12orf51        GCN1L1  RPLP0   RPSAP54 PARP4-AS1       KCTD4   TPT1
ZC3H13  LPAR6   CHD8    U6      C14orf166       IGHD    GOLGA8IP        HERC2
RPS3AP47        SPG11   POLR2M  RPS3AP6 HERC1   RPL4    RPL13   TOM1L2  MTRNR2L1
RPS7P1  RPL23A  TBC1D3H RPL27   DHX8    RPS2P48 TNRC6C  ROCK1P1 IER3IP1 ZNF737
KCNK6   CEACAM5 SULT2B1 KLK1    RPS5    BFSP1   CEP250  ZNFX1   PEX26   NF2
LDOC1L  GNL3L   ZC3H12B MED12   RPL36A  RPL39   FLNA    MT
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GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0006414	4.81E-34	71.99596774	0.632136184	25	105	translational elongation
GO:0006415	7.10E-34	81.29068941	0.54785136	24	91	translational termination
GO:0000184	1.54E-32	61.21310913	0.716421009	25	119	"nuclear-transcribed mRNA catabolic process, nonsense-mediated decay"
GO:0006614	3.37E-32	67.17460317	0.632136184	24	105	SRP-dependent cotranslational protein targeting to membrane

GO:0006613	4.33E-32	66.35075494	0.638156529	24	106
cotranslational protein targeting to membrane					
GO:0045047	4.33E-32	66.35075494	0.638156529	24	106
protein targeting to ER					
GO:0072599	4.33E-32	66.35075494	0.638156529	24	106
establishment of protein localization to endoplasmic reticulum					
GO:0070972	7.36E-31	57.83181358	0.710400664	24	118
protein localization to endoplasmic reticulum					
GO:0006413	1.14E-29	45.20256541	0.915092381	25	152

						translational initiation
GO:0006612	1.36E-29	44.84627016	0.921112726	25	153	protein targeting to membrane
GO:0000956	1.87E-28	39.81854839	1.01743824	25	169	nuclear-transcribed mRNA catabolic process
GO:0019080	4.26E-28	42.70566179	0.909072037	24	151	viral genome expression
GO:0019083	4.26E-28	42.70566179	0.909072037	24	151	viral transcription

GO:0043624	5.94E-28	42.03765227	0.921112726	24	153	cellular protein complex disassembly
GO:0006402	7.29E-28	37.45256167	1.071621341	25	178	mRNA catabolic process
GO:0043241	1.34E-27	40.45486851	0.951214449	24	158	protein complex disassembly
GO:0034623	1.52E-26	36.09904762	1.047539963	24	174	cellular macromolecular complex disassembly
GO:0072594	2.50E-26	31.95395567	1.228150301	25	204	establishment of protein localization to organelle

GO:0006401	2.84E-26	31.77419355	1.234170646	25	205	RNA catabolic process
GO:0032984	3.08E-26	34.92227343	1.077641686	24	179	macromolecular complex disassembly
GO:0019058	6.02E-25	27.71296586	1.390699606	25	231	viral infectious cycle
GO:0022415	1.20E-23	24.24330817	1.565289599	25	260	viral reproductive process

GO:0071845	1.09E-22	21.95945946	1.70977787	25	284	cellular component disassembly at cellular level
GO:0022411	1.55E-22	21.61934257	1.733859248	25	288	cellular component disassembly
GO:0033365	1.46E-19	14.04282511	2.847623002	27	473	protein localization to organelle
GO:0006605	1.54E-19	14.01040268	2.853643346	27	474	protein targeting
GO:0016032	8.53E-18	13.19286688	2.71517542	25	451	viral reproduction

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Tissue: Artery_Tibial=>Muscle_Skeletal  Type:   asymmetric

SourceGene:     GAS8(ENSG00000141013.10)        growth arrest-specific 8

TargetGeneSet:  FAM41C  H6PD    SNRNP40 IPP     ALG6    SGIP1   RP11    GAPDHP32
EFNA4   MSTO1   B4GALT3 HSPA6   POU2F1  TOR1AIP1        ZNF678  JMJD4   RNASEH1
IGKJ4   ARL6IP6 ICA1L   CRBN    GHRL    KIAA1143        MON1A   PROS1   TMEM45A
ZDHHC23 CCNL1   H1FX    PLD1    DCAF16  SLC30A9 POLR2B  ENAM    EXOSC9  GARS
FHDC1   LPCAT1  CTD     ZFR     SKP2    YTHDC2  HNRNPA0 IK      GALNT10 NHLRC1
TOB2P1  TRIM39  VPS52   MAPK13  RP1     SCAF8   TATDN2P2        WDR27   AP5Z1
WIPI2   CCDC126 GPC2    SPDYE3  CTA     C8orf42 PPP2R2A BRF2    RNF170  KIAA0196
ZNF7    RCL1    SLC44A1 C9orf148        STXBP1  C9orf106        USP20   NUP214
SEC16A  FAM21C  STOX1   RRP12   C10orf32        PLEKHA1 BET1L   ART1    CHRNA10 RIC3
PPP2R5B SART1   ANKRD13D        ATG16L2 SRSF8   TTC12   RPL23AP64       NPFF
THAP2   ANO4    PLBD2   FBXO21  TPTE2   CDK8    MTRF1   LINC00452       C14orf21
ZBTB1   ATPBD4  GCHFR   ZFYVE19 CLPX    U6      FAM103A1        ZNF75A  DOC2A   FUS
MMP15   SETD6   CMC2    GAS8    PIGS    SUPT6H  TP53I13 NSRP1   PGAP3   GSDMB
H3F3B   ZNF236  C19orf6 CIRBP   VMAC    TNFSF14 MEF2BNB ZNF681  ZNF30   HNRNPL
MED29   SUPT5H  HNRNPUL1        TSKS    C19orf48        PPP2R1A LENG8   ZNF324B
C20orf96        FAM110A UBOX5   RP4     CDH4    PRPF6   IGLL5   IGLC1   PES1    H1F0
7SK     GSPT2   TSR2    ACRC

GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
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GO:0008380	6.72E-07	6.328650711	2.369247803	13	323	RNA splicing
GO:0006397	1.25E-06	5.517786561	2.926717874	14	399	mRNA processing
GO:0000377	2.47E-06	7.598260309	1.496367033	10	204	"RNA splicing, via transesterification reactions with bulged adenosine as nucleophile"
GO:0000398	2.47E-06	7.598260309	1.496367033	10	204	"nuclear mRNA splicing, via spliceosome"

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GO:0000375      3.07E-06        7.404731993     1.533042696     10      209     "RNA
splicing, via transesterification reactions"
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Tissue: Artery_Tibial=>Muscle_Skeletal  Type:   asymmetric
SourceGene:     KRT8P46(ENSG00000248971.1)
TargetGeneSet:  FAM41C  IPP     RP11    JTB     RABIF   RNASEH1 EMX1    DCAF17  MREG
CRBN    KIAA1143        CTD     UBA3    C3orf58 METTL15P1       PHC3    AFAP1
RG9MTD2 RPS3A   SKP2    TTC37   RAPGEF6 IK      CDKAL1  ZNF192  WDR11   SNX14
USP45   DCBLD1  SCAF8   TATDN2P2        FOXK1   GLCCI1  RALA    TMEM60  C8orf42
PPP2R2A BRF2    RALGAPA1P       USP20   NUP214  RPL7A   SEC16A  DUPD1   GBF1
SART1   NPFF    THAP2   NOC4L   CDK8    EBPL    ALG11   C14orf21        HERC2
HERC1   FAM108C1        NMB     CCDC113 TOM1L2  SUPT6H  TAOK1   DHX8    SLC16A5 SGSH
METTL4  GNA11   HSH2D   DDA1    RYR1    MED29   SUPT5H  DYRK1B  HNRNPUL1        RP4
TGM2    PRPF6   SON     MCM5    RAB9A   RBM10   SUV39H1 TSR2    APOOL   RPL39
IDH3G
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
Tissue: Muscle_Skeletal=>Artery_Tibial  Type:   asymmetric
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SourceGene:     MTRNR2L1(ENSG00000256618.1)     MT-RNR2-like 1
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TargetGeneSet:  MTND2P28        ISG15   DFFA    CELA2A  CHCHD2P6        EIF1AX  RP1
CELA3B  CELA3A  PHACTR4 YRDC    MFI2    CLDN19  AMY2A   CLCC1   TARS2   JTB
RPS27   VAMP4   ZBTB37  RP11    PIGR    PTPN14  PREPL   EPCAM   CEP68   AAK1
REG1B   REG1A   REG3A   POLR1A  EIF5B   H3F3AP4 ORMDL1  TRIP12  HDLBP   NR2C2   CTD
ZBTB20  STAG1   CPB1    MIR943  ABLIM2  FRG1    NUP155  CTB     MTND5P11
PCDHGA5 GEMIN5  CLPS    FTH1P5  MTRNR2L9        WDR11   PHACTR2 IYD     PHF14
STK31   CBX3    NUDCD3  TRIM56  CPA2    CPA1    BRAF    PRSS1   PRSS3P1 PRSS3P2
MTMR9   VAT1    ELP3    PRKDC   NFIB    PRSS3   RGP1    ZNF462  ARPC5L  C9orf16
ATOH7   FBXL15  PDCD11  PNLIP   SLC22A18AS      OR52E8  NAT10   TRIM44  CKAP5   DDB1
DLAT    SLC38A1 RP3     DAZAP2  HIGD1AP1        PLA2G1B STRN3   KLHL28  L2HGDH
YLPM1   GOLGA8IP        USP8    MYO9A   IQGAP1  RPL21P119       GP2     LONP2
SLC12A4 NFATC3  CHTF8   CTRB2   CTRB1   VPS53   TSR1    RNASEK  MYH1    TAOK1   LIG3
CDC27   KPNB1   DYNLL2  RNF126  ALKBH7  TRAPPC5 ADAMTS10        SYCN    LINC00085
RBPJL   URB1    CBR3    NBEAP3  FAM108A5P       CTA     GS1     HUWE1   PAGE2B
RPL39   MT

GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
















GO:0007586      7.23E-08        13.78935484     0.769358522     9       109
digestion
















Tissue: Muscle_Skeletal=>Artery_Tibial  Type:   asymmetric









SourceGene:     PABPC3(ENSG00000151846.6)       "poly(A) binding protein,
cytoplasmic 3"
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TargetGeneSet: CELA2B ZMYM1 TXNIP GLUL SUCLG1 SLC25A12 NIF3L1 ING5
PDHB GTF2E1 KLF15 C3orf70 RASL11B ARL9 AREG USP53 ARHGAP26
ADRA1B LY6G6C MED20 GAPDHP15 LYRM2 FAXC QRSL1 LAMA4 RP1 RP11
UST FAM103A2P NDUFA4 MEOX2 ACN9 PMS2P1 NEIL2 VDAC3 LAPTM4B
DENND3 RANBP6 ALDH1B1 KLF9 TLR4 CISD1 ADO NODAL SLC16A12
FAM118B COPS7A COX14 TSFM IRAK3 TPCN1 ZCCHC8 SFSWAP QRSL1P3 NID2
SLC25A29 ATP10A ARID3B CTD FAM108C1 IL16 IDH2 PER1
NDEL1 COX10 PSMB3 C17orf89 ATP5A1 NDUFA7 NXNL1 ITPKC RBM39
ARFGAP3 KLHL13 NDUFA1

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0045333	1.22E-10	24.01346801	0.540447028	10	142	cellular respiration
GO:0015980	1.73E-08	11.90878378	1.16843125	11	307	energy derivation by oxidation of organic compounds
GO:0006091	5.00E-07	8.380695444	1.628953014	11	428	generation of precursor metabolites and energy
GO:0022904	1.64E-06	19.46394558	0.365372639	6	96	respiratory electron transport chain
GO:0022900	1.13E-05	13.64923469	0.509999308	6	134	electron transport chain

GO:0009060	1.89E-05	29.63467492	0.159850529	4	42	aerobic respiration

Tissue: Artery_Tibial=>Muscle_Skeletal Type: asymmetric

SourceGene: PPIG(ENSG00000138398.10) peptidylprolyl isomerase G (cyclophilin G)

TargetGeneSet: MINOS1 TMSB4XP1 APOA1BP RP4 LBR GNPAT RP11
MRPL33 MDH1 SLC1A4 TPRKB SUCLG1 NDUFB3 COL4A3 GIGYF2 ABHD14A CCNL1
CKMT2 IK MNF1 PHACTR2 WDR27 EEF1A1P6 RPS2P32 CYCS GATS
NDUFA5 WASL MRPS33 GSTK1 KIAA0196 ST13P6 ERP44 MRPL41 FAM21C
NDUFB8 GBF1 NRAP PLEKHA1 SART1 NDUFS8 C11orf73 SDHD LIN7A
NDUFA12 SLC25A3 LINC00441 ARHGEF7-IT1 C14orf21 FOXN3 GLRX5
COX5A NDUFB10 GOT2 CA7 SUPT6H TP53I13 ATP5G1 NDUFV2 CCDC68 ATP5D
WDR88 SUPT5H ESF1 PRPF6 ATP5J C21orf33 RAB9A

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0045333	1.19E-18	45.5586295	0.510968099	15	142	cellular respiration
GO:0022904	1.09E-17	57.4939759	0.345443222	13	96	respiratory electron transport chain

GO:0022900	9.67E-16	39.33333333	0.482181164	13	134	electron transport chain
GO:0015980	1.27E-13	19.58580155	1.104698637	15	307	energy derivation by oxidation of organic compounds
GO:0006091	1.04E-12	15.08845739	1.540101031	16	428	generation of precursor metabolites and energy
GO:0006119	2.68E-11	52.17818182	0.20870528	8	58	oxidative phosphorylation
GO:0042773	2.89E-10	55.84055556	0.169123244	7	47	ATP synthesis coupled electron transport
GO:0042775	2.89E-10	55.84055556	0.169123244	7	47	mitochondrial ATP synthesis coupled electron transport
GO:0006120	2.89E-09	62.47391304	0.129541208	6	36	"mitochondrial electron transport, NADH to ubiquinone"

GO:0042776 1.23E-05 88.09591837 0.04677877 3 13
mitochondrial ATP synthesis coupled proton transport

Tissue: Artery_Tibial=>Muscle_Skeletal Type: asymmetric

SourceGene: PVRL3-AS1(ENSG00000242242.1) PVRL3 antisense RNA 1 (MiscRNA)

TargetGeneSet: PPIH MRPL9 RP11 LRRN2 DYNC2LI1 UBC MPHOSPH10
RPL31 METTL5 RPL37A FAM208A RPL24 RAB6B PARL RPL35A FRYL RPL34
BRIX1 RPL37 MAN2A1 NOL7 PRRC2A NOTCH4 RPL10A C6orf57 L3MBTL3 MRPS12
PNLDC1 PINX1 HOOK3 RPS20 C8orf59 RPL30 POLR2K RPS13 C11orf10
RCOR2 FAU RPS25 ERC1 RPL41 RAP2A ARHGEF7-AS2 HEATR5A ERH
ADAM20 BTBD7 UNC45A FBXL19 GIT1 TMEM106A PPP1R9B SOGA2 C18orf21
SNRPD2 MID1 NKAP RPL7P56 PLXNA3

GOBPID Pvalue OddsRatio ExpCount Count Size Term

GO:0006415 5.35E-21 86.84848485 0.277074251 14 91
translational termination

GO:0006414 4.47E-20 73.41538462 0.319701059 14 105
translational elongation

GO:0006614 4.47E-20 73.41538462 0.319701059 14 105
SRP-dependent cotranslational protein targeting to membrane

GO:0006613	5.15E-20	72.61231884	0.322745831	14	106	cotranslational protein targeting to membrane
GO:0045047	5.15E-20	72.61231884	0.322745831	14	106	protein targeting to ER
GO:0072599	5.15E-20	72.61231884	0.322745831	14	106	establishment of protein localization to endoplasmic reticulum
GO:0019080	1.69E-19	54.27611562	0.45976057	15	151	viral genome expression
GO:0019083	1.69E-19	54.27611562	0.45976057	15	151	viral transcription
GO:0043624	2.07E-19	53.482009	0.465850114	15	153	cellular protein complex disassembly
GO:0070972	2.48E-19	64.18012821	0.359283095	14	118	protein localization to endoplasmic reticulum
GO:0000184	2.81E-19	63.56444444	0.362327867	14	119	"nuclear-transcribed mRNA catabolic process, nonsense-mediated decay"

GO:0043241	3.39E-19	51.59392332	0.481073974	15	158	protein complex disassembly
GO:0034623	1.49E-18	46.35003253	0.529790326	15	174	cellular macromolecular complex disassembly
GO:0032984	2.30E-18	44.92115223	0.545014186	15	179	macromolecular complex disassembly
GO:0006413	9.67E-18	48.252657	0.462805342	14	152	translational initiation
GO:0006612	1.06E-17	47.90215827	0.465850114	14	153	protein targeting to membrane
GO:0000956	4.40E-17	42.90924731	0.514566466	14	169	nuclear-transcribed mRNA catabolic process
GO:0006402	9.20E-17	40.52886179	0.541969414	14	178	mRNA catabolic process
GO:0019058	1.10E-16	33.98227969	0.703342329	15	231	viral infectious cycle

GO:0072594	6.31E-16	34.91894737	0.621133486	14	204	establishment of protein localization to organelle
GO:0022415	6.46E-16	29.89866291	0.791640717	15	260	viral reproductive process
GO:0006401	6.76E-16	34.73368237	0.624178258	14	205	RNA catabolic process
GO:0071845	2.40E-15	27.18497629	0.864715245	15	284	cellular component disassembly at cellular level
GO:0022411	2.96E-15	26.77908299	0.876894333	15	288	cellular component disassembly
GO:0016032	2.07E-12	16.57426447	1.373192167	15	451	viral reproduction
GO:0033365	4.09E-12	15.75327511	1.44017715	15	473	protein localization to organelle
GO:0006605	6.43E-11	14.14913043	1.443221922	14	474	protein targeting

Tissue: Artery_Tibial=>Muscle_Skeletal Type: asymmetric

SourceGene: RAB32(ENSG00000118508.4) "RAB32, member RAS oncogene family"

TargetGeneSet: RP1 UBC RPL31 EEF1B2 RPL37A RP11 RPL35A RPL34 LSM6
CTD MRPS12 RPS20 U6 RPS13 RPS25 PFDN5 RPL41 HERC2 NDNL2
RPS3AP6 MED31 RPL23A RPL27 RPS5 EEF1B2P3

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0006414	1.42E-23	253.2527174	0.152584596	13	105	translational elongation
GO:0006415	5.14E-22	242.2109705	0.132239983	12	91	translational termination
GO:0006614	3.15E-21	205.5483871	0.152584596	12	105	SRP-dependent cotranslational protein targeting to membrane
GO:0006613	3.55E-21	203.3475177	0.154037783	12	106	cotranslational protein targeting to membrane
GO:0045047	3.55E-21	203.3475177	0.154037783	12	106	protein targeting to ER
GO:0072599	3.55E-21	203.3475177	0.154037783	12	106	establishment of protein localization to endoplasmic reticulum
GO:0000956	9.00E-21	148.6875	0.245588541	13	169	nuclear-transcribed mRNA catabolic process
GO:0070972	1.37E-20	180.1761006	0.171476022	12	118	protein localization to endoplasmic reticulum
GO:0000184	1.52E-20	178.4797508	0.172929209	12	119	"nuclear-transcribed mRNA catabolic process, nonsense-mediated decay"

GO:0006402	1.80E-20	140.4886364	0.25866722	13	178	mRNA catabolic process
GO:0006401	1.18E-19	120.5039063	0.297903259	13	205	RNA catabolic process
GO:0019080	2.95E-19	137.0839329	0.219431181	12	151	viral genome expression
GO:0019083	2.95E-19	137.0839329	0.219431181	12	151	viral transcription
GO:0006413	3.20E-19	136.0952381	0.220884368	12	152	translational initiation
GO:0006612	3.47E-19	135.1205674	0.222337554	12	153	protein targeting to membrane
GO:0043624	3.47E-19	135.1205674	0.222337554	12	153	cellular protein complex disassembly
GO:0043241	5.16E-19	130.4474886	0.229603488	12	158	protein complex disassembly
GO:0034623	1.69E-18	117.4320988	0.252854474	12	174	cellular macromolecular complex disassembly
GO:0032984	2.40E-18	113.8762475	0.260120407	12	179	macromolecular complex disassembly
GO:0072594	1.19E-17	98.875	0.296450073	12	204	establishment of protein localization to organelle
GO:0019058	5.41E-17	86.52054795	0.335686112	12	231	viral infectious cycle
GO:0022415	2.27E-16	76.24731183	0.377828524	12	260	viral reproductive process
GO:0071845	6.61E-16	69.40196078	0.412705003	12	284	cellular component disassembly at cellular level

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GO:0022411      7.83E-16        68.37681159     0.41851775      12      288
cellular component disassembly



GO:0016032      1.68E-13        42.49354594     0.65538717      12      451
viral reproduction


GO:0033365      2.96E-13        40.40202458     0.687357276     12      473
protein localization to organelle



GO:0006605      3.04E-13        40.31168831     0.688810463     12      474
protein targeting


Tissue: Muscle_Skeletal=>Artery_Tibial  Type:   asymmetric
SourceGene:     RP1-159M24.1(ENSG00000225580.2)
TargetGeneSet:  PIK3CD  CELA2B  RP11    MECR    CRTC2   MIR4426 ODC1    KLHL29  RBKS
RPLP0P6 MAP4K3  ASB3    TET3    BTF3L4P2        FARSB   LSM3    ZNF662  KRBOX1
RPL10AP6        LMOD3   DZIP3   DDX50P2 AASDH   NDUFC1  ANXA2P1 CTD     GPR150
RNF145  CREBRF  BNIP1   SUMO2P1 RPL24P4 RP3     LYRM2   UFL1    PMS2P1  C7orf61
C7orf60 MRPS33  AGAP3   PPP3CC  KIF13B  TRIM55  NDUFB9  C9orf123        FKTN
SYNPO2L RP13    COX15   UROS    CHST1   CLNS1A  C11orf70        ATP5L   SPA17   GPD1
NDUFA12 RPS7P10 C14orf39        NDUFB1  C14orf2 HMGN2P5 BMF     FURIN   MYLPF
CCDC113 PSMB10  PPM1D   WDR83   SNRPB2  C20orf43        OGFR    COMT    PNPLA4  SMPX
EEF1B2P3        RPS2P55 ITGB1BP2        COX7B   DOCK11  NDUFA1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      3.5669491973475e-09     26.5417439703154        0.37865891633797
8       96      respiratory electron transport chain
GO:0022900      4.99586841258498e-08    18.4878522837706        0.528544737388416
8       134     electron transport chain
GO:0045333      7.84983626824484e-08    17.3743527261651        0.560099647083247
8       142     cellular respiration
GO:0042773      1.07881748832632e-06    32.8571428571429        0.185385094457131
5       47      ATP synthesis coupled electron transport
GO:0042775      1.07881748832632e-06    32.8571428571429        0.185385094457131
5       47      mitochondrial ATP synthesis coupled electron transport
GO:0006119      3.11798050635669e-06    26.0177793904209        0.228773095287523
5       58      oxidative phosphorylation
GO:0006120      1.16615178243753e-05    33.872641509434 0.141997093626739       4
36      mitochondrial electron transport, NADH to ubiquinone
Tissue: Muscle_Skeletal=>Artery_Tibial  Type:   asymmetric
SourceGene:     RP11-350G8.5(ENSG00000228013.1)
TargetGeneSet:  HMGN2   SERINC2 SFPQ    PPIE    RP3     MUTYH   CMPK1   OSBPL9
PRPF38A GNG12   RP11    NSRP1P1 FAM69A  AGL     NBPF6   BCAS2   MAN1A2  RAB7L1  RD3
SMYD2   ANKS1B  CAPN2   DEGS1   ZRANB3  COBLL1  BBS5    NCKAP1  RPL7P14 FARSB
TMEM43  BTD     OSBPL10 ZDHHC3  RBM5    EIF4E3  SCHIP1  AP2M1   CHRD    CCDC50
STK32B  CC2D2A  MED28   PARM1   SH3D19  HADHAP1 FBXL7   OXCT1   ARL15   MAP1B   HEXB
FBXL17  ERGIC1  MAPK9   MRPS18B SCUBE3  NFYA    MRPL2   HSP90AB1        SLC35B2
FKBP9   DPY19L1 ANKIB1  MEPCE   RBM28   OPN1SW  KCNH2   NEIL2   ZMAT4   PTDSS1  APTX
SMU1    VPS13A  C9orf156        EXOSC2  DDX31   SURF6   EDF1    CHAF1B  FAM35A
ZFYVE27 CWF19L1 PDCD11  C10orf137       BET1L   OR51A9P FAM160A2        NAT10
PPME1   GDPD5   FAT3    GUCY1A2 DIXDC1  SIDT2   FEZ1    WNT5B   NECAP1  ART4
TMEM117 CACNB3  DCTN2   GNS     CHPT1   SART3   PLBD2   CDK2AP1 SETD8   MTUS2
RBM26   PRMT5-AS1       MED6    EML1    ULK4P3  SLC30A4 NEO1    UBE2Q2  HMG20A  AEN
FANCI   C16orf91        TELO2   NTAN1   GDE1    KIF22   INO80E  CCDC102A        CTU2
METTL16 SPAG5   UTP6    SRSF1   NAT9    THOC1   TTC39C  MBD1    FZR1    HNRNPM
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OLFM2   DDX49   U2AF1L4 C19orf55        SUPT5H  ZNF546  RTN2    SYMPK   CCDC9
DHX34   ZNF324B FAM83D  DDX27   COL20A1 USP25   ITSN1   PKNOX1  U2AF1   GAS2L1  DRG1
RASD2   TRIOBP  XPNPEP3 TRMU    SCML1   RAI2    RBM10   LAS1L   TAF1    ENOX2   EMD
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006397      4.68594899917893e-07    5.19955240581872        3.53414988582105
16      399     mRNA processing
Tissue: Artery_Tibial=>Muscle_Skeletal  Type:   asymmetric
SourceGene:     RP11-370B11.1(ENSG00000236739.2)
TargetGeneSet:  CELA2A  CELA3B  CELA3A  TMSB4XP1        RP4     AMYP1   RPS27
MIR4426 PTPN14  PPP1CB  RHOQ    MCM6    RPL29   CTBP1-AS1       RPL7AP31        ZFR
RP11    CLPS    MTRNR2L9        EEF1A1P6        TRIM56  PRSS1   YWHAZP3 PNLIP
MTRNR2L8        CARD16  LINC00441       IGHA2   GP2     CTRB2   CTRB1   ADAMTS18
CYP2F1P SON     RP1     WASF4P  RP6
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0007586      1.93179639713465e-08    46.3559870550162        0.181025534565082
6       109     digestion
Tissue: Artery_Tibial=>Muscle_Skeletal  Type:   asymmetric
SourceGene:     RP11-452F19.3(ENSG00000228106.1)
TargetGeneSet:  RPL22   RP4     SRGAP2P1        SNX18P15        RPS27   FAM189B
ACBD6   RP11    UBC     RPL31   RPL37A  RPL14   CCDC72  FAM208A RPL24   RPL35A
RPL34   RPL37   NNT     BTF3    NSA2    TBCA    RPS23   CTD     RELL2   HCP5
CSNK2B  NOTCH4  RPS18   SYNGAP1 RPL10A  MRPS12  RPS20   C8orf59 RPL30   THNSL1
RPL27A  RPS13   LPXN    C11orf10        FAU     RPS25   PFDN5   WIBG    RPL41
SLC24A6 TPT1    MED4-AS1        BIVM    RPL4    TCEB2   ZCCHC14 RPS7P1  SPAG5-AS1
RPL23A  RPL27   IER3IP1 HMHA1   MAP3K10 SNRPD2  RPS11   CPT1C   EEF1B2P3
TCEAL3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      2.06633390345245e-40    183.351812366738        0.327451387447236
24      91      translational termination
GO:0000184      2.12166164030355e-39    140.908195429472        0.428205660507923
25      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006414      1.01286699559936e-38    151.513227513228        0.377828523977579
24      105     translational elongation
GO:0006614      1.01286699559936e-38    151.513227513228        0.377828523977579
24      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.30686375341027e-38    149.655052264808        0.381426890872604
24      106     cotranslational protein targeting to membrane
GO:0045047      1.30686375341027e-38    149.655052264808        0.381426890872604
24      106     protein targeting to ER
GO:0072599      1.30686375341027e-38    149.655052264808        0.381426890872604
24      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      2.28287588990214e-37    130.440729483283        0.424607293612899
24      118     protein localization to endoplasmic reticulum
GO:0019080      1.42021310224845e-36    104.88683127572 0.543353401148709       25
151     viral genome expression
GO:0019083      1.42021310224845e-36    104.88683127572 0.543353401148709       25
151     viral transcription
GO:0000956      2.90698812152579e-35    91.6602366255144        0.608124005259152
25      169     nuclear-transcribed mRNA catabolic process
GO:0006402      1.15547026151555e-34    86.2139917695473        0.640509307314373
25      178     mRNA catabolic process
GO:0006413      1.69049505340889e-34    95.5647321428571        0.546951768043734
24      152     translational initiation
GO:0006612      2.0012394252553e-34     94.8172757475083        0.550550134938759
24      153     protein targeting to membrane
GO:0043624      2.0012394252553e-34     94.8172757475083        0.550550134938759
24      153     cellular protein complex disassembly
GO:0043241      4.57092535173956e-34    91.2473347547974        0.568541969413881
24      158     protein complex disassembly
GO:0006401      4.78976746455963e-33    73.1430041152263        0.737665213480036
25      205     RNA catabolic process
GO:0034623      5.364037335902e-33      81.4228571428571        0.626115839734274
24      174     cellular macromolecular complex disassembly
```

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GO:0032984      1.10112153428467e-32    78.76866359447  0.644107674209397       24
179     macromolecular complex disassembly
GO:0019058      1.08040811381849e-31    63.794498381877 0.831222752750675       25
231     viral infectious cycle
GO:0072594      2.97522236261082e-31    67.7095238095238        0.734066846585011
24      204     establishment of protein localization to organelle
GO:0022415      2.30178622896268e-30    55.8077226162333        0.935575392706387
25      260     viral reproductive process
GO:0071845      1.08055864628249e-27    46.6120879120879        1.02193619818698
24      284     cellular component disassembly at cellular level
GO:0022411      1.52173021425648e-27    45.8928571428571        1.03632966576707
24      288     cellular component disassembly
GO:0016032      2.58745487499351e-24    30.3708050773778        1.62286346965608
25      451     viral reproduction
GO:0033365      2.34727705743791e-22    26.63060769965  1.70202754134662        24
473     protein localization to organelle
GO:0006605      2.46772339950581e-22    26.5695238095238        1.70562590824164
24      474     protein targeting
GO:0022613      1.49006029914864e-05    10.1189602446483        0.809632551380527
7       225     ribonucleoprotein complex biogenesis
Tissue: Muscle_Skeletal=>Artery_Tibial  Type:   asymmetric
SourceGene:     RP11-56B16.2(ENSG00000259556.1)
TargetGeneSet:  KHDRBS1 CYP4A11 FPGT-TNNI3K     PSMB4   C1orf61 RPL15   C3orf37 RP11
EXOSC9  RXFP1   MRPS18B MRPL2   RSPH9   AGPAT4  TRGV5   EIF4H   KRT8P3  PYCRL
TMEM38B OPALIN  SH3PXD2A        ARL2    SF3B2   RPL18AP3        ARHGAP5-AS1     RPS2
MIR4519 LDHD    SPIRE2  WNK4    NT5C    HNRNPM  CTD     RPS5    PSMF1   MT1P3
U2AF1   XRCC6   RP13    RPS23P8
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
Tissue: Artery_Tibial=>Muscle_Skeletal  Type:   asymmetric







SourceGene:     S100A6(ENSG00000197956.4)       S100 calcium binding protein A6








TargetGeneSet:  WDTC1   CCDC23  KDM4A   INADL   IL6R    MTX1    PRRC2C  PPP2R5A PUM2
UBC     ORMDL1  NIF3L1  FAM117B PAX3    D2HGDH  NR1D2   OR7E94P RP11    CTD
MAN2A1  FAM53C  FOXP4   PEX6    PHF3    MDN1    STXBP5  ARID1B  TNRC18  C7orf41
BAZ1B   CUX1    OPN1SW  MLL3    SEPT7P6 RPS20   C8orf59 FAM91A1 FAM83H  MPDZ
FAM13C  LDB1    HBE1    OR52E8  RPL27A  RPS13   PIGCP1  UCP2    MLL     RPS25
DSTNP2  ITPR2   RP3     NR2C1   ACAD10  LRRC43  PARP4-AS1       RFXAP   MED4-AS1
HERC1   TNFRSF12A       TXNDC11 RPL7P47 GDPD3   SULT1A3 FBXL19  ANKFY1  TOM1L2
TMEM11  RPS7P1  RPL27   FAM171A2        TNRC6C  IER3IP1 MAP3K10 SNRPD2  SYMPK   BAX
RP1     SLC16A8 XPNPEP3 WWC3    MED12   RPL39   BCORL1

GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
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GO:0006415	7.20E-08	23.38071895	0.36523424	7	91
translational termination					
GO:0072594	1.09E-07	13.3733124	0.818766867	9	204
establishment of protein localization to organelle					
GO:0006414	1.94E-07	20.0210084	0.421424123	7	105
translational elongation					
GO:0006614	1.94E-07	20.0210084	0.421424123	7	105
SRP-dependent cotranslational protein targeting to membrane					
GO:0006613	2.07E-07	19.81738958	0.425437686	7	106
cotranslational protein targeting to membrane					
GO:0045047	2.07E-07	19.81738958	0.425437686	7	106
protein targeting to ER					

GO:0072599	2.07E-07	19.81738958	0.425437686	7	106	establishment of protein localization to endoplasmic reticulum
GO:0070972	4.31E-07	17.66013072	0.473600443	7	118	protein localization to endoplasmic reticulum
GO:0034623	4.32E-07	13.71277108	0.698359975	8	174	cellular macromolecular complex disassembly
GO:0000184	4.57E-07	17.50122549	0.477614006	7	119	"nuclear-transcribed mRNA catabolic process, nonsense-mediated decay"
GO:0032984	5.36E-07	13.3071345	0.71842779	8	179	macromolecular complex disassembly
GO:0071845	1.77E-06	9.429461967	1.139851913	9	284	cellular component disassembly at cellular level
GO:0022411	1.98E-06	9.291639236	1.155906166	9	288	cellular component disassembly

GO:0019080	2.28E-06	13.58156318	0.606048024	7	151	viral genome expression
GO:0019083	2.28E-06	13.58156318	0.606048024	7	151	viral transcription
GO:0006413	2.38E-06	13.48695064	0.610061587	7	152	translational initiation
GO:0006612	2.49E-06	13.39363417	0.614075151	7	153	protein targeting to membrane
GO:0043624	2.49E-06	13.39363417	0.614075151	7	153	cellular protein complex disassembly
GO:0043241	3.08E-06	12.94559148	0.634142966	7	158	protein complex disassembly

```
GO:0000956      4.81E-06        12.05725006     0.67829216      7       169
nuclear-transcribed mRNA catabolic process



GO:0006402      6.77E-06        11.41543401     0.714414227     7       178     mRNA
catabolic process



GO:0006401      1.70E-05        9.84006734      0.82278043      7       205     RNA
catabolic process



Tissue: Muscle_Skeletal=>Artery_Tibial  Type:   asymmetric
SourceGene:     TMED4(ENSG00000158604.9)
TargetGeneSet:  FAM132A GNB1    PANK4   GPR157  SLC25A34        RP4     FAM43B
EIF4G3  RP1     SYF2    DLGAP3  STK40   KCNQ4   IPO13   SLC6A9  ZFYVE9  RP11
FPGT-TNNI3K     LRRC39  SLC16A1 GDAP2   NOTCH2  PMF1    SMG5    PEA15   FAM78B
TATDN3  LIN9    NUP133  TOMM20  LYST-IT1        PXDN    TRAPPC12-AS1    KHK     PREB
EXOC6B  SPR     FAHD2A  STARD7  ACVR1   BTF3L4P2        FASTKD1 UBE2V1  NCKAP1  KLF7
INHA    AGAP1   MTMR14  UBP1    GOLGA4  TRAK1   PHF7    PBRM1   SPCS1   TMEM110
RPL10AP6        PTPLB   LRRC34  ABCC5   VPS8    TM4SF19-AS1     TMEM128 SHROOM3
NUDT10  EXOSC9  SPATA5  NAA15   OTUD4   WWC2    CTD     C7      FBXO4   RNF138P1
PPIP5K2 SEC24A  SLU7    ARL10   C6orf228        LST1    AGER    RPL10A  SRPK1
ASCC3   BVES    C6orf72 MTRF1L  PSMB1   C7orf50 TMEM196 TMED4   GTF2I   GTF2IRD2B
TAF6    FBXO24  PMPCB   COG5    WDR91   SLC4A2  LMBR1   ARHGEF10        CHMP7
SGK196  CHD7    C8orf46 MYBL1   FBXO43  C8orf33 SNAPC3  ACO1    DCTN3   VPS13A
BICD2   FSD1L   STXBP1  AK8     CAMSAP1 C9orf69 RNF224  NOXA1   PFKP    FAM208B CDNF
FAM190B C10orf12        MGEA5   SFR1    ACADSB  PWWP2B  CARS    TRIM44  PEX16   DDB2
PLCB3   KDM2A   PANX1   FAM76B  TIMM8B  TTC12   CCDC84  DPAGT1  ERC1    C12orf33
LRP6    C12orf69        LMO3    KIF21A  H1FNT   LETMD1  PRR13   HOXC13  HOXC5
B4GALNT1        XPOT    RIC8B   SSH1    TAOK3   MLEC    ZNF605  TPTE2   SACS    DGKH
LINC00441       DIAPH3-AS1      OXA1L   EAPP    FANCM   EXOC5   CHURC1  EXD2
SRSF5   GSTZ1   PTPN21  TTC7B   MEG8    TYRO3   TP53BP1 UBAP1L  HEXA    NEO1
C15orf27        ZNF592  RHOT2   ADCY9   GLIS2   CLEC16A NDE1    KIF22   TBX6
GNAO1   MMP15   DDX19B  GAN     MPRIP   ALKBH5  LLGL1   CCDC144C        C17orf51
ANKRD13B        CCT6B   PGAP3   SMARCE1 DUSP3   CDK5RAP3        BPTF    NT5C
SOGA2   GNAL    WDR7    APC2    REEP6   LMNB2   PIP5K1C CATSPERD        CARM1
SYCE2   SAMD1   U2AF1L4 ALKBH6  ZNF345  SIPA1L3 ZNF226  EHD2    CYTH2   C19orf48
NLRP9   ZNF460  ZNF552  ZSCAN22 ZNF446  SNPH    TASP1   POLR3F  RP3     SLC35C2
USP25   CHAF1B  MICAL3  ZNF74   CRKL    MAPK1   ZNF70   GAS2L1  PICK1   CTA
```

```
RANGAP1 C22orf32        TCF20   ZBED4   POLA1   RBM3    SUV39H1 RRAGB   THOC2
RBMX2   RBMX    RP13
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
Tissue: Artery_Tibial=>Muscle_Skeletal  Type:   asymmetric
```

```
SourceGene:     TMEM106C(ENSG00000134291.7)     ?
```

```
TargetGeneSet:  C1orf174        RPL22   H6PD    CTNNBIP1        IPP     CPT2    RP4
GBP3    SLC35A3 RP11    S100A12 CHTOP   POU2F1  JMJD4   IBA57   UBC     POLE4   RPIA
RPL31   ARL6IP6 BBS5    EEF1B2  D2HGDH  CHCHD4  RPL29   PTPRG   RPL24   RAB41   H1FX
VPS8    RPL34   PHF17   RTN3P1  GARS    RPS3A   LPCAT1  LEAP2   ZFP2    CCDC90A
TOB2P1  RPS18   MRPS12  IYD     TATDN2P2        FBXL18  EEF1A1P6        LINC00265
RPS3AP26        IFRD1   PPP2R2A ASPH    SLC26A7 ZNF707  C9orf106        USP20
NUP214  NKX2-1  RPL7A   SEC16A  VDAC2   ART1    CHRNA10 RNF141  NAALADL1
ATG16L2 MMP8    TTC12   RPS25   TBCEL   PFDN5   ARHGAP9 DDIT3   THAP2   TRAFD1  CDK8
TPT1    C14orf21        SFTA3   DDX24   WDR25   RPS3AP47        TGM7    RPS3AP6
NAGPA   ITGAX   CKLF    DYNC1LI2        TMEM170A        CMC2    MTHFSD  RPS7P1  PIGS
RPL23A  RPL27   GNG8    COG1    CTD     ADNP2   PRR22   EMR1    PEX11G  C19orf59
KLHL26  ZNF30   FXYD7   PRR19   VASP    PYGB    CDH4    RAC2    LDOC1L  GPR64
SUV39H1 PQBP1   RPL39

GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
```

```
GO:0006414      9.75E-16        31.37582418     0.610338385     14      105
translational elongation
```

GO:0006415	4.38E-15	33.54225352	0.528959934	13	91	translational termination
GO:0000184	5.90E-15	27.16571429	0.691716836	14	119	"nuclear-transcribed mRNA catabolic process, nonsense-mediated decay"
GO:0006614	2.99E-14	28.41013472	0.610338385	13	105	SRP-dependent cotranslational protein targeting to membrane
GO:0006613	3.40E-14	28.1026806	0.616151131	13	106	cotranslational protein targeting to membrane
GO:0045047	3.40E-14	28.1026806	0.616151131	13	106	protein targeting to ER

GO:0072599	3.40E-14	28.1026806	0.616151131	13	106	establishment of protein localization to endoplasmic reticulum
GO:0070972	1.40E-13	24.87002012	0.68590409	13	118	protein localization to endoplasmic reticulum
GO:0072594	6.61E-13	16.30779848	1.185800291	15	204	establishment of protein localization to organelle
GO:0000956	8.12E-13	18.33806452	0.982354162	14	169	nuclear-transcribed mRNA catabolic process
GO:0006402	1.66E-12	17.32073171	1.034668881	14	178	mRNA catabolic process

GO:0019080 viral genome expression	3.47E-12	18.87905695	0.877724725	13	151
GO:0019083 viral transcription	3.47E-12	18.87905695	0.877724725	13	151
GO:0006413 translational initiation	3.78E-12	18.74191914	0.883537471	13	152
GO:0006612 protein targeting to membrane	4.11E-12	18.60674044	0.889350218	13	153
GO:0043624 cellular protein complex disassembly	4.11E-12	18.60674044	0.889350218	13	153

GO:0043241	6.21E-12	17.95881496	0.918413951	13	158	protein complex disassembly
GO:0006401	1.14E-11	14.84397906	1.191613037	14	205	RNA catabolic process
GO:0034623	2.12E-11	16.15589187	1.011417895	13	174	cellular macromolecular complex disassembly
GO:0032984	3.04E-11	15.66375361	1.040481628	13	179	macromolecular complex disassembly
GO:0019058	7.29E-10	11.88377051	1.342744447	13	231	viral infectious cycle

GO:0071845	8.63E-10	10.44222222	1.650820012	14	284
cellular component disassembly at cellular level					
GO:0022411	1.03E-09	10.28686131	1.674070999	14	288
cellular component disassembly					
GO:0022415	3.08E-09	10.4670126	1.511314096	13	260
viral reproductive process					
GO:0033365	1.11E-08	7.161796885	2.749429105	16	473
protein localization to organelle					

```
GO:0006605      1.14E-08        7.145646031     2.755241852     16      474
protein targeting



GO:0016032      2.93E-07        6.375286041     2.621548682     14      451
viral reproduction



Tissue: Muscle_Skeletal=>Artery_Tibial  Type:   asymmetric
SourceGene:     all_source
TargetGeneSet:  MIR133A2        RPL36P4 MT1P2   APLP1   SLC7A11 CALCRL  MAGI2
PMP22   ELOVL3  RBM38   TPH1    SNAI1   C6orf25 C10orf99        PRMT8   GK5
FHDC1   CTB     HSD11B2 MAP3K1  DGCR2   OXSM    LINC00452       CCL21   ITIH4-AS1
ICOS    DUTP7   ZBTB34  LRRC6   APAF1   TSPYL6  LSR     B3GALTL C10orf32
TRIB1   NHSL1   LCE2A   PQBP1   RPS12P26        ART1    C1orf229        CD247   CSF3
GALNT14 EEF1A1P12       NUAK1   PBK     TELO2   ATP6V1A NF2     RP13    HBEGF
FAM174A WDR25   TBC1D2B RP1     DOPEY1  MPO     CLVS2   SORBS1  ZC3HC1  RNF122
SAMD15  PROM1   TM4SF1  TMED4   PRICKLE2        PHEX-AS1        WISP3   FAM46A
MCRS1   USP20   RNF141  MAPK13  MAFK    HOMEZ   PLCXD2  GPRC5C  C1orf174        KLF4
PIGL    BUD13   NFE2L3  NACA2   GABRB2  NPPB    EEPD1   U6      LSM14B  MTERFD2 CINP
IGHV3-74        ZSWIM3  RASD1   NPFF    RBAK    C15orf57        PPP1R10 C15orf23
MYO18B  ADAM33  PDZK1IP1-AS1    PITX3   PITX2   KLLN    FAM173A DNAJC12 GIT1
HIBADH  PDF     MTHFD1P1        FAM181A-AS1     ABCA9   RALGAPA2        DNAH11  FOS
VEZF1P1 LYL1    SNORA7A SRGAP2-IT1      CDH4    PCBP2P1 RALGPS1 PDK1    NOG
ARPC3P1 MTRNR2L1        USP54   GPR124  C2CD2   GAPDHP44        CHAD    MMP28
SLC35A3 C8orf42 BACE2   DNM1P33 CTD     JAKMIP1 UBOX5   SVIP    HIPK4   C1orf9
CCDC57  SH2B1   RP4     U1      TRAF3IP1        MYSM1   C6orf162        ARFGAP3
AP5Z1   SOCS1   AVIL    CHRNA10 PABPC3  C16orf45        PDCD6   FAM53C  MTA2
TRAPPC9 C15orf44        CYB5R1  IQSEC2  ADPRHL1 POLH    JMJD4   SULT1A3 MRPS2
PAFAH1B2        IRF2BPL POLR2B  TTLL7-IT1       AIF1L   APOBEC2 CACNG1  PCP2
MTHFSD  RP11    SYT12   TMEM140 TMEM171 HCG20   CEBPE   NR1I3   PTGDR2  COX7A2P1
RNASEH1 IL13    SLC22A13        ZNF678  EBF2    GAPDHP62        VGLL4   LIPJ
EIF4A1P7        HNRNPH2 PITPNM3 FAM181A KLHL26  TAF1C   GLTPD1  TEAD3   ZNF689  PBX1
C3orf37 SPHK2   WIPI2   TYMP    IFNG    TNFAIP8L1       PHLDA1  ZNF329  TCEB1P2 IL6R
PEX10   PUF60   EBF1    BMP4    E2F3    BMP5    TMEM50B HMOX1   DFFB    FTLP3
MTND4P24        MT
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0048660      2.77023798858757e-08    15.7433660933661        0.695315203100132
9       64      regulation of smooth muscle cell proliferation
GO:0048659      4.18321374063363e-08    14.925908667288 0.72790810324545        9
67      smooth muscle cell proliferation
GO:0033002      7.86852492477653e-08    11.3717486994798        1.03210850460176
10      95      muscle cell proliferation
GO:0048661      3.62512358780466e-06    17.1715833835039        0.423707701889143
6       39      positive regulation of smooth muscle cell proliferation
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Tissue: Artery_Tibial=>Nerve_Tibial     Type:   asymmetric
SourceGene:     C10orf35(ENSG00000171224.7)
TargetGeneSet:  RPL22   ZMYND12 PPCS    LRRC41  ATPAF1  BTF3L4  RP11    RPL5    RP4
ATP5F1  RPS27   CAMSAP2 KLHL12  SNRPE   SOX13   PLXNA2  BROX    ARV1    CNST
PPM1B   MTHFD2  COA5    UNC50   CCDC115 NIF3L1  RPL37A  SETD5   RPL15   KIF9
TRAIP   RPL29   SPCS1   RNF7    MBNL1   RSRC1   FNDC3B  METTL19 C4orf52 THAP6
COPS4   MRPS18C RPL34   KIAA0922        TAF9    BTF3    XRCC4   HINT1   AFF4    SKP1
SH3PXD2B        NOL7    MRPS18B RPL10A  GAPDHP15        RPL39P3 MRPS12  RP1
ARID1B  TMEM181 BUD31   FAM200A FBXO24  KAT6A   C8orf40 C8orf22 XKR4    RPS20
RPL30   POLR2K  ZHX1    C9orf123        DCTN3   RPL12   MRPL41  COX15   SFR1
RPS13   EIF3M   DDB2    POLR2G  FCHSD2  C11orf1 ATP5L   RPS25   C12orf57
C12orf47        ELF1    COMMD6  STK24   LTB4R   KTN1    ISCA2   PSMC1   C14orf142
RPL3P4  DTWD1   CARHSP1 CTA     LCMT1   NAE1    DERL2   RPL26   MAPK7   RPL17
RPL38   DUS1L   FOXK2   CTD     RPL36   BRD4    JPH2    ATP5J   CSDC2   C22orf40
RPS2P55 ATRX
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006614      1.38481720267066e-21    41.5978630403108        0.646668050653934
18      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.6602657582738e-21     41.1222791293214        0.652826793993495
18      106     cotranslational protein targeting to membrane
GO:0045047      1.6602657582738e-21     41.1222791293214        0.652826793993495
18      106     protein targeting to ER
GO:0072599      1.6602657582738e-21     41.1222791293214        0.652826793993495
18      106     establishment of protein localization to endoplasmic reticulum
GO:0006415      4.21536756381393e-21    45.5885885885886        0.560445643900076
17      91      translational termination
GO:0070972      1.27463902762592e-20    36.1571830985916        0.726731714068231
18      118     protein localization to endoplasmic reticulum
GO:0019080      4.3944017071538e-20     29.2608225108225        0.929970244273753
19      151     viral genome expression
GO:0019083      4.3944017071538e-20     29.2608225108225        0.929970244273753
19      151     viral transcription
GO:0006414      5.62679419065913e-20    38.2982954545455        0.646668050653934
17      105     translational elongation
GO:0000184      5.23620634255959e-19    33.0092592592593        0.732890457407792
17      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006413      1.42411153623148e-18    26.9186462055918        0.936128987613314
18      152     translational initiation
GO:0006612      1.60641818017974e-18    26.7173708920188        0.942287730952875
18      153     protein targeting to membrane
GO:0019058      7.75988172814626e-18    19.4395219451885        1.42266971143865
20      231     viral infectious cycle
GO:0043624      4.213261542162e-17      24.6979166666667        0.942287730952875
17      153     cellular protein complex disassembly
GO:0043241      7.32595854230213e-17    23.813731284476 0.973081447650682       17
158     protein complex disassembly
GO:0022415      7.96107871597996e-17    17.0555555555556        1.60127326828593
20      260     viral reproductive process
GO:0000956      2.31817905642901e-16    22.0732821637427        1.04082762438586
17      169     nuclear-transcribed mRNA catabolic process
GO:0072594      2.92975829806545e-16    19.3221263062244        1.2563836412705 18
204     establishment of protein localization to organelle
GO:0034623      3.80902046211827e-16    21.3627919320594        1.07162134108366
17      174     cellular macromolecular complex disassembly
GO:0006402      5.60386723225121e-16    20.8261732229124        1.09625631444191
17      178     mRNA catabolic process
GO:0032984      6.16251868877569e-16    20.696159122085 1.10241505778147        17
179     macromolecular complex disassembly
GO:0016032      2.34714639752683e-15    11.3452987822147        2.77759324614214
23      451     viral reproduction
GO:0006401      6.04928694818813e-15    17.8012706855792        1.26254238461006
17      205     RNA catabolic process
GO:0071845      6.78592096436273e-15    14.4389757412399        1.7490831084354 19
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284     cellular component disassembly at cellular level
GO:0022411      8.76344183537776e-15    14.220233669676 1.77371808179365        19
288     cellular component disassembly
GO:0033365      5.79041800110511e-11    8.31504090623033        2.91308559961248
19      473     protein localization to organelle
GO:0006605      6.00373783552746e-11    8.29616954474097        2.91924434295204
19      474     protein targeting
Tissue: Nerve_Tibial=>Artery_Tibial     Type:   asymmetric
SourceGene:     CROCCP3(ENSG00000080947.9)
TargetGeneSet:  RP13    RP11    KHDRBS1 IPP     BEND5   LYPLAL1 TOMM20  ABHD1
DDIT3   EIF3FP3 FAHD2B  MCM6    FMNL2   PPIG    LRRN4   RPL15   SPCS1   CPOX
RPL24   NDUFB4  ITGB5-AS1       DHX36   ATP5G1P4        ABCC5   WDFY3-AS1
OTUD4   EPB41L4A-AS1    CCT5P1  CTB     RPL26L1 ARL10   TBC1D9B RPS10   RPL10A
C6orf226        MRPL2   RP1     DDO     SOGA3   SPDYE1  RP4     RHBDD2  STAG3
HMBOX1  C8orf40 PRKDC   RPS20   CHCHD7  SNHG6   TATDN1  EEF1D   TONSL   RPL8
RPL35   RPL12   NOXA1   CDNF    ZNF37BP DDIT4   CTD     EIF3F   RPL27A  NDUFV1  PHB2
ZCRB1   TIMELESS        NACA    YEATS4  ISCU    C12orf51        SMAD9-AS1
C13orf44-IT1    DHRS12  SYNE2   CEP152  GS1     SMG1    GTF3C1  NUDT21  DDX19B
COX4I1  RPL13   C17orf108       ACACA   RPL19   CCR10   ZADH2   RPL36   PRR24
RPL18   ZNF341  MT1P3   SCAND1  SLC2A4RG        USP16   URB1    CHCHD10 CTA
PLCXD1  RP3     FAM122C RPL10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      6.90619840747159e-20    45.0668243642815        0.530413120199294
16      105     translational elongation
GO:0006614      6.90619840747159e-20    45.0668243642815        0.530413120199294
16      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      8.10359646248825e-20    44.562962962963 0.535464673725002       16
106     cotranslational protein targeting to membrane
GO:0045047      8.10359646248825e-20    44.562962962963 0.535464673725002       16
106     protein targeting to ER
GO:0072599      8.10359646248825e-20    44.562962962963 0.535464673725002       16
106     establishment of protein localization to endoplasmic reticulum
GO:0006415      3.14843541559965e-19    48.6683303085299        0.459691370839388
15      91      translational termination
GO:0070972      4.89284304868317e-19    39.2872377020984        0.596083316033493
16      118     protein localization to endoplasmic reticulum
GO:0000184      5.63177529675806e-19    38.9030829500937        0.6011348695592 16
119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006413      3.16844260983172e-17    29.3952528379773        0.76783613590755
16      152     translational initiation
GO:0006612      3.52523541807684e-17    29.1786400307338        0.772887689433257
16      153     protein targeting to membrane
GO:0043241      5.94358273078551e-17    28.1413392636521        0.798145457061795
16      158     protein complex disassembly
GO:0072594      1.583500418993e-16      23.0373376623377        1.03051691924434
17      204     establishment of protein localization to organelle
GO:0000956      1.76493880694697e-16    26.0979245499369        0.853712545844578
16      169     nuclear-transcribed mRNA catabolic process
GO:0006402      4.06609441071111e-16    24.6324453108079        0.899176527575946
16      178     mRNA catabolic process
GO:0032984      4.44848468912443e-16    24.4796039177699        0.904228081101654
16      179     macromolecular complex disassembly
GO:0019080      8.244973911826e-16      27.0829107505071        0.762784582381842
15      151     viral genome expression
GO:0019083      8.244973911826e-16      27.0829107505071        0.762784582381842
15      151     viral transcription
GO:0043624      1.00652448871285e-15    26.6866566716642        0.772887689433257
15      153     cellular protein complex disassembly
GO:0006401      3.86587428900499e-15    21.0734243014945        1.03556847277005
16      205     RNA catabolic process
GO:0034623      6.98680755445834e-15    23.1278464541314        0.878970313473116
15      174     cellular macromolecular complex disassembly
GO:0019058      4.61240226551949e-13    16.9564176245211        1.16690886443845
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15      231     viral infectious cycle
GO:0022411      7.76646211009645e-13    14.5572755417957        1.45484741540378
16      288     cellular component disassembly
GO:0022415      2.56567103853682e-12    14.9187192118227        1.31340391668397
15      260     viral reproductive process
GO:0071845      9.11819223887337e-12    13.5646071016536        1.43464120130095
15      284     cellular component disassembly at cellular level
GO:0033365      1.40679287257283e-11    10.0145454545455        2.38938481765968
18      473     protein localization to organelle
GO:0006605      1.4569105049423e-11     9.99186602870813        2.39443637118538
18      474     protein targeting
GO:0016032      6.3932193816875e-10     8.99729784230692        2.27825064009411
16      451     viral reproduction
Tissue: Nerve_Tibial=>Artery_Tibial     Type:   asymmetric
SourceGene:     CTA-520D8.2(ENSG00000237445.1)
TargetGeneSet:  RP11    ARNT    EEF1B2  GPR55   TMEM43  RPL29   RPL24   GPRIN3
ITGA1   CTB     RPS10   RPL7    EIF3H   EEF1D   NAA35   EDF1    PIK3AP1 RPS3
BUD13   RPL18AP3        RPL6    RPL13   RPL23A  RPL17   RPL19   RPL18A  RPS16
RPL18   CD33    UBE2M   CHMP4B  RALY    RPS21   SH3KBP1 NUP62CL
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      5.02934023179459e-27    171.757303370787        0.225243927755865
16      105     translational elongation
GO:0006415      1.31799727206099e-23    153.401069518717        0.195211404055083
14      91      translational termination
GO:0006614      1.11465811618562e-22    129.674208144796        0.225243927755865
14      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.28286079883624e-22    128.255754475703        0.227389108020206
14      106     cotranslational protein targeting to membrane
GO:0045047      1.28286079883624e-22    128.255754475703        0.227389108020206
14      106     protein targeting to ER
GO:0072599      1.28286079883624e-22    128.255754475703        0.227389108020206
14      106     establishment of protein localization to endoplasmic reticulum
GO:0006413      2.74222482694532e-22    97.7395072992701        0.326067400179918
15      152     translational initiation
GO:0070972      6.24825863287656e-22    113.361990950226        0.253131271192305
14      118     protein localization to endoplasmic reticulum
GO:0000184      7.07352833397243e-22    112.274509803922        0.255276451456647
14      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      2.27927918353134e-20    85.8574495491627        0.323922219915577
14      151     viral genome expression
GO:0019083      2.27927918353134e-20    85.8574495491627        0.323922219915577
14      151     viral transcription
GO:0006612      2.75724644608103e-20    84.6102412187897        0.32821258044426
14      153     protein targeting to membrane
GO:0043624      2.75724644608103e-20    84.6102412187897        0.32821258044426
14      153     cellular protein complex disassembly
GO:0043241      4.3880052088887e-20     81.6437908496732        0.338938481765968
14      158     protein complex disassembly
GO:0000956      1.15722733570687e-19    75.7912713472486        0.362535464673725
14      169     nuclear-transcribed mRNA catabolic process
GO:0034623      1.75945658274205e-19    73.3970588235294        0.373261365995433
14      174     cellular macromolecular complex disassembly
GO:0006402      2.43793015979867e-19    71.5868005738881        0.381842087052799
14      178     mRNA catabolic process
GO:0032984      2.6418492968021e-19     71.1479500891266        0.383987267317141
14      179     macromolecular complex disassembly
GO:0072594      1.71051515428738e-18    61.6780185758514        0.43761677392568
14      204     establishment of protein localization to organelle
GO:0006401      1.83385229797468e-18    61.3507853403141        0.439761954190021
14      205     RNA catabolic process
GO:0019058      9.98733941194616e-18    53.9013282732448        0.495536641062902
14      231     viral infectious cycle
GO:0022415      5.30005349293814e-17    47.4500239120038        0.557746868728808
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14      260     viral reproductive process
GO:0071845      1.83128841043921e-16    43.1590413943355        0.609231195073005
14      284     cellular component disassembly at cellular level
GO:0022411      2.22765937577193e-16    42.516960068699 0.617811916130372       14
288     cellular component disassembly
GO:0016032      1.11223409867631e-13    26.3510566698075        0.967476299218047
14      451     viral reproduction
GO:0033365      2.13374419548453e-13    25.0485710624119        1.01467026503356
14      473     protein localization to organelle
GO:0006605      2.19619968406647e-13    24.9923273657289        1.0168154452979 14
474     protein targeting
Tissue: Artery_Tibial=>Nerve_Tibial     Type:   asymmetric
SourceGene:     DCTN3(ENSG00000137100.10)
TargetGeneSet:  RP11    RPL22   ZBTB17  KPNA7   EIF3I   RP4     MAP7D1  UQCRH
DIRAS3  PIGK    COL24A1 ATP5F1  ANKRD35 APH1A   MRPS21  SMG5    MNDA    TSTD1
TMCO1   DENND1B CAMSAP2 SNRPE   TMEM81  IKBKE   BROX    LYST-IT1        ZNF692
YWHAQ   TTC32   SLC5A6  RPLP0P6 DHX57   MORN2   NFU1    TPRKB   CAPG    GGCX
RPL31   SMPD4   CCDC115 FMNL2   SPC25   SCRN3   CHRNA1  HOXD-AS2        RBM45
KCTD18  NDUFB3  IMPDH1P10       LANCL1  GPR55   OR6B3   SETD5   ZNF197  PTPN23  RBM6
VPRBP   SPCS1   ARL6IP5 GXYLT2  CLDN18  ARID4A  MRPL47  NDUFB5  EIF4G1  KIAA0226
RPL35A  MYL5    NOP14   TLR1    UTP3    MRPS18C RPL34   PLK4    MGST2   OTUD4   BTF3
XRCC4   CTD     UQCRQ   UBE2D2  CTB     TCOF1   CD74    RPS14   ARL10   TMEM14C
TMEM14B PRSS16  PPP1R10 LST1    C6orf48 HLA-DMB HLA-DMA RPS10   HNRNPC  RP3
KIAA0240        C6orf226        MAD2L1BP        VEGFA   RPL39P3 COX7A2  ASF1A
SLC18B1 MRPS12  ARID1B  C6orf70 SNX8    NDUFA4  LSM5    SEC61G  GS1     ACN9    PUS7
NDUFA5  KAT6A   MRPL15  RPS20   PENK    C8orf59 FAM82B  TP53INP1        UQCRB
COX6C   POLR2K  KIAA0196        RP13    FAM83H  C9orf123        DCTN3   GBA2
LINC00475       SEC61B  STXBP1  ODF2    ZDHHC12 C9orf114        FAM78A  FAM208B
FBXO18  ATP5C1  COMMD3  PARD3   TMEM26  PBLD    IFIT2   RPP30   RPL13AP5
PPRC1   MRPL23  NUP98   ZNF143  RPS13   NDUFS3  FNBP4   MRPL16  CPSF7   SDHAF2
INCENP  MTA2    SF1     KLC2    LAMTOR1 CLPB    C11orf30        INTS4   USP28
PCSK7   ATP5L   RPS25   DPAGT1  TBCEL   KCNJ5   RAD52   C12orf57        DDX23
SPRYD3  PHC1P1  SLC25A3 SART3   TMEM119 COX6A1  RPS7P10 SACS    LPAR6   COMMD6
ACIN1   RPS29   BCRP2   ERH     NEK9    POMT2   NDUFB1  GLRX5   RPL3P4  BTBD6   NDN
SLC24A5 RSL24D1 PIGB    GTF2A2  FAM96A  NDUFB10 NPIPL3  POLR3E  NDUFAB1 KIF22
BCL7C   MIR4519 PYCARD  C16orf57        NAE1    RANBP10 AARS    DDX19A  SF3B3
USP10   ZNF469  NDEL1   CDRT4   FAM106B LIG3    MLLT6   RPL17   PGAP3   VPS25
RPL27   SAMD14  HILS1   SUPT4H1 SKA2    H3F3B   CBX4    C17orf90        ZFP161
IMPACT  UQCR11  C19orf10        C19orf70        RPL36   TRIP10  PEX11G  CARM1   BRD4
PGLS    ZNF85   UQCRFS1 ANKRD27 CLASRP  TRAPPC6A        RTN2    SNRPD2  ZNF541
TBC1D17 CLEC11A CNOT3   RPS9    NLRP9   ZIK1    ZNF552  TBC1D20 ZNF343  FTLP3
SNRPB2  TM9SF4  ROMO1   SNHG11  PFDN4   STMN3   ATP5J   MIS18A  C21orf67
MRPL40  DGCR6L  PI4KA   BCR     CRYBB3  UQCR10  PIK3IP1 APOBEC3H        RANGAP1
GTPBP6  SLC25A6 EEF1B2P3        ATP6AP2 RPS2P55 TIMP1   RPL7P57 PHF8    PDZD11
RPS23P8 MED12   RGAG4   TREX2   ARHGAP4
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      1.88458437076499e-18    18.9515789473684        1.52792194311812
21      96      respiratory electron transport chain
GO:0022900      2.47680787658444e-15    12.5446923826057        2.13272437893571
21      134     electron transport chain
GO:0045333      8.25666345961817e-15    11.7086480287872        2.26005120752889
21      142     cellular respiration
GO:0006614      7.07593781295201e-13    12.8180217669654        1.67116462528545
17      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      8.30987319424839e-13    12.6731022841167        1.68708047885959
17      106     cotranslational protein targeting to membrane
GO:0045047      8.30987319424839e-13    12.6731022841167        1.68708047885959
17      106     protein targeting to ER
GO:0072599      8.30987319424839e-13    12.6731022841167        1.68708047885959
17      106     establishment of protein localization to endoplasmic reticulum
GO:0006119      5.01854264201393e-12    18.8722990271377        0.923119507300533
13      58      oxidative phosphorylation
GO:0070972      5.0241719492898e-12     11.1579045228467        1.87807072174936
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17      118     protein localization to endoplasmic reticulum
GO:0042773      6.33921836763452e-12    22.310878112713 0.748045117984915       12
47      ATP synthesis coupled electron transport
GO:0042775      6.33921836763452e-12    22.310878112713 0.748045117984915       12
47      mitochondrial ATP synthesis coupled electron transport
GO:0006612      3.84007161473665e-11    8.85911949685535        2.43512559684451
18      153     protein targeting to membrane
GO:0000184      6.33694622180209e-11    10.2480718628074        1.89398657532351
16      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006414      1.05640758098325e-10    10.9542635658915        1.67116462528545
15      105     translational elongation
GO:0015980      1.26958528003733e-10    5.73796699715256        4.88616704726317
24      307     energy derivation by oxidation of organic compounds
GO:0006415      1.62733343099736e-10    11.9057239057239        1.44834267524739
14      91      translational termination
GO:0000956      2.03489396210353e-10    7.91140822191678        2.68977925403086
18      169     nuclear-transcribed mRNA catabolic process
GO:0006413      3.05447468900562e-10    8.32766475395583        2.41920974327036
17      152     translational initiation
GO:0006402      4.79192681795886e-10    7.46161556603774        2.83302193619819
18      178     mRNA catabolic process
GO:0019080      2.30109816367139e-09    7.80117687781239        2.40329388969621
16      151     viral genome expression
GO:0019083      2.30109816367139e-09    7.80117687781239        2.40329388969621
16      151     viral transcription
GO:0072594      4.3470597684874e-09     6.40672550213025        3.24683412912601
18      204     establishment of protein localization to organelle
GO:0006401      4.69892492085097e-09    6.37201089698315        3.26274998270016
18      205     RNA catabolic process
GO:0019058      5.12462939122301e-09    5.95034874362872        3.67656217562798
19      231     viral infectious cycle
GO:0006091      2.10454133579994e-08    4.1814440476911 6.81198532973497        25
428     generation of precursor metabolites and energy
GO:0043624      2.14279131117529e-08    7.11981799797775        2.43512559684451
15      153     cellular protein complex disassembly
GO:0043241      3.3111925186411e-08     6.86843389168971        2.51470486471524
15      158     protein complex disassembly
GO:0022415      3.51702201328691e-08    5.22349609643861        4.13812192927825
19      260     viral reproductive process
GO:0006120      7.51400194916751e-08    18.2664092664093        0.572970728669296
8       36      mitochondrial electron transport, NADH to ubiquinone
GO:0034623      1.19904119548825e-07    6.17025010969724        2.7693585219016 15
174     cellular macromolecular complex disassembly
GO:0006605      1.52243093578566e-07    3.74056168178608        7.54411459414573
25      474     protein targeting
GO:0032984      1.74020569964455e-07    5.98000567214974        2.84893778977233
15      179     macromolecular complex disassembly
GO:0071845      6.79424322897455e-07    4.45435522769187        4.52010241505778
18      284     cellular component disassembly at cellular level
GO:0022411      8.32543055384426e-07    4.38710691823899        4.58376582935437
18      288     cellular component disassembly
GO:0033365      1.9965500502194e-06     3.40024691358025        7.52819874057159
23      473     protein localization to organelle
GO:0016032      3.2040933158498e-06     3.40039447731755        7.17804996194035
22      451     viral reproduction
GO:0006122      1.57328230397114e-05    187.929515418502        0.0636634142965885
3       4       mitochondrial electron transport, ubiquinol to cytochrome c
Tissue: Nerve_Tibial=>Artery_Tibial     Type:   asymmetric
SourceGene:     ENSG00000258604.1
TargetGeneSet:  MTND1P23        RPL22   KHDRBS1 RP11    ADORA3  KCNT2   UBC
PLEKHB2 SATB2   EEF1B2  AGFG1   RPL15   RPL14   STAB1   RPL10AP6        RPL24
SEC62   RAC1P2  CTD     RPL10A  MRPL2   EIF4H   FAM71F1 CLEC5A  RPL7    RPS6
RPL35   RPS13   SAA2-SAA4       SAA1    RPL41   RPL14P1 CHPT1   RPL7AP6 NETO2
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ZNF29P  RPS7P1  RPL23A  RPL17   RPL19   RAB31   CRLF1   FXYD1   HNRNPL  PRR24
RPL18   SYP     RPL10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      4.60435519401376e-28    153.772727272727        0.254307660369525
17      105     translational elongation
GO:0006613      5.47734464382063e-28    152.034332084894        0.25672963808733
17      106     cotranslational protein targeting to membrane
GO:0006415      5.61898119021901e-27    161.021754385965        0.220399972320255
16      91      translational termination
GO:0006614      6.63757336611401e-26    135.560023654642        0.254307660369525
16      105     SRP-dependent cotranslational protein targeting to membrane
GO:0045047      7.80784890738954e-26    134.044444444444        0.25672963808733
16      106     protein targeting to ER
GO:0072599      7.80784890738954e-26    134.044444444444        0.25672963808733
16      106     establishment of protein localization to endoplasmic reticulum
GO:0006413      3.64041620113799e-25    99.9082304526749        0.368140613106359
17      152     translational initiation
GO:0006612      4.09060402366082e-25    99.1666666666667        0.370562590824164
17      153     protein targeting to membrane
GO:0070972      4.85756512067118e-25    118.175438596491        0.28579337070099
16      118     protein localization to endoplasmic reticulum
GO:0000184      5.60514234428549e-25    117.019928461932        0.288215348418795
16      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      3.06778938257395e-23    89.082261208577 0.365718635388554       16
151     viral genome expression
GO:0019083      3.06778938257395e-23    89.082261208577 0.365718635388554       16
151     viral transcription
GO:0043624      3.81957819605949e-23    87.7694967345371        0.370562590824164
16      153     cellular protein complex disassembly
GO:0043241      6.52086191731666e-23    84.6493699036323        0.382672479413189
16      158     protein complex disassembly
GO:0000956      1.99037797474661e-22    78.5029239766082        0.409314234309044
16      169     nuclear-transcribed mRNA catabolic process
GO:0034623      3.22294709479738e-22    75.9920053297801        0.421424122898069
16      174     cellular macromolecular complex disassembly
GO:0006402      4.68991096999289e-22    74.0948667966212        0.431112033769289
16      178     mRNA catabolic process
GO:0032984      5.14382636216027e-22    73.6351307717146        0.433534011487094
16      179     macromolecular complex disassembly
GO:0072594      4.40408747444263e-21    63.7312430011198        0.494083454432219
16      204     establishment of protein localization to organelle
GO:0006401      4.77093386266361e-21    63.3895850737956        0.496505432150024
16      205     RNA catabolic process
GO:0019058      3.3435978412586e-20     55.6220318237454        0.559476852812954
16      231     viral infectious cycle
GO:0022415      2.27217933231035e-19    48.9111302847282        0.629714206629299
16      260     viral reproductive process
GO:0071845      9.42866345048754e-19    44.4556166535742        0.687841671856619
16      284     cellular component disassembly at cellular level
GO:0022411      1.18057012549749e-18    43.7894736842105        0.697529582727839
16      288     cellular component disassembly
GO:0006605      1.16826820766969e-16    28.8479212253829        1.14801743823957
17      474     protein targeting
GO:0016032      1.46671598495031e-15    27.0654567453116        1.09231195073005
16      451     viral reproduction
GO:0033365      3.09473638919039e-15    25.7219854888863        1.14559546052176
16      473     protein localization to organelle
Tissue: Nerve_Tibial=>Artery_Tibial     Type:   asymmetric
SourceGene:     GBA2(ENSG00000070610.10)
TargetGeneSet:  RPL22   ZBTB40  PPIE    RPS8    RP11    WDR77   BCAS2   HIST2H2AC
SMG5    HDGF    KCNJ9   SMYD2   LYPLAL1 PSEN2   DDIT3   HAAO    RPL31   ANKRD44
SATB2   TATDN2  RPL15   CTDSPL  KRBOX1  ZDHHC3  RNF123  RPL29   ZNF717  DZIP3
NDUFB4  ALG1L   EIF4G1  TRA2B   OCIAD1  CLOCK   MAPK10  NDUFC1  TAF9    PCDHB16
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ARL10	RPS10	RPL10A	XPO5	MICAL1	C7orf50	IQCE	GPNMB	CDK13	IMPDH1	RP4
DCTN6	C8orf40	PAF1	GS1	ZNF706	DCTN3	FAM27D1	VPS13A	RABGAP1	RPL35
RPL12	SLC27A4	CAMSAP1	CXCL12	RP13	ACTR1A	RPL27A	MRVI1-AS1		MRVI1
RPS13	RARRES3	CPT1A	CTD	CBL	LTBR	RARG	STAT2	TIMELESS
PIP4K2C	YEATS4	RP1	CHPT1	EID3	C12orf51		MLEC	DIABLO	TPTE2P6
KATNAL1	DGKZP1	MED4	DHRS12	POMT2	AKT1	KIAA0284		AVEN	RPLP1
ZNF592	NUDT21	DOK4	FHOD1	WWOX	COX4I1	RPL13	KIF1C	KCTD11	FLII
C17orf108		SPAG5-AS1		KIAA0100		RPL23A	PIP4K2B	RPL19	MSL1	ACLY
ATXN7L3	TRIM65	RPL36	DNMT1	KCTD15	RPL18	TBC1D20	DUSP15	SOGA1	RALGAPB
DHX35	ELMO2	COL18A1	CECR5	PI4KA	RANGAP1	TCF20	SYP	MAGED2	KLF8
NAP1L2	TCEAL7
GOBPID	Pvalue	OddsRatio		ExpCount		Count	Size	Term
GO:0000184		4.19812441977784e-20	29.0904301075269		0.922289114940143
19	119	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006415		2.67184523221966e-19	34.4957325746799		0.705279911424815
17	91	translational termination
GO:0006414		3.49151455770065e-18	28.9793062200957		0.813784513182479
17	105	translational elongation
GO:0006614		3.49151455770065e-18	28.9793062200957		0.813784513182479
17	105	SRP-dependent cotranslational protein targeting to membrane
GO:0006613		4.13247995207642e-18	28.6516853932584		0.821534841879455
17	106	cotranslational protein targeting to membrane
GO:0045047		4.13247995207642e-18	28.6516853932584		0.821534841879455
17	106	protein targeting to ER
GO:0072599		4.13247995207642e-18	28.6516853932584		0.821534841879455
17	106	establishment of protein localization to endoplasmic reticulum
GO:0070972		2.74357353697432e-17	25.2262636789995		0.914538786243167
17	118	protein localization to endoplasmic reticulum
GO:0000956		3.85574698609524e-17	19.3255197132616		1.30980554978894
19	169	nuclear-transcribed mRNA catabolic process
GO:0006402		1.03274059701408e-16	18.2200581591939		1.37955850806173
19	178	mRNA catabolic process
GO:0006413		1.08657065817354e-16	20.2993013655129		1.17804996194035
18	152	translational initiation
GO:0043624		1.22379974471189e-16	20.1475177304965		1.18580029063733
18	153	cellular protein complex disassembly
GO:0043241		2.1899510816277e-16	19.4211246200608		1.22455193412221
18	158	protein complex disassembly
GO:0034623		1.23826262812777e-15	17.4095744680851		1.34855719327382
18	174	cellular macromolecular complex disassembly
GO:0006401		1.4638504110895e-15	15.5455543993525		1.58881738288008
19	205	RNA catabolic process
GO:0019080		1.94316001343214e-15	18.9697564807541		1.17029963324337
17	151	viral genome expression
GO:0019083		1.94316001343214e-15	18.9697564807541		1.17029963324337
17	151	viral transcription
GO:0032984		2.05195752714321e-15	16.8629575789613		1.3873088367587	18
179	macromolecular complex disassembly
GO:0006612		2.43064543588102e-15	18.6881578947368		1.18580029063733
17	153	protein targeting to membrane
GO:0072594		2.0648227822419e-14	14.5706932052162		1.5810670541831	18
204	establishment of protein localization to organelle
GO:0019058		2.25520135315448e-12	11.8113625184456		1.79032592900145
17	231	viral infectious cycle
GO:0071845		6.0318344171858e-12	10.130939049752	2.20109334994118		18
284	cellular component disassembly at cellular level
GO:0022411		7.62577873374238e-12	9.97801418439716		2.23209466472908
18	288	cellular component disassembly
GO:0006605		1.05901152812948e-11	7.51017699115044		3.67365580236662
22	474	protein targeting
GO:0022415		1.50265383879605e-11	10.3804201862681		2.01508546121376
17	260	viral reproductive process
GO:0033365		3.57356105773459e-09	6.2482828856994	3.66590547366964		19
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473     protein localization to organelle
GO:0016032      1.06978778669909e-08    6.14977150999951        3.49539824233617
18      451     viral reproduction
Tissue: Nerve_Tibial=>Artery_Tibial     Type:   asymmetric
SourceGene:     HDAC6(ENSG00000094631.13)
TargetGeneSet:  RPL22   HMGN2   KHDRBS1 RPS8    IPP     RP11    CD53    DPM3
KCNJ9   FCER1G  FCGR3A  SFT2D2  KCNT2   SNRPE   SRGAP3  CAPN8   LRPPRC  CAMKMT  UBC
RPL31   TTL     MZT2A   ANKRD44 SATB2   STK36   SLC23A3 RPL15   RPL14   RPL24
ALCAM   ALG1L   FAM86HP PCOLCE2 PARL    CLOCK   NAP1L5  RXFP1   CTD     THOC3   RP1
RPS10   RPL10A  MRPL2   EFHC1   MRAP2   SNHG5   MICAL1  MRPS12  C7orf50 ABCB5
TOMM7   OSBPL3  EIF4H   GTF2IP1 SSBP1   RARRES2 RPL7    EIF3H   EEF1D   RPS6
POLR1E  C9orf103        SLC44A1 C9orf43 RPL35   RPL12   AKR1C2  DDIT4   EIF3F
RPS13   MS4A7   RARRES3 RPS3    PHB2    AEBP2   CYP27B1 STAT2   RPL18AP3        RPL6
MLEC    MED4    TMCO3   RPS29   GS1     RPS3AP6 RPLP1   BCL7C   NETO2   NUDT21
FHOD1   EXOSC6  COX4I1  RPL13   C17orf108       KIAA0100        RPL23A  RPL17
RPL19   CCR10   HEXIM2  PPP4R1  RPS15   SNRPEP4 RPL36   RPL18A  FXYD1   OVOL3
HNRNPL  RPS16   PRR24   RPL18   SIGLEC9 RPL28   ZNF530  RPL24P2 NDRG3   ELMO2
PPDPF   SLC2A4RG        CLIC6   GPKOW   SYP     SRPX2   RBMX    RPL10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      1.82808473763696e-41    91.5428634555899        0.642308490761885
29      91      translational termination
GO:0006414      2.94892989231113e-41    79.3    0.741125181648329       30      105
translational elongation
GO:0006614      2.27785307734369e-39    74.6065248738284        0.741125181648329
29      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006413      2.67922162204485e-39    54.2057142857143        1.07286692962425
32      152     translational initiation
GO:0006613      3.12033054069613e-39    73.6324497420388        0.748183516711646
29      106     cotranslational protein targeting to membrane
GO:0045047      3.12033054069613e-39    73.6324497420388        0.748183516711646
29      106     protein targeting to ER
GO:0072599      3.12033054069613e-39    73.6324497420388        0.748183516711646
29      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      1.05707251201559e-37    63.6509158072957        0.832883537471455
29      118     protein localization to endoplasmic reticulum
GO:0000184      1.39080826296839e-37    62.9392694063927        0.839941872534773
29      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0043241      5.24348696189237e-37    48.8945325496285        1.11521694000415
31      158     protein complex disassembly
GO:0043624      8.84432528147779e-36    48.1910569105691        1.07992526468756
30      153     cellular protein complex disassembly
GO:0032984      3.3630335073767e-35     41.8948420251237        1.26344197633382
31      179     macromolecular complex disassembly
GO:0000956      2.19848923185318e-34    42.5959232613909        1.19285862570064
30      169     nuclear-transcribed mRNA catabolic process
GO:0019080      2.76508618823873e-34    46.3264091623625        1.06580859456093
29      151     viral genome expression
GO:0019083      2.76508618823873e-34    46.3264091623625        1.06580859456093
29      151     viral transcription
GO:0006612      4.17468835703725e-34    45.5728015908087        1.07992526468756
29      153     protein targeting to membrane
GO:0034623      5.59434162136755e-34    41.1024305555556        1.22815030101723
30      174     cellular macromolecular complex disassembly
GO:0006402      1.15585282491115e-33    39.9802927927928        1.2563836412705 30
178     mRNA catabolic process
GO:0072594      8.61177604755942e-32    33.9439655172414        1.43990035291675
30      204     establishment of protein localization to organelle
GO:0006401      1.00388074289027e-31    33.747619047619 1.44695868798007        30
205     RNA catabolic process
GO:0019058      1.19180948039549e-28    27.8219856232199        1.63047539962632
29      231     viral infectious cycle
GO:0022411      1.48329247308381e-28    23.9410314024223        2.03280049823542
31      288     cellular component disassembly
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GO:0022415      1.56525903941967e-28    25.5778985507246        1.83516711646253
30      260     viral reproductive process
GO:0071845      2.29052558913642e-27    23.121719160105 2.00456715798215        30
284     cellular component disassembly at cellular level
GO:0016032      1.9413471071617e-21     13.784639746635 3.18330911355616        30
451     viral reproduction
GO:0033365      7.61119892224637e-21    13.0793829947329        3.33859248494914
30      473     protein localization to organelle
GO:0006605      8.08510821876735e-21    13.0489864864865        3.34565082001246
30      474     protein targeting
GO:0042274      6.63466085483646e-06    41.7930029154519        0.127050031139714
4       18      ribosomal small subunit biogenesis
GO:0006364      8.60311641238993e-06    10.8262615301139        0.734066846585011
7       104     rRNA processing
GO:0016072      1.24500930613032e-05    10.1913132345427        0.776416856964916
7       110     rRNA metabolic process
Tissue: Nerve_Tibial=>Artery_Tibial     Type:   asymmetric
SourceGene:     HLA-DMA(ENSG00000204257.8)
TargetGeneSet:  RP11    HMGN2   KHDRBS1 STK40   RPS8    IPP     POMGNT1 SMG5    HDGF
LYPLAL1 EIF3FP3 RPL31   MAP3K2  SATB2   PPP1R7  TATDN2  CHDH    RPL10AP6
DZIP3   LIAS    OTUD4   COX7C   CTD     ARL10   RPS10   RPL10A  XPO5    MRPS12
GTF2H5  C7orf50 TOMM7   SLC4A2  AGPAT6  CHCHD7  RPL7    COX6C   EIF3H   RPS6
DCTN3   C9orf103        RPL35   RPL12   VAV2    RP13    CARS    RPS13   DAK     NXF1
PRDM10  TULP3   TNFRSF1A        STAT2   XPOT    NDUFA12 CHPT1   EID3    C12orf51
DHRS12  CMTM5   RPS29   RPL7AP6 AKT1    KIAA0284        HERC2P3 HMGN2P5 RPLP1
MAN2A2  C16orf79        FHOD1   HSDL1   COX4I1  CYB5D2  MINK1   FLII    C17orf108
RPL17   RPL19   HEXIM2  MRPL45P2        NPEPPS  BAHCC1  PPP4R1  DNMT1   PRKCSH
SUGP2   COX6B1  NDUFA3  RPS9    RPL28   ZNF667  ZSCAN1  TBC1D20 ELMO2   RPS21
APOBEC3G        RANGAP1 EFCAB6  SYP     KLF8    RP3     RPL10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      1.81110837456362e-21    48.2837837837838        0.535257075634904
17      91      translational termination
GO:0000184      6.10927534779988e-21    37.9444362346682        0.699951560445644
18      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006414      2.42646128577078e-20    40.5625 0.617604318040274       17      105
translational elongation
GO:0006614      2.42646128577078e-20    40.5625 0.617604318040274       17      105
SRP-dependent cotranslational protein targeting to membrane
GO:0006613      2.87702575868489e-20    40.1039325842697        0.623486263926372
17      106     cotranslational protein targeting to membrane
GO:0045047      2.87702575868489e-20    40.1039325842697        0.623486263926372
17      106     protein targeting to ER
GO:0072599      2.87702575868489e-20    40.1039325842697        0.623486263926372
17      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      1.95134119188602e-19    35.3094059405941        0.694069614559546
17      118     protein localization to endoplasmic reticulum
GO:0006413      5.87161916046592e-19    28.5337491646246        0.894055774686873
18      152     translational initiation
GO:0000956      4.09461599280805e-18    25.2910941978847        0.994048854750536
18      169     nuclear-transcribed mRNA catabolic process
GO:0006402      1.05140400979372e-17    23.8533582089552        1.04698636772542
18      178     mRNA catabolic process
GO:0019080      1.46579017978226e-17    26.5522388059701        0.888173828800775
17      151     viral genome expression
GO:0019083      1.46579017978226e-17    26.5522388059701        0.888173828800775
17      151     viral transcription
GO:0006612      1.84006815045489e-17    26.1580882352941        0.899937720572971
17      153     protein targeting to membrane
GO:0043624      1.84006815045489e-17    26.1580882352941        0.899937720572971
17      153     cellular protein complex disassembly
GO:0043241      3.20371381281421e-17    25.2216312056738        0.92934745000346
17      158     protein complex disassembly
GO:0072594      1.22472715482202e-16    20.4814636494945        1.19991696076396
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18      204     establishment of protein localization to organelle
GO:0006401      1.3366520779621e-16     20.3705004389816        1.20579890665006
18      205     RNA catabolic process
GO:0034623      1.67278171419204e-16    22.625796178344 1.02345858418103        17
174     cellular macromolecular complex disassembly
GO:0032984      2.70993198091825e-16    21.9197530864198        1.05286831361151
17      179     macromolecular complex disassembly
GO:0019058      1.11617743754793e-15    17.8511667017028        1.3587294996886 18
231     viral infectious cycle
GO:0022415      8.90746454878533e-15    15.6797829036635        1.52930593038544
18      260     viral reproductive process
GO:0006605      2.57460605906515e-14    10.7496839443742        2.78804235001038
22      474     protein targeting
GO:0071845      5.80436860630791e-13    13.2013108614232        1.67047263165179
17      284     cellular component disassembly at cellular level
GO:0022411      7.28058789392234e-13    13.0027675276753        1.69400041519618
17      288     cellular component disassembly
GO:0033365      2.6233042470814e-12     9.45016131771099        2.78216040412428
20      473     protein localization to organelle
GO:0016032      1.07578100071674e-11    9.28542368125702        2.65275759463013
19      451     viral reproduction
Tissue: Artery_Tibial=>Nerve_Tibial     Type:   asymmetric
SourceGene:     LAMC3(ENSG00000050555.11)
TargetGeneSet:  THBS3   BZW1    RPL37A  C3orf39 SEC61A1 EEF1A1P19       RPS23
HLA-DOA RPS10   FOXP4   EEF1A1  AHCYL2  MTFR1   EEF1D   RPS6    RPL12   LRP10   FAU
TM7SF3  RPS3AP6 OSTBETA UBA52   RPS16   NUMBL   RPS9    RPS21   CTA     SLC16A2
RPL10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      1.70532207841082e-22    184.145256916996        0.17438239568196
13      105     translational elongation
GO:0045047      3.21172747861733e-20    152.478723404255        0.17604318040274
12      106     protein targeting to ER
GO:0072599      3.21172747861733e-20    152.478723404255        0.17604318040274
12      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      1.23360123967505e-19    135.103773584906        0.195972597052107
12      118     protein localization to endoplasmic reticulum
GO:0006415      7.71872065757033e-19    151.747115384615        0.151131409591032
11      91      translational termination
GO:0006614      4.01661343482609e-18    129.020458265139        0.17438239568196
11      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      4.47797614809388e-18    127.653441295547        0.17604318040274
11      106     cotranslational protein targeting to membrane
GO:0000184      1.68002490885081e-17    112.185897435897        0.197633381772888
11      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0072594      1.05491597867372e-16    74.140625       0.338800083039236       12
204     establishment of protein localization to organelle
GO:0019080      2.49118165200418e-16    86.35   0.250778492837866       11      151
viral genome expression
GO:0019083      2.49118165200418e-16    86.35   0.250778492837866       11      151
viral transcription
GO:0006413      2.68329475132038e-16    85.7315875613748        0.252439277558646
11      152     translational initiation
GO:0006612      2.88874998161738e-16    85.1218851570964        0.254100062279427
11      153     protein targeting to membrane
GO:0043624      2.88874998161738e-16    85.1218851570964        0.254100062279427
11      153     cellular protein complex disassembly
GO:0043241      4.14666655261344e-16    82.1978021978022        0.26240398588333
11      158     protein complex disassembly
GO:0000956      8.82122496932847e-16    76.4162609542356        0.280672617811916
11      169     nuclear-transcribed mRNA catabolic process
GO:0034623      1.22248223566935e-15    74.0462482302973        0.288976541415819
11      174     cellular macromolecular complex disassembly
GO:0006402      1.57610865522108e-15    72.2524182404422        0.295619680298941
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11      178     mRNA catabolic process
GO:0032984      1.67790682697873e-15    71.8173076923077        0.297280465019722
11      179     macromolecular complex disassembly
GO:0006401      7.60023279136492e-15    62.078905630452 0.340460867760017       11
205     RNA catabolic process
GO:0019058      2.85353956380093e-14    54.6423076923077        0.383641270500311
11      231     viral infectious cycle
GO:0022415      1.05121680674353e-13    48.179796107507 0.431804027402948       11
260     viral reproductive process
GO:0071845      2.77153128770952e-13    43.8698224852071        0.471662860701682
11      284     cellular component disassembly at cellular level
GO:0022411      3.23054316537605e-13    43.2241044154402        0.478305999584804
11      288     cellular component disassembly
GO:0033365      2.49276638795817e-12    30.295010845987 0.785551172929209       12
473     protein localization to organelle
GO:0006605      2.55549620889547e-12    30.2272727272727        0.78721195764999
12      474     protein targeting
GO:0016032      4.19569745135523e-11    26.8980769230769        0.749013909072037
11      451     viral reproduction
GO:0042274      3.23105168313163e-06    137.257142857143        0.0298941249740502
3       18      ribosomal small subunit biogenesis
Tissue: Artery_Tibial=>Nerve_Tibial     Type:   asymmetric
SourceGene:     NGFRAP1(ENSG00000166681.9)
TargetGeneSet:  ZCCHC17 PSMB2   NDUFS5  UQCRH   ST6GALNAC5      ALG14   CAPZA1
MRPS21  TMCO1   RP4     PFN1P1  SNRPE   LINC00467       RP11    TARBP1  PTRHD1  OST4
MRPL33  MORN2   MDH1    NFU1    TPRKB   TMSB10  NDUFB3  BRK1    UBE2E1  CCDC72
VPRBP   SPCS1   NEK4    MRPL47  NDUFB5  ATP5I   STX18   EVC2    MAN2B2  OCIAD1
NDUFC1  MGST2   FSTL5   NEIL3   SUB1    CTD     UQCRQ   PHF15   PDF     DIAPH1
TCOF1   ATOX1   PTTG1   AIF1    C6orf48 KIFC1   COX6A1P2        FOXP4   KIAA0240
RPL39P3 COX7A2  HMGN3   PRSS35  PEX7    NUDT1   NDUFA4  TOMM7   MALSU1  LSM5
SEC61G  TP53TG1 ECD     PMS2P1  AP1S1   GSTK1   MRPL15  PENK    C8orf59 DECR1
UQCRB   COX6C   MRPL13  C9orf123        SEC61B  TXN     ATP5C1  TAF3    POLR2L
NUP98   IMMP1L  SLC43A3 C11orf10        SNX15   RELA    ARAP1-AS1       CLNS1A
ATP5L   ZC3H10  C12orf45        GCN1L1  CCDC92  POMP    COMMD6  ACIN1   RPS29   ERH
RP3     EFCAB11 NDUFB1  IFI27L1 C14orf2 HMGN2P5 SRP14   GTF2A2  COX5A   WASH3P
NDUFAB1 NSMCE1  MIR4519 PSMB10  TRAPPC1 ATP5H   H3F3B   SEC11C  UQCR11  C19orf70
C19orf79        MAP2K7  PIN1    RAVER1  ZNF653  ZNF625  ZNF726  ANKRD27 COX6B1
POLR2I  MIA     CCDC97  SNRPD2  SLC17A7 TBC1D17 NDUFA3  C20orf7 SNRPB2  ROMO1
PFDN4   ATP5J   SNRPD3  UQCR10  LGALS1  CBX7    RP6     EEF1B2P3        NDUFB11
TIMP1   PRICKLE3        PDZD11  BCORL1  SSR4    DKC1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      3.60072593790556e-26    43.2506894649752        0.797176665974673
22      96      respiratory electron transport chain
GO:0022900      3.16534702822751e-24    30.3761493452215        1.11272576292298
23      134     electron transport chain
GO:0045333      1.28520448731778e-23    28.3181148748159        1.1791571517542 23
142     cellular respiration
GO:0015980      3.892942073092e-18      13.1103023516237        2.54930454639817
25      307     energy derivation by oxidation of organic compounds
GO:0006091      1.01142087492698e-15    9.58383613845665        3.55407930247042
26      428     generation of precursor metabolites and energy
GO:0006119      3.96541852571518e-14    34.5048309178744        0.481627569026365
12      58      oxidative phosphorylation
GO:0042773      1.09909586770632e-13    40.072629969419 0.390284409383434       11
47      ATP synthesis coupled electron transport
GO:0042775      1.09909586770632e-13    40.072629969419 0.390284409383434       11
47      mitochondrial ATP synthesis coupled electron transport
GO:0006120      4.45026373362782e-10    36.4872448979592        0.298941249740502
8       36      mitochondrial electron transport, NADH to ubiquinone
GO:0042776      4.43127881906548e-08    77.8423913043478        0.107951006850737
5       13      mitochondrial ATP synthesis coupled proton transport
GO:0015985      2.85361870179688e-07    47.8862876254181        0.149470624870251
5       18      energy coupled proton transport, down electrochemical gradient
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GO:0015986      2.85361870179688e-07    47.8862876254181        0.149470624870251
5       18      ATP synthesis coupled proton transport
GO:0006122      2.22034742164306e-06    367.435897435897        0.0332156944156114
3       4       mitochondrial electron transport, ubiquinol to cytochrome c
GO:0006200      2.84068659625795e-06    12.9933628318584        0.622794270292713
7       75      ATP catabolic process
GO:0000387      5.19105516446692e-06    23.9214046822742        0.257421631720988
5       31      spliceosomal snRNP assembly
Tissue: Nerve_Tibial=>Artery_Tibial     Type:   cluster
SourceGene:     NUP98(ENSG00000110713.11)
TargetGeneSet:  CDK11A  PARK7   UBR4    WBP1    CNKSR1  SRSF4   PPT1    PPCS
UQCRH   ATPAF1  SCP2    RP4     LRRC40  CRYZ    PIGK    RWDD3   ACTG1P4 TAF13
HBXIP   RP11    ATP5F1  SIKE1   C1orf54 CRTC2   PMVK    C1orf85 HDGF    DCAF8   SDHC
MGST3   CREG1   BRP44   DNM3OS  TIMM17A IKBKE   NSL1    LYPLAL1 ARV1    RRM2    OST4
CGREF1  MPV17   RBKS    USP34   COMMD1  MDH1    NFU1    TPRKB   BOLA3   SNRNP200
TXNDC9  CCDC74A PSMD14  H3F3AP4 ATP5G3  DUSP19  MOB4    C2orf47 NDUFB3  IMPDH1P10
SENP2   MYEOV2  BRK1    LSM3    MLH1    ENTPD3-AS1      LZTFL1  ARIH2   ABHD14A
SPCS1   ACOX2   TFG     ABHD10  SLC35A5 NDUFB4  RPL32P3 MRPL3   ANAPC13 HLTF
LRRC34  MRPL47  NDUFB5  DNAJC19 RNF168  KIAA0226        FAM193A GNPDA2  OCIAD1
MRPL1   MRPS18C SLC10A6 LAMTOR3 PPA2    TRAM1L1 NUDT6   NDUFC1  SCOC    ANAPC10
PET112  SCRG1   FBXO8   C5orf55 FASTKD3 SUB1    C5orf43 MAST4-AS1       COX7C
CETN3   COMMD10 UQCRQ   LEAP2   SKP1    SIL1    PDF     PCDHB9  PCDHB10 DIAPH1  GM2A
ATOX1   UBLCP1  NUDCD2  HMMR    RPL26L1 HIGD2A  UIMC1   FGFR4   LY86    TMEM14B NOL7
HMGN4   BAG6    HNRNPC  BRPF3   PNPLA1  MRPS10  MRPS18A TMEM14A PHF3    COX7A2
IRAK1BP1        HMGN3   CYB5R4  GTF3C6  ASF1A   PKIB    MRPS12  AIG1    PEX3
SF3B5   RPA3    NDUFA4  RPS2P32 LSM5    SEPT7   EPDR1   PPIA    SEC61G  CHCHD2
SKP1P1  STAG3L4 TRIM74  UPK3B   TP53TG1 SRI     SMURF1  ZNHIT1  RABL5   CAPZA2
NDUFA5  C7orf73 NDUFB2  MRPS33  KIAA1147        MLL3    RBM33   NAT1    SORBS3
KIF13B  DCTN6   LSM1    ATP6V1H RAB2A   C8orf45 COPS5   TCEB1   TMEM70  PAF1
MRPS35  DECR1   HRSP12  COX6C   MRPL13  ASAP1   CTD     RLN2    DENND4C NDUFB6
DCTN3   CCL19   GBA2    SHC3    KIAA0368        ATP6V1G1        CDK9    CIZ1
RALGDS  LINC00094       NOTCH1  TMEM141 ATP5C1  CDC123  MSRB2   C10orf68
PARD3   MRPS16  GHITM   ZRANB1  ECHS1   NUP98   SMPD1   C11orf58        IMMP1L  ELP4
C11orf74        ETFA    FNBP4   PATL1   MTA2    BAD     SF1     FRMD8   RNASEH2C
MRPL11  NDUFS8  MYEOV   PPFIA1  CLNS1A  CCDC90B TMEM126B        TMEM126A
C11orf70        DCUN1D5 SIK3    ATP5L   MLL     TBCEL   FEZ1    NFRKB   DYRK4   ATN1
ALG1L2  MAGOHB  CCDC91  COX14   POU6F1  PCBP2   SMARCC2 BAZ2A   R3HDM2  C12orf29
TMTC3   UBE2N   MRPL42  CCDC53  ARPC3   C12orf51        MED13L  COX6A1  TRIAP1  POP5
TRAC    RAN     MPHOSPH8        MRP63   EFHA1   TPTE2P1 MTMR6   POMP    MED4
COMMD6  A2LD1   C14orf126       BAZ1A   MBIP    MGAT2   AP5M1   ACTR10  PSMA3
ATP6V1D BCRP2   SLIRP   TTC8    NDUFB1  C14orf129       C14orf2 NDN     SRP14
SERF2   DYX1C1-CCPG1    GTF2A2  FAM96A  PPIB    ZNF609  PARP6   WDR61   TMED3
C15orf40        MRPS11  MAN2A2  NDUFB10 SRRM2   SMG1    NDUFAB1 ATXN2L  ITFG1
CNOT1   FAM65A  SLC12A4 DHX38   COX4NB  PITPNA  PFN1    C17orf61-PLSCR3 FLII    GIT1
MLLT6   STARD3  CASC3   STAT5A  VPS25   GPATCH8 EFTUD2  SCRN2   SPAG9   ICT1
ATP5H   ANAPC11 IER3IP1 C18orf32        RBFA    BSG     UQCR11  MRPL54  SAFB
C19orf70        NDUFA11 PIN1    DNM2    ASNA1   PRDX2   NDUFB7  ZNF333  AKAP8L
EPS15L1 NDUFA13 RPSAP58 POP4    CYP2G1P GEMIN7  AP2S1   C19orf63        JOSD2
TMEM230 SNRPB2  COMMD7  MAPRE1  CTSA    ZNF334  ATP5E   PPIAP22 ATP5J   SCAF4   CBR1
ERVH48-1        CSTB    MCM3AP  DIP2A   MRPL40  DGCR6L  PI4KAP2 UQCR10  MTMR3
EIF4ENIF1       RP1     TXN2    LGALS1  GTPBP1  COX5BP7 RBX1    NDUFA6  PRDX4
ATP6AP2 FUNDC1  OTUD5   PHF8    PDZD11  MED12   ITGB1BP2        COX7B   TAF9B
NAP1L3  TCEAL8  NGFRAP1 RPL39   C1GALT1C1       THOC2   FAM127C CETN2   SSR4
MECP2   FUNDC2  VAMP7
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      4.81829348728712e-29    23.6666666666667        2.18559269254723
32      96      respiratory electron transport chain
GO:0045333      1.95904953081311e-25    14.9553044569994        3.23285585772611
34      142     cellular respiration
GO:0022900      3.86376520601551e-25    15.4767527428419        3.05072313334717
33      134     electron transport chain
GO:0042773      2.87665841927614e-15    23.2357002988766        1.07002975572625
16      47      ATP synthesis coupled electron transport
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GO:0042775      2.87665841927614e-15    23.2357002988766        1.07002975572625
16      47      mitochondrial ATP synthesis coupled electron transport
GO:0015980      3.07145615883108e-15    6.06179971988796        6.98934329804166
35      307     energy derivation by oxidation of organic compounds
GO:0006119      6.66748543546713e-15    18.713023764853 1.32046225174728        17
58      oxidative phosphorylation
GO:0006120      1.84479784875503e-14    28.4848484848485        0.819597259705211
14      36      mitochondrial electron transport, NADH to ubiquinone
GO:0006091      2.74007973506067e-12    4.44983883964545        9.74410075427306
37      428     generation of precursor metabolites and energy
GO:0015985      7.63100566924428e-08    27.8873517786561        0.409798629852605
7       18      energy coupled proton transport, down electrochemical gradient
GO:0015986      7.63100566924428e-08    27.8873517786561        0.409798629852605
7       18      ATP synthesis coupled proton transport
GO:0042776      1.99560289510032e-07    37.4568774878372        0.295965677115771
6       13      mitochondrial ATP synthesis coupled proton transport
GO:0015992      2.22247353014058e-06    7.87393640841917        1.50259497612622
10      66      proton transport
GO:0006818      2.94185482576975e-06    7.6013403956329 1.54812815722095        10
68      hydrogen transport
Tissue: Nerve_Tibial=>Artery_Tibial     Type:   asymmetric
SourceGene:     PIK3IP1(ENSG00000100100.7)
TargetGeneSet:  HMGN2   RPS8    CCDC17  RP11    C1orf54 CREB3L4 RPS27   SSR2
NCOA1   EIF3FP3 SATB2   RPL15   CTDSPL  RPL14   ZBTB47  RPL29   RPL10AP6
PCOLCE2 EIF4G1  GPR125  LIAS    C5orf34 SIL1    CTB     ARL10   LYRM4   RPL15P3
RPS10   RPL10A  SNHG5   BEND3   MRPS12  C7orf50 FBXO24  RPS20   RPL7    C8orf73
DCTN3   VPS13A  RPL35   RPL12   RPL7A   FAM208B STIM1   RPL27A  RPS13   PTPRCAP
CHPT1   RPL18AP3        EID3    RPL6    RPLP0   DYNC1H1 AKT1    RPLP1   C16orf57
RPL13   KIF1C   KIAA0100        RPL19   MRPL45P2        BAHCC1  FASN    RPL17
RPS15   PRKCSH  CTD     RPL18A  C19orf12        RPL18   RPS9    RPL28   A1BG    RPS5
RPL12P4 PPDPF   EIF3FP1 MICALL1 CTA     GLUD2   RPL10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006614      4.11941428480046e-45    157.719008264463        0.443221922358314
28      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      5.58574977734701e-45    155.686091686092        0.447443083523632
28      106     cotranslational protein targeting to membrane
GO:0045047      5.58574977734701e-45    155.686091686092        0.447443083523632
28      106     protein targeting to ER
GO:0072599      5.58574977734701e-45    155.686091686092        0.447443083523632
28      106     establishment of protein localization to endoplasmic reticulum
GO:0006415      7.17549268866088e-45    177.758272058824        0.384125666043872
27      91      translational termination
GO:0070972      1.69411579208698e-43    134.814814814815        0.498097017507439
28      118     protein localization to endoplasmic reticulum
GO:0000184      2.21045964572133e-43    133.324009324009        0.502318178672756
28      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006414      6.22826737110555e-43    145.710407239819        0.443221922358314
27      105     translational elongation
GO:0006413      4.33690436240561e-40    97.6168132942326        0.641616497128226
28      152     translational initiation
GO:0006612      5.29654982714096e-40    96.8290909090909        0.645837658293544
28      153     protein targeting to membrane
GO:0000956      1.07861822522739e-38    85.7451106812809        0.71337623693862
28      169     nuclear-transcribed mRNA catabolic process
GO:0019080      3.36234410657138e-38    91.361954459203 0.637395335962909       27
151     viral genome expression
GO:0019083      3.36234410657138e-38    91.361954459203 0.637395335962909       27
151     viral transcription
GO:0043624      4.94201641057437e-38    89.8991596638655        0.645837658293544
27      153     cellular protein complex disassembly
GO:0006402      5.12968344097234e-38    80.549494949495 0.751366687426476       28
178     mRNA catabolic process
GO:0043241      1.26368164806305e-37    86.4375841939829        0.66694346412013
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27      158     protein complex disassembly
GO:0034623      2.07136599701717e-36    76.9429771908763        0.734482042765207
27      174     cellular macromolecular complex disassembly
GO:0072594      2.97174463481531e-36    68.5247933884298        0.861116877724725
28      204     establishment of protein localization to organelle
GO:0006401      3.43416062535662e-36    68.1328539633624        0.865338038890042
28      205     RNA catabolic process
GO:0032984      4.68495160608245e-36    74.3858359133127        0.755587848591793
27      179     macromolecular complex disassembly
GO:0019058      6.60041849918665e-33    55.2223183391003        0.975088229188292
27      231     viral infectious cycle
GO:0022415      1.80574338752716e-31    48.2503155768745        1.09750190298249
27      260     viral reproductive process
GO:0071845      2.09364027324473e-30    43.6702906843671        1.19880977095011
27      284     cellular component disassembly at cellular level
GO:0022411      3.08201273765649e-30    42.9888438133874        1.21569441561138
27      288     cellular component disassembly
GO:0033365      3.05041458481956e-27    28.4652308558559        1.99660923119507
29      473     protein localization to organelle
GO:0006605      3.2420308424832e-27     28.3992275280899        2.00083039236039
29      474     protein targeting
GO:0016032      6.09273795948175e-25    26.1571864594895        1.90374368555809
27      451     viral reproduction
GO:0022613      4.41542322260067e-06    9.85862098947918        0.949761262196388
8       225     ribonucleoprotein complex biogenesis
GO:0071843      6.88629834733271e-06    9.25198072367884        1.00885751851083
8       239     cellular component biogenesis at cellular level
Tissue: Nerve_Tibial=>Artery_Tibial     Type:   asymmetric
SourceGene:     PLXNA2(ENSG00000076356.6)
TargetGeneSet:  RPL22   RP11    RHCE    HMGN2   KHDRBS1 RPS8    IPP     RP4
CHI3L2  ANP32E  CREB3L4 SSR2    TOMM20  NCAPH   RPL31   FMNL2   EEF1B2  RPL15
CTDSPL  RPL14   RNF123  RPL10AP6        PSMC1P1 RPL24   PLXNA1  PARL    TFRC
YTHDC1  AIMP1   METTL14 COX7C   RIOK2   CTD     NPM1    MRPS18B RPL10A  MRPL2
MRPS12  C7orf50 TOMM7   EIF4H   SSBP1   CHCHD7  EIF3H   RPL8    RPS6    RPL35
RPL12   RPL7A   C10orf35        C10orf116       AGAP11  CCDC147 WDR11   C11orf58
RPS13   PLA2G16 U4      RPS3    C11orf1 NRGN    RPL41   RPL14P1 RPL18AP3        TCHP
DIABLO  IFT88   SAP18   DIAPH3-AS1      RPL7AP6 SLC30A4 RSL24D1 RPLP1   PEAK1   RPS2
NUDT21  RPL13   ALDOC   RPL23A  ACACA   RPL17   RPL19   SMARCE1 ZNF385C HEXIM2
PTPRM   PPP4R1  RPL36   DNMT1   RPS16   RPL18   RPL28   RPS5    SNPH    DTD1
CHMP4B  DHX35   RPS21   PPDPF   GRIK1   PIGP    USP51   BEX4    RPL10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      6.1703430167461e-42     109.593869731801        0.541554217701197
28      91      translational termination
GO:0006414      6.87236085561065e-42    95.6558171745152        0.624870251193689
29      105     translational elongation
GO:0006614      6.87236085561065e-42    95.6558171745152        0.624870251193689
29      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      9.42433443774958e-42    94.4069264069264        0.630821396443153
29      106     cotranslational protein targeting to membrane
GO:0045047      9.42433443774958e-42    94.4069264069264        0.630821396443153
29      106     protein targeting to ER
GO:0072599      9.42433443774958e-42    94.4069264069264        0.630821396443153
29      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      3.23440990448545e-40    81.6093041592746        0.702235139436717
29      118     protein localization to endoplasmic reticulum
GO:0006413      1.76944804945208e-38    62.5424473067916        0.904574077918483
30      152     translational initiation
GO:0000184      3.344037340499e-38      75.7241379310345        0.708186284686181
28      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006612      1.3267439040668e-36     58.4308149405772        0.910525223167947
29      153     protein targeting to membrane
GO:0072594      4.99225871832265e-36    46.2377299001576        1.2140336308906 31
204     establishment of protein localization to organelle
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GO:0019080      5.08201334118564e-35    55.8979534622932        0.898622932669019
28      151     viral genome expression
GO:0019083      5.08201334118564e-35    55.8979534622932        0.898622932669019
28      151     viral transcription
GO:0034623      7.33260248617606e-35    49.8947368421053        1.03549927340668
29      174     cellular macromolecular complex disassembly
GO:0043624      7.56543424743669e-35    54.9958620689655        0.910525223167947
28      153     cellular protein complex disassembly
GO:0032984      1.75977086521413e-34    48.2146198830409        1.065254999654  29
179     macromolecular complex disassembly
GO:0043241      1.99496508092307e-34    52.8620689655172        0.940280949415265
28      158     protein complex disassembly
GO:0000956      1.49951507432058e-33    48.700415749572 1.00574354715937        28
169     nuclear-transcribed mRNA catabolic process
GO:0006402      7.02352240549742e-33    45.7494252873563        1.05930385440454
28      178     mRNA catabolic process
GO:0006401      4.49166690403213e-31    38.6970582505357        1.21998477614006
28      205     RNA catabolic process
GO:0019058      1.44054718261466e-29    33.678953626635 1.37471455262612        28
231     viral infectious cycle
GO:0071845      1.91139572050037e-28    28.1520467836257        1.69012525084769
29      284     cellular component disassembly at cellular level
GO:0022411      2.88393105145004e-28    27.7094086567771        1.71392983184555
29      288     cellular component disassembly
GO:0022415      4.2927540672964e-28     29.4087395957194        1.54729776486056
28      260     viral reproductive process
GO:0033365      8.35406024658428e-26    18.7103384563702        2.81489170299633
32      473     protein localization to organelle
GO:0006605      8.92540399046233e-26    18.6666666666667        2.8208428482458 32
474     protein targeting
GO:0016032      1.9244691752017e-21     15.9116328360642        2.68396650750813
28      451     viral reproduction
GO:0042254      2.84611120448856e-06    10.346608474268 0.886720642170092       8
149     ribosome biogenesis
GO:0042274      3.35689577045844e-06    50.0034843205575        0.107120614490347
4       18      ribosomal small subunit biogenesis
GO:0022613      7.44969396446811e-06    7.65638528138528        1.33900768112933
9       225     ribonucleoprotein complex biogenesis
GO:0071843      1.21044720135613e-05    7.1832298136646 1.42232371462183        9
239     cellular component biogenesis at cellular level
Tissue: Artery_Tibial=>Nerve_Tibial     Type:   asymmetric
SourceGene:     RPL35(ENSG00000136942.9)
TargetGeneSet:  RPL22   MTOR    CROCCP3 PHACTR4 ZMYND12 RNU5E-6P        NASP    MSH4
GTF2B   FAM40A  RP4     NOTCH2NL        GPR89A  NBPF16  CREB3L4 ARHGEF11        LHX4
RP11    SOX13   PLXNA2  NENF    NVL     NTPCR   SLC5A6  THADA   CAMKMT  PNPT1   TIA1
LINC00152       RPL31   RFX8    CCDC115 R3HDM1  KIAA1715        RPL37A  ABCB6
OR6B3   RPL32   UBE2E1  APEH    RBM6    IFRD2   MYH15   WDR52   RNF7    U2SURP
MCCC1   EIF4G1  RPL35A  MYL5    LETM1   SOD3    CLOCK   IL8     CXCL1   RPL34
NDUFC1  MED10   CCDC152 NDUFS4  MCCC2   BTF3    RPS23   CTD     PHF15   CAMLG   HARS
ARHGAP26        TCERG1  TCOF1   LYRM4   PAK1IP1 GABBR1  PPT2    HLA-DMA VPS52
RPS10   TCP11   C6orf226        RPL39P3 BCKDHB  MICAL1  SERINC1 HINT3   MRPS12
ALDH8A1 AIG1    TOMM7   HNRNPA2B1       CDK13   GS1     TMEM120A        C7orf59
TRIP6   ABCF2   INTS10  C8orf40 RPS20   RPL30   POP1    COX6C   EIF3E   KIFC2
MFSD3   GBA2    FAM120A ZNF169  IKBKAP  IKBKAP-IT1      C5      RPL35   PRPS1P2
SLC27A4 ODF2    WDR34   C9orf114        NUP188  FAM208B FBXO18  CDNF    AGAP6
TSPAN14 MMS19   SFXN2   TUBGCP2 ZNF195  RPS13   FAM111A CPSF7   MTA2    GANAB   FAU
CCL13   RPS6KB2 CHKA    C2CD3   PIWIL4  RNF214  DPAGT1  KLHDC5  PHC1P1  TIMELESS
MARS    POLR3B  ANAPC7  RBM19   ANAPC5  PXMP2   MRPS31P2        POMP    KLF12
COMMD6  RALGAPA1        RPS29   DHRS7   NEK9    POMT2   RPL3P4  TMEM85  SRP14
RSL24D1 SLTM    VPS13C  PIAS1   C16orf79        GSPT1   NPIPL3  MIR4519 C16orf57
CTCF    RANBP10 HAS3    DDX19A  SF3B3   GALNS   AFG3L1P CTNS    C17orf85
MYBBP1A ZMYND15 FAM106B RPL19   PNMT    RPL27   GPATCH8 ZNF652  MTMR4   SLC39A11
RPL38   ASPSCR1 HEXDC   RAB12   RPL36   ZNF558  DNMT1   RAVER1  SMARCA4 ZNF69
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SAMD1   MAST3   ARMC6   U2AF1L4 ZNF781  SMG9    TOMM40  QPCTL   PPP5C   BCAT2
SNRNP70 RPS9    TRAPPC2 LINC00493       TM9SF4  NCOA6   TAF4    RPS21   ATP5J
IFNGR2  TMEM50B PI4KA   CCDC116 BCR     CABIN1  PIK3IP1 NOL12   RP3     L3MBTL2
TTLL12  PPARA   GTPBP6  ZNF81   HDAC6   FAM156A GPR173  MAMLD1  G6PD
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0000184      1.1190553214695e-22     23.1068251273345        1.47401563905612
24      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006414      7.07099984389583e-20    22.4493670886076        1.30060203446128
21      105     translational elongation
GO:0006614      7.07099984389583e-20    22.4493670886076        1.30060203446128
21      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006415      7.50866062168435e-20    25.1590043405085        1.12718842986645
20      91      translational termination
GO:0006613      8.72545248415072e-20    22.1836932241251        1.31298872050377
21      106     cotranslational protein targeting to membrane
GO:0045047      8.72545248415072e-20    22.1836932241251        1.31298872050377
21      106     protein targeting to ER
GO:0072599      8.72545248415072e-20    22.1836932241251        1.31298872050377
21      106     establishment of protein localization to endoplasmic reticulum
GO:0006402      1.52369410364955e-19    14.9806892453951        2.20483011556294
25      178     mRNA catabolic process
GO:0006401      3.77488203989601e-19    13.3792675356921        2.53927063871012
26      205     RNA catabolic process
GO:0000956      6.53020082084425e-19    15.0855617352614        2.09334994118054
24      169     nuclear-transcribed mRNA catabolic process
GO:0006413      8.46080250430692e-19    16.164231763069 1.88277627845824        23
152     translational initiation
GO:0070972      9.20132139045525e-19    19.4228761581626        1.46162895301363
21      118     protein localization to endoplasmic reticulum
GO:0043624      1.56413266464346e-17    15.1262702387319        1.89516296450073
22      153     cellular protein complex disassembly
GO:0034623      1.89801598067534e-17    13.7876974019358        2.15528337139298
23      174     cellular macromolecular complex disassembly
GO:0043241      3.17356756115267e-17    14.5650056200824        1.95709639471317
22      158     protein complex disassembly
GO:0032984      3.61245688578415e-17    13.3410585141354        2.21721680160543
23      179     macromolecular complex disassembly
GO:0019080      1.77903389701337e-16    14.4587147030185        1.87038959241575
21      151     viral genome expression
GO:0019083      1.77903389701337e-16    14.4587147030185        1.87038959241575
21      151     viral transcription
GO:0006612      2.34259044725607e-16    14.2376294591484        1.89516296450073
21      153     protein targeting to membrane
GO:0072594      6.78280275089811e-16    11.47800679983  2.52688395266764        23
204     establishment of protein localization to organelle
GO:0019058      1.03212754697973e-13    9.42876299027824        2.86132447581482
22      231     viral infectious cycle
GO:0071845      8.56361057481229e-13    7.91465271637685        3.51781883606671
23      284     cellular component disassembly at cellular level
GO:0022411      1.14741289271562e-12    7.79296081277213        3.56736558023666
23      288     cellular component disassembly
GO:0022415      1.153664293109e-12      8.26280575924637        3.22053837104699
22      260     viral reproductive process
GO:0016032      3.23326928406376e-10    5.27635510029876        5.58639540516227
25      451     viral reproduction
GO:0033365      8.7095212843007e-10     5.00927643784787        5.85890249809702
25      473     protein localization to organelle
GO:0006605      9.09802069589796e-10    4.99775836635525        5.87128918413951
25      474     protein targeting
Tissue: Nerve_Tibial=>Artery_Tibial     Type:   asymmetric
SourceGene:     SNORD14E(ENSG00000200879.1)
TargetGeneSet:  RPS8    GAS5    EIF3FP3 IWS1    RPL15   RPL14   RPL24   EPB41L4A-AS1
MIR4454 RPS10   RPL10A  RPS20   RPL7A   RPS13   RP11    U6      MARS    DHRS12
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RPL23A  ACACA   RPL19   RPS10P2 PHEX-AS1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      4.41889237162837e-22    493.4875        0.0944571309943949      11
91      translational termination
GO:0006414      2.31803923774973e-21    419.579787234043        0.108988997301225
11      105     translational elongation
GO:0006614      2.31803923774973e-21    419.579787234043        0.108988997301225
11      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      2.58578316147057e-21    415.134210526316        0.110026987751713
11      106     cotranslational protein targeting to membrane
GO:0045047      2.58578316147057e-21    415.134210526316        0.110026987751713
11      106     protein targeting to ER
GO:0072599      2.58578316147057e-21    415.134210526316        0.110026987751713
11      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      8.87277980524406e-21    368.268691588785        0.122482873157567
11      118     protein localization to endoplasmic reticulum
GO:0000184      9.77398975571312e-21    364.833333333333        0.123520863608055
11      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      1.47625530308852e-19    280.814285714286        0.156736558023666
11      151     viral genome expression
GO:0019083      1.47625530308852e-19    280.814285714286        0.156736558023666
11      151     viral transcription
GO:0006413      1.59101650924014e-19    278.803191489362        0.157774548474154
11      152     translational initiation
GO:0006612      1.71382512639667e-19    276.820422535211        0.158812538924642
11      153     protein targeting to membrane
GO:0043624      1.71382512639667e-19    276.820422535211        0.158812538924642
11      153     cellular protein complex disassembly
GO:0043241      2.46721559375237e-19    267.311224489796        0.164002491177081
11      158     protein complex disassembly
GO:0000956      5.28191363405507e-19    248.509493670886        0.175420386132448
11      169     nuclear-transcribed mRNA catabolic process
GO:0034623      7.34103891523919e-19    240.802147239264        0.180610338384887
11      174     cellular macromolecular complex disassembly
GO:0006402      9.48644375554893e-19    234.968562874251        0.184762300186838
11      178     mRNA catabolic process
GO:0032984      1.01049864840513e-18    233.553571428571        0.185800290637326
11      179     macromolecular complex disassembly
GO:0072594      4.39820261133927e-18    202.944300518135        0.211750051899523
11      204     establishment of protein localization to organelle
GO:0006401      4.64639077626831e-18    201.884020618557        0.21278804235001
11      205     RNA catabolic process
GO:0019058      1.77093774552353e-17    177.7   0.239775794062695       11      231
viral infectious cycle
GO:0022415      6.63448392011275e-17    156.683734939759        0.269877517126842
11      260     viral reproductive process
GO:0071845      1.77370479174115e-16    142.667582417582        0.294789287938551
11      284     cellular component disassembly at cellular level
GO:0022411      2.07226688558269e-16    140.567689530686        0.298941249740502
11      288     cellular component disassembly
GO:0016032      2.95985130748601e-14    87.475  0.468133693170023       11      451
viral reproduction
GO:0033365      4.99810743614271e-14    83.1785714285714        0.490969483080756
11      473     protein localization to organelle
GO:0006605      5.11551529694795e-14    82.9929805615551        0.492007473531244
11      474     protein targeting
Tissue: Nerve_Tibial=>Artery_Tibial     Type:   asymmetric
SourceGene:     TCERG1(ENSG00000113649.7)
TargetGeneSet:  MTND1P23        RBBP4   BTBD19  PRPF38A DDAH1   RP11    RP4
WDR77   CD58    GAPDHP32        SF3B4   RPRD2   KCNJ9   TRAF5   CAPN2   TOMM20
COX20   PXDN    DDIT3   LRPPRC  EIF3FP3 TIA1    TTL     KIF5C   FMNL2   ANKRD44
SATB2   CLN5    RPL15   RPL14   KIAA1143        MFSD1   PARL    YTHDC1  METTL14 INTU
RXFP1   OXCT1   ITGA1   HNRNPA0 RBM27   ATXN1   RPL10A  EFHC1   SNHG5   MICAL1  DDO
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RNF217  SCAF8   OSBPL3  EIF4H   MEPCE   CBLL1   EEF1D   POLR1E  VPS13A  RPL35
RPL12   NUP214  UCK1    ARHGAP12        HECTD2  WDR11   RPS3    SIK2    BCAT1
RPL14P1 CRADD   RPL18AP3        BRAP    KATNAL1 VPS36   CARS2   OXA1L   PRKD1
L2HGDH  ATP6V1D STRCP1  GS1     NUDT21  FHOD1   TERF2   ATXN1L  COX4I1  METTL16
PELP1   POLR2A  ATP1B2  RPL23A  RPL19   HEXIM2  ROCK1P1 SF3A2   KHSRP   ZNF426
RPL18A  FXYD7   ZNF383  RPS16   FBL     HNRNPUL1        BCAT2   RPL18   ATF5
RPL28   PSMF1   NSFL1C  DHX35   STX16   SF3A1   ARSA    SYP     USP51   GPRASP2
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      1.56335372159536e-13    24.5800636267232        0.690263649574424
13      105     translational elongation
GO:0006415      6.56816657422186e-13    26.1284123837121        0.598228496297834
12      91      translational termination
GO:0006614      3.77056663558359e-12    22.1733385153517        0.690263649574424
12      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      4.22928844262792e-12    21.9359138682389        0.69683758909418
12      106     cotranslational protein targeting to membrane
GO:0045047      4.22928844262792e-12    21.9359138682389        0.69683758909418
12      106     protein targeting to ER
GO:0072599      4.22928844262792e-12    21.9359138682389        0.69683758909418
12      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      1.53784848908999e-11    19.43623550807  0.775724863331257       12
118     protein localization to endoplasmic reticulum
GO:0000184      1.70121226068845e-11    19.2532372480577        0.782298802851014
12      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      1.75656333887671e-11    16.3338635560269        0.992664867483219
13      151     viral genome expression
GO:0019083      1.75656333887671e-11    16.3338635560269        0.992664867483219
13      151     viral transcription
GO:0006413      1.91066564467994e-11    16.2152131952974        0.999238807002976
13      152     translational initiation
GO:0043624      2.0770172462924e-11     16.0982578397213        1.00581274652273
13      153     cellular protein complex disassembly
GO:0043241      3.12506272799019e-11    15.5376787216148        1.03868244412151
13      158     protein complex disassembly
GO:0034623      1.05506307305378e-10    13.9778063929708        1.14386547643762
13      174     cellular macromolecular complex disassembly
GO:0032984      1.50448375706582e-10    13.5520129297679        1.1767351740364 13
179     macromolecular complex disassembly
GO:0006612      3.29941084523034e-10    14.5757498077416        1.00581274652273
12      153     protein targeting to membrane
GO:0072594      7.62029550948366e-10    11.7574383859022        1.34108366203031
13      204     establishment of protein localization to organelle
GO:0000375      1.02626805736932e-09    11.4534594325535        1.37395335962909
13      209     RNA splicing, via transesterification reactions
GO:0000956      1.04297389651935e-09    13.0755889801243        1.11099577883883
12      169     nuclear-transcribed mRNA catabolic process
GO:0006402      1.89125595617685e-09    12.3588329220496        1.17016123451664
12      178     mRNA catabolic process
GO:0008380      2.75953277936573e-09    8.55194805194805        2.12338246488132
15      323     RNA splicing
GO:0019058      3.47914056166851e-09    10.2816066234057        1.51858002906373
13      231     viral infectious cycle
GO:0006397      6.36362819839496e-09    7.38896784215223        2.62300186838281
16      399     mRNA processing
GO:0000377      8.87693882294628e-09    10.6656626506024        1.34108366203031
12      204     RNA splicing, via transesterification reactions with bulged
adenosine as nucleophile
GO:0000398      8.87693882294628e-09    10.6656626506024        1.34108366203031
12      204     nuclear mRNA splicing, via spliceosome
GO:0006401      9.37855334306275e-09    10.6096510393907        1.34765760155007
12      205     RNA catabolic process
GO:0022415      1.44200116716393e-08    9.05584082156611        1.70922427513667
13      260     viral reproductive process
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GO:0071845      4.10392679977806e-08    8.23980739807398        1.86699882361082
13      284     cellular component disassembly at cellular level
GO:0022411      4.83723793618626e-08    8.11764966740576        1.89329458168985
13      288     cellular component disassembly
GO:0033365      6.88199245180791e-08    6.1597097194139 3.10947339284479        16
473     protein localization to organelle
GO:0016032      2.30380449189281e-07    5.98623853211009        2.96484672341014
15      451     viral reproduction
GO:0006605      4.34989579975314e-07    5.67687908496732        3.11604733236454
15      474     protein targeting
Tissue: Nerve_Tibial=>Artery_Tibial     Type:   asymmetric
SourceGene:     UBE2E1(ENSG00000170142.7)
TargetGeneSet:  SDHB    ATPIF1  TAF12   ZCCHC17 MACF1   RP1     PPCS    RPS8
UQCRH   RWDD3   RP11    HBXIP   NOTCH2  C1orf54 SCNM1   PSMB4   RPS27   DPM3
PFDN2   NAV1    SNRPE   LYST-IT2        RPS7    UBC     NFU1    SNRNP27 SNRPG
TPRKB   DGUOK   MITD1   RPL31   MZT2B   MZT2A   BTF3L4P2        EEF1B2  MYEOV2
CCDC72  SPCS1   RPL24   NDUFB4  SEC22A  RNF7    PDCD10  DNAJC19 TMEM128 OCIAD1
CLOCK   BDH2    NDUFC1  ANAPC10 LSM6    NDUFS4  NDUFAF2 CHCHD2P2        TAF9
MAP1B   TBCA    COX7C   CTD     MRPL22  RPL26L1 RAB24   TMEM14B NOL7    C6orf48
RPS10   RPL10A  MEA1    MRPL2   C6orf162        MRPS12  PSMB1   YAE1D1  MPLKIP
CHCHD2  BUD31   C7orf59 PMS2P1  MOSPD3  POP7    TRIP6   ZNHIT1  FIS1    NAA38   ARF5
SSBP1   DCTN6   C8orf40 FNTA    RPS20   SNHG6   TCEB1   PAF1    TTC35   MRPL13
TATDN1  C9orf133        NDUFB6  VPS13A  SEC61B  ATP6V1G1        OR1N1   RPL35
RPL12   SWI5    NUP188  VPS26A  GSTO1   MRPL23  RPL27A  DENND5A RPS13   IMMP1L
C11orf31        C11orf10        GANAB   POLR2G  COX8A   GAL     CWC15   AASDHPPT
UBE4A   ATP5L   COX14   RPL41   RPL18AP3        ISCU    GPN3    C12orf47
MED13L  DIABLO  ARL6IP4 POMP    MED4    RPS29   CGRRF1  ERH     COX16   SIPA1L1
NDUFB1  DYNC1H1 C14orf2 SRP14   RSL24D1 GTF2A2  RPS3AP6 VPS13C  RPLP1   BBS4
RPS17L  IQGAP1  RPS15A  TERF2IP RPL13   RPAIN   KIAA0100        ACACA   RPL17
RPL19   RPS7P11 BPTF    TRIM65  ANAPC11 C18orf32        UQCR11  RPL36   TRAPPC5
NDUFA7  PIN1    NDUFA13 ALKBH6  EID2    SEPW1   RPL18   LIN7B   RPS9    TRAPPC2 A1BG
RPS5    LINC00493       ROMO1   UQCR10  RPS19BP1        SLC25A17        USP9X   UXT
TIMM17B HUWE1   TCEAL8  NGFRAP1 PSMD10  NDUFA1  SSR4
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006614      1.93501935783393e-35    46.6360655737705        1.10442183931908
30      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      2.67665026944318e-35    46.0191975841242        1.11494014255069
30      106     cotranslational protein targeting to membrane
GO:0045047      2.67665026944318e-35    46.0191975841242        1.11494014255069
30      106     protein targeting to ER
GO:0072599      2.67665026944318e-35    46.0191975841242        1.11494014255069
30      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      1.0070255646683e-33     39.7103204172876        1.24115978133001
30      118     protein localization to endoplasmic reticulum
GO:0006414      3.82515260888377e-32    41.7067448680352        1.10442183931908
28      105     translational elongation
GO:0006415      9.22894034660175e-31    45.1873015873016        0.957165594076534
26      91      translational termination
GO:0072594      3.98518260107929e-30    22.9113961374023        2.14573385924849
33      204     establishment of protein localization to organelle
GO:0006612      4.93071587865502e-30    28.3406637345062        1.60930039443637
30      153     protein targeting to membrane
GO:0000184      2.13947470155618e-27    31.5203959720089        1.25167808456162
26      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      2.48046465937381e-27    26.0246525045896        1.58826378797315
28      151     viral genome expression
GO:0019083      2.48046465937381e-27    26.0246525045896        1.58826378797315
28      151     viral transcription
GO:0043624      9.2406972904508e-26     24.2965714285714        1.60930039443637
27      153     cellular protein complex disassembly
GO:0043241      2.29121967989197e-25    23.3609770992366        1.66189191059442
27      158     protein complex disassembly
GO:0000956      1.51151156239037e-24    21.5345915492958        1.77759324614214
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27      169     nuclear-transcribed mRNA catabolic process
GO:0006413      1.85405285265539e-24    23.2110103300579        1.59878209120476
26      152     translational initiation
GO:0033365      2.50837908810917e-24    11.0259573426859        4.97515742855166
39      473     protein localization to organelle
GO:0034623      3.40309038164766e-24    20.7947755102041        1.83018476230019
27      174     cellular macromolecular complex disassembly
GO:0006402      6.39148121649979e-24    20.2381986754967        1.87225797522663
27      178     mRNA catabolic process
GO:0032984      7.46337920381415e-24    20.1036315789474        1.88277627845824
27      179     macromolecular complex disassembly
GO:0019058      3.01553722160842e-23    16.4538758753924        2.42972804650197
29      231     viral infectious cycle
GO:0006401      3.06751891538302e-22    17.135595505618 2.15625216248011        27
205     RNA catabolic process
GO:0006605      3.11520177880595e-22    10.2058302656452        4.98567573178327
37      474     protein targeting
GO:0016032      5.90534725579859e-22    10.3827170751973        4.74375475745623
36      451     viral reproduction
GO:0022415      9.02941465379931e-22    14.3586386513216        2.73475884021867
29      260     viral reproductive process
GO:0071845      1.10110053202151e-20    12.9850470269409        2.98719811777732
29      284     cellular component disassembly at cellular level
GO:0022411      1.63163906717007e-20    12.7808644881816        3.02927133070376
29      288     cellular component disassembly
GO:0022904      6.67156536268756e-14    19.2187077588537        1.00975711023459
15      96      respiratory electron transport chain
GO:0022900      9.91866284412494e-12    13.0466785254248        1.40945263303578
15      134     electron transport chain
GO:0045333      2.31037940751085e-11    12.2179435599747        1.49359905888866
15      142     cellular respiration
GO:0042773      1.20364804133444e-09    23.6196172248804        0.494360251885683
9       47      ATP synthesis coupled electron transport
GO:0042775      1.20364804133444e-09    23.6196172248804        0.494360251885683
9       47      mitochondrial ATP synthesis coupled electron transport
GO:0015980      3.72440504716403e-09    6.51190414708465        3.22911909210435
18      307     energy derivation by oxidation of organic compounds
GO:0006119      8.52537130747957e-09    18.3031254459826        0.610061587433396
9       58      oxidative phosphorylation
GO:0006120      8.01587204193473e-08    23.7550535077289        0.37865891633797
7       36      mitochondrial electron transport, NADH to ubiquinone
GO:0006091      1.1846145623813e-07     4.851554313657  4.50183378312919        19
428     generation of precursor metabolites and energy
Tissue: Artery_Tibial=>Nerve_Tibial     Type:   asymmetric
SourceGene:     YAE1D1(ENSG00000241127.3)
TargetGeneSet:  MRPL20  MINOS1  CDC42   ZCCHC17 RP11    PSMB2   PPCS    CCDC30
MAGOH   SLC35D1 COL24A1 ACTG1P4 BCAS2   U1      FAM72C  MRPS21  RP1     ALDH9A1
TMCO1   XPR1    SNRPE   TARBP1  YWHAQ   SLC4A1AP        MORN2   PPM1B   CCDC115 AGPS
UBE2E3  C2orf47 NDUFB3  MRPL44  SEPT2   CNTN4-AS1       TPRXL   UBE2E1  CCDC72  RBM6
SPCS1   PSMC1P1 RNF7    MRPL47  NDUFB5  MYL5    EVC2    UTP3    MRPS18C TMSB4XP8
NDUFC1  NDUFS6  RBBP4P1 ZNF622  SUB1    TAF9    CTD     PRRC1   UQCRQ   TCOF1   CTB
FGFR4   TMEM14B NHLRC1  HIST1H1E        PPP1R10 HNRNPC  COX6A1P2        FRS3
KIAA0240        C6orf226        MAD2L1BP        RPL39P3 COX7A2  FAM54A  PSMB1
FTSJ2   NUDT1   NDUFA4  TOMM7   MALSU1  POM121C GNG11   BUD31   PMS2P1  PSMC2
MRPS33  LSM1    KAT6A   MRPL15  TCEB1   C8orf59 COX6C   POLR2K  C9orf123
C9orf133        CTSL1   SEC61B  MSANTD3 CTNNAL1 TXN     DFNB31  FBXW2   ODF2
C9orf104        FBXO18  ATP5C1  CDC123  SAR1A   POLR2L  ARNTL   IMMP1L  FNBP4
MRPL16  FEN1    C11orf30        SNORA32 ATP5L   PANX3   PHC1P1  MYL6    MED13L  PXN
RPL31P52        DIABLO  RPS7P10 POMP    COMMD6  RPS29   PSMA3   ERH     NDUFB1
C14orf2 HMGN2P5 TMEM85  SRP14   GTF2A2  ANXA2   COX5A   FAM100A NDUFAB1 HMGN2P3
KIF22   TBX6    MIR4519 RANBP10 MLLT6   MSI2    ATP5H   MRPS7   H3F3B   USP36
MYL12B  IER3IP1 DYM     C19orf70        PIN1    ZNF653  C19orf44        UQCRFS1
COX6B1  POLR2I  TBC1D17 NDUFA3  MCM8    SNRPB2  ROMO1   RP3     PFDN4   ATP5J   PIGP
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BCR     BCRP8   SNRPD3  UQCR10  MORC2   LGALS1  NDUFA6  EEF1B2P3        FATE1
HMGN1P26
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      1.08446173673158e-20    31.6644436644437        0.863608054805896
19      96      respiratory electron transport chain
GO:0022900      3.66206446297357e-19    22.658692185008 1.20545290983323        20
134     electron transport chain
GO:0045333      1.20307042226636e-18    21.1609538002981        1.27742024773372
20      142     cellular respiration
GO:0015980      4.10583548678421e-14    10.032228719948 2.76174659193135        22
307     energy derivation by oxidation of organic compounds
GO:0006119      3.23436620881736e-12    28.0733059181119        0.521763199778562
11      58      oxidative phosphorylation
GO:0006091      4.297180398149e-12      7.38590054228684        3.85025257767629
23      428     generation of precursor metabolites and energy
GO:0042773      9.54978224417832e-12    32.1711711711712        0.422808110165386
10      47      ATP synthesis coupled electron transport
GO:0042775      9.54978224417832e-12    32.1711711711712        0.422808110165386
10      47      mitochondrial ATP synthesis coupled electron transport
GO:0006120      2.23648849422177e-11    39.3774104683196        0.323853020552211
9       36      mitochondrial electron transport, NADH to ubiquinone
GO:0000375      2.87742340673222e-06    6.59337068160598        1.88014670265034
11      209     RNA splicing, via transesterification reactions
GO:0042776      4.19856001155518e-06    50.4832451499118        0.116946924088298
4       13      mitochondrial ATP synthesis coupled proton transport
GO:0015985      1.73520865905422e-05    32.4421768707483        0.161926510276105
4       18      energy coupled proton transport, down electrochemical gradient
GO:0015986      1.73520865905422e-05    32.4421768707483        0.161926510276105
4       18      ATP synthesis coupled proton transport
Tissue: Artery_Tibial=>Nerve_Tibial     Type:   asymmetric
SourceGene:     YEATS4(ENSG00000127337.2)
TargetGeneSet:  RP11    RP13    SLC45A1 TMEM201 FAM131C CROCCP3 RPL11   MAP7D1
MFSD2A  RP3     SNORD46 TMEM69  CSRP3   CELSR2  GDAP2   CCT3    ATP1A2  RCSD1
KDM5B-AS1       TMEM81  ST13P19 ZNF692  LPIN1   SRSF7   EIF3FP3 NFU1    CAPG
RPL31   RFX8    SLC6A6  PLCL2   RPL14   QARS    PHF7    SHQ1    P2RY13  EIF4G1
RPL35A  MYL5    RPL7AP31        PAICS   RPL34   INTU    NPY1R   EXOC3   MTRR    CCT5
BTF3    F2RL1   FBXL17  CAMLG   CD74    RPS14   GAPDHP71        BTN2A3P RPS10
C6orf226        SLC18B1 MRPS12  PERP    RPL23P8 GS1     TMEM120A        MKRN1
ABCF2   C8orf40 RPS20   RPL30   POP1    COX6C   CTHRC1  SCRIB   GBA2    ZNF169
IKBKAP  GGTA1P  PRPS1P2 C9orf114        ABCA2   PARD3   ZNF37A  TSPAN14 RPL13AP5
SFRP5   PLEKHA1 ZNF195  EIF3F   RPS13   MTA2    DNAJC4  FAU     CDK2AP2 UNC93B1
CEP57   RPS25   HYOU1   KCNJ5   FKBP4   RP4     KLRF1   FMNL3   ATP5G2  MARS
RPL14P1 KRT8P22 YEATS4  SLC25A3 GLT8D2  ISCU    PUS1    RPS7P10 WBP4    OXA1L
NUBPL   RPS6KL1 NEK9    TTLL5   GLRX5   MEG8    BTBD6   IGHV3-7 OIP5-AS1
PLA2G4B GRAMD2  HEXA    C16orf79        ERVK13-1        HCFC1R1 CLEC16A CTD
PYCARD  C16orf46        ZNF469  RP1     CTNS    MYBBP1A ALDOC   GPR179  RPL17
RPL19   KRT223P GHDC    RPL27   HILS1   RPL38   FBF1    ZFP161  RAB12   DSC2
ZCCHC2  RPL36   SMARCA4 UBA52   ZNF708  RPS16   ZNF541  BCAT2   ZNF808  RPS9
ZNF470  NOP56   ELMO2   RPS21   RTN4R   ZNF280B RANGAP1 CRELD2  STS     ZNF81
RPL7P57 DIAPH2  CXorf1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      3.1428413168975e-24     38.8636363636364        0.824925610684382
21      91      translational termination
GO:0000184      4.60956574832672e-23    29.5948169866641        1.07874887551035
22      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006414      8.19925129889536e-23    32.3545454545455        0.951837243097364
21      105     translational elongation
GO:0006614      8.19925129889536e-23    32.3545454545455        0.951837243097364
21      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.01502290635405e-22    31.9716577540107        0.960902359698291
21      106     cotranslational protein targeting to membrane
GO:0045047      1.01502290635405e-22    31.9716577540107        0.960902359698291
21      106     protein targeting to ER
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GO:0072599      1.01502290635405e-22    31.9716577540107        0.960902359698291
21      106     establishment of protein localization to endoplasmic reticulum
GO:0006413      5.48981075299118e-22    23.4275768016078        1.37789772334095
23      152     translational initiation
GO:0034623      6.32326500172459e-22    21.188785046729 1.57733028856135        24
174     cellular macromolecular complex disassembly
GO:0043624      6.41441462649512e-22    23.2457264957265        1.38696283994187
23      153     cellular protein complex disassembly
GO:0070972      1.11243590681068e-21    27.9927835051546        1.06968375890942
21      118     protein localization to endoplasmic reticulum
GO:0032984      1.26394354349116e-21    20.49804039795  1.62265587156598        24
179     macromolecular complex disassembly
GO:0043241      1.37344324543283e-21    22.3768861454047        1.43228842294651
23      158     protein complex disassembly
GO:0019080      1.09227039286321e-20    22.2033994737216        1.36883260674002
22      151     viral genome expression
GO:0019083      1.09227039286321e-20    22.2033994737216        1.36883260674002
22      151     viral transcription
GO:0006612      1.46997069689745e-20    21.8613348273689        1.38696283994187
22      153     protein targeting to membrane
GO:0000956      1.3648602001262e-19     19.4599013917494        1.53200470555671
22      169     nuclear-transcribed mRNA catabolic process
GO:0006402      4.31521714479814e-19    18.3255704540108        1.61359075496505
22      178     mRNA catabolic process
GO:0006401      5.82224420843747e-19    16.5432437932438        1.85834890319009
23      205     RNA catabolic process
GO:0071845      7.0820758368039e-17     12.1294033069734        2.57449311466334
24      284     cellular component disassembly at cellular level
GO:0022411      9.76231353416179e-17    11.9422259983008        2.61075358106705
24      288     cellular component disassembly
GO:0019058      1.24754327370916e-16    13.6272332206663        2.0940419348142 22
231     viral infectious cycle
GO:0072594      1.32874576152819e-16    14.7479880774963        1.84928378658916
21      204     establishment of protein localization to organelle
GO:0022415      1.5313899745717e-15     11.9421787063449        2.35693031624109
22      260     viral reproductive process
GO:0006605      8.02267033340791e-13    7.28610749254108        4.29686526883953
25      474     protein targeting
GO:0033365      3.84720495659742e-11    6.56399176954733        4.2878001522386 23
473     protein localization to organelle
GO:0016032      1.01508531448093e-10    6.535403434486  4.0883675870182 22      451
viral reproduction
GO:0006364      4.56921504894388e-06    9.63685636856369        0.942772126496436
8       104     rRNA processing
GO:0016072      6.94523902936424e-06    9.06615654391838        0.997162826102  8
110     rRNA metabolic process
GO:0042254      8.39393584807817e-06    7.47189695550351        1.35070237353816
9       149     ribosome biogenesis
GO:0034660      1.08073032336964e-05    5.18866007941638        2.58355823126427
12      285     ncRNA metabolic process
GO:0071843      1.11563267010338e-05    5.6656432748538 2.16656286762162        11
239     cellular component biogenesis at cellular level
GO:0034470      1.38935912753098e-05    6.14615050021749        1.81302332018545
10      200     ncRNA processing
GO:0042274      1.7884689744967e-05     32.1844769403825        0.163172098816691
4       18      ribosomal small subunit biogenesis
Tissue: Skin_Sun_Exposed_Lower_leg=>Artery_Tibial       Type:   cluster
SourceGene:     ACTG1P3(ENSG00000215388.3)
TargetGeneSet:  RP11    NBPF5   SNAPIN  FLAD1   LAMTOR2 MRPL24  TIMM17A PYCR2
TFB2M   OST4    TRIM54  GEMIN6  COMMD1  SNRPG   TANC1   ATP5G3  IQSEC1  UMPS
ETV5-AS1        NDUFC1  NDUFS6  SKP2    EGFLAM  POC5    CETN3   ASS1P10 EEF1E1
TBC1D7  MED20   COX7A2  YAE1D1  MTERF   PMS2P1  POP7    NDUFB2  TMEM74  PCBD1
MRPS16  SRP9P1  PTPRE   POLR2L  HARBI1  COX8A   EI24    SMUG1   MMAB    POP5    DENR
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MRPL52  ARG2    COX16   SLIRP   C14orf2 MRPS11  POLR3K  C16orf91        NDUFAB1
PSMB6   TXNDC17 ATP5G1  PHB     C17orf89        UQCR11  NDUFA7  PIN1    LSM4
DDX49   NDUFA13 COX6B1  GEMIN7  AP2S1   PLCB1   RPS27AP2        ZNFX1   ATP5E
TUBA8   UQCR10  HDHD1   NDUFA1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      3.24556440118388e-16    42.2655148897477        0.43844716628607
13      96      respiratory electron transport chain
GO:0022900      2.79075475944671e-14    28.9150163729924        0.61199916960764
13      134     electron transport chain
GO:0045333      5.97504778100445e-14    27.106625713032 0.648536433464812       13
142     cellular respiration
GO:0015980      1.03829670147942e-09    11.756064690027 1.402117500519  13      307
energy derivation by oxidation of organic compounds
GO:0042773      1.62773256372155e-09    42.5487288135593        0.214656425160889
7       47      ATP synthesis coupled electron transport
GO:0042775      1.62773256372155e-09    42.5487288135593        0.214656425160889
7       47      mitochondrial ATP synthesis coupled electron transport
GO:0006119      7.48133722625455e-09    33.345962113659 0.264895162964501       7
58      oxidative phosphorylation
GO:0006120      1.25847848280961e-08    47.85   0.164417687357276       6       36
mitochondrial electron transport, NADH to ubiquinone
GO:0006091      5.5191971543385e-08     8.25687656285519        1.95474361635873
13      428     generation of precursor metabolites and energy
GO:0000387      1.13792270258561e-05    34.3082437275986        0.141581897446543
4       31      spliceosomal snRNP assembly
Tissue: Skin_Sun_Exposed_Lower_leg=>Artery_Tibial       Type:   cluster
SourceGene:     CNOT6(ENSG00000113300.7)
TargetGeneSet:  AURKAIP1        XKR8    GPBP1L1 MAGOH   RWDD3   RP11    PYCR2
MRPL33  SNRPG   MYEOV2  GTPBP8  RNF7    PDCD6   SKP2    FST     ATOX1   HNRNPC
KLHDC3  COX7A2  GPR126  RP1     TMEM242 SEC61G  SKP1P1  BRI3    POP7    ADCK2
C7orf29 BAG4    MRPS35  ZBTB34  CACFD1  C9orf69 CHCHD1  BUB3    C11orf10
COX8A   PPP1R14B        PHLDB1  MRPL51  FAM86FP COX14   ESRRAP1 MRPL52  C14orf167
COX16   GTF2A2  CORO2B  COX5A   POLR3K  NDUFAB1 CNEP1R1 TMEM208 C17orf59
SNX11   MRPL27  ATP5H   UQCR11  SIRT6   CLPP    C19orf79        PIN1    LSM4
NDUFA13 COX6B1  CTU1    ATP5E   UQCR10  RPS19BP1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      2.83657356242712e-11    37.0215517241379        0.325513805272992
9       96      respiratory electron transport chain
GO:0022900      5.80245845438919e-10    25.6986 0.454363019860217       9       134
electron transport chain
GO:0045333      9.73660960242165e-10    24.1392857142857        0.481489170299633
9       142     cellular respiration
GO:0015980      7.63431626646694e-07    10.6489932885906        1.04096602311259
9       307     energy derivation by oxidation of organic compounds
GO:0006091      1.15696279473892e-05    7.50877088305489        1.45124904850875
9       428     generation of precursor metabolites and energy
Tissue: Artery_Tibial=>Skin_Sun_Exposed_Lower_leg       Type:   asymmetric
SourceGene:     CTD-2547L16.3(ENSG00000253384.1)
TargetGeneSet:  C1QC    C1QB    LAPTM5  BMP8A   CD53    FCER1G  PTPRC   CR1
HS1BP3-IT1      BRE     U6      CHST13  CP      SPOCK1  DOCK2   CTB     SDCBP
HRCT1   SVEP1   SUSD1   APBB1IP HPS1    SERPING1        MS4A7   SLC15A3 ALDH3B1 NNMT
C1S     C3AR1   LRP1    SELPLG  CHST14  TEPP    IRF8    CYBA    CD68    NSF
ANKFN1  C19orf59        LRRC25  TYROBP  ZSCAN18 CTSA    ATP6AP2 FAM120C GLA
SASH3   TMLHE
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0002460      7.41189648208857e-10    25.6954691259022        0.475953221230365
9       181     adaptive immune response based on somatic recombination of immune
receptors built from immunoglobulin superfamily domains
GO:0002250      1.64056603770991e-09    23.3563218390805        0.520656009964708
9       198     adaptive immune response
GO:0002449      9.79027258973292e-09    23.9060796645702        0.439139159919729
8       167     lymphocyte mediated immunity
GO:0002252      3.99113913874788e-08    13.3330167173252        1.01501626185039
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10      386     immune effector process
GO:0002443      6.07249161939955e-08    18.6666666666667        0.554840495467442
8       211     leukocyte mediated immunity
GO:0006958      1.85988125384329e-07    48.3771043771044        0.131478790395128
5       50      complement activation, classical pathway
GO:0016064      4.05110284594765e-07    25.55   0.291882914677185       6       111
immunoglobulin mediated immune response
GO:0019724      4.74438212221084e-07    24.8350694444444        0.299771642100893
6       114     B cell mediated immunity
GO:0006956      6.0190430144779e-07     37.5    0.165663275897862       5       63
complement activation
GO:0002455      7.04631537401598e-07    36.2449494949495        0.170922427513667
5       65      humoral immune response mediated by circulating immunoglobulin
GO:0072376      2.25343803708071e-06    28.2093663911846        0.215625216248011
5       82      protein activation cascade
GO:0050778      3.78880573433601e-06    10.5295880149813        0.957165594076534
8       364     positive regulation of immune response
GO:0002253      1.10142986865853e-05    10.9199072028281        0.786243166562868
7       299     activation of immune response
GO:0002697      1.28020566668088e-05    13.6711538461538        0.528544737388416
6       201     regulation of immune effector process
GO:0006959      1.58627604246756e-05    18.5133385133385        0.320808248564113
5       122     humoral immune response
Tissue: Artery_Tibial=>Skin_Sun_Exposed_Lower_leg       Type:   asymmetric
SourceGene:     ENSG00000225059.1
TargetGeneSet:  DENND2D FLG2    LCE1F   LCE1E   LCE1C   LCE1B   LCE1A   HMCN1   GDF7
ADAMTS9-AS1     BCL6    BTC     ANKRD32 GLIS3   CCDC77  PLEKHG6 NFE2    LRCH1   RP11
G2E3    CES4A   VN2R10P GSDMA   CALR    SYS1-DBNDD2     MIS18A  ETS2    GRPR
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0031424      1.82922189146044e-09    138.947876447876        0.0552210919659539
5       42      keratinization
GO:0030216      1.13167210273534e-07    57.5561797752809        0.123590062971421
5       94      keratinocyte differentiation
GO:0009913      2.49078956408045e-07    48.7312925170068        0.144626669434641
5       110     epidermal cell differentiation
GO:0030855      1.14741895604588e-06    23.6722408026756        0.370770188914262
6       282     epithelial cell differentiation
GO:0008544      1.62241952436155e-05    20.0963718820862        0.33790049131548
5       257     epidermis development
Tissue: Skin_Sun_Exposed_Lower_leg=>Artery_Tibial       Type:   asymmetric
SourceGene:     IGFBP5(ENSG00000115461.4)
TargetGeneSet:  FOXO6   RPL5    RPS7    COX7A2L NCAPH   RPL15   MAP1B   RP11    NPM1
RPL15P3 MICA    RPL10A  SPDYE1  SEMA3C  EIF3E   RPL7A   VTI1A   RPL27A  FAT3
PLBD2   RSL24D1 SEC11A  NLRP12
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006614      9.33838843882724e-11    73.1224489795918        0.152584596221715
7       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      9.99015863106583e-11    72.3787878787879        0.154037782852398
7       106     cotranslational protein targeting to membrane
GO:0045047      9.99015863106583e-11    72.3787878787879        0.154037782852398
7       106     protein targeting to ER
GO:0072599      9.99015863106583e-11    72.3787878787879        0.154037782852398
7       106     establishment of protein localization to endoplasmic reticulum
GO:0070972      2.13927239416294e-10    64.5    0.171476022420594       7       118
protein localization to endoplasmic reticulum
GO:0000184      2.27103890190469e-10    63.9196428571429        0.172929209051277
7       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006413      1.27428244380048e-09    49.2586206896552        0.220884367863816
7       152     translational initiation
GO:0006612      1.33423773257923e-09    48.9178082191781        0.222337554494499
7       153     protein targeting to membrane
GO:0043624      1.33423773257923e-09    48.9178082191781        0.222337554494499
7       153     cellular protein complex disassembly
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GO:0043241      1.67139039472262e-09    47.2814569536424        0.229603487647914
7       158     protein complex disassembly
GO:0006415      2.65350413836654e-09    67.5058823529412        0.132239983392153
6       91      translational termination
GO:0000956      2.67584712446114e-09    44.037037037037 0.245588540585427       7
169     nuclear-transcribed mRNA catabolic process
GO:0034623      3.27969306330938e-09    42.7035928143713        0.252854473738842
7       174     cellular macromolecular complex disassembly
GO:0006402      3.84282202852439e-09    41.6929824561403        0.258667220261574
7       178     mRNA catabolic process
GO:0032984      3.99579626860457e-09    41.4476744186046        0.260120406892257
7       179     macromolecular complex disassembly
GO:0006414      6.32691400295807e-09    57.9030303030303        0.152584596221715
6       105     translational elongation
GO:0072594      9.91149384902272e-09    36.1243654822335        0.296450072659332
7       204     establishment of protein localization to organelle
GO:0006401      1.02531144534909e-08    35.9393939393939        0.297903259290015
7       205     RNA catabolic process
GO:0019080      5.61716063210416e-08    39.4068965517241        0.219431181233133
6       151     viral genome expression
GO:0019083      5.61716063210416e-08    39.4068965517241        0.219431181233133
6       151     viral transcription
GO:0071845      9.65983470197068e-08    25.5469314079422        0.412705003113971
7       284     cellular component disassembly at cellular level
GO:0022411      1.06279105736804e-07    25.1761565836299        0.418517749636703
7       288     cellular component disassembly
GO:0033365      1.73630693240662e-07    18.4813895781638        0.687357276313058
8       473     protein localization to organelle
GO:0006605      1.76466691210442e-07    18.4404093760317        0.688810462943741
8       474     protein targeting
GO:0022613      5.9483776486576e-07     25.9561643835616        0.326966991903675
6       225     ribonucleoprotein complex biogenesis
GO:0019058      6.9406123036348e-07     25.2533333333333        0.335686111687772
6       231     viral infectious cycle
GO:0071843      8.47127712974072e-07    24.3725321888412        0.347311604733236
6       239     cellular component biogenesis at cellular level
GO:0022415      1.38494421022697e-06    22.3244094488189        0.377828523977579
6       260     viral reproductive process
GO:0042254      1.94069486231348e-06    31.0026041666667        0.216524807971767
5       149     ribosome biogenesis
Tissue: Artery_Tibial=>Skin_Sun_Exposed_Lower_leg       Type:   asymmetric
SourceGene:     MIR590(ENSG00000207741.1)
TargetGeneSet:  MXRA8   DNAJC16 EYA3    CCDC23  RP4     CTSS    UFC1    DNM3OS
GPR37L1 RAB4A   IAH1    SPDYA   UBC     SP5     NIF3L1  EEF1B2  RPL15   CP
TTC14   PPP1R2  RP11    FAM190A RPS3A   SPCS3   BDP1    ADAMTS19        F13A1
KLHDC3  EEF1A1  UBE2J1  BRD7P3  HEBP2   PSMB1   EEF1A1P6        SBDS    NCF1B
CCL26   RPS3AP26        LY96    CHMP4C  DAPK1   RPS3AP5 SLC35G1 TSSC2   EIF3F
RPS13   HPS5    LMO2    RP1     FTH1    RBM14   JRKL    GAPDH   DAZAP2  PFDN5
APPL2   RPL6    TPT1    CCNB1IP1        TRDC    EXD2    PAPLN   TRPM7   PKM2
NTAN1   RPS15A  GOT2    CHTF8   CTD     RNF167  CD68    RPL26   COX10   ZNHIT3
RPL17   FTL     RP3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      1.47673546624249e-11    30.0968421052632        0.435955989204899
10      105     translational elongation
GO:0006614      4.32985424798658e-10    26.2775735294118        0.435955989204899
9       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      4.71651216055801e-10    26.0048514251061        0.440107951006851
9       106     cotranslational protein targeting to membrane
GO:0045047      4.71651216055801e-10    26.0048514251061        0.440107951006851
9       106     protein targeting to ER
GO:0072599      4.71651216055801e-10    26.0048514251061        0.440107951006851
9       106     establishment of protein localization to endoplasmic reticulum
GO:0070972      1.23586942312019e-09    23.1225040474906        0.489931492630268
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9       118     protein localization to endoplasmic reticulum
GO:0006415      3.53907690704808e-09    26.5208526413346        0.377828523977579
8       91      translational termination
GO:0006413      1.16255483641681e-08    17.5828877005348        0.631098193896616
9       152     translational initiation
GO:0006612      1.23127224219466e-08    17.4595588235294        0.635250155698568
9       153     protein targeting to membrane
GO:0043624      1.23127224219466e-08    17.4595588235294        0.635250155698568
9       153     cellular protein complex disassembly
GO:0043241      1.63102119620009e-08    16.8677457560205        0.656009964708325
9       158     protein complex disassembly
GO:0000184      2.98491410807608e-08    19.7920997920998        0.494083454432219
8       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0034623      3.7730360310148e-08     15.2149732620321        0.722441353539547
9       174     cellular macromolecular complex disassembly
GO:0032984      4.8202817690404e-08     14.7622837370242        0.743201162549305
9       179     macromolecular complex disassembly
GO:0072594      1.48031863913011e-07    12.8470588235294        0.84700020759809
9       204     establishment of protein localization to organelle
GO:0019080      1.90639954577891e-07    15.3286713286713        0.626946232094665
8       151     viral genome expression
GO:0019083      1.90639954577891e-07    15.3286713286713        0.626946232094665
8       151     viral transcription
GO:0000956      4.52078350387159e-07    13.5977066411849        0.70168154452979
8       169     nuclear-transcribed mRNA catabolic process
GO:0006402      6.70898009617185e-07    12.8696832579186        0.739049200747353
8       178     mRNA catabolic process
GO:0006401      1.9446719025694e-06     11.0847325263569        0.851152169400042
8       205     RNA catabolic process
GO:0071845      2.36772714650336e-06    9.05839572192513        1.1791571517542 9
284     cellular component disassembly at cellular level
GO:0022411      2.65586737324971e-06    8.92599620493359        1.19576499896201
9       288     cellular component disassembly
GO:0019058      4.72285749714866e-06    9.77440496723008        0.959103176250778
8       231     viral infectious cycle
GO:0022415      1.12341186163975e-05    8.63186813186813        1.07951006850737
8       260     viral reproductive process
Tissue: Artery_Tibial=>Skin_Sun_Exposed_Lower_leg       Type:   cluster
SourceGene:     MIR590(ENSG00000207741.1)
TargetGeneSet:  MXRA8   DNAJC16 EYA3    CCDC23  RP4     CTSS    UFC1    DNM3OS
GPR37L1 RAB4A   IAH1    SPDYA   UBC     SP5     NIF3L1  EEF1B2  RPL15   CP
TTC14   PPP1R2  RP11    FAM190A RPS3A   SPCS3   BDP1    ADAMTS19        F13A1
KLHDC3  EEF1A1  UBE2J1  BRD7P3  HEBP2   PSMB1   EEF1A1P6        SBDS    NCF1B
CCL26   RPS3AP26        LY96    CHMP4C  DAPK1   RPS3AP5 SLC35G1 TSSC2   EIF3F
RPS13   HPS5    LMO2    RP1     FTH1    RBM14   JRKL    GAPDH   DAZAP2  PFDN5
APPL2   RPL6    TPT1    CCNB1IP1        TRDC    EXD2    PAPLN   TRPM7   PKM2
NTAN1   RPS15A  GOT2    CHTF8   CTD     RNF167  CD68    RPL26   COX10   ZNHIT3
RPL17   FTL     RP3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      1.47673546624249e-11    30.0968421052632        0.435955989204899
10      105     translational elongation
GO:0006614      4.32985424798658e-10    26.2775735294118        0.435955989204899
9       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      4.71651216055801e-10    26.0048514251061        0.440107951006851
9       106     cotranslational protein targeting to membrane
GO:0045047      4.71651216055801e-10    26.0048514251061        0.440107951006851
9       106     protein targeting to ER
GO:0072599      4.71651216055801e-10    26.0048514251061        0.440107951006851
9       106     establishment of protein localization to endoplasmic reticulum
GO:0070972      1.23586942312019e-09    23.1225040474906        0.489931492630268
9       118     protein localization to endoplasmic reticulum
GO:0006415      3.53907690704808e-09    26.5208526413346        0.377828523977579
8       91      translational termination
```

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GO:0006413      1.16255483641681e-08    17.5828877005348        0.631098193896616
9       152     translational initiation
GO:0006612      1.23127224219466e-08    17.4595588235294        0.635250155698568
9       153     protein targeting to membrane
GO:0043624      1.23127224219466e-08    17.4595588235294        0.635250155698568
9       153     cellular protein complex disassembly
GO:0043241      1.63102119620009e-08    16.8677457560205        0.656009964708325
9       158     protein complex disassembly
GO:0000184      2.98491410807608e-08    19.7920997920998        0.494083454432219
8       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0034623      3.7730360310148e-08     15.2149732620321        0.722441353539547
9       174     cellular macromolecular complex disassembly
GO:0032984      4.8202817690404e-08     14.7622837370242        0.743201162549305
9       179     macromolecular complex disassembly
GO:0072594      1.48031863913011e-07    12.8470588235294        0.84700020759809
9       204     establishment of protein localization to organelle
GO:0019080      1.90639954577891e-07    15.3286713286713        0.626946232094665
8       151     viral genome expression
GO:0019083      1.90639954577891e-07    15.3286713286713        0.626946232094665
8       151     viral transcription
GO:0000956      4.52078350387159e-07    13.5977066411849        0.70168154452979
8       169     nuclear-transcribed mRNA catabolic process
GO:0006402      6.70898009617185e-07    12.8696832579186        0.739049200747353
8       178     mRNA catabolic process
GO:0006401      1.9446719025694e-06     11.0847325263569        0.851152169400042
8       205     RNA catabolic process
GO:0071845      2.36772714650336e-06    9.05839572192513        1.1791571517542 9
284     cellular component disassembly at cellular level
GO:0022411      2.65586737324971e-06    8.92599620493359        1.19576499896201
9       288     cellular component disassembly
GO:0019058      4.72285749714866e-06    9.77440496723008        0.959103176250778
8       231     viral infectious cycle
GO:0022415      1.12341186163975e-05    8.63186813186813        1.07951006850737
8       260     viral reproductive process
Tissue: Artery_Tibial=>Skin_Sun_Exposed_Lower_leg       Type:   asymmetric
SourceGene:     MYL6P3(ENSG00000227173.1)
TargetGeneSet:  AURKAIP1        ARHGEF16        FBXO44  SIKE1   C2CD4D  SLC19A2
SNRPG   ARL5A   FASTKD1 MTX2    ZC3H15  DNAJC19 NDUFS6  HMGCR   RPL26L1 7SK     FUT9
RN5S216 ZFAND2A PSMG3   ACTB    NDUFA4  POP7    RABL5   NDUFB2  COX6C   C8orf55
EXOSC4  ARHGAP39        AK1     FAM73B  ZMYND19 CHCHD1  HECTD2  USMG5   TSSC4
CTNND1  ESRRA   EFHA1   RP11    CTD     SNRPA1  FAM195A NARFL   MRPS34  TCEB2
SPIRE2  ITGAE   MIS12   COASY   LLGL2   SCARNA17        UQCR11  CSNK1G2 TJP3
DDX39A  NDUFB7  UQCRFS1 U2AF1L4 GNG8    EHD2    ATP5J   MAPK1   CRYBB3  RPS19BP1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0045333      5.35321403002086e-10    26.1020117862223        0.452010241505778
9       142     cellular respiration
GO:0022904      5.97919403603125e-10    34.2511961722488        0.305584388623625
8       96      respiratory electron transport chain
GO:0022900      8.59309419206233e-09    23.8579782790309        0.426544875787143
8       134     electron transport chain
GO:0015980      4.32947608406704e-07    11.514873934337 0.977233409452633       9
307     energy derivation by oxidation of organic compounds
GO:0006120      4.91239267601197e-06    42.7767857142857        0.114594145733859
4       36      mitochondrial electron transport, NADH to ubiquinone
GO:0006091      6.71209554667473e-06    8.11933174224344        1.36239706594699
9       428     generation of precursor metabolites and energy
GO:0042773      1.44991914134624e-05    31.8095238095238        0.149609023596983
4       47      ATP synthesis coupled electron transport
GO:0042775      1.44991914134624e-05    31.8095238095238        0.149609023596983
4       47      mitochondrial ATP synthesis coupled electron transport
Tissue: Skin_Sun_Exposed_Lower_leg=>Artery_Tibial       Type:   cluster
SourceGene:     PTPRU(ENSG00000060656.14)
TargetGeneSet:  MRPL20  RPL22   ATPIF1  RPS8    UQCRH   PRPF38A MAGOH   RP4     RP11
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BCAS2   C1orf54 MRPS21  GAS5    SNRPE   DNAJC27-AS1     HAAO    TTC7A   MPHOSPH10
DGUOK   DGUOK-AS1       RPL31   PPIG    FKBP7   EEF1B2  LSM3    RPL15   LZTFL1
RPL10AP6        C3orf15 METTL14 CEP44   BRIX1   MAP1B   COX7C   RFESD   RPL15P3 NOL7
RPS10   RPL10A  ENPP5   C6orf225        MRPS12  C7orf50 TOMM7   RABL5   JHDM1D
SSBP1   R3HCC1  RPS6    RPL7A   EDF1    AGAP11  DPCD    MRPL23  RPL27A  C11orf58
SVIP    CELF1   TRMT112 EHD1    C11orf70        RPS25   DYRK4   C12orf57        EID3
DIABLO  MRPS31  ERH     SLIRP   LRRC49  PPCDC   ANPEP   SNHG9   HSDL1   ALDOC   SDF2
EIF1    RPL27   COIL    RPL38   H3F3B   TRIM47  CTD     PTPRM   RPL17   RPS15
ZNF559  ZNF226  RPL18   ZNF548  ZNF274  RPS5    SLC27A5 RPL12P4 PPDPF   PIGP
SNRPD3  RP6     NAP1L2  RPL10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      3.61800527309792e-23    52.7955665024631        0.537679053352709
18      105     translational elongation
GO:0006415      1.37298687599072e-22    57.6460407776197        0.465988512905681
17      91      translational termination
GO:0000184      3.95990920916677e-22    45.4328147100424        0.609369593799737
18      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006614      1.85824725656262e-21    48.4276315789474        0.537679053352709
17      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      2.20489973980139e-21    47.8801498127341        0.542799806241783
17      106     cotranslational protein targeting to membrane
GO:0045047      2.20489973980139e-21    47.8801498127341        0.542799806241783
17      106     protein targeting to ER
GO:0072599      2.20489973980139e-21    47.8801498127341        0.542799806241783
17      106     establishment of protein localization to endoplasmic reticulum
GO:0000956      8.59039655703612e-21    32.7652121212121        0.865407238253408
19      169     nuclear-transcribed mRNA catabolic process
GO:0070972      1.50854685816494e-20    42.1559840194546        0.604248840910664
17      118     protein localization to endoplasmic reticulum
GO:0006402      2.35386601763777e-20    30.8910234419668        0.911494014255069
19      178     mRNA catabolic process
GO:0006413      3.89847881365398e-20    34.1649786780384        0.77835443913916
18      152     translational initiation
GO:0043624      4.4019142455727e-20     33.9095238095238        0.783475192028233
18      153     cellular protein complex disassembly
GO:0043241      7.97693921172502e-20    32.6869897959184        0.8090789564736 18
158     protein complex disassembly
GO:0006401      3.57244086218085e-19    26.3566959921799        1.04975434226005
19      205     RNA catabolic process
GO:0034623      4.6959898820806e-19     29.301510989011 0.891011002698775       18
174     cellular macromolecular complex disassembly
GO:0032984      7.88056609561584e-19    28.3815439219166        0.916614767144142
18      179     macromolecular complex disassembly
GO:0019080      1.16065392194971e-18    31.7008379156847        0.773233686250086
17      151     viral genome expression
GO:0019083      1.16065392194971e-18    31.7008379156847        0.773233686250086
17      151     viral transcription
GO:0006612      1.45913639667665e-18    31.2302631578947        0.783475192028233
17      153     protein targeting to membrane
GO:0072594      8.44615921303806e-18    24.5236175115207        1.04463358937098
18      204     establishment of protein localization to organelle
GO:0019058      1.64697046410397e-15    19.738563698967 1.18289391737596        17
231     viral infectious cycle
GO:0071845      3.0200856157906e-15     17.0514232008593        1.45429382049685
18      284     cellular component disassembly at cellular level
GO:0022411      3.85700023655921e-15    16.7940476190476        1.47477683205315
18      288     cellular component disassembly
GO:0022415      1.18047761501009e-14    17.3473395422713        1.33139575115909
17      260     viral reproductive process
GO:0016032      8.18141692971715e-12    10.35103926097  2.30945955297211        18
451     viral reproduction
GO:0033365      1.8035401165751e-11     9.83500784929356        2.42211611653173
18      473     protein localization to organelle
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GO:0006605      1.86766659472713e-11    9.81273496240602        2.4272368694208 18
474     protein targeting
GO:0022613      1.80417516525998e-08    11.5556297285269        1.15216940004152
11      225     ribonucleoprotein complex biogenesis
GO:0071843      3.36134997539575e-08    10.8353522695628        1.22385994048855
11      239     cellular component biogenesis at cellular level
GO:0042274      1.83593780917654e-06    58.6244897959184        0.0921735520033216
4       18      ribosomal small subunit biogenesis
GO:0008380      5.47716940716468e-06    7.02076677316294        1.65400318317071
10      323     RNA splicing
GO:0022618      8.89474588802644e-06    14.1652346331791        0.486471524461975
6       95      ribonucleoprotein complex assembly
GO:0042254      1.08641351200467e-05    10.4735127180996        0.76299218047194
7       149     ribosome biogenesis
GO:0000375      1.11299866289987e-05    8.54877129503995        1.07023735381634
8       209     RNA splicing, via transesterification reactions
GO:0071826      1.19563278429271e-05    13.407071339174 0.512075288907342       6
100     ribonucleoprotein complex subunit organization
Tissue: Artery_Tibial=>Skin_Sun_Exposed_Lower_leg       Type:   asymmetric
SourceGene:     RP11-54D18.2(ENSG00000215237.5)
TargetGeneSet:  KCNAB2  RP11    CDCA8   IQGAP3  CKAP2L  HJURP   CAND2   POC1A
NCAPG   PALLD   TTK     CALD1   JPH1    DNAJB5  TPP1    VWA5A   CDCA3   ESPL1
KNTC1   LINC00427       CASC4   AURKB   SPAG5   NDC80   KANK2   UBE2C   C21orf58
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0000280      1.70149855514261e-11    37.6737967914438        0.508615320739049
10      350     nuclear division
GO:0007067      1.70149855514261e-11    37.6737967914438        0.508615320739049
10      350     mitosis
GO:0000087      2.2474302087212e-11     36.5714285714286        0.523147187045879
10      360     M phase of mitotic cell cycle
GO:0048285      2.94510377886324e-11    35.530303030303 0.537679053352709       10
370     organelle fission
GO:0007051      1.20806651538886e-09    77.6    0.11625493045464        6       80
spindle organization
GO:0051301      5.5714723193295e-09     23.6800225733634        0.656840357068715
9       452     cell division
GO:0007059      3.57457495212115e-08    42.6746268656716        0.20344612829562
6       140     chromosome segregation
GO:0000070      6.69163696986665e-07    75.2156862745098        0.0712061449034669
4       49      mitotic sister chromatid segregation
GO:0000819      8.52610879416797e-07    70.5    0.0755657047955159      4       52
sister chromatid segregation
GO:0000226      1.68825441609451e-06    21.5467680608365        0.390907203653726
6       269     microtubule cytoskeleton organization
GO:0008608      1.7751076400133e-06     171.619047619048        0.024704172721611
3       17      attachment of spindle microtubules to kinetochore
GO:0051313      2.52480397672365e-06    150.145833333333        0.027610545982977
3       19      attachment of spindle microtubules to chromosome
GO:0051983      5.2490984608998e-06     114.357142857143        0.0348764791363919
3       24      regulation of chromosome segregation
GO:0000236      6.1814169372142e-06     41.681917211329 0.123520863608055       4
85      mitotic prometaphase
GO:0010948      1.00368476133952e-05    36.6700767263427        0.139505916545568
4       96      negative regulation of cell cycle process
GO:0007052      1.40312171277173e-05    80      0.0479551588125389      3       33
mitotic spindle organization
GO:0007017      1.49419123300948e-05    14.5147286821705        0.571102345858418
6       393     microtubule-based process
GO:0034453      1.68003697599912e-05    74.9895833333333        0.0508615320739049
3       35      microtubule anchoring
Tissue: Artery_Tibial=>Skin_Sun_Exposed_Lower_leg       Type:   asymmetric
SourceGene:     RP11-800K23.2(ENSG00000237350.1)
TargetGeneSet:  CTRC    CELA2A  CELA3B  CELA3A  AKIRIN1 TPI1P1  AMY2A   RP11
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APOA2   SSFA2   DPH3    RN5S155 FGB     FGA     GPBP1   SFTA2   CLPS    RP1     PLG
PSMG3   CPA2    CPA1    PRSS1   PRSS3P2 TMUB1   FGL1    DMRT2   BAG1    ARPC5L
PNLIP   PNLIPRP1        PNLIPRP2        INS     APOC3   APOA1   PLA2G1B NMB
C15orf42        GP2     CTRB2   CTRB1   BTG3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0007586      6.63892895159599e-16    69.879769299024 0.256452840633866       11
109     digestion
GO:0044241      5.24796719084791e-13    343.047619047619        0.0352916753165871
6       15      lipid digestion
GO:0010903      1.1899789965411e-08     Inf     0.00705833506331742     3       3
negative regulation of very-low-density lipoprotein particle remodeling
GO:0010901      1.18615230345785e-07    697.5   0.0117638917721957      3       5
regulation of very-low-density lipoprotein particle remodeling
GO:0035376      2.36848744672549e-07    464.967741935484        0.0141166701266348
3       6       sterol import
GO:0035382      2.36848744672549e-07    464.967741935484        0.0141166701266348
3       6       sterol transmembrane transport
GO:0070508      2.36848744672549e-07    464.967741935484        0.0141166701266348
3       6       cholesterol import
GO:0034384      9.89971067513112e-07    232.435483870968        0.0211750051899523
3       9       high-density lipoprotein particle clearance
GO:0016042      1.23887328377334e-06    15.6460204885737        0.569372361774272
7       242     lipid catabolic process
GO:0033700      1.41196926651202e-06    199.216589861751        0.0235277835443914
3       10      phospholipid efflux
GO:0022617      1.42607879604727e-06    59.9375 0.084700020759809       4       36
extracellular matrix disassembly
GO:0050709      1.42607879604727e-06    59.9375 0.084700020759809       4       36
negative regulation of protein secretion
GO:0034370      1.93833465391372e-06    174.302419354839        0.0258805618988305
3       11      triglyceride-rich lipoprotein particle remodeling
GO:0034372      1.93833465391372e-06    174.302419354839        0.0258805618988305
3       11      very-low-density lipoprotein particle remodeling
GO:0030299      2.5802890055433e-06     154.924731182796        0.0282333402532697
3       12      intestinal cholesterol absorption
GO:0008202      2.83207296481381e-06    13.7397697322791        0.644661269116324
7       274     steroid metabolic process
GO:0034377      3.34898032474373e-06    139.422580645161        0.0305861186077088
3       13      plasma lipoprotein particle assembly
GO:0065005      3.34898032474373e-06    139.422580645161        0.0305861186077088
3       13      protein-lipid complex assembly
GO:0034375      4.25548315102518e-06    126.739002932551        0.0329388969621479
3       14      high-density lipoprotein particle remodeling
GO:0008203      5.94554982932334e-06    23.0583306477602        0.263511175697184
5       112     cholesterol metabolic process
GO:0050708      7.06079297055722e-06    22.2211867039453        0.27292228911494
5       116     regulation of protein secretion
GO:0043691      7.91151056259763e-06    99.5599078341014        0.0399972320254654
3       17      reverse cholesterol transport
GO:0050995      7.91151056259763e-06    99.5599078341014        0.0399972320254654
3       17      negative regulation of lipid catabolic process
GO:0016125      7.99987331388902e-06    21.6318814277072        0.279980624178258
5       119     sterol metabolic process
GO:0015918      1.21199112232295e-05    33.5906432748538        0.143519479620787
4       61      sterol transport
GO:0030301      1.21199112232295e-05    33.5906432748538        0.143519479620787
4       61      cholesterol transport
GO:0050892      1.31995368287061e-05    81.9734345351044        0.0470555670887828
3       20      intestinal absorption
GO:0018158      1.60955815335276e-05    901     0.00705833506331742     2       3
protein oxidation
GO:0060620      1.60955815335276e-05    901     0.00705833506331742     2       3
regulation of cholesterol import
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GO:2000909      1.60955815335276e-05    901     0.00705833506331742     2       3
regulation of sterol import
Tissue: Skin_Sun_Exposed_Lower_leg=>Artery_Tibial       Type:   asymmetric
SourceGene:     RP11-874J12.2(ENSG00000177337.2)
TargetGeneSet:  PARK7   PPCS    MRPL9   RP11    COX5B   WDSUB1  BRK1    LSM3    RP4
ZMYND10 THOC7   NDUFB4  MRPS18C NDUFC1  C5orf42 CDK7    COX7C   TTC1    PNPLA1
MRPS18A OGFRL1  C6orf203        MRPS12  ZDHHC4  SKP1P1  COPS5   C10orf31
USMG5   MRPL11  ACER3   SRGAP1  MRP63   MRPS31  DGKH    HEATR4  GLRX5   TMEM121
TMEM85  RPL9P25 MT1H    COIL    SUPT4H1 ATP5H   COX6B1  FAM71E1 SNRPB2  FAM182A
ATP5J   PIGP    SNRPD3  CBY1    NDUFA6
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      9.28994304269143e-11    44.9090909090909        0.245796138675524
8       96      respiratory electron transport chain
GO:0022900      1.36360471479738e-09    31.2818828680898        0.343090443567919
8       134     electron transport chain
GO:0045333      2.16383598522514e-09    29.3978383942357        0.363573455124213
8       142     cellular respiration
GO:0015980      8.55415930448744e-07    13.022719409526 0.78603556847277        8
307     energy derivation by oxidation of organic compounds
GO:0006091      1.0064653866618e-05     9.19146141215107        1.09584111826171
8       428     generation of precursor metabolites and energy
Tissue: Skin_Sun_Exposed_Lower_leg=>Artery_Tibial       Type:   cluster
SourceGene:     RP3-393E18.2(ENSG00000237927.1)
TargetGeneSet:  C1QA    CD53    RP4     FCGR1A  CTSS    FCER1G  FCGR2A  PTPRC   PLEK
ITGA4   CCR1    EEF1A1P25       RP11    SFRP2   SLC1A3  GAPT    YTHDC2  CD14    DOK3
AIF1    CLEC5A  REPIN1  SYK     PIK3AP1 SLK     SPI1    MS4A7   EFEMP2  KCNE3   BIN2
LCP1    GPR65   ITGAM   GFOD2   SLC16A11        PIK3R6  TEX2    CD300A  IMPA2
GNA15   VAV1    IFI30   LRRC25  TYROBP  FPR3    LAIR1   HCK     FAM207CP
TRPM2   CTA     CRYBB1  RAC2    CYBB    GPR82
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0007229      2.00025953351907e-11    54.6590476190476        0.202338938481766
8       68      integrin-mediated signaling pathway
GO:0006909      5.58738652465578e-09    35.2682841068917        0.255899245726939
7       86      phagocytosis
GO:0030168      1.19105452995402e-08    18.0712669683258        0.645699259566812
9       217     platelet activation
GO:0007596      1.42457603637426e-08    11.0888092393469        1.48183516711646
12      498     blood coagulation
GO:0050900      4.66788626629229e-07    13.9055793991416        0.717113002560376
8       241     leukocyte migration
GO:0002252      1.59135061919244e-06    9.85169293181464        1.1485710331465 9
386     immune effector process
GO:0042590      3.5142206581175e-06     25.4871977240398        0.235070237353816
5       79      antigen processing and presentation of exogenous peptide antigen via
MHC class I
GO:0002283      3.98256092190817e-06    135     0.0327312988720504      3       11
neutrophil activation involved in immune response
GO:0002478      4.48771252450626e-06    24.1734143049933        0.246972527852744
5       83      antigen processing and presentation of exogenous peptide antigen
GO:0019884      5.04778463581109e-06    23.5657894736842        0.252923673102207
5       85      antigen processing and presentation of exogenous antigen
GO:0050867      6.18133996269474e-06    11.8293991416309        0.714137429935645
7       240     positive regulation of cell activation
GO:0002474      1.067374454247e-05      20.0363941769317        0.294581689848453
5       99      antigen processing and presentation of peptide antigen via MHC class
I
GO:0006911      1.08913549185673e-05    89.975  0.0446335893709778      3       15
phagocytosis, engulfment
GO:0010324      1.62097344171137e-05    77.1107142857143        0.0505847346204415
3       17      membrane invagination
GO:0048002      1.6309931321023e-05     18.2741440981093        0.32136184347104
5       108     antigen processing and presentation of peptide antigen
Tissue: Skin_Sun_Exposed_Lower_leg=>Artery_Tibial       Type:   asymmetric
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SourceGene:     SLC26A11(ENSG00000181045.10)
TargetGeneSet:  RP3     ZNF362  INSL3   TNNI1   KDM3A   SMYD1   NEB     KBTBD10 PDK1
OXSM    SLC22A14        WNT5A   LMOD3   SPINK1  HIST1H2BH       ADCYAP1R1       AVL9
FZD9    RELN    LRRN3   RP11    DLGAP2  ZNF395  C9orf95 IPMK    SLC35G1 NRAP
BNIP3   ADM     TULP3   CD27    MYF6    MYL2    ZMYM5   MYH7    GRIN2A  FA2H
SMTNL2  JMJD6   TGIF1   ANGPTL4 MYBPC2  TNNC2   PVALB   MAFF    FAM155B
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0030049      9.271688710528e-10      76.8877005347594        0.107951006850737
6       39      muscle filament sliding
GO:0033275      9.271688710528e-10      76.8877005347594        0.107951006850737
6       39      actin-myosin filament sliding
GO:0070252      1.48173203631027e-09    70.4656862745098        0.11625493045464
6       42      actin-mediated cell contraction
GO:0030048      1.22971324712985e-08    47.8068812430633        0.163310497543423
6       59      actin filament-based movement
GO:0006936      2.42527363012568e-07    15.3463203463203        0.661545913777593
8       239     muscle contraction
GO:0060415      2.42552850360207e-07    45.6063492063492        0.138398726731714
5       50      muscle tissue morphogenesis
GO:0048644      4.32016652732376e-07    40.2240896358543        0.15500657393952
5       56      muscle organ morphogenesis
GO:0003012      5.4774389387088e-07     13.7141472868217        0.736281226212719
8       266     muscle system process
GO:0006941      1.87847787915929e-06    29.2673469387755        0.207598090097571
5       75      striated muscle contraction
GO:0007507      3.59997407179999e-06    10.5366766467066        0.946647290844924
8       342     heart development
GO:0055008      6.90807921637003e-06    38.9430894308943        0.124558854058543
4       45      cardiac muscle tissue morphogenesis
GO:0048729      1.22150628670457e-05    8.84785353535353        1.11826171199225
8       404     tissue morphogenesis
Tissue: Artery_Tibial=>Skin_Sun_Exposed_Lower_leg       Type:   asymmetric
SourceGene:     TBL2(ENSG00000106638.9)
TargetGeneSet:  CPSF3L  CAMK2N1 HTR1D   RPL11   ATPIF1  EIF2C4  RPS8    RP4     RP11
RBM8A   MRPL55  GUK1    RPS7    UBC     WBP1    TXNDC9  RPL31   UGGT1   EEF1B2
CXCR2   CRBN    TTLL3   EXOSC7  THOC7   C3orf70 RPL34   UBE2B   CAMLG   FAM193B
RWDD1   MAP3K4  BRAT1   RALA    WBSCR17 HIPK2   OR9A3P  COPS5   CDC37L1 RPS6
UBAC1   ANAPC2  TET1    RPS24   LDB1    HRAS    C11orf35        FBXO3   CCS
RPS25   CLEC2B  HMGB1   N4BP2L1 COMMD6  NDFIP2  ABCD4   IFT43   PLDN    SHC4
SPSB3   NUPR1   FUK     ZFHX3   NEURL4  RPL26   UTP18   FN3KRP  C18orf21
HAUS1   RPL17   LSM7    MLL4    ARHGAP33        ZNF224  ARFGAP3 SLC2A4RG
UCKL1   BTG3    PISD    AKAP17A RP3     CXorf56 GPC4
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006402      2.48818502035394e-15    25.1669419537518        0.825271607501211
15      178     mRNA catabolic process
GO:0006401      2.04842705634507e-14    21.5495951417004        0.950453255830046
15      205     RNA catabolic process
GO:0000956      2.97119394913301e-14    24.2490566037736        0.783544391391599
14      169     nuclear-transcribed mRNA catabolic process
GO:0006414      4.89025394882655e-14    33.5272727272727        0.486817521278804
12      105     translational elongation
GO:0006614      4.89025394882655e-14    33.5272727272727        0.486817521278804
12      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      5.49507456161732e-14    33.1682785299807        0.491453878624317
12      106     cotranslational protein targeting to membrane
GO:0045047      5.49507456161732e-14    33.1682785299807        0.491453878624317
12      106     protein targeting to ER
GO:0072599      5.49507456161732e-14    33.1682785299807        0.491453878624317
12      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      2.0417290081453e-13     29.388679245283 0.547090166770466       12
118     protein localization to endoplasmic reticulum
GO:0000184      2.26268763505438e-13    29.1119796091759        0.551726524115978
12      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
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GO:0006415      3.19175769529315e-13    35.1214285714286        0.42190851844163
11      91      translational termination
GO:0006413      4.31463379196058e-12    22.1984415584416        0.704726316517888
12      152     translational initiation
GO:0006612      4.66527642874167e-12    22.0394584139265        0.7093626738634 12
153     protein targeting to membrane
GO:0019080      8.73681239153119e-11    19.9852040816327        0.700089959172376
11      151     viral genome expression
GO:0019083      8.73681239153119e-11    19.9852040816327        0.700089959172376
11      151     viral transcription
GO:0043624      1.00755954318332e-10    19.7009557344064        0.7093626738634 11
153     cellular protein complex disassembly
GO:0072594      1.37585044045365e-10    16.1272727272727        0.945816898484534
12      204     establishment of protein localization to organelle
GO:0043241      1.42656683439314e-10    19.0241739552964        0.732544460590963
11      158     protein complex disassembly
GO:0022415      1.64029906771953e-10    13.7787524366472        1.20545290983323
13      260     viral reproductive process
GO:0034623      4.02469233199967e-10    17.1374890446976        0.806726178119161
11      174     cellular macromolecular complex disassembly
GO:0032984      5.44861896223371e-10    16.6215986394558        0.829907964846723
11      179     macromolecular complex disassembly
GO:0071845      6.02781333295069e-09    11.3197860962567        1.31672548612553
12      284     cellular component disassembly at cellular level
GO:0022411      7.0518130646347e-09     11.1525691699605        1.33527091550758
12      288     cellular component disassembly
GO:0019058      8.03056910643846e-09    12.6464285714286        1.07099854681337
11      231     viral infectious cycle
GO:0042274      1.50494185231174e-08    89.1501240694789        0.0834544322192236
5       18      ribosomal small subunit biogenesis
GO:0006364      2.51599543897936e-08    20.180790960452 0.482181163933292       8
104     rRNA processing
GO:0042254      2.65558944957181e-08    15.787684729064 0.690817244481351       9
149     ribosome biogenesis
GO:0016072      3.91547118036927e-08    18.9857095380525        0.509999308006366
8       110     rRNA metabolic process
GO:0022613      7.8293624186879e-08     11.561811505508 1.04318040274029        10
225     ribonucleoprotein complex biogenesis
GO:0016032      1.22484734410462e-07    7.66522915609674        2.0909971628261 13
451     viral reproduction
GO:0071843      1.37753688339582e-07    10.844250363901 1.10808940557747        10
239     cellular component biogenesis at cellular level
GO:0033365      1.53598385943145e-06    6.58946953263656        2.19299702442738
12      473     protein localization to organelle
GO:0006605      1.57023409742074e-06    6.57473435655254        2.19763338177289
12      474     protein targeting
GO:0034470      3.79294432966074e-06    10.0225988700565        0.927271469102484
8       200     ncRNA processing
Tissue: Artery_Tibial=>Skin_Sun_Exposed_Lower_leg       Type:   asymmetric
SourceGene:     TYRP1(ENSG00000107165.7)
TargetGeneSet:  CTNNBIP1        RPL11   MEAF6   YBX1    RPS8    PSMD4   B3GALT2
RAB4A   TOMM20  RPS7    UBC     KCMF1   RPL31   MZT2A   BBS5    EIF2S2P4
EEF1B2  RPL15   RPL24   GRK7    EIF2S1  NCBP2   RPL35A  RP11    CTD     EEF1A1
MRPS12  ZFAND2A POP7    DNAJC2  CHMP4C  MTDH    RPS6    SURF2   CCNY    RPS13   FAU
KRT8P26 RPS25   METAP2  RPL6    MRP63   GTF3A   TPT1    C14orf166       MOAP1
HAUS2   RPS3AP6 BTBD1   AXIN1   GFER    PALB2   EXOSC6  TAF1C   IFT20   RPS7P1
RPL17   RPL19   RPL27   HOXB4   RP13    NAA20   EIF2S2  C20orf24        EEF1B2P3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      8.00011629816487e-26    80.0130475302889        0.399626323437824
18      105     translational elongation
GO:0006413      1.6705875399692e-24     56.5992063492063        0.578506677738565
19      152     translational initiation
GO:0006415      3.73230934449678e-23    78.337094017094 0.346342813646114       16
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91      translational termination
GO:0000184      5.92378821595437e-23    62.6929824561403        0.452909833229534
17      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006614      4.32864406170196e-22    65.9498703543647        0.399626323437824
16      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      5.0851515085895e-22     65.2125356125356        0.403432288422946
16      106     cotranslational protein targeting to membrane
GO:0045047      5.0851515085895e-22     65.2125356125356        0.403432288422946
16      106     protein targeting to ER
GO:0072599      5.0851515085895e-22     65.2125356125356        0.403432288422946
16      106     establishment of protein localization to endoplasmic reticulum
GO:0000956      6.59679309573166e-22    45.8940397350993        0.643208082485641
18      169     nuclear-transcribed mRNA catabolic process
GO:0006402      1.72451866100566e-21    43.2851351351351        0.67746176735174
18      178     mRNA catabolic process
GO:0070972      3.11421270420208e-21    57.492207139266 0.449103868244412       16
118     protein localization to endoplasmic reticulum
GO:0019080      4.08181428053345e-21    47.614689709348 0.574700712753443       17
151     viral genome expression
GO:0019083      4.08181428053345e-21    47.614689709348 0.574700712753443       17
151     viral transcription
GO:0072594      2.1155673178974e-20     37.1665213600697        0.776416856964916
18      204     establishment of protein localization to organelle
GO:0006401      2.31350997401875e-20    36.9651683769331        0.780222821950038
18      205     RNA catabolic process
GO:0006612      2.33863422759867e-19    42.6996069623807        0.582312642723687
16      153     protein targeting to membrane
GO:0043624      2.33863422759867e-19    42.6996069623807        0.582312642723687
16      153     cellular protein complex disassembly
GO:0043241      3.96637940556713e-19    41.1816540267245        0.601342467649298
16      158     protein complex disassembly
GO:0034623      1.91952148295049e-18    36.9698149951315        0.662237907411252
16      174     cellular macromolecular complex disassembly
GO:0032984      3.0434441731485e-18     35.823187037911 0.681267732336863       16
179     macromolecular complex disassembly
GO:0019058      6.40484091892523e-18    29.6475651746188        0.879177911563214
17      231     viral infectious cycle
GO:0022415      4.76156532692629e-17    26.0559887372753        0.989550896131756
17      260     viral reproductive process
GO:0071845      2.10519686334829e-16    23.6736644983245        1.08089405577469
17      284     cellular component disassembly at cellular level
GO:0022411      2.66173745686471e-16    23.3176344921344        1.09611791571518
17      288     cellular component disassembly
GO:0033365      4.01932061762941e-15    16.2076603034753        1.80022143796277
19      473     protein localization to organelle
GO:0006605      4.17696218883589e-15    16.1708791208791        1.80402740294789
19      474     protein targeting
GO:0016032      2.80398946136548e-14    15.687784782473 1.71649020829008        18
451     viral reproduction
GO:0022613      1.56445492953574e-07    12.8442028985507        0.856342121652481
9       225     ribonucleoprotein complex biogenesis
GO:0071843      2.61152742793885e-07    12.0504725897921        0.909625631444191
9       239     cellular component biogenesis at cellular level
GO:0042274      5.52277506078789e-07    80.5714285714286        0.0685073697321985
4       18      ribosomal small subunit biogenesis
GO:0042254      1.44249463700459e-06    14.6387910798122        0.567088782783198
7       149     ribosome biogenesis
GO:0006364      2.61706669591879e-06    17.8650562265723        0.395820358452702
6       104     rRNA processing
GO:0016072      3.63014331363447e-06    16.8273155416013        0.418656148363435
6       110     rRNA metabolic process
GO:0034470      1.01251906931225e-05    10.7319732297064        0.761192997024427
7       200     ncRNA processing
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GO:0034660      1.13038814308804e-05    8.67593517167217        1.08470002075981
8       285     ncRNA metabolic process
Tissue: Skin_Sun_Exposed_Lower_leg=>Artery_Tibial       Type:   asymmetric
SourceGene:     ZNF826P(ENSG00000231205.6)
TargetGeneSet:  RPL22   CAMTA1-IT1      RPS8    RP11    RPL31   MAP4K4  MZT2A
MRPS18B LY6G5C  MRPS12  PMS2P4  RPS6    RPS3AP5 RPS25   KLHDC5  HOXC4   UBC
MCF2L   ARHGEF40        RPS5    RPL12P4 ASB9
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      1.91762679497595e-12    149.5   0.0944571309943949      7       91
translational termination
GO:0006414      5.35581710072394e-12    128.017857142857        0.108988997301225
7       105     translational elongation
GO:0006614      5.35581710072394e-12    128.017857142857        0.108988997301225
7       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      5.73171739753588e-12    126.715909090909        0.110026987751713
7       106     cotranslational protein targeting to membrane
GO:0045047      5.73171739753588e-12    126.715909090909        0.110026987751713
7       106     protein targeting to ER
GO:0072599      5.73171739753588e-12    126.715909090909        0.110026987751713
7       106     establishment of protein localization to endoplasmic reticulum
GO:0070972      1.23276970424851e-11    112.922297297297        0.122482873157567
7       118     protein localization to endoplasmic reticulum
GO:0000184      1.30917922215508e-11    111.90625       0.123520863608055       7
119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      7.09604372233481e-11    86.84375        0.156736558023666       7
151     viral genome expression
GO:0019083      7.09604372233481e-11    86.84375        0.156736558023666       7
151     viral transcription
GO:0006413      7.43497825634392e-11    86.2387931034483        0.157774548474154
7       152     translational initiation
GO:0006612      7.78764418694332e-11    85.6421232876712        0.158812538924642
7       153     protein targeting to membrane
GO:0043624      7.78764418694332e-11    85.6421232876712        0.158812538924642
7       153     cellular protein complex disassembly
GO:0043241      9.77339101656688e-11    82.7773178807947        0.164002491177081
7       158     protein complex disassembly
GO:0000956      1.57100332169022e-10    77.0972222222222        0.175420386132448
7       169     nuclear-transcribed mRNA catabolic process
GO:0034623      1.92905229329879e-10    74.7627245508982        0.180610338384887
7       174     cellular macromolecular complex disassembly
GO:0006402      2.26358693985382e-10    72.9934210526316        0.184762300186838
7       178     mRNA catabolic process
GO:0032984      2.35455743001986e-10    72.5639534883721        0.185800290637326
7       179     macromolecular complex disassembly
GO:0072594      5.89417708112577e-10    63.2442893401015        0.211750051899523
7       204     establishment of protein localization to organelle
GO:0006401      6.09956796824973e-10    62.9204545454545        0.21278804235001
7       205     RNA catabolic process
GO:0019058      1.40565670508218e-09    55.515625       0.239775794062695       7
231     viral infectious cycle
GO:0022415      3.20411362178548e-09    49.0518774703557        0.269877517126842
7       260     viral reproductive process
GO:0071845      5.91575276257488e-09    44.726083032491 0.294789287938551       7
284     cellular component disassembly at cellular level
GO:0022411      6.51819085454377e-09    44.0769572953737        0.298941249740502
7       288     cellular component disassembly
GO:0016032      1.42629435581143e-07    27.5743243243243        0.468133693170023
7       451     viral reproduction
GO:0033365      1.97334860926187e-07    26.2312231759657        0.490969483080756
7       473     protein localization to organelle
GO:0006605      2.0019322032261e-07     26.1731798715203        0.492007473531244
7       474     protein targeting
GO:0042274      7.31458391870453e-07    240.35  0.0186838281087814      3       18
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ribosomal small subunit biogenesis
GO:0000028      1.50488235864716e-05    555.076923076923        0.00622794270292713
2       6       ribosomal small subunit assembly
Tissue: Whole_Blood=>Artery_Tibial      Type:   cluster
SourceGene:     C6orf226(ENSG00000221821.2)
TargetGeneSet:  CTNNBIP1        PPCS    HBXIP   TMCO1   RP11    SNRPE   SLC41A1
TATDN3  LYST-IT1        C2orf28 MORN2   MGAT5   BTF3L4P2        NDUFB3  ARMC9
MYEOV2  GLYCTK  SPCS1   NIT2    TCTEX1D2        EXOSC9  NDUFC1  FRG1    PDCD6
RBBP4P1 POC5    COX7C   CTD     HINT1   SYNPO   ATOX1   TMEM14B AGER    PPP1R2P1
COX7A2  RP1     PEX7    RP4     PSMB1   NDUFA4  YAE1D1  CLIP2   GTPBP10 C7orf59
PMS2P1  ARF5    CHCHD7  HNRNPA1P4       DECR1   VPS28   NDUFB6  NUDT2   DCTN3
BICD2   SEC61B  ATP6V1G1        FAM208B KCNMA1  USMG5   POLR2L  IMMP1L  CFL1
LAMTOR1 ATP5L   SPA17   FOXRED1 FAM60A  PRR13   NUP37   PEBP1   RPS7P10 MED4
AKAP6   ERH     SLIRP   TTC7B   NDUFB1  C14orf2 SRP14   FAM96A  WDR61   C15orf40
GNAO1   GAN     TXNDC17 ARHGAP44        MPRIP   C17orf75        PSMB3   MRPS23  BPTF
NT5C    ELAC1   UQCR11  NDUFA11 TRAPPC5 NDUFA7  PIN1    NDUFB7  RASAL3  EPS15L1 LSM4
NDUFA13 ALKBH6  SNRPD2  ZNF552  PRNP    ROMO1   EPB41L1 ATP5E   ABHD16B ATP5J   DDT
ADORA2A RP3     RP6     PSMA6P2 EEF1B2P3        RPS2P55 PDZD11  NDUFA1  SSR4
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      2.52654969692243e-17    34.7928849902534        0.604525638364127
15      96      respiratory electron transport chain
GO:0022900      4.37148497605088e-15    23.6195267580717        0.843817036883261
15      134     electron transport chain
GO:0045333      1.05130405045952e-14    22.1192498963945        0.894194173413605
15      142     cellular respiration
GO:0015980      6.54425517789902e-12    11.145852749301 1.93322261435195        17
307     energy derivation by oxidation of organic compounds
GO:0006120      4.73293577437247e-11    49.3356282271945        0.226697114386548
8       36      mitochondrial electron transport, NADH to ubiquinone
GO:0042773      4.64895699389261e-10    35.393265369169 0.295965677115771       8
47      ATP synthesis coupled electron transport
GO:0042775      4.64895699389261e-10    35.393265369169 0.295965677115771       8
47      mitochondrial ATP synthesis coupled electron transport
GO:0006091      1.16324885284373e-09    7.79683698296837        2.6951768043734 17
428     generation of precursor metabolites and energy
GO:0006119      2.67859930206568e-09    27.5855421686747        0.365234239844993
8       58      oxidative phosphorylation
Tissue: Artery_Tibial=>Whole_Blood      Type:   cluster
SourceGene:     CPLX2(ENSG00000145920.9)
TargetGeneSet:  CACNA1A HAPLN2  KCNJ9   MYOC    ASTN1   C1orf95 ARID4B-IT1      GNG4
MYT1L   VSNL1   DPYSL5  CTNNA2  SCN2A   NEUROD1 CDK5R2  MEN1    DNER    KIF1A
ATP2B2  SLC6A1  ARPP21  CAMKV   CADPS   SYNPR   TAGLN3  GAP43   STXBP5L ZIC1
SOX2-OT PPP2R2C SYNPO2  GRIA2   CTNND2  SOWAHA  CAMK2A  GABRB2  GABRA6  GABRA1  SNCB
NRSN1   MOG     GRM4    RUNX2   RIMS1   SNAP91  FABP7   DGKB    VSTM2A  WBSCR17
CALN1   SRRM3   TMEM130 DPP6    RP11    NEFM    STMN4   STMN2   SH3GL2  DIRAS2
GABBR2  DBC1    NCS1    GRIN1   GPR158  GAD2    INA     CALY    PTPN5   ANO3
LRRC10B CHRM1   PIH1D2  KCNA1   LMO3    FAIM2   KCNC2   SYT1    N4BP2L2 DCLK1   ZIC2
PPP4R4  CYP46A1 SCG5    CKMT1B  RBFOX1  CBLN1   JPH3    PPP1R1B CA10    NPTX1
SOGA2   SYT4    ST8SIA3 CDH20   CELF5   ELAVL3  UNC13A  NCAN    MAG     APLP1
SLC8A2  PRKCG   CHGB    SNAP25  SLC32A1 PCP4    RASD2   RP1     SEPT3   SULT4A1
TMEM35  TCEAL2  TCEAL5  TCEAL7  PLP1    GRIA3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0007269      1.12636120430139e-11    24.3517829457364        0.577261089197979
11      86      neurotransmitter secretion
GO:0006836      4.0501787538111e-10     16.8718776916451        0.798768251332088
11      119     neurotransmitter transport
GO:0001505      5.79176591583528e-10    16.2647425249169        0.82561760431804
11      123     regulation of neurotransmitter levels
GO:0003001      2.34256424736022e-08    7.8484002234102 2.12109888589025        14
316     generation of a signal involved in cell-cell signaling
GO:0023061      2.34256424736022e-08    7.8484002234102 2.12109888589025        14
316     signal release
GO:0007214      9.8184283972011e-08     59.9540133779264        0.120822088436786
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5       18      gamma-aminobutyric acid signaling pathway
GO:0048489      7.64673956903262e-07    22.4678178963893        0.32219223583143
6       48      synaptic vesicle transport
GO:0016079      1.53219011289151e-06    31.15   0.201370147394644       5       30
synaptic vesicle exocytosis
GO:0007270      2.00961671328466e-06    13.7052126200274        0.590685765690956
7       88      neuron-neuron synaptic transmission
GO:0007611      4.68254573777622e-06    9.61121905888316        0.946439692754827
8       141     learning or memory
GO:0050890      8.98410609145878e-06    8.74742188702478        1.03370008995917
8       154     cognition
GO:0050808      1.13040743836982e-05    10.3560747663551        0.765206560099647
7       114     synapse organization
Tissue: Whole_Blood=>Artery_Tibial      Type:   asymmetric
SourceGene:     CPSF1(ENSG00000071894.9)
TargetGeneSet:  RPL22   NDUFS5  C1orf50 RPS8    RP4     RPL5    RP11    C1orf54
PSMB4   ACBD6   CYB5R1  RPS7    RNF181  CHCHD5  BRK1    RPL15   EIF1B   SPCS1
RPL10AP6        C3orf33 COX7C   CTD     BOD1    TMEM14C CSNK2B  C6orf48 RPS10
RPL10A  MRPS12  SF3B5   RPA3    CHCHD2  TMEM60  C7orf59 ZNHIT1  TERF1   EIF3H
CPSF1   RPS6    CLTA    RPL7A   ST13P13 MRPL23  RNASEH2C        MRPL11  FTH1P16
ATP5L   U6      WNT1    YEATS4  SLC25A3 RPL18AP3        RPL6    PEBP1   ARL6IP4
NUFIP1  TRAV13-2        AP4S1   COX16   SRP14   RSL24D1 RPS3AP6 COMMD4  SEC11A
TM2D3   ECI1    BCL7C   LDHD    COX4I1  RPAIN   SAT2    RPS7P1  CCDC56  RPL27
SUMO2   ALKBH7  WDR83OS NDUFB7  MYO9B   RPL18A  SNRPD2  SEPW1   RPS5    FTLP3
MT1P3   YBEY    TXN2    XRCC6   C22orf32        UXT     PQBP1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006614      3.81818462543385e-21    55.8866634098681        0.450487855511729
16      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      4.48341940480774e-21    55.2618357487923        0.454778216040412
16      106     cotranslational protein targeting to membrane
GO:0045047      4.48341940480774e-21    55.2618357487923        0.454778216040412
16      106     protein targeting to ER
GO:0072599      4.48341940480774e-21    55.2618357487923        0.454778216040412
16      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      2.7306000495633e-20     48.7195225916454        0.50626254238461
16      118     protein localization to endoplasmic reticulum
GO:0006612      2.01779658634231e-18    36.1840685496668        0.65642516088852
16      153     protein targeting to membrane
GO:0006414      1.01774915410727e-17    45.8269230769231        0.450487855511729
14      105     translational elongation
GO:0006413      6.43430904318494e-17    33.2008075788166        0.652134800359837
15      152     translational initiation
GO:0006415      6.50171905539358e-17    48.6768707482993        0.390422808110165
13      91      translational termination
GO:0072594      2.12482464322994e-16    26.2738205365402        0.87523354785136
16      204     establishment of protein localization to organelle
GO:0000184      2.42343410352065e-15    35.7487485560262        0.510552902913293
13      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      5.61422610328355e-14    27.3976634131914        0.647844439831154
13      151     viral genome expression
GO:0019083      5.61422610328355e-14    27.3976634131914        0.647844439831154
13      151     viral transcription
GO:0043624      6.66687276281697e-14    27.0024781341108        0.65642516088852
13      153     cellular protein complex disassembly
GO:0043241      1.01386702052561e-13    26.0622097114708        0.677876963531935
13      158     protein complex disassembly
GO:0006401      1.36798618509885e-13    21.6810645724258        0.879523908380043
14      205     RNA catabolic process
GO:0000956      2.42934209262384e-13    24.2057823129252        0.72507092934745
13      169     nuclear-transcribed mRNA catabolic process
GO:0034623      3.54202475228955e-13    23.4458106223856        0.746522731990866
13      174     cellular macromolecular complex disassembly
GO:0006402      4.74940310853451e-13    22.8709956709957        0.763684174105598
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13      178     mRNA catabolic process
GO:0032984      5.10507677451707e-13    22.731620358987 0.767974534634281       13
179     macromolecular complex disassembly
GO:0019058      7.06772061132108e-13    19.0483870967742        0.991073282125804
14      231     viral infectious cycle
GO:0022415      3.53630696857751e-12    16.7684620596206        1.11549373745762
14      260     viral reproductive process
GO:0033365      8.12075047112856e-12    11.5429337231969        2.02934053006712
17      473     protein localization to organelle
GO:0006605      8.39739015155602e-12    11.5168490153173        2.03363089059581
17      474     protein targeting
GO:0071845      1.74322364236693e-10    13.8213720912719        1.21846239014601
13      284     cellular component disassembly at cellular level
GO:0022411      2.0723769572223e-10     13.6164749536178        1.23562383226074
13      288     cellular component disassembly
GO:0016032      4.99245580574251e-10    10.2134979504197        1.93495259843609
15      451     viral reproduction
GO:0022613      4.54143754582648e-07    11.1422955974843        0.965331118953706
9       225     ribonucleoprotein complex biogenesis
GO:0071843      7.53473849246801e-07    10.4537325676784        1.02539616635527
9       239     cellular component biogenesis at cellular level
Tissue: Whole_Blood=>Artery_Tibial      Type:   cluster
SourceGene:     CPSF1(ENSG00000071894.9)
TargetGeneSet:  RPL22   NDUFS5  C1orf50 RPS8    RP4     RPL5    RP11    C1orf54
PSMB4   ACBD6   CYB5R1  RPS7    RNF181  CHCHD5  BRK1    RPL15   EIF1B   SPCS1
RPL10AP6        C3orf33 COX7C   CTD     BOD1    TMEM14C CSNK2B  C6orf48 RPS10
RPL10A  MRPS12  SF3B5   RPA3    CHCHD2  TMEM60  C7orf59 ZNHIT1  TERF1   EIF3H
CPSF1   RPS6    CLTA    RPL7A   ST13P13 MRPL23  RNASEH2C        MRPL11  FTH1P16
ATP5L   U6      WNT1    YEATS4  SLC25A3 RPL18AP3        RPL6    PEBP1   ARL6IP4
NUFIP1  TRAV13-2        AP4S1   COX16   SRP14   RSL24D1 RPS3AP6 COMMD4  SEC11A
TM2D3   ECI1    BCL7C   LDHD    COX4I1  RPAIN   SAT2    RPS7P1  CCDC56  RPL27
SUMO2   ALKBH7  WDR83OS NDUFB7  MYO9B   RPL18A  SNRPD2  SEPW1   RPS5    FTLP3
MT1P3   YBEY    TXN2    XRCC6   C22orf32        UXT     PQBP1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006614      3.81818462543385e-21    55.8866634098681        0.450487855511729
16      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      4.48341940480774e-21    55.2618357487923        0.454778216040412
16      106     cotranslational protein targeting to membrane
GO:0045047      4.48341940480774e-21    55.2618357487923        0.454778216040412
16      106     protein targeting to ER
GO:0072599      4.48341940480774e-21    55.2618357487923        0.454778216040412
16      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      2.7306000495633e-20     48.7195225916454        0.50626254238461
16      118     protein localization to endoplasmic reticulum
GO:0006612      2.01779658634231e-18    36.1840685496668        0.65642516088852
16      153     protein targeting to membrane
GO:0006414      1.01774915410727e-17    45.8269230769231        0.450487855511729
14      105     translational elongation
GO:0006413      6.43430904318494e-17    33.2008075788166        0.652134800359837
15      152     translational initiation
GO:0006415      6.50171905539358e-17    48.6768707482993        0.390422808110165
13      91      translational termination
GO:0072594      2.12482464322994e-16    26.2738205365402        0.87523354785136
16      204     establishment of protein localization to organelle
GO:0000184      2.42343410352065e-15    35.7487485560262        0.510552902913293
13      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      5.61422610328355e-14    27.3976634131914        0.647844439831154
13      151     viral genome expression
GO:0019083      5.61422610328355e-14    27.3976634131914        0.647844439831154
13      151     viral transcription
GO:0043624      6.66687276281697e-14    27.0024781341108        0.65642516088852
13      153     cellular protein complex disassembly
GO:0043241      1.01386702052561e-13    26.0622097114708        0.677876963531935
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13      158     protein complex disassembly
GO:0006401      1.36798618509885e-13    21.6810645724258        0.879523908380043
14      205     RNA catabolic process
GO:0000956      2.42934209262384e-13    24.2057823129252        0.72507092934745
13      169     nuclear-transcribed mRNA catabolic process
GO:0034623      3.54202475228955e-13    23.4458106223856        0.746522731990866
13      174     cellular macromolecular complex disassembly
GO:0006402      4.74940310853451e-13    22.8709956709957        0.763684174105598
13      178     mRNA catabolic process
GO:0032984      5.10507677451707e-13    22.731620358987 0.767974534634281       13
179     macromolecular complex disassembly
GO:0019058      7.06772061132108e-13    19.0483870967742        0.991073282125804
14      231     viral infectious cycle
GO:0022415      3.53630696857751e-12    16.7684620596206        1.11549373745762
14      260     viral reproductive process
GO:0033365      8.12075047112856e-12    11.5429337231969        2.02934053006712
17      473     protein localization to organelle
GO:0006605      8.39739015155602e-12    11.5168490153173        2.03363089059581
17      474     protein targeting
GO:0071845      1.74322364236693e-10    13.8213720912719        1.21846239014601
13      284     cellular component disassembly at cellular level
GO:0022411      2.0723769572223e-10     13.6164749536178        1.23562383226074
13      288     cellular component disassembly
GO:0016032      4.99245580574251e-10    10.2134979504197        1.93495259843609
15      451     viral reproduction
GO:0022613      4.54143754582648e-07    11.1422955974843        0.965331118953706
9       225     ribonucleoprotein complex biogenesis
GO:0071843      7.53473849246801e-07    10.4537325676784        1.02539616635527
9       239     cellular component biogenesis at cellular level
Tissue: Artery_Tibial=>Whole_Blood      Type:   asymmetric
SourceGene:     EIF1AP1(ENSG00000236698.1)
TargetGeneSet:  CELA2A  CELA3B  CELA3A  COL9A2  TCTEX1D4        AMY2A   ARHGAP30
RP11    REG1A   RAB3GAP1        TMEM45A CPB1    BASP1   SREK1IP1        CTB
ADAMTS2 TAPBP   ARMC12  CLPS    PKIB    EEPD1   TPST1   CPA2    CPA1    PRSS1
ST13P6  KLF9    OLAH    YWHAZP3 PNLIP   PNLIPRP1        PNLIPRP2        HTRA1
PTGDR2  BIRC3   IL18    CD163   ERGIC2  CPM     PLA2G1B HDC     GP2     CTD
CTRB2   CTRB1   WRAP53  NF1     ZNF385C CACNA1A CYP4F22 RAB3A   SYCN    CEACAM3
CALM3   SIRPG   PRAF2   F8A1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0007586      4.93335756690257e-11    34.7959459459459        0.346965607916407
9       109     digestion
GO:0044241      1.19534012668532e-07    124.623376623377        0.0477475607224414
4       15      lipid digestion
Tissue: Whole_Blood=>Artery_Tibial      Type:   asymmetric
SourceGene:     ENSG00000205233.4
TargetGeneSet:  RPL22   EIF4G3  RP11    AGL     TOMM20  DGUOK-AS1       HDLBP
RPL15   EIF1B   RPL15P3 DDAH2   RPL10A  SRPK1   ASCC3   FAM120B GTF2I   COG5
LUC7L2  EIF3H   NFIB    ALAD    PFKP    DAZAP2  TMEM19  NME2P1  OXA1L   GMPR2
RSL24D1 SEC11A  CEP95   TSEN34  BACH1   EIF3D   RRAGB   TTC3P1  RBMX2
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006413      1.21995167857677e-08    32.8229885057471        0.294512490485088
7       152     translational initiation
Tissue: Whole_Blood=>Artery_Tibial      Type:   asymmetric
SourceGene:     HERC2P2(ENSG00000140181.10)
TargetGeneSet:  KLHL17  RPL22   HMGN2   PPCS    SLC6A9  RPS8    RP11    FGGY
SGIP1   RPL5    BCAS2   PRKAB2  MRPL9   GBAP1   PEX19   PPFIA4  ANKS1B  NUP133
TMEM18  RPS7    C2orf28 MEMO1   GFPT1   SFXN5   CHCHD5  PTPN4   MAP3K2  NCKAP1
SATB2   RAB17   XPC     ACAA1   SPCS1   RPL10AP6        CNTN3   PVRL3-AS1
SPICE1  ZMAT3   CHRD    EXOSC9  NDUFC1  NSA2    COX7C   CTD     P4HA2   SEPT8   IK
CPEB4   ARL10   TMEM14B BTN2A3P GPANK1  DDAH2   RPS18   RPS10   RPL10A  RPL24P4
MRPL2   VEGFA   MRPS12  PSMB1   C7orf50 MICALL2 TOMM7   DPY19L1 GTF2I   C7orf59
PMS2P1  MUC3A   ARF5    MRPS33  SLC4A2  CHCHD7  DECR1   C9orf123        RPS6
CHMP5   NUDT2   FAM219A VPS13A  FSD1L   VAV2    EDF1    RP13    USMG5   OCRL
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EIF3M   ALKBH3  PLCB3   UCP2    USP35   C11orf1 ATP5L   CACNA1C-AS1     LEPREL2
ADCY6   CACNB3  LETMD1  DGKA    SLC25A3 CKAP4   PEBP1   SETD8   SAP18   RPS7P10
COMMD6  OXA1L   GMPR2   RPS29   DDHD1   SNW1    C14orf2 HERC2P2 HMGN2P5 SRP14
MAPKBP1 DUOX1   RPS3AP6 MAN2A2  GLIS2   UBFD1   NSMCE1  FBXL8   KIAA0513
COX4I1  CYB5D2  LLGL1   RPS7P1  SMARCE1 RPL27   TBKBP1  SLC16A3 CIRBP   REEP6
MRPL54  NDUFA7  MYO9B   USE1    DPY19L3 FXYD1   ZNF226  SNRPD2  RPL28   RPS5    SNPH
EBF4    VPS16   LINC00493       DTD1    C20orf43        ATP5J   CRYZL1  C21orf33
FAM118A ARSD    EEF1B2P3        UXT     FGD1    PDZD11  RPS23P8 PIN4    RPS6KA6
CXorf56 RP3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006614      2.35395294561711e-13    20.0945659844742        0.893709777870044
14      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      2.69299584376163e-13    19.8747506980455        0.902221299564044
14      106     cotranslational protein targeting to membrane
GO:0045047      2.69299584376163e-13    19.8747506980455        0.902221299564044
14      106     protein targeting to ER
GO:0072599      2.69299584376163e-13    19.8747506980455        0.902221299564044
14      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      1.22070507063295e-12    17.5666901905434        1.00435955989205
14      118     protein localization to endoplasmic reticulum
GO:0006612      3.0908997356395e-12     14.2814009661836        1.30226281918206
15      153     protein targeting to membrane
GO:0006414      4.65713112799928e-12    18.2873517786561        0.893709777870044
13      105     translational elongation
GO:0006415      1.49929257841184e-11    19.4991447143346        0.774548474154038
12      91      translational termination
GO:0072594      1.73193862839245e-11    11.2467687413005        1.73635042557608
16      204     establishment of protein localization to organelle
GO:0000184      3.69256863969297e-10    14.3682748168729        1.01287108158605
12      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006413      5.22731058408295e-10    12.0638979725311        1.29375129748806
13      152     translational initiation
GO:0000956      1.94036717768034e-09    10.7363636363636        1.43844716628607
13      169     nuclear-transcribed mRNA catabolic process
GO:0034623      2.77379799910712e-09    10.3992659514399        1.48100477475607
13      174     cellular macromolecular complex disassembly
GO:0006402      3.66104137082604e-09    10.1442975206612        1.51505086153207
13      178     mRNA catabolic process
GO:0032984      3.91970579103365e-09    10.0824753559693        1.52356238322607
13      179     macromolecular complex disassembly
GO:0019080      5.80069085687583e-09    11.0355823449349        1.28523977579406
12      151     viral genome expression
GO:0019083      5.80069085687583e-09    11.0355823449349        1.28523977579406
12      151     viral transcription
GO:0043624      6.73699148366134e-09    10.877515813686 1.30226281918206        12
153     cellular protein complex disassembly
GO:0043241      9.70034631340651e-09    10.5012958163643        1.34482042765207
12      158     protein complex disassembly
GO:0006401      2.01161612809203e-08    8.70113636363636        1.74486194727009
13      205     RNA catabolic process
GO:0071843      1.22741358088792e-07    7.37433628318584        2.0342536848661 13
239     cellular component biogenesis at cellular level
GO:0019058      6.30297826240347e-07    6.96482784154017        1.9661615113141 12
231     viral infectious cycle
GO:0071845      8.84326593732462e-07    6.13019121100302        2.41727216109612
13      284     cellular component disassembly at cellular level
GO:0022411      1.03484073380331e-06    6.03930578512397        2.45131824787212
13      288     cellular component disassembly
GO:0022415      2.18850039024828e-06    6.13775065387969        2.21299564044011
12      260     viral reproductive process
GO:0033365      2.54245048213041e-06    4.53866132231743        4.0259497612622 16
473     protein localization to organelle
GO:0006605      2.61261196657949e-06    4.52842509080521        4.0344612829562 16
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474     protein targeting
GO:0022613      3.41149192836991e-06    6.47755340453939        1.91509238115009
11      225     ribonucleoprotein complex biogenesis
GO:0015980      1.19544966232335e-05    5.14264773247824        2.61303716005813
12      307     energy derivation by oxidation of organic compounds
GO:0022904      1.73595233003197e-05    9.65449438202247        0.81710608262404
7       96      respiratory electron transport chain
Tissue: Whole_Blood=>Artery_Tibial      Type:   cluster
SourceGene:     HERC2P2(ENSG00000140181.10)
TargetGeneSet:  KLHL17  RPL22   HMGN2   PPCS    SLC6A9  RPS8    RP11    FGGY
SGIP1   RPL5    BCAS2   PRKAB2  MRPL9   GBAP1   PEX19   PPFIA4  ANKS1B  NUP133
TMEM18  RPS7    C2orf28 MEMO1   GFPT1   SFXN5   CHCHD5  PTPN4   MAP3K2  NCKAP1
SATB2   RAB17   XPC     ACAA1   SPCS1   RPL10AP6        CNTN3   PVRL3-AS1
SPICE1  ZMAT3   CHRD    EXOSC9  NDUFC1  NSA2    COX7C   CTD     P4HA2   SEPT8   IK
CPEB4   ARL10   TMEM14B BTN2A3P GPANK1  DDAH2   RPS18   RPS10   RPL10A  RPL24P4
MRPL2   VEGFA   MRPS12  PSMB1   C7orf50 MICALL2 TOMM7   DPY19L1 GTF2I   C7orf59
PMS2P1  MUC3A   ARF5    MRPS33  SLC4A2  CHCHD7  DECR1   C9orf123        RPS6
CHMP5   NUDT2   FAM219A VPS13A  FSD1L   VAV2    EDF1    RP13    USMG5   OCRL
EIF3M   ALKBH3  PLCB3   UCP2    USP35   C11orf1 ATP5L   CACNA1C-AS1     LEPREL2
ADCY6   CACNB3  LETMD1  DGKA    SLC25A3 CKAP4   PEBP1   SETD8   SAP18   RPS7P10
COMMD6  OXA1L   GMPR2   RPS29   DDHD1   SNW1    C14orf2 HERC2P2 HMGN2P5 SRP14
MAPKBP1 DUOX1   RPS3AP6 MAN2A2  GLIS2   UBFD1   NSMCE1  FBXL8   KIAA0513
COX4I1  CYB5D2  LLGL1   RPS7P1  SMARCE1 RPL27   TBKBP1  SLC16A3 CIRBP   REEP6
MRPL54  NDUFA7  MYO9B   USE1    DPY19L3 FXYD1   ZNF226  SNRPD2  RPL28   RPS5    SNPH
EBF4    VPS16   LINC00493       DTD1    C20orf43        ATP5J   CRYZL1  C21orf33
FAM118A ARSD    EEF1B2P3        UXT     FGD1    PDZD11  RPS23P8 PIN4    RPS6KA6
CXorf56 RP3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006614      2.35395294561711e-13    20.0945659844742        0.893709777870044
14      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      2.69299584376163e-13    19.8747506980455        0.902221299564044
14      106     cotranslational protein targeting to membrane
GO:0045047      2.69299584376163e-13    19.8747506980455        0.902221299564044
14      106     protein targeting to ER
GO:0072599      2.69299584376163e-13    19.8747506980455        0.902221299564044
14      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      1.22070507063295e-12    17.5666901905434        1.00435955989205
14      118     protein localization to endoplasmic reticulum
GO:0006612      3.0908997356395e-12     14.2814009661836        1.30226281918206
15      153     protein targeting to membrane
GO:0006414      4.65713112799928e-12    18.2873517786561        0.893709777870044
13      105     translational elongation
GO:0006415      1.49929257841184e-11    19.4991447143346        0.774548474154038
12      91      translational termination
GO:0072594      1.73193862839245e-11    11.2467687413005        1.73635042557608
16      204     establishment of protein localization to organelle
GO:0000184      3.69256863969297e-10    14.3682748168729        1.01287108158605
12      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006413      5.22731058408295e-10    12.0638979725311        1.29375129748806
13      152     translational initiation
GO:0000956      1.94036717768034e-09    10.7363636363636        1.43844716628607
13      169     nuclear-transcribed mRNA catabolic process
GO:0034623      2.77379799910712e-09    10.3992659514399        1.48100477475607
13      174     cellular macromolecular complex disassembly
GO:0006402      3.66104137082604e-09    10.1442975206612        1.51505086153207
13      178     mRNA catabolic process
GO:0032984      3.91970579103365e-09    10.0824753559693        1.52356238322607
13      179     macromolecular complex disassembly
GO:0019080      5.80069085687583e-09    11.0355823449349        1.28523977579406
12      151     viral genome expression
GO:0019083      5.80069085687583e-09    11.0355823449349        1.28523977579406
12      151     viral transcription
GO:0043624      6.73699148366134e-09    10.877515813686 1.30226281918206        12
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153     cellular protein complex disassembly
GO:0043241      9.70034631340651e-09    10.5012958163643        1.34482042765207
12      158     protein complex disassembly
GO:0006401      2.01161612809203e-08    8.70113636363636        1.74486194727009
13      205     RNA catabolic process
GO:0071843      1.22741358088792e-07    7.37433628318584        2.0342536848661 13
239     cellular component biogenesis at cellular level
GO:0019058      6.30297826240347e-07    6.96482784154017        1.9661615113141 12
231     viral infectious cycle
GO:0071845      8.84326593732462e-07    6.13019121100302        2.41727216109612
13      284     cellular component disassembly at cellular level
GO:0022411      1.03484073380331e-06    6.03930578512397        2.45131824787212
13      288     cellular component disassembly
GO:0022415      2.18850039024828e-06    6.13775065387969        2.21299564044011
12      260     viral reproductive process
GO:0033365      2.54245048213041e-06    4.53866132231743        4.0259497612622 16
473     protein localization to organelle
GO:0006605      2.61261196657949e-06    4.52842509080521        4.0344612829562 16
474     protein targeting
GO:0022613      3.41149192836991e-06    6.47755340453939        1.91509238115009
11      225     ribonucleoprotein complex biogenesis
GO:0015980      1.19544966232335e-05    5.14264773247824        2.61303716005813
12      307     energy derivation by oxidation of organic compounds
GO:0022904      1.73595233003197e-05    9.65449438202247        0.81710608262404
7       96      respiratory electron transport chain
Tissue: Whole_Blood=>Artery_Tibial      Type:   cluster
SourceGene:     MED24(ENSG00000008838.11)
TargetGeneSet:  RPL22   ATPIF1  NDUFS5  C1orf50 MAGOH   RP11    PSMB4   RPS27   DPM3
SNRPE   CAPN2   RPL35P1 ACP1    MPHOSPH10       RNF181  CHCHD5  BRK1    C3orf37
GRPEL1  MED10   BRIX1   COX7C   RIOK2   CTD     RP1     ZNRD1   GPANK1  RPL10A
MRPL2   COX7A2  C6orf203        MRPS12  FTSJ2   PMS2CL  TOMM7   YAE1D1  SEC61G
CHCHD2  BUD31   C7orf59 R3HCC1  BRF2    RPL7    VPS13B  EBAG9   EIF3H   EDF1
AGAP11  TSSC4   EIF3F   GSTP1   C11orf1 ATP5L   CACNB3  SLC9A7P1        RPL18AP3
ARL6IP4 SAP18   CHMP4B  RPS29   SLIRP   NDUFB1  GLRX5   C14orf2 SIVA1   SRP14
RSL24D1 SNRNP25 C16orf91        ECI1    TRAPPC2L        RPL27   UTP18   COIL
UQCR11  ZNF554  MRPL54  TIMM44  NDUFA7  PIN1    C19orf42        FXYD1   ZNF568
SNRPD2  SEPW1   A1BG    RPS5    MRPS26  LINC00493       ATP5J   PIGP    THAP7
MAPK1   C22orf32        RAB40A
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0072594      3.31379968836637e-10    14.778125       1.01640024911771        12
204     establishment of protein localization to organelle
GO:0006614      2.31969129398839e-09    21.2544642857143        0.523147187045879
9       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      2.52494744947732e-09    21.0338733431517        0.528129541208221
9       106     cotranslational protein targeting to membrane
GO:0045047      2.52494744947732e-09    21.0338733431517        0.528129541208221
9       106     protein targeting to ER
GO:0072599      2.52494744947732e-09    21.0338733431517        0.528129541208221
9       106     establishment of protein localization to endoplasmic reticulum
GO:0070972      6.55689224613394e-09    18.7024901703801        0.587917791156321
9       118     protein localization to endoplasmic reticulum
GO:0006414      4.83291413978044e-08    18.4046391752577        0.523147187045879
8       105     translational elongation
GO:0006413      6.01280058429219e-08    14.2217782217782        0.757317832675939
9       152     translational initiation
GO:0006612      6.3634435923876e-08     14.1220238095238        0.762300186838281
9       153     protein targeting to membrane
GO:0000184      1.28622128383345e-07    16.0675675675676        0.592900145318663
8       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0000956      1.49643787481541e-07    12.6955357142857        0.842017853435748
9       169     nuclear-transcribed mRNA catabolic process
GO:0006402      2.32952248574824e-07    12.0118343195266        0.886859040896824
9       178     mRNA catabolic process
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GO:0006415      3.28291819940666e-07    18.3269230769231        0.453394228773095
7       91      translational termination
GO:0022904      4.74001401796263e-07    17.2912705272256        0.478305999584804
7       96      respiratory electron transport chain
GO:0033365      5.10693945824097e-07    6.6671702284451 2.35665351878763        13
473     protein localization to organelle
GO:0006605      5.23063420198314e-07    6.65222986139196        2.36163587294997
13      474     protein targeting
GO:0006401      7.6718164493642e-07     10.3374635568513        1.02138260328005
9       205     RNA catabolic process
GO:0022613      1.66498998425485e-06    9.36706349206349        1.12102968652688
9       225     ribonucleoprotein complex biogenesis
GO:0071843      2.73842229720722e-06    8.78819875776398        1.19078264479967
9       239     cellular component biogenesis at cellular level
GO:0022900      4.49330549730544e-06    12.0852816474864        0.667635457753789
7       134     electron transport chain
GO:0045333      6.59343012241467e-06    11.362735042735 0.707494291052522       7
142     cellular respiration
GO:0019080      9.8734089327833e-06     10.6458333333333        0.752335478513598
7       151     viral genome expression
GO:0019083      9.8734089327833e-06     10.6458333333333        0.752335478513598
7       151     viral transcription
GO:0043624      1.0761109893349e-05     10.4985247629083        0.762300186838281
7       153     cellular protein complex disassembly
GO:0043241      1.32738544957744e-05    10.14732552216  0.78721195764999        7
158     protein complex disassembly
Tissue: Whole_Blood=>Artery_Tibial      Type:   asymmetric
SourceGene:     NCCRP1(ENSG00000188505.3)
TargetGeneSet:  SPEN    FBXO42  WASF2   MECR    FCRLA   TSEN15  RP11    TET3
BOLA3   UXS1    MTX2    U6      NDUFB3  PTH1R   SETD2   GOLGB1  BCL6    FAM193A
WDR19   ANKRD20A17P     CICP16  NDUFC1  MGST2   NIPBL   C5orf43 RPS23P5 MAN2A1
EEF1E1  LRRC16A HCG23   UBR2    FKBP1C  ARID1B  CYCS    EPDR1   CHCHD2  ACN9
PMS2P1  TRIM56  NAT2    COX6C   COL14A1 C9orf123        NDUFB6  KLF9    SEC61B  RSU1
KIAA0913        UROS    METTL15 NUMA1   MLL     CRABP1  GS1     CPM     UBE2N
MED13L  DENR    ULK1    POLE    GTF2F2  GLRX5   DUOX1   WDR61   IFT140  SRCAP
NUTF2   PSMB10  SLC12A4 GLG1    ANKRD11 GLOD4   CCL13   C17orf96        IER3IP1
NDUFA13 CYP2A7  FKBP1A  MAVS    TMEM230 ARFGEF2 ATP5J   PSMG1   LSS     SLC25A18
SBF1    SYAP1   ACTG1P10        COX7B   C1GALT1C1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      1.18070954806934e-08    22.4090909090909        0.43844716628607
8       96      respiratory electron transport chain
GO:0022900      1.61923684969259e-07    15.6091954022988        0.61199916960764
8       134     electron transport chain
GO:0045333      2.53300312874695e-07    14.6690684508492        0.648536433464812
8       142     cellular respiration
GO:0018023      3.14349433431358e-06    171.202380952381        0.031970105875026
3       7       peptidyl-lysine trimethylation
Tissue: Whole_Blood=>Artery_Tibial      Type:   cluster
SourceGene:     NCCRP1(ENSG00000188505.3)
TargetGeneSet:  SPEN    FBXO42  WASF2   MECR    FCRLA   TSEN15  RP11    TET3
BOLA3   UXS1    MTX2    U6      NDUFB3  PTH1R   SETD2   GOLGB1  BCL6    FAM193A
WDR19   ANKRD20A17P     CICP16  NDUFC1  MGST2   NIPBL   C5orf43 RPS23P5 MAN2A1
EEF1E1  LRRC16A HCG23   UBR2    FKBP1C  ARID1B  CYCS    EPDR1   CHCHD2  ACN9
PMS2P1  TRIM56  NAT2    COX6C   COL14A1 C9orf123        NDUFB6  KLF9    SEC61B  RSU1
KIAA0913        UROS    METTL15 NUMA1   MLL     CRABP1  GS1     CPM     UBE2N
MED13L  DENR    ULK1    POLE    GTF2F2  GLRX5   DUOX1   WDR61   IFT140  SRCAP
NUTF2   PSMB10  SLC12A4 GLG1    ANKRD11 GLOD4   CCL13   C17orf96        IER3IP1
NDUFA13 CYP2A7  FKBP1A  MAVS    TMEM230 ARFGEF2 ATP5J   PSMG1   LSS     SLC25A18
SBF1    SYAP1   ACTG1P10        COX7B   C1GALT1C1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      1.18070954806934e-08    22.4090909090909        0.43844716628607
8       96      respiratory electron transport chain
GO:0022900      1.61923684969259e-07    15.6091954022988        0.61199916960764
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8       134     electron transport chain
GO:0045333      2.53300312874695e-07    14.6690684508492        0.648536433464812
8       142     cellular respiration
GO:0018023      3.14349433431358e-06    171.202380952381        0.031970105875026
3       7       peptidyl-lysine trimethylation
Tissue: Whole_Blood=>Artery_Tibial      Type:   asymmetric
SourceGene:     PCBP1(ENSG00000169564.5)
TargetGeneSet:  ATPIF1  SLC16A1 DPM3    NAV1    RP11    MAPKAPK2        RPL35P1
CHRM3-AS2       STEAP3  PDE11A  ARMC9   LSM3    C3orf78 CNTN3   PDGFC   GLRB    CTD
ANKH    DAB2    MAN2A1  CPEB4   ECI2    COX6A1P2        SLC29A1 COX7A2  TRAF3IP2
GJA1    HDAC7   AEBP1   AUTS2   CHCHD7  DECR1   COX6C   C9orf123        C9orf133
PLXDC2  HK1     USMG5   POLR2L  NAV2    ODZ4    ATP5L   CLMP    ADCY6   SAP18
RPS29   ERH     NDUFB1  C14orf2 THBS1   SRP14   MYEF2   ALPK3   EIF3C   BCAR1
MMP28   TOB1    UQCR11  NDUFA7  PIN1    NDUFA13 EPS8L1  ROMO1   ATP5E   ATP5J
RBFOX2  RP6     PIN4    NDUFA1  GRIA3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      7.14548993627377e-11    32.8965517241379        0.358729499688603
9       96      respiratory electron transport chain
GO:0022900      1.44440940593033e-09    22.8352 0.500726593315342       9       134
electron transport chain
GO:0045333      2.41768474624567e-09    21.4496240601504        0.530620718289392
9       142     cellular respiration
GO:0006091      4.34195864528954e-08    9.60233516483516        1.59933568611169
12      428     generation of precursor metabolites and energy
GO:0015980      1.69250226508262e-07    10.7897153351699        1.14718704587918
10      307     energy derivation by oxidation of organic compounds
GO:0042776      1.37381713630155e-05    84.6294117647059        0.0485779530828316
3       13      mitochondrial ATP synthesis coupled proton transport
Tissue: Whole_Blood=>Artery_Tibial      Type:   cluster
SourceGene:     PISD(ENSG00000241878.4)
TargetGeneSet:  NPHP4   SPEN    RP11    UBR4    ATPIF1  SRSF4   ZCCHC17 INPP5B
SCMH1   PPCS    RPS8    NSUN4   SCP2    ACOT11  JAK1    PIGK    RWDD3   HBXIP
LRIG2   S100A6  UBQLN4  SMG5    ARHGEF11        BRP44   CEP350  TSEN15  C1orf132
NSL1    ARV1    AHCTF1  PQLC3   PTRHD1  SLC5A6  C2orf28 RPLP0P6 MORN2   CALM2
COMMD1  MDH1    SUCLG1  RNF181  SNRNP200        SMPD4   DAPL1   BTF3L4P2
NDUFB3  TTLL4   SETD5   TATDN2  LSM3    SCAP    SPCS1   PDHB    LRRC34  LETM1
SLC30A9 TMSB4XP8        LAMTOR3 PPA2    HIGD1AP14       NDUFC1  MGST2   SUB1
NIPBL   COX7C   CTD     RFESD   HINT1   PDF     ATOX1   TTC1    ARL10   TMEM14C
TMEM14B ABCF1   BAG6    RPS18   RP3     BRPF3   XPO5    SLC29A1 COX7A2  WDR11
ECHDC1  MRPS12  RP1     HIVEP2  ZDHHC14 RP4     PSMB1   FBXL18  RPA3    NDUFA4
SEPT7   EPDR1   SPDYE1  CHCHD2  POM121C PMS2P1  TRIM56  RABL5   ARF5    C7orf73
MRPS33  VDAC3   CHCHD7  DECR1   COX6C   C9orf123        MPDZ    LINC00032
NDUFB6  CHMP5   DCTN3   SNX18P3 FAM27D1 KIF27   TSTD2   TXN     ATP6V1G1
ZNF79   FAM102A CIZ1    HMGA1P4 SETX    FAM208B SEC24C  KIAA0913        RP13    LGI1
DPCD    USMG5   PDCD11  PHRF1   CYB5R2  AKIP1   NAV2-AS2        IMMP1L  ELP4
NAT10   INCENP  NXF1    MARK2   KLC2    BBS1    KDM2A   LAMTOR1 ARHGEF17
CLNS1A  TAGLN   ATP5L   IGSF9B  NCAPD3  CACNA1C-AS2     ADCY6   POU6F1  SRGAP1
NDUFA12 CCDC53  NUP37   RBM19   RPLP0   POP5    KDM2B   POLE    POMP    RFXAP   DGKH
MED4    COMMD6  A2LD1   RASA3   ACIN1   C14orf166       HEATR4  MLH3    NDUFB1
C14orf2 KIAA0284        SRP14   MAPKBP1 DYX1C1-CCPG1    GTF2A2  KIAA0101
RAB11A  RPLP1   MYO9A   WDR61   C15orf40        ZNF592  KIF7    RPL36AP43
MAN2A2  ZNF598  CREBBP  CLEC16A PDXDC1  SRCAP   RNF40   ITFG1   EDC4    SLC12A4 AARS
FBXO31  ZC3H18  VPS53   MINK1   LSMD1   AURKB   STX8    FLCN    SUPT6H  MMP28
MLLT6   TOP2A   SMARCE1 STAT5B  STAT3   HSD17B1P1       ICT1    UNK     UBE2O
TNRC6C  USP36   MYL12B  ZNF397  EPG5    CYB5A   UQCR11  DOT1L   NDUFA11 TRAPPC5
NDUFA7  ZNF317  PIN1    KRI1    TNPO2   NDUFB7  MYO9B   NDUFA13 RPSAP58 MLL4
SAMD4B  SYMPK   ZNF841  ZNF417  RPS5    EBF4    MAVS    SNRPB2  DTD1    ZNF334
ZNFX1   PFDN4   RPL12P4 C20orf43        ATP5E   PPIAP22 LINC00515       ATP5J
SCAF4   URB1    LRRC3-AS1       MCM3AP  DIP2A   MTMR3   CTA     GTPBP1  TTLL12  SBF1
TAB3-AS1        ATP6AP2 RPS2P55 FUNDC1  UBA1    PAGE2B  PDZD11  PIN4    COX7B
RPSAP9  NGFRAP1 NDUFA1  VAMP7   MT
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0045333      3.07183877498828e-15    12.3687703481092        2.15196180195142
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21      142     cellular respiration
GO:0022904      4.24854673243702e-15    16.2502870264064        1.45484741540378
18      96      respiratory electron transport chain
GO:0022900      1.20300542110449e-14    12.4464427400159        2.03072451733444
20      134     electron transport chain
GO:0015980      2.74983792662288e-10    5.76322219028456        4.65248079717667
23      307     energy derivation by oxidation of organic compounds
GO:0006091      1.67109622141055e-09    4.6345990255974 6.48619472700851        26
428     generation of precursor metabolites and energy
GO:0006120      5.14275840883601e-08    19.2335815842925        0.545567780776417
8       36      mitochondrial electron transport, NADH to ubiquinone
GO:0042773      4.63091380783589e-07    13.7980313525337        0.712269047124766
8       47      ATP synthesis coupled electron transport
GO:0042775      4.63091380783589e-07    13.7980313525337        0.712269047124766
8       47      mitochondrial ATP synthesis coupled electron transport
GO:0006119      2.44649806854381e-06    10.7541232227488        0.878970313473116
8       58      oxidative phosphorylation
Tissue: Whole_Blood=>Artery_Tibial      Type:   asymmetric
SourceGene:     RP11-403P17.2(ENSG00000260650.1)
TargetGeneSet:  C1orf122        PPCS    MAGOH   USP24   HBXIP   ARV1    OST4
MORN2   MDH1    BOLA3   NIF3L1  NDUFB3  MYEOV2  BRK1    CMC1    SPTSSB  MRPL47
NDUFC1  PDCD6   SLC9A3  C5orf43 COMMD10 ATOX1   FAM114A2        COX6A1P2
COX7A2  WDR11   RPA3    NDUFA4  MPLKIP  SEC61G  PMS2P1  ZNHIT1  C7orf73 TCEB1
DECR1   COX6C   HAS2    C9orf123        NDUFB6  SEC61B  RP11    UROS    IMMP1L
TMEM126B        TMEM126A        ATP5L   HIGD1AP1        NDUFA12 CCDC53  POP5    DENR
ULK1    ERH     SLIRP   NDUFB1  ATG2B   C14orf2 DYX1C1-CCPG1    GTF2A2  ANKRD11
TXNDC17 ICT1    NDUFA7  PIN1    NDUFB7  NDUFA13 COX7A1  SNRPD2  ATP5E   PPIAP22
ATP5J   FAM104B PDZD11  COX7B   NXT2    NDUFA1  C1GALT1C1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      2.1771608472011e-20     60.2314814814815        0.391945194104214
15      96      respiratory electron transport chain
GO:0045333      2.43668636871758e-19    42.1291989664083        0.57975226627915
16      142     cellular respiration
GO:0022900      4.07883718536453e-18    40.8890374331551        0.547090166770466
15      134     electron transport chain
GO:0015980      5.61468734236273e-14    18.0305282506194        1.25340806864577
16      307     energy derivation by oxidation of organic compounds
GO:0006091      6.71170885717984e-13    13.7687985169737        1.74742232371462
17      428     generation of precursor metabolites and energy
GO:0006120      1.30518094614004e-12    80.4705882352941        0.14697944778908
8       36      mitochondrial electron transport, NADH to ubiquinone
GO:0042773      1.31017536476418e-11    57.7295123177476        0.191889834613522
8       47      ATP synthesis coupled electron transport
GO:0042775      1.31017536476418e-11    57.7295123177476        0.191889834613522
8       47      mitochondrial ATP synthesis coupled electron transport
GO:0006119      7.71454992997175e-11    44.9945098039216        0.236800221437963
8       58      oxidative phosphorylation
GO:0042776      1.79589970093787e-05    77.0464285714286        0.0530759117016123
3       13      mitochondrial ATP synthesis coupled proton transport
Tissue: Whole_Blood=>Artery_Tibial      Type:   cluster
SourceGene:     RP11-403P17.2(ENSG00000260650.1)
TargetGeneSet:  C1orf122        PPCS    MAGOH   USP24   HBXIP   ARV1    OST4
MORN2   MDH1    BOLA3   NIF3L1  NDUFB3  MYEOV2  BRK1    CMC1    SPTSSB  MRPL47
NDUFC1  PDCD6   SLC9A3  C5orf43 COMMD10 ATOX1   FAM114A2        COX6A1P2
COX7A2  WDR11   RPA3    NDUFA4  MPLKIP  SEC61G  PMS2P1  ZNHIT1  C7orf73 TCEB1
DECR1   COX6C   HAS2    C9orf123        NDUFB6  SEC61B  RP11    UROS    IMMP1L
TMEM126B        TMEM126A        ATP5L   HIGD1AP1        NDUFA12 CCDC53  POP5    DENR
ULK1    ERH     SLIRP   NDUFB1  ATG2B   C14orf2 DYX1C1-CCPG1    GTF2A2  ANKRD11
TXNDC17 ICT1    NDUFA7  PIN1    NDUFB7  NDUFA13 COX7A1  SNRPD2  ATP5E   PPIAP22
ATP5J   FAM104B PDZD11  COX7B   NXT2    NDUFA1  C1GALT1C1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      2.1771608472011e-20     60.2314814814815        0.391945194104214
15      96      respiratory electron transport chain
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GO:0045333      2.43668636871758e-19    42.1291989664083        0.57975226627915
16      142     cellular respiration
GO:0022900      4.07883718536453e-18    40.8890374331551        0.547090166770466
15      134     electron transport chain
GO:0015980      5.61468734236273e-14    18.0305282506194        1.25340806864577
16      307     energy derivation by oxidation of organic compounds
GO:0006091      6.71170885717984e-13    13.7687985169737        1.74742232371462
17      428     generation of precursor metabolites and energy
GO:0006120      1.30518094614004e-12    80.4705882352941        0.14697944778908
8       36      mitochondrial electron transport, NADH to ubiquinone
GO:0042773      1.31017536476418e-11    57.7295123177476        0.191889834613522
8       47      ATP synthesis coupled electron transport
GO:0042775      1.31017536476418e-11    57.7295123177476        0.191889834613522
8       47      mitochondrial ATP synthesis coupled electron transport
GO:0006119      7.71454992997175e-11    44.9945098039216        0.236800221437963
8       58      oxidative phosphorylation
GO:0042776      1.79589970093787e-05    77.0464285714286        0.0530759117016123
3       13      mitochondrial ATP synthesis coupled proton transport
Tissue: Whole_Blood=>Artery_Tibial      Type:   cluster
SourceGene:     RP11-84A14.5(ENSG00000223989.1)
TargetGeneSet:  TPRG1L  RP11    NDUFS5  RP4     GTF2B   BCAS2   PSMB4   DPM3    STX6
MIR4426 RPS7    FAHD2A  MGAT5   DNPEP   ZNF385D SPCS1   RPL10AP6        ZMAT3
NDUFC1  SEMA5A  COX7C   CTD     HINT1   P4HA2   TMEM14B RPS18   RPS10   RPL10A
RPL24P4 MRPL2   ASCC3   RP1     MRPS12  TOMM7   PMS2P1  ARF5    NDUFB9  PUF60
C9orf133        NUDT2   IER5L   USMG5   PEX16   LAMTOR1 ATP5L   FAM60A  PRKAG1
PRR13   PEBP1   RPS7P10 EAPP    RPS29   ERH     COQ6    SLIRP   NDUFB1  C14orf2
SRP14   SEC11A  FAM192A MIR22HG SLC52A1 ZSWIM7  MPRIP-AS1       RPS7P1  SMARCE1
RPL27   SLC16A3 MADCAM1 UQCR11  NDUFA7  NDUFB7  EID2    SNRPD2  NLRP9   RPS5
LINC00493       ROMO1   C20orf43        ATP5J   U2AF1   EEF1B2P3        PIN4
CXorf56 NDUFA1  RP3     PLAC1   MTCP1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      5.84239041621181e-13    33.0439075630252        0.445090305169192
11      96      respiratory electron transport chain
GO:0070972      5.85953004275699e-12    26.2094459279039        0.547090166770466
11      118     protein localization to endoplasmic reticulum
GO:0022900      2.37721101989593e-11    22.7745354239257        0.621271884298664
11      134     electron transport chain
GO:0045333      4.47957813120369e-11    21.3717284623773        0.658362743062764
11      142     cellular respiration
GO:0006614      4.65758776247962e-11    26.387811634349 0.486817521278804       10
105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      5.12424242892513e-11    26.1111111111111        0.491453878624317
10      106     cotranslational protein targeting to membrane
GO:0045047      5.12424242892513e-11    26.1111111111111        0.491453878624317
10      106     protein targeting to ER
GO:0072599      5.12424242892513e-11    26.1111111111111        0.491453878624317
10      106     establishment of protein localization to endoplasmic reticulum
GO:0006612      1.00755954318332e-10    19.7009557344064        0.7093626738634 11
153     protein targeting to membrane
GO:0072594      1.37585044045365e-10    16.1272727272727        0.945816898484534
12      204     establishment of protein localization to organelle
GO:0006120      2.50508621655278e-10    57.75   0.166908864438447       7       36
mitochondrial electron transport, NADH to ubiquinone
GO:0015980      1.26395112380204e-09    11.5375409423028        1.42336170507231
13      307     energy derivation by oxidation of organic compounds
GO:0042773      1.81322448644403e-09    41.8366666666667        0.217908795239084
7       47      ATP synthesis coupled electron transport
GO:0042775      1.81322448644403e-09    41.8366666666667        0.217908795239084
7       47      mitochondrial ATP synthesis coupled electron transport
GO:0006091      7.55600629287101e-09    8.91349922523015        1.98436094387932
14      428     generation of precursor metabolites and energy
GO:0006119      8.3283323725346e-09     32.787908496732 0.26890872603972        7
58      oxidative phosphorylation
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GO:0006414      2.71359653037751e-08    19.9713437008562        0.486817521278804
8       105     translational elongation
GO:0006415      1.98806726427512e-07    19.8611111111111        0.42190851844163
7       91      translational termination
GO:0000184      1.24253009417208e-06    14.8666666666667        0.551726524115978
7       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0034623      1.33958056585863e-06    11.6136410046968        0.806726178119161
8       174     cellular macromolecular complex disassembly
GO:0033365      1.53598385943145e-06    6.58946953263656        2.19299702442738
12      473     protein localization to organelle
GO:0006605      1.57023409742074e-06    6.57473435655254        2.19763338177289
12      474     protein targeting
GO:0032984      1.65764254102156e-06    11.2700961443156        0.829907964846723
8       179     macromolecular complex disassembly
GO:0019080      6.08834441710184e-06    11.537037037037 0.700089959172376       7
151     viral genome expression
GO:0019083      6.08834441710184e-06    11.537037037037 0.700089959172376       7
151     viral transcription
GO:0006413      6.35906666054627e-06    11.4566666666667        0.704726316517888
7       152     translational initiation
GO:0043624      6.63973181469041e-06    11.377397260274 0.7093626738634 7       153
cellular protein complex disassembly
GO:0043241      8.20245376989087e-06    10.9967991169978        0.732544460590963
7       158     protein complex disassembly
GO:0000956      1.27355058579536e-05    10.2421810699588        0.783544391391599
7       169     nuclear-transcribed mRNA catabolic process
GO:0006402      1.78367876385405e-05    9.69697855750487        0.825271607501211
7       178     mRNA catabolic process
Tissue: Nerve_Tibial=>Heart_Left_Ventricle      Type:   cluster
SourceGene:     AIFM3(ENSG00000183773.10)
TargetGeneSet:  NUDC    NR0B2   CDC20   NEDD4   RP4     HSD3BP3 FAM72B  SNX18P15
IQGAP3  USP21   ASPM    NEK2    CEP170  STARD7  NCAPH   HJURP   JAGN1   KCTD6
IFT122  CTA     GLRB    KIF20A  CDC25C  LSM11   HMMR    GPANK1  LY6G6E  KIFC1
MTCH1   FKBP9   ANLN    NSUN5   POR     ASB15   FZD3    RP11    MELK    GKAP1
COBRA1  CEP55   MKI67   TSSC4   CDCA5   CARNS1  MPP2    FANCB   CGRRF1  DLGAP5
BUB1B   CASC5   NUSAP1  KIAA0101        PKM2    FANCI   C15orf42        ZNF48   DEF8
GGT6    AURKB   TOP2A   KIF18B  MRPL45P2        BIRC5   NDC80   ASXL3   SKA1    CTD
MAN2B1  UNC13A  LGALS4  SNPH    SIRPG   TPX2    UBE2C   PHEX    RBM10   SPIN4
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0000087      5.77840233219617e-20    22.3048058882956        1.56944156113764
22      360     M phase of mitotic cell cycle
GO:0051301      4.18480609018208e-19    18.7096153846154        1.97052107120614
23      452     cell division
GO:0000280      7.0432102634161e-19     21.3662613981763        1.52584596221715
21      350     nuclear division
GO:0007067      7.0432102634161e-19     21.3662613981763        1.52584596221715
21      350     mitosis
GO:0048285      2.21082121499435e-18    20.1131805157593        1.61303716005813
21      370     organelle fission
GO:0007059      8.25432922759039e-16    32.3401360544218        0.610338384886859
14      140     chromosome segregation
GO:0010564      1.28904743512527e-12    13.0241485050925        1.80485779530828
17      414     regulation of cell cycle process
GO:0000819      5.33240829785879e-11    47.4181818181818        0.226697114386548
8       52      sister chromatid segregation
GO:0007346      4.7916273970545e-10     12.6395862068966        1.32094664729084
13      303     regulation of mitotic cell cycle
GO:0007017      1.07010218486297e-09    10.5608744817188        1.71330703757525
14      393     microtubule-based process
GO:0000070      1.5802192543395e-09     42.6964285714286        0.213618434710401
7       49      mitotic sister chromatid segregation
GO:0000236      3.04867722569876e-09    27.0337662337662        0.370562590824164
8       85      mitotic prometaphase
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GO:0000910      6.83952572361645e-09    24.1894291754757        0.409798629852605
8       94      cytokinesis
GO:0051313      1.48596772101876e-08    88.5098522167488        0.0828316379489309
5       19      attachment of spindle microtubules to chromosome
GO:0000226      1.98210574086758e-08    11.5854203935599        1.17272161096118
11      269     microtubule cytoskeleton organization
GO:0007088      1.02282884249281e-07    22.0787037037037        0.383641270500311
7       88      regulation of mitosis
GO:0051783      1.02282884249281e-07    22.0787037037037        0.383641270500311
7       88      regulation of nuclear division
GO:0051656      2.65134781667083e-07    19.0079787234043        0.440315549096948
7       101     establishment of organelle localization
GO:0051640      2.67051307331495e-07    14.5925736235595        0.653933983807349
8       150     organelle localization
GO:0034453      3.93211835776371e-07    41.2586206896552        0.152584596221715
5       35      microtubule anchoring
GO:0051329      6.32935923564417e-07    8.05915551839465        1.65227319908657
11      379     interphase of mitotic cell cycle
GO:0008608      7.48018024905164e-07    74.9674054758801        0.0741125181648329
4       17      attachment of spindle microtubules to kinetochore
GO:0051325      7.7772033780125e-07     7.88318330605565        1.68714967822296
11      387     interphase
GO:0031577      1.00651369015586e-06    33.4366262814539        0.183101515466058
5       42      spindle checkpoint
GO:0007051      1.25766306931074e-06    20.3613086770982        0.348764791363919
6       80      spindle organization
GO:0050000      1.85661134868087e-06    57.3120638085743        0.0915507577330289
4       21      chromosome localization
GO:0051303      1.85661134868087e-06    57.3120638085743        0.0915507577330289
4       21      establishment of chromosome localization
GO:0071156      1.97760347735792e-06    9.23725490196078        1.15092381150093
9       264     regulation of cell cycle arrest
GO:0000086      2.92583069556219e-06    13.0027372262774        0.627776624455055
7       144     G2/M transition of mitotic cell cycle
GO:0007050      3.99539455496947e-06    7.37320649603195        1.60867760016608
10      369     cell cycle arrest
GO:0051651      6.90324640129683e-06    14.8900468994268        0.466472908449242
6       107     maintenance of location in cell
GO:0030261      8.25500485226602e-06    37.4498044328553        0.13078679676147
4       30      chromosome condensation
GO:0000075      9.64188258652613e-06    8.7981351981352 1.05501349387586        8
242     cell cycle checkpoint
GO:0071173      1.37882324114023e-05    32.4474576271186        0.148225036329666
4       34      spindle assembly checkpoint
GO:0007096      1.68925712656398e-05    79.8833333333333        0.0523147187045879
3       12      regulation of exit from mitosis
GO:0045786      1.75605492402451e-05    6.16897176439397        1.90512767282541
10      437     negative regulation of cell cycle
GO:0033043      1.89948618539111e-05    6.10996804272644        1.92256591239361
10      441     regulation of organelle organization
Tissue: Nerve_Tibial=>Heart_Left_Ventricle      Type:   cluster
SourceGene:     CCDC90B(ENSG00000137500.5)
TargetGeneSet:  RP11    GPX6    MTMR11  PRELP   ETNK2   KIAA1383        RPL31   TSPO
RPL37A  SNED1   RBMS3   ZBTB47  RPL10AP6        BBX     ITGB5   ABTB1   FGF12
GMPSP1  RPL34   USP53   MSNP1   RPL37   JMY     CREBRF  RPS18   ADCYAP1R1
YAE1D1  SRI     CTB     ATP5J2  GSTK1   GS1     GRIP1   TMEM55A RPL30   YWHAZ
CYHR1   C9orf156        SLC44A1 NTNG2   ARRDC1  RSU1    PRTFDC1 ZNF22   ERCC6
RPL13AP5        FXC1    NR1H3   ZBTB16  DYRK4   TMTC1   FGD4    RPL14P1 C12orf26
GNPTAB  ULK1    STXBP6  RPL36A  NEK9    JDP2    POLR2M  FAM81A  SEC11A  CTD
JMJD5   SLC7A6OS        MON1B   FXR2    PER1    RPL26   HS3ST3A1        RPL23A  GIT1
RPL17   PLEKHM1 SLC38A10        OSBPL1A TRAPPC8 SBNO2   MKNK2   C19orf43
UBA52   SLC25A42        CCDC9   MYH7B   ATP9A   URB1    BCL2L13 PLA2G6  EEF1B2P3
RP3     FAM127B
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GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0072594	2.58412319246211e-13	20.5102167182663	0.917583558231264
14	204	establishment of protein localization to organelle
GO:0006614	1.12668141048972e-12	30.9716312056738	0.472285654971974
11	105	SRP-dependent cotranslational protein targeting to membrane
GO:0006613	1.25281388558025e-12	30.643469785575 0.476783613590755	11
106	cotranslational protein targeting to membrane
GO:0045047	1.25281388558025e-12	30.643469785575 0.476783613590755	11
106	protein targeting to ER
GO:0072599	1.25281388558025e-12	30.643469785575 0.476783613590755	11
106	establishment of protein localization to endoplasmic reticulum
GO:0006612	3.19068225975015e-12	22.8743476515456	0.688187668673448
12	153	protein targeting to membrane
GO:0070972	4.13732373446474e-12	27.1839736933195	0.530759117016123
11	118	protein localization to endoplasmic reticulum
GO:0006415	7.95881032947131e-12	32.1099887766554	0.409314234309044
10	91	translational termination
GO:0006414	3.40266175495566e-11	27.3511961722488	0.472285654971974
10	105	translational elongation
GO:0000184	1.19525470078418e-10	23.814845704754 0.535257075634904	10
119	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080	1.25866887322011e-09	18.3687943262411	0.679191751435887
10	151	viral genome expression
GO:0019083	1.25866887322011e-09	18.3687943262411	0.679191751435887
10	151	viral transcription
GO:0006413	1.34262074072221e-09	18.2381562099872	0.683689710054667
10	152	translational initiation
GO:0043624	1.43151305453085e-09	18.1093452002543	0.688187668673448
10	153	cellular protein complex disassembly
GO:0043241	1.95929027695537e-09	17.4914004914005	0.710677461767352
10	158	protein complex disassembly
GO:0000956	3.76806827694243e-09	16.2687249857061	0.76015500657394
10	169	nuclear-transcribed mRNA catabolic process
GO:0034623	4.99601276650178e-09	15.7671840354767	0.782644799667843
10	174	cellular macromolecular complex disassembly
GO:0006402	6.2214483141093e-09	15.3874458874459	0.800636634142966
10	178	mRNA catabolic process
GO:0032984	6.56663903908814e-09	15.2953200645508	0.805134592761747
10	179	macromolecular complex disassembly
GO:0033365	1.76727736295494e-08	8.32918962792088	2.12753442668327
14	473	protein localization to organelle
GO:0006605	1.81492378685088e-08	8.31048593350384	2.13203238530206
14	474	protein targeting
GO:0006401	2.40589720690824e-08	13.2317016317016	0.922081516850045
10	205	RNA catabolic process
GO:0019058	7.43844078156544e-08	11.6536404771699	1.03902844093834
10	231	viral infectious cycle
GO:0022415	2.24268094993652e-07	10.2807272727273	1.16946924088298
10	260	viral reproductive process
GO:0071845	5.06134324788978e-07	9.364299933643  1.27742024773372	10
284	cellular component disassembly at cellular level
GO:0022411	5.75315735175906e-07	9.22694571615435	1.29541208220884
10	288	cellular component disassembly
Tissue: Nerve_Tibial=>Heart_Left_Ventricle	Type:	asymmetric
SourceGene:	CNTD2(ENSG00000105219.3)
TargetGeneSet:	RP11	MRPL20	RPL22	DNAJC11	RPL11	EIF2C3	SZT2	BEND5
ANXA9	INSRR	SRP9	UBC	EIF3FP3	RPL15	HIGD1A	CHMP2B	RPL24	C3orf27
C3orf37	RPL35A	ANAPC10	RPS3A	C5orf22	BRIX1	BTF3	SKP1	SPOCK1	TMEM14B
RPS10	RPL10A	RPL39P3	MRPS12	SNHG6	RPL30	EEF1D	KANK1	DCTN3	FAM22G	ASB6
POLR3A	RPS24	RPL27A	RPS13	HTATIP2	FAU	RPS25	KDM5A	PFDN5	OR10P1
SYCP3	RILPL1	STARD13	RNASEH2B		RPS3AP6	RPLP1	ZZEF1	KIAA0100
RPL19	EIF3G	RPL18A	RPS16	EID2B	EXOSC3P1		RGN	RPS23P8	RPS4X
RAB11FIP1P1		EMD
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GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0006414	1.12426377239108e-34	130.857498961363	0.370562590824164	22	105	translational elongation
GO:0006614	1.40619194885409e-32	119.3	0.370562590824164	21	105	SRP-dependent cotranslational protein targeting to membrane
GO:0006613	1.75010579333706e-32	117.888235294118	0.374091758355823	21	106	cotranslational protein targeting to membrane
GO:0045047	1.75010579333706e-32	117.888235294118	0.374091758355823	21	106	protein targeting to ER
GO:0072599	1.75010579333706e-32	117.888235294118	0.374091758355823	21	106	establishment of protein localization to endoplasmic reticulum
GO:0006415	6.84356161348383e-32	130.204452521581	0.321154245380943	20	91	translational termination
GO:0070972	2.04497673012893e-31	103.217525773196	0.416441768735728	21	118	protein localization to endoplasmic reticulum
GO:0000184	2.42741266830333e-29	93.1964809384164	0.419970936267386	20	119	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006413	6.07258898491126e-29	76.2465648854962	0.536433464812124	21	152	translational initiation
GO:0006612	7.02459986295605e-29	75.6636363636364	0.539962632343782	21	153	protein targeting to membrane
GO:0006401	7.5833112102058e-28	58.936122102883	0.723479343990035	22	205	RNA catabolic process
GO:0006402	1.97950146336038e-27	63.503821656051	0.62819182063525	21	178	mRNA catabolic process
GO:0019080	3.87415982015813e-27	70.2733316917016	0.532904297280465	20	151	viral genome expression
GO:0019083	3.87415982015813e-27	70.2733316917016	0.532904297280465	20	151	viral transcription
GO:0043624	5.11085612430377e-27	69.2068881882125	0.539962632343782	20	153	cellular protein complex disassembly
GO:0043241	1.00453714998166e-26	66.6760168302945	0.557608470002076	20	158	protein complex disassembly
GO:0072594	3.87001346254351e-26	54.3819672131148	0.719950176458377	21	204	establishment of protein localization to organelle
GO:0000956	4.10822896760333e-26	61.7059969690409	0.596429312850322	20	169	nuclear-transcribed mRNA catabolic process
GO:0034623	7.54415845132792e-26	59.6816087138668	0.614075150508615	20	174	cellular macromolecular complex disassembly
GO:0032984	1.35990178644407e-25	57.7845404747413	0.631720988166909	20	179	macromolecular complex disassembly
GO:0019058	2.58758551892479e-23	43.3848035468583	0.815237699813162	20	231	viral infectious cycle
GO:0022415	2.85800587275904e-22	38.0645161290323	0.917583558231264	20	260	viral reproductive process
GO:0071845	1.6961335005656e-21	34.5454545454545	1.00228357899107	20	284	cellular component disassembly at cellular level
GO:0022411	2.24675214330027e-21	34.0202214732788	1.01640024911771	20	288	cellular component disassembly
GO:0033365	3.47241803156095e-21	25.4642857142857	1.66929624247457	23	473	protein localization to organelle
GO:0006605	3.64251793132596e-21	25.4060025340513	1.67282541000623	23	474	protein targeting
GO:0016032	7.30222353574565e-19	22.7418604651163	1.59165455677808	21	451	viral reproduction
GO:0022613	1.30660656937396e-05	10.3496663886572	0.794062694623209	7	225	ribonucleoprotein complex biogenesis
GO:0042254	1.33451810417935e-05	13.2932400932401	0.525845962217148	6	149	ribosome biogenesis
GO:0071843	1.93101608071394e-05	9.71551724137931	0.843471040066431	7	239	cellular component biogenesis at cellular level

Tissue: Nerve_Tibial=>Heart_Left_Ventricle	Type:	asymmetric
SourceGene:	ENSG00000215346.3

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TargetGeneSet:  CCNL2   NPHP4   SRRM1   KHDRBS1 PTGFR   CNN3    RNPC3   PIAS3
TIPRL   RAB10   NRXN1   AHSA2   PPP3R1  ANTXR1  RABL2A  GALNT13 NDUFB3  STK36
COX17   ZXDC    RP11    NPHP3   TMEM14E MAP3K13 METTL19 C4orf3  CPE     NDUFS6
EGFLAM  COX7C   PPIC    WDR55   HMGXB3  ATF6B   NUDT3   TBCC    EFHC1   MARCKS
TOMM7   MRPS24  UBE2D4  CCT6P1  SGCE    FAM71F2 NDUFB2  RBM33   GFRA2   KIAA1875
IL33    C9orf123        CDK9    ANAPC2  MLLT10  RET     C10orf102       USMG5
MRPL23  TMEM138 COX8A   VEGFB   CCL13   PCNXL3  NDUFS8  C11orf67        KIAA1731
MAML2   VPS11   FEZ1    COX14   CAPS2   GLTP    ARL6IP4 LTB4R   RDH11   SLIRP
NDUFB1  RAB8B   LUC7L   TCEB2   POLR3E  CTD     NDUFAB1 SETD6   SLC7A6  YWHAE
MYBBP1A VMO1    KIAA0753        NXPH3   SUMO2   C17orf89        CTDP1   CFD
UQCR11  C19orf70        CAPS    C3      C19orf79        TRAPPC5 ADAMTS10
GPATCH1 USF2    COX6B1  POLR2I  COX7A1  QPCTL   LENG8   XRN2    ROMO1   ZMYND8
RPS21   SLC2A4RG        PCP4    NDUFV3  CHCHD10 DDX17   RP1     TOMM22  TUBGCP6
PRPS2   NDUFA1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      2.67348502771974e-12    22.8988764044944        0.67095702719535
12      96      respiratory electron transport chain
GO:0006120      1.10616062802446e-10    44      0.251608885198256       8       36
mitochondrial electron transport, NADH to ubiquinone
GO:0022900      1.450782056823e-10      15.7244428071468        0.936544183793509
12      134     electron transport chain
GO:0006119      2.22073209059671e-10    28.5512422360248        0.40536987059719
9       58      oxidative phosphorylation
GO:0045333      2.86203743916216e-10    14.7484874675886        0.992457269393122
12      142     cellular respiration
GO:0042773      1.07918168525966e-09    31.5654811138682        0.328489377897723
8       47      ATP synthesis coupled electron transport
GO:0042775      1.07918168525966e-09    31.5654811138682        0.328489377897723
8       47      mitochondrial ATP synthesis coupled electron transport
GO:0006091      4.22139006051641e-08    6.36801827527127        2.99135007957927
16      428     generation of precursor metabolites and energy
GO:0015980      2.12874277364463e-07    7.06277056277056        2.14566465988513
13      307     energy derivation by oxidation of organic compounds
Tissue: Nerve_Tibial=>Heart_Left_Ventricle      Type:   asymmetric
SourceGene:     ENSG00000223442.1
TargetGeneSet:  ISG15   AGRN    MXRA8   ZBTB48  MT1XP1  MFAP2   ATPIF1  RP11
FAM176B FTH1P1  CYP4B1  SPATA6  ALG6    HHLA3   IFI44L  IFI44   TGFBR3  AMIGO1
AMPD2   INTS3   CRABP2  KIRREL  GLUL    CNST    TRAPPC12-AS1    C2orf18 EMILIN1 XPO1
ATOH8   IL1B    INHBB   METAP1D ITGAV   COL3A1  FN1     TMBIM1  SERPINE2
MTMR14  TIMP4   GALNTL2 TRANK1  ABHD6   SLC9C1  CCDC80  KLF15   GOLIM4  PHF17
ZDHHC11 CDH6    NREP    CDX1    SPARC   PDLIM7  RMND5B  SCAND3  RXRB    FKBP5
MAPK14  BYSL    CCND3   MTO1    COL12A1 SH3BGRL2        PGM3    KIAA1009
SESN1   FAN1    SEPT7   HGF     SAMD9L  COL1A2  MKLN1   ADCK2   LOXL2   DRP2
PROSC   MSC     CRISPLD1        CTHRC1  SYBU    SNTB1   OGN     ASPN    ANKS6
COL15A1 ZFP37   IER5L   COL5A1  LCN6    ECHDC3  ZNF438  ITGB1   ARHGAP22
MICU1   IFIT1   PANK1   POLL    LSP1    PRKCDBP DCHS1   ZNF214  FJX1    PRR5L
NR1H3   LRRC55  SLC43A1 TMEM223 NRXN2   DPF2    KAT5    OAF     MGST1   LIMA1
TENC1   PAN2    IRAK3   LRRC10  LUM     BRAP    LPAR6   LINC00346       ARHGEF40
PRMT5-AS1       ZFHX2   C14orf101       ARID4A  DACT1   MTA1    NIPA2   GPR176  CILP
LOXL1   FAM174B CCDC101 MT1A    FOXC2   DEF8    SERPINF2        RP1     ZMYND15
ZNF594  CCR10   EZH1    ARL17B  COL1A1  TMEM100 MRC2    CDC42EP4        BAIAP2
ABHD3   C19orf6 TCF3    CSNK1G2 MOB3A   PLIN4   XAB2    ZNF844  ZNF564  ARRDC2
ISYNA1  ZNF233  HIF3A   RCN3    VRK3    CLEC11A SSC5D   ZNF274  C20orf202
CSRP2BP BCL2L1  TTI1    KIAA1755        SLCO4A1 ADAMTS5 FAM176C RUNX1   CBS
SCARF2  DRG1    C1QTNF6 NOL12   TRIOBP  GTPBP1  MXRA5   RP3     TSC22D3 KIAA1210
SEPT6   NLGN4Y
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0030199      2.52257794560002e-11    39.3805147058824        0.331118953705626
9       33      collagen fibril organization
GO:0030198      6.52673092890722e-07    7.74706467661692        1.61545913777593
11      161     extracellular matrix organization
GO:0043062      6.94264786395083e-07    7.69521597311456        1.62549304546398
11      162     extracellular structure organization
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Tissue: Heart_Left_Ventricle=>Nerve_Tibial      Type:   asymmetric
SourceGene:     ENSG00000228404.1
TargetGeneSet:  C1QA    C1QC    C1QB    RPS6KA1 LAPTM5  BRD8    CD53    C1orf162
ADORA3  DENND4B ARHGAP30        FCER1G  NPL     CHIT1   FAM177B ENAH    CCDC75
RAB11FIP5       VAMP8   ARID5A  BUB1    SLC11A1 IRS1    ATRIP   STAB1   LRIG1
GAP43   HCLS1   TM4SF1  TLR6    RBM47   CXCL13  TLR2    SAP30   KCNN2   P4HA2-AS1
ERGIC1  ATP6V0E1        MUTED   GPSM3   CYB5R4  RP3     C6orf123        TWISTNB
IKZF1   MTERF   GAL3ST4 TFEC    TES     IRF5    TBXAS1  RP11    PREX2   SLA
CDKN2A  CDKN2B-AS1      GNA14   SYK     FGD3    ARRDC1  ITIH5   ASCC1   SAA2-SAA4
SAA1    MS4A6A  MS4A7   SLC15A3 FERMT3  PGM2L1  SLCO2B1 MYO7A   GPR162  PTPN6
CD163   C3AR1   ERP27   IRAK4   BIN2    MSRB3   HSPB8   ALOX5AP RNASE6  RNASE2
SLC7A7  FMN1    ANP32A  APOBR   CORO1A  RPH3AL  CD68    ALOX15B PIK3R5  EVI2A
FMNL1   YES1    ABHD3   STXBP2  CD97    RASAL3  ZNF738  RASGRP4 SHKBP1  SIGLEC9
SIGLEC7 NLRP12  SIRPG   NNAT    PKIG    ATP9A   SLC17A9 SAMSN1  TLR8    WAS
WDR44   SASH3   MTM1    ARHGAP4
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0002250      1.14803998294445e-08    10.3848973607038        1.37014739464397
12      198     adaptive immune response
GO:0050778      2.00383920420658e-07    6.51209302325581        2.5188568265172 14
364     positive regulation of immune response
GO:0002460      4.84306528829036e-07    9.21377517868746        1.25250847692201
10      181     adaptive immune response based on somatic recombination of immune
receptors built from immunoglobulin superfamily domains
GO:0006954      6.21981120977108e-07    5.48914330833004        3.1970105875026 15
462     inflammatory response
GO:0050900      8.47628373614584e-07    7.58822667318026        1.66770465711715
11      241     leukocyte migration
GO:0050865      4.25529148021367e-06    5.77588574567427        2.3735381634489 12
343     regulation of cell activation
GO:0002253      6.83481194313715e-06    6.0351513732834 2.06906096463913        11
299     activation of immune response
GO:0002694      1.33374702695963e-05    5.59807901413556        2.22129956404401
11      321     regulation of leukocyte activation
GO:0002443      1.53366305529808e-05    6.92748340768143        1.46010656701958
9       211     leukocyte mediated immunity
Tissue: Heart_Left_Ventricle=>Nerve_Tibial      Type:   cluster
SourceGene:     ENSG00000232821.1
TargetGeneSet:  HSPB7   PTGER3  PXDN    RETSAT  MOGAT1  CIDEC   TIMP4   PPARG
ADIPOQ  ADIPOQ-AS1      HSP90AB2P       KLB     RP11    ACSL1   PPARGC1B
KLHL31  SLC29A4 MLXIPL  CD36    LEP     PRRT4   DUSP4   FABP4   AQP9    AGPAT2
O3FAR1  SCD     KCNIP2  GPAM    PNPLA2  LGALS12 DGAT2   THRSP   GPD1    PPP1R1A
PLIN1   ABCC6   SPIRE2  TUSC5   SCN4A   FASN    PLIN4   PLIN5   OLFM2   RFXANK
CEBPA   LIPE    RPL12L3 BLCAP   PCK1    RP1     GYG2    TMEM164
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006641      2.38359895737063e-18    66.367201426025 0.311950730053283       13
98      triglyceride metabolic process
GO:0006639      4.69741644196249e-18    62.6582491582492        0.327866583627431
13      103     acylglycerol metabolic process
GO:0006638      5.3570268371576e-18     61.965367965368 0.33104975434226        13
104     neutral lipid metabolic process
GO:0019432      5.83776216399773e-14    79.3912776412776        0.168708047885959
9       53      triglyceride biosynthetic process
GO:0046460      8.33727060110283e-14    75.9289071680376        0.175074389315618
9       55      neutral lipid biosynthetic process
GO:0046463      8.33727060110283e-14    75.9289071680376        0.175074389315618
9       55      acylglycerol biosynthetic process
GO:0046486      8.76471418799091e-13    22.6739344666174        0.824441215140821
13      259     glycerolipid metabolic process
GO:0045017      1.23681112604198e-09    23.5929398786542        0.49657463151339
9       156     glycerolipid biosynthetic process
GO:0044262      1.47954503401583e-07    16.1820768136558        0.614351947962079
8       193     cellular carbohydrate metabolic process
GO:0019216      1.5395511703538e-07     16.0939445387663        0.617535118676908
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8       194     regulation of lipid metabolic process
GO:0006071      6.30229179542734e-07    76.1216931216931        0.0700297557262473
4       22      glycerol metabolic process
GO:0019433      7.61135957108558e-07    72.1102756892231        0.0732129264410767
4       23      triglyceride catabolic process
GO:0019400      9.11240520275404e-07    68.5    0.0763960971559062      4       24
alditol metabolic process
GO:0046461      9.11240520275404e-07    68.5    0.0763960971559062      4       24
neutral lipid catabolic process
GO:0046464      9.11240520275404e-07    68.5    0.0763960971559062      4       24
acylglycerol catabolic process
GO:0050873      9.11240520275404e-07    68.5    0.0763960971559062      4       24
brown fat cell differentiation
GO:0055089      2.50194174192626e-06    167.43023255814 0.0286485364334648      3
9       fatty acid homeostasis
GO:0046503      3.02691826860864e-06    48.9013605442177        0.101861462874542
4       32      glycerolipid catabolic process
GO:0006631      3.05314827031352e-06    10.6203007518797        0.916753165870874
8       288     fatty acid metabolic process
GO:0019751      3.88556489186654e-06    45.6349206349206        0.1082278043042 4
34      polyol metabolic process
GO:0032787      3.95504925652452e-06    8.69532542746829        1.2764514566466 9
401     monocarboxylic acid metabolic process
GO:0044242      4.46166843388477e-06    16.3442748091603        0.436094387931631
6       137     cellular lipid catabolic process
GO:0010876      4.78571076242548e-06    12.2508629191321        0.684381703688326
7       215     lipid localization
GO:0046339      4.89262644019665e-06    125.55523255814 0.0350148778631237      3
11      diacylglycerol metabolic process
GO:0050872      4.89262644019665e-06    125.55523255814 0.0350148778631237      3
11      white fat cell differentiation
GO:0055088      5.59022469380387e-06    22.9926187419769        0.257836827901183
5       81      lipid homeostasis
GO:0006637      7.55092524771267e-06    38.0132275132275        0.127326828593177
4       40      acyl-CoA metabolic process
GO:0035383      7.55092524771267e-06    38.0132275132275        0.127326828593177
4       40      thioester metabolic process
GO:0045834      1.04540248717122e-05    20.0700869077656        0.292851705764307
5       92      positive regulation of lipid metabolic process
GO:0010035      1.53444045941357e-05    8.42944969260759        1.14275828662376
8       359     response to inorganic substance
GO:0034383      1.64209495918165e-05    77.2379248658318        0.0509307314372708
3       16      low-density lipoprotein particle clearance
GO:0071285      1.64209495918165e-05    77.2379248658318        0.0509307314372708
3       16      cellular response to lithium ion
GO:0019915      1.71434037712978e-05    30.3915343915344        0.155975365026642
4       49      lipid storage
Tissue: Nerve_Tibial=>Heart_Left_Ventricle      Type:   asymmetric
SourceGene:     ENSG00000239935.1
TargetGeneSet:  DFFB    RBP7    UBE4B   HNRNPR  RP1     KHDRBS1 NDUFS5  TAL1    NRD1
RP4     FAM69A  WNT2B   BCAS2   ITGA10  C1orf54 SPRR1A  S100A4  INTS3   RP11
CRTC2   RGS5    TIPRL   CEP350  MIR4426 HHAT    LYST    SOS1    KDM3A   COX5B
RABL2A  INHBB   MAP3K2  SLC40A1 STK36   STK11IP ASB1    ING5    MRPS36P1
MTMR14  CCDC72  SNORD19B        PDHB    ROBO1   CD200R1 CCDC58  ITGB5   ABTB1
UBQLN4P1        RTP4    BCL6    ATP5I   METTL19 QDPR    FAM184B WDR19   RPL7AP31
FAM13A-AS1      TMSB4XP8        ENPEP   PDE5A   LSM6    CTSO    PTGER4  C5orf43
PIK3R1  COX7C   CTD     KIF3A   SOX4    ANKS1A  FKBP5   ETV7    PEX6    PPP2R5D NT5E
MARCKS  GTF2H5  AGPAT4  FAM120B IQCE    AGR2    DNAH11  CDK14   SGCE    ECD
ATP5J2  GFRA2   BIN3    EBF2    UBE2V2  ENY2    DENND3  IL33    GLIPR2  ZNF169
COL15A1 GRIN3A  C9orf114        USP20   CAMSAP1 RET     CXCL12  ZNF22   RHOBTB1
CALM2P2 BLNK    TM9SF3  C10orf82        POLR2L  LSP1    PHLDA2  OLFML1  ATG13
LRRN4CL COX8A   FAU     SYVN1   PRCP    FEZ1    TSPAN11 C12orf35        PKP2    TWF1
TENC1   ITGA5   NDUFA12 RPS11P5 RPS7P10 MED4    MED4-AS1        MRPL52  AP1G2
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FITM1   ARF6    GNG2    MAX     ERH     MLH3    SLIRP   NDUFB1  SLC25A29        PLDN
FBN1    SCAND2  IFT140  SEPHS2  MT1JP   PSMB10  SLC7A6  DHX38   ZC3H18  INPP5K
WDR81   DPH1    MNT     SPAG7   FXR2    PER1    LRRC48  EZH1    MTMR4   SLC16A6
RPL38   RECQL5  SMCHD1  ZNF397  MBD1    DPP9    SNRPEP4 CAPS    GPR108  C19orf60
GPATCH1 COX6B1  POLR2I  COX7A1  ZNF428  HIF3A   NDUFA3  ZNF274  ZNF341  ROMO1
PTPRT   BCAS4   RPS21   ATP5J   URB1    NDUFV3  CHCHD10 TPST2   EIF4ENIF1
PLA2G6  TOMM22  EEF1B2P3        MAGEH1  SH3BGRL PGRMC1  NDUFA1  RP3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      2.38067494063953e-11    15.9031841652324        1.01640024911771
13      96      respiratory electron transport chain
GO:0045333      3.05580499993376e-10    11.1499550359712        1.50342536848661
14      142     cellular respiration
GO:0022900      1.65293176557921e-09    10.8796340023613        1.4187253477268 13
134     electron transport chain
GO:0015980      2.67741731030971e-08    6.03793103448276        3.25036329665767
17      307     energy derivation by oxidation of organic compounds
GO:0006091      1.31625266919999e-07    4.81500200707952        4.53145111064978
19      428     generation of precursor metabolites and energy
Tissue: Nerve_Tibial=>Heart_Left_Ventricle      Type:   asymmetric
SourceGene:     ENSG00000243172.1
TargetGeneSet:  RBP7    UBE4B   HNRNPR  RP1     KHDRBS1 NDUFS5  TAL1    BCAS2
SPRR1A  S100A4  MIR4426 HHAT    SOS1    KDM3A   SH3RF3  RABL2A  INHBB   NDUFB3  ING5
MTMR14  PDHB    ROBO1   CCDC58  UBQLN4P1        RP11    BCL6    ATP5I   METTL19 QDPR
FAM184B COX7C   CTD     ADAMTS19        RP3     ETV7    USP49   PPP2R5D MARCKS  IQCE
AGR2    DNAH11  GFRA2   EBF2    GLIPR2  COL15A1 C9orf114        USP20   CAMSAP1 RET
CXCL12  CALM2P2 BLNK    PHLDA2  ATG13   OR4C3   COX8A   SYVN1   UCP2    PRCP
TSPAN11 PKP2    ITGA5   RIC8B   RPS11P5 RPS7P10 MRPL52  ARF6    U3      MAX
SLIRP   NDUFB1  FBN1    SCAND2  IFT140  POLR3E  MT1JP   PSMB10  DHX38   ZC3H18
INPP5K  MNT     SPAG7   LRRC48  EZH1    MTMR4   SLC16A6 SMCHD1  ZNF397  DPP9
SNRPEP4 CAPS    C19orf60        GPATCH1 COX6B1  NDUFA3  ZNF274  ROMO1   BCAS4
RPS21   ATP5J   CHCHD10 PLA2G6  TOMM22  MAGEH1  HDAC8   RP13    PGRMC1  NDUFA1
PNMA6C
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      6.72920021658114e-12    25.6720588235294        0.551380527299149
11      96      respiratory electron transport chain
GO:0045333      2.70262888587389e-11    18.5109425785482        0.815583696629991
12      142     cellular respiration
GO:0022900      2.63392577042806e-10    17.6936540198735        0.769635319355062
11      134     electron transport chain
GO:0015980      2.01036838139178e-09    9.7467477865163 1.7632689779254 14      307
energy derivation by oxidation of organic compounds
GO:0006091      1.7873964604507e-08     7.45353226036177        2.45823818420871
15      428     generation of precursor metabolites and energy
GO:0006119      9.53058109375238e-07    21.4525474525475        0.333125735243236
6       58      oxidative phosphorylation
GO:0006120      1.81379446212975e-06    29.6464019851117        0.206767697737181
5       36      mitochondrial electron transport, NADH to ubiquinone
GO:0042773      7.02387280262989e-06    21.8650793650794        0.269946716490208
5       47      ATP synthesis coupled electron transport
GO:0042775      7.02387280262989e-06    21.8650793650794        0.269946716490208
5       47      mitochondrial ATP synthesis coupled electron transport
Tissue: Heart_Left_Ventricle=>Nerve_Tibial      Type:   asymmetric
SourceGene:     ENSG00000258953.2
TargetGeneSet:  C1QC    RPS6KA1 ADORA3  RP11    SLAMF8  ARHGAP30        FCER1G
TRMT1L  TLR5    VAMP8   SLC4A3  CCR2    HCLS1   KLHL7   PDE6B   SLC2A9  RBM47   ARSJ
RP13    SLC1A3  GNPDA1  LCP2    HLA-DRB5        FGD2    ZC3H12D TFEC    IRF5
TBXAS1  SLA     SYK     ENG     SFMBT2  ASCC1   VENTX   MS4A6A  MS4A4E  MS4A7
CCDC88B SLCO2B1 LRRC32  SLC37A2 C11orf45        PTPN6   CD163   C3AR1   IRAK4
RNASE6  SLC7A7  FMN1    PMFBP1  BCAR1   HIC1    ZFP3    ALOX15B PIK3R5  AKAP10
STXBP2  ZNF812  NUDT19  NR1H2   SIGLEC9 SIGLEC7 CD33    SIGLEC10        CTD
LILRB2  HCK     TLR8    WAS     BTK     SASH3   ARHGAP4
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0050778      2.48504833504871e-11    12.8391147960739        1.56169123244066
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15      364     positive regulation of immune response
GO:0002764      5.05636428672103e-10    14.3928813559322        1.06400941111342
12      248     immune response-regulating signaling pathway
GO:0002757      4.07884376650866e-09    13.6392682072829        1.00823472424054
11      235     immune response-activating signal transduction
GO:0002253      4.23671184581676e-09    11.7926132404181        1.28281779807626
12      299     activation of immune response
GO:0001816      9.6346617077943e-09     9.72812266267764        1.69469240882984
13      395     cytokine production
GO:0002250      1.53746943109868e-07    12.7583108715184        0.849491384679261
9       198     adaptive immune response
GO:0002768      1.71706727782569e-07    15.5261437908497        0.617811916130372
8       144     immune response-regulating cell surface receptor signaling pathway
GO:0050865      1.9773336970043e-07     9.1322348216395 1.47159366133832        11
343     regulation of cell activation
GO:0002443      2.63990345932064e-07    11.9263030076593        0.905266071552142
9       211     leukocyte mediated immunity
GO:0001817      3.12044145533633e-07    8.70244534595447        1.54023942979725
11      359     regulation of cytokine production
GO:0043299      5.55191241907973e-07    38.160552897395 0.163033700089959       5
38      leukocyte degranulation
GO:0050867      7.80228360848356e-07    10.407743200196 1.02968652688395        9
240     positive regulation of cell activation
GO:0002694      9.82156060142484e-07    8.7051694286421 1.37720572970729        10
321     regulation of leukocyte activation
GO:0002460      9.85128122379462e-07    12.1738385784629        0.776555255691648
8       181     adaptive immune response based on somatic recombination of immune
receptors built from immunoglobulin superfamily domains
GO:0045055      1.17774441339446e-06    32.2762033288349        0.188775863262058
5       44      regulated secretory pathway
GO:0002429      1.54053548353115e-06    14.4070707070707        0.570617950314857
7       133     immune response-activating cell surface receptor signaling pathway
GO:0043300      1.74037131440556e-06    58.3042596348884        0.0900975711023459
4       21      regulation of leukocyte degranulation
GO:0002886      2.55844426015257e-06    52.1597096188748        0.0986782921597121
4       23      regulation of myeloid leukocyte mediated immunity
GO:0002703      2.60592313300984e-06    17.8193521594684        0.394713168638849
6       92      regulation of leukocyte mediated immunity
GO:0042129      4.49497462692755e-06    16.1210526315789        0.433326413396997
6       101     regulation of T cell proliferation
GO:0002252      5.12654125636125e-06    7.16704173486088        1.65607916407169
10      386     immune effector process
GO:0002696      6.46907816332389e-06    9.32609053497942        0.999654003183171
8       233     positive regulation of leukocyte activation
GO:0042098      1.10449759516756e-05    13.6578443877551        0.50626254238461
6       118     T cell proliferation
GO:0002283      1.21088113765642e-05    91.4046610169491        0.0471939658155145
3       11      neutrophil activation involved in immune response
GO:0050851      1.40087942779846e-05    13.0695970695971        0.527714345028026
6       123     antigen receptor-mediated signaling pathway
GO:0045576      1.45564056343773e-05    31.9421579532814        0.15016261850391
4       35      mast cell activation
Tissue: Nerve_Tibial=>Heart_Left_Ventricle      Type:   asymmetric
SourceGene:     FAM132A(ENSG00000184163.3)
TargetGeneSet:  DNAJC11 RP11    SLC39A1 LRRC71  TNFAIP6 BTF3L4P2        RPL15   LNP1
OSBPL11 PPP1R2  LETM1   SLC2A9  RPS3A   NDUFAF2 SKP1    MATR3   RPS14   TMEM14C RDBP
RXRB    RPS10   RPL10A  RPL39P3 MTO1    ELMO1   ZNF706  SYBU    RPL8    CHMP5
FRMPD1  RPL35   TRMT112 SNX32   CCDC59  RILPL1  ZNF605  ESR2    RPS3AP6 BCL7C
MIR4519 SLC12A4 RPL26   RPL19   KCNH4   BAIAP2  LAMA3   CABYR   GPX4    RPS15
MOB3A   RPL18A  ZNF790  ZNF585B OPA3    SNRPD2  SIGLEC10        UBE2S   CTD
SLC5A1  XRCC6   RAB11FIP1P1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      3.68790031645846e-15    56.2767857142857        0.289668535049478
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11      91      translational termination
GO:0006414      1.88173460707377e-14    47.8483282674772        0.334232925057089
11      105     translational elongation
GO:0006614      1.88173460707377e-14    47.8483282674772        0.334232925057089
11      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      2.09493349418219e-14    47.3413533834586        0.337416095771919
11      106     cotranslational protein targeting to membrane
GO:0045047      2.09493349418219e-14    47.3413533834586        0.337416095771919
11      106     protein targeting to ER
GO:0072599      2.09493349418219e-14    47.3413533834586        0.337416095771919
11      106     establishment of protein localization to endoplasmic reticulum
GO:0019080      3.12135750018348e-14    36.2234447735929        0.480658777939243
12      151     viral genome expression
GO:0019083      3.12135750018348e-14    36.2234447735929        0.480658777939243
12      151     viral transcription
GO:0070972      7.01974491092106e-14    41.9967957276369        0.375614144349872
11      118     protein localization to endoplasmic reticulum
GO:0000184      7.71744494046882e-14    41.6050264550265        0.378797315064701
11      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019058      2.02553255535598e-13    25.6367806505421        0.735312435125597
13      231     viral infectious cycle
GO:0022415      9.20617414433382e-13    22.5805422647528        0.82762438585565
13      260     viral reproductive process
GO:0006413      1.17672574858471e-12    31.7941236068896        0.483841948654072
11      152     translational initiation
GO:0006612      1.26504439078283e-12    31.5680080482897        0.487025119368902
11      153     protein targeting to membrane
GO:0043624      1.26504439078283e-12    31.5680080482897        0.487025119368902
11      153     cellular protein complex disassembly
GO:0043241      1.8031805503896e-12     30.4835762876579        0.502940972943049
11      158     protein complex disassembly
GO:0000956      3.77697590408088e-12    28.3394213381555        0.537955850806173
11      169     nuclear-transcribed mRNA catabolic process
GO:0016032      4.34289999368037e-12    15.5027374963007        1.43560999238807
15      451     viral reproduction
GO:0034623      5.19756755499635e-12    27.4604732690622        0.55387170438032
11      174     cellular macromolecular complex disassembly
GO:0006402      6.66341867427501e-12    26.7952095808383        0.566604387239637
11      178     mRNA catabolic process
GO:0032984      7.08381264271001e-12    26.633843537415 0.569787557954467       11
179     macromolecular complex disassembly
GO:0072594      2.9338328188775e-11     23.1431532198372        0.649366825825202
11      204     establishment of protein localization to organelle
GO:0006401      3.09323206622306e-11    23.0222385861561        0.652549996540032
11      205     RNA catabolic process
GO:0071845      1.00890170914966e-09    16.269178440607 0.904020483011556       11
284     cellular component disassembly at cellular level
GO:0022411      1.16935669744987e-09    16.0297060340382        0.916753165870874
11      288     cellular component disassembly
GO:0033365      1.94678745871024e-07    9.48503401360544        1.50563974811432
11      473     protein localization to organelle
GO:0006605      1.98851357911984e-07    9.46386917618019        1.50882291882915
11      474     protein targeting
Tissue: Nerve_Tibial=>Heart_Left_Ventricle      Type:   asymmetric
SourceGene:     NDP(ENSG00000124479.8)
TargetGeneSet:  LCE1B   SPRR1B  LOR     RASGRP3 ATP13A5-AS1     RP11    C8orf40
RPL35   TTC40   ALDH3B2 TRIM29  KRT2    KRT1    BRF1    KRT15   KRT14   CD300E  SBSN
NCOA3   MT
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0008544      5.18751359582003e-11    65.1153184165232        0.266763545775379
8       257     epidermis development
GO:0030216      2.98334499526174e-08    80.6011235955056        0.0975711023458584
5       94      keratinocyte differentiation
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GO:0009913      6.59063634319035e-08    68.2428571428571        0.114178949553664
5       110     epidermal cell differentiation
GO:0031424      8.21897370340797e-08    137.77990430622 0.0435955989204899      4
42      keratinization
GO:0030855      2.26069284363087e-07    34.2028985507246        0.292713307037575
6       282     epithelial cell differentiation
Tissue: Heart_Left_Ventricle=>Nerve_Tibial      Type:   asymmetric
SourceGene:     NLGN4Y(ENSG00000165246.7)
TargetGeneSet:  ZNF684  RPS8    ITGB3BP RP11    RPL5    TLR5    C2orf43 LTBP1   FEZ2
C2orf40 CXCR2P1 BCS1L   RPL14   CTNNB1  NME6    RPL29   CPOX    RPS3A   BRD9    ANKH
CTD     LYRM7   NDST1   RPL10A  LRRC1   MALSU1  SGCE    RP4     DYNLL1  RPS6
MICU1   OAT     TUT1    KLRD1   LETMD1  RPL18AP3        LINC00327       CARS2
OSTBETA RPS2    RPS15A  LYRM1   WDR81   ALOX15B MYO19   HAP1    TMEM101 CDK5RAP3
TMC6    RPL17   ZNF44   RLN3    LPAR2   ZC3H4   RPL18   RPL13A  RPS9    RPS5    ESF1
CXADR   TUBGCP6
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      1.10615651250552e-20    81.4090909090909        0.289668535049478
14      91      translational termination
GO:0006414      9.22812056959534e-20    68.8173076923077        0.334232925057089
14      105     translational elongation
GO:0006614      9.22812056959534e-20    68.8173076923077        0.334232925057089
14      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.06102922106085e-19    68.0645380434783        0.337416095771919
14      106     cotranslational protein targeting to membrane
GO:0045047      1.06102922106085e-19    68.0645380434783        0.337416095771919
14      106     protein targeting to ER
GO:0072599      1.06102922106085e-19    68.0645380434783        0.337416095771919
14      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      5.10763590601569e-19    60.1604567307692        0.375614144349872
14      118     protein localization to endoplasmic reticulum
GO:0000184      5.77660916999985e-19    59.5833333333333        0.378797315064701
14      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      1.80407109799649e-17    45.5638686131387        0.480658777939243
14      151     viral genome expression
GO:0019083      1.80407109799649e-17    45.5638686131387        0.480658777939243
14      151     viral transcription
GO:0006413      1.98295052106258e-17    45.2305253623188        0.483841948654072
14      152     translational initiation
GO:0006612      2.17812191695451e-17    44.9019784172662        0.487025119368902
14      153     protein targeting to membrane
GO:0043624      2.17812191695451e-17    44.9019784172662        0.487025119368902
14      153     cellular protein complex disassembly
GO:0043241      3.44944755146313e-17    43.3276909722222        0.502940972943049
14      158     protein complex disassembly
GO:0000956      8.99965785951009e-17    40.2217741935484        0.537955850806173
14      169     nuclear-transcribed mRNA catabolic process
GO:0034623      1.36163269298018e-16    38.951171875    0.55387170438032        14
174     cellular macromolecular complex disassembly
GO:0006402      1.87932361720925e-16    37.9904725609756        0.566604387239637
14      178     mRNA catabolic process
GO:0032984      2.03452495739994e-16    37.7575757575758        0.569787557954467
14      179     macromolecular complex disassembly
GO:0072594      1.28541013487958e-15    32.7319078947368        0.649366825825202
14      204     establishment of protein localization to organelle
GO:0006401      1.37674422062526e-15    32.5582460732984        0.652549996540032
14      205     RNA catabolic process
GO:0071845      5.1628724778575e-15     25.4275092936803        0.904020483011556
15      284     cellular component disassembly at cellular level
GO:0022411      6.34974776454939e-15    25.047855370436 0.916753165870874       15
288     cellular component disassembly
GO:0019058      7.30900396665305e-15    28.6048387096774        0.735312435125597
14      231     viral infectious cycle
GO:0022415      3.76975017475305e-14    25.1811483739837        0.82762438585565
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14      260     viral reproductive process
GO:0016032      6.55042999470477e-11    13.9839816933638        1.43560999238807
14      451     viral reproduction
GO:0033365      1.22949274315806e-10    13.2927559912854        1.50563974811432
14      473     protein localization to organelle
GO:0006605      1.26422343196093e-10    13.2629076086957        1.50882291882915
14      474     protein targeting
GO:0042273      6.50895150443359e-06    111.596899224806        0.0381980485779531
3       12      ribosomal large subunit biogenesis
Tissue: Heart_Left_Ventricle=>Nerve_Tibial      Type:   asymmetric
SourceGene:     RP1-64K7.4(ENSG00000229472.1)
TargetGeneSet:  C1QA    C1QC    C1QB    RUNX3   C1orf38 LAPTM5  BRD8    CD2
TBX15   LYSMD1  RP11    SLAMF6  CD84    CD48    RGS1    PTPRC   TLR5    PPM1B
IGKV2-28        DUSP2   ZAP70   RNF149  LAP3    CD28    TRAT1   HCLS1   FNDC3B
KLHL7   SH3TC1  DTHD1   DAPP1   BBS12   TLR2    IL7R    FYB     EMB     GZMK    GZMA
C5orf56 HAVCR2  RPS15AP18       STK38   FGD2    PRDM1   WASF1   MAN1A1  CTGF
CARD11  AOAH    IKZF1   TFEC    IRF5    TBXAS1  C8orf80 SLA     DOCK8   AQP7P4  FGD3
SLC31A2 AKNA    MRC1    PRF1    FIBIN   MS4A6A  MS4A4E  MS4A7   CCDC88B TBC1D10C
MYO7A   IL10RA  CD3E    LPAR5   CD4     CD163   CD69    SAT2    ARHGAP9 SELPLG
ALOX5AP GPR183  RNASE6  U6      RIN3    FMN1    PSTPIP1 SPN     RNF166  ARRB2
ACAP1   GUCY2D  TMEM106A        HMHA1   LINGO3  EBI3    STXBP2  RASAL3  IL12RB1 HCST
TGFB1   C5AR1   CD37    SIGLEC11        CD33    HCK     STK4    CASS4   ZNF831
RGS19   ITGB2   CECR1   NCF4    MKL1    WAS     IL2RG   BTK     TSC22D3 MTCP1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0050867      6.16703954911104e-13    12.9761737533092        1.66078472078057
17      240     positive regulation of cell activation
GO:0002696      5.04670518126635e-12    12.4064077243801        1.61234516642447
16      233     positive regulation of leukocyte activation
GO:0050778      5.41880613303461e-12    9.52277688316336        2.5188568265172 19
364     positive regulation of immune response
GO:0030098      9.28197829187571e-12    13.2231559290383        1.41166701266348
15      204     lymphocyte differentiation
GO:0002252      1.50708337585715e-11    8.93786793151008        2.67109542592208
19      386     immune effector process
GO:0050865      1.91997384763899e-11    9.47347091932458        2.3735381634489 18
343     regulation of cell activation
GO:0051251      1.97286924531344e-11    12.4861764705882        1.48778631236593
15      215     positive regulation of lymphocyte activation
GO:0002694      6.42392528192572e-11    9.46413284717819        2.22129956404401
17      321     regulation of leukocyte activation
GO:0051249      9.43043132679043e-11    10.0474406991261        1.95834198325375
16      283     regulation of lymphocyte activation
GO:0002697      9.96774978837845e-11    12.3303071757244        1.39090720365373
14      201     regulation of immune effector process
GO:0002253      2.1294807690829e-10     9.46861854282349        2.06906096463913
16      299     activation of immune response
GO:0002521      2.4671329272346e-10     9.36729936729937        2.08982077364888
16      302     leukocyte differentiation
GO:0002703      7.17720097508706e-10    19.3346883468835        0.636634142965885
10      92      regulation of leukocyte mediated immunity
GO:0030217      7.58713217794386e-10    13.4535984848485        1.07951006850737
12      156     T cell differentiation
GO:0046649      8.54058368578435e-10    7.37137819570967        2.99633243374161
18      433     lymphocyte activation
GO:0002449      1.66273990593222e-09    12.4891495601173        1.15562936820981
12      167     lymphocyte mediated immunity
GO:0002706      1.69853349330778e-09    22.078125       0.505155352570756       9
73      regulation of lymphocyte mediated immunity
GO:0002443      2.20446041873009e-09    10.6808893533031        1.46010656701958
13      211     leukocyte mediated immunity
GO:0046651      2.3307192597608e-09     12.0946022727273        1.19022904989274
12      172     lymphocyte proliferation
GO:0030097      2.47490834918128e-09    6.85963277610304        3.20393052383918
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18      463     hemopoiesis
GO:0032943      2.65963372781222e-09    11.9436026936027        1.20406892256591
12      174     mononuclear cell proliferation
GO:0050863      3.87037939776661e-09    10.1602011494253        1.52930593038544
13      221     regulation of T cell activation
GO:0050670      4.34613577562348e-09    13.2126383374166        0.996470832468341
11      144     regulation of lymphocyte proliferation
GO:0070661      4.43571420482504e-09    11.3751336898396        1.2594284132586 12
182     leukocyte proliferation
GO:0032944      4.67626092337837e-09    13.1131142042596        1.00339076880493
11      145     regulation of mononuclear cell proliferation
GO:0042110      4.83737255784548e-09    8.15421826625387        2.20745969137084
15      319     T cell activation
GO:0070663      6.68777336065435e-09    12.6369735672136        1.03799045048786
11      150     regulation of leukocyte proliferation
GO:0048534      7.05979434556716e-09    6.38472158306489        3.42536848660992
18      495     hemopoietic or lymphoid organ development
GO:0002757      8.1218685742489e-09     9.51004452728591        1.62618503909764
13      235     immune response-activating signal transduction
GO:0002250      1.14803998294445e-08    10.3848973607038        1.37014739464397
12      198     adaptive immune response
GO:0045058      1.14820459955949e-08    50.8262411347518        0.166078472078057
6       24      T cell selection
GO:0002764      1.54722792979759e-08    8.97569087796527        1.71614421147325
13      248     immune response-regulating signaling pathway
GO:0042102      1.63340291382369e-08    21.4287856071964        0.456715798214656
8       66      positive regulation of T cell proliferation
GO:0050671      1.99022653682482e-08    16.2152330428192        0.664313888312227
9       96      positive regulation of lymphocyte proliferation
GO:0032946      2.18132883609966e-08    16.0298451548452        0.671233824648813
9       97      positive regulation of mononuclear cell proliferation
GO:0050870      2.62938137882742e-08    10.9621488764045        1.18330911355616
11      171     positive regulation of T cell activation
GO:0002429      2.65982143388681e-08    12.8527551942186        0.920351532765899
10      133     immune response-activating cell surface receptor signaling pathway
GO:0070665      2.85428414469622e-08    15.498128245381 0.69199363365857        9
100     positive regulation of leukocyte proliferation
GO:0042129      3.11573362566166e-08    15.3285953177258        0.698913569995156
9       101     regulation of T cell proliferation
GO:0002460      4.72833113101083e-08    10.3100462656973        1.25250847692201
11      181     adaptive immune response based on somatic recombination of immune
receptors built from immunoglobulin superfamily domains
GO:0002768      5.68250300970559e-08    11.7885572139303        0.996470832468341
10      144     immune response-regulating cell surface receptor signaling pathway
GO:0045061      8.31079430657567e-08    62.890350877193 0.117638917721957       5
17      thymic T cell selection
GO:0006917      8.31237658421176e-08    6.48808049535604        2.73337485295135
15      395     induction of apoptosis
GO:0050871      8.33834134099843e-08    22.9073438572409        0.373676562175628
7       54      positive regulation of B cell activation
GO:0012502      9.17451499795423e-08    6.43587774535402        2.75413466196111
15      398     induction of programmed cell death
GO:0042113      1.00907522818003e-07    11.039627039627 1.05875025949761        10
153     B cell activation
GO:0042098      1.2109996796369e-07     12.9224720233895        0.816552487717113
9       118     T cell proliferation
GO:0042108      1.56154634860335e-07    20.6974772539289        0.408276243858556
7       59      positive regulation of cytokine biosynthetic process
GO:0050851      1.73242213071227e-07    12.3513591671486        0.851152169400042
9       123     antigen receptor-mediated signaling pathway
GO:0045619      4.03748991580462e-07    13.6263736263736        0.685073697321985
8       99      regulation of lymphocyte differentiation
GO:0050852      4.03748991580462e-07    13.6263736263736        0.685073697321985
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8       99      T cell receptor signaling pathway
GO:0045060      6.86340650750316e-07    85.3809523809524        0.0761192997024427
4       11      negative thymic T cell selection
GO:0001909      8.05595548383086e-07    22.2781525687597        0.325237007819528
6       47      leukocyte mediated cytotoxicity
GO:0050900      8.47628373614584e-07    7.58822667318026        1.66770465711715
11      241     leukocyte migration
GO:0043383      1.02404447386817e-06    74.703125       0.0830392360390284      4
12      negative T cell selection
GO:0002822      1.29170712742541e-06    14.7217557814111        0.553594906926856
7       80      regulation of adaptive immune response based on somatic
recombination of immune receptors built from immunoglobulin superfamily domains
GO:0050864      1.40594890246263e-06    14.5217959895379        0.560514843263442
7       81      regulation of B cell activation
GO:0002704      1.4713225342121e-06     66.3981481481482        0.0899591723756141
4       13      negative regulation of leukocyte mediated immunity
GO:0002707      1.4713225342121e-06     66.3981481481482        0.0899591723756141
4       13      negative regulation of lymphocyte mediated immunity
GO:0045086      1.4713225342121e-06     66.3981481481482        0.0899591723756141
4       13      positive regulation of interleukin-2 biosynthetic process
GO:0001910      1.78219897861988e-06    30.16   0.207598090097571       5       30
regulation of leukocyte mediated cytotoxicity
GO:0006959      1.99315232100243e-06    10.859649122807 0.844232233063456       8
122     humoral immune response
GO:0046641      2.04891780529454e-06    59.7541666666667        0.0968791087121998
4       14      positive regulation of alpha-beta T cell proliferation
GO:0046634      2.08004396836927e-06    18.6304819800261        0.380596498512214
6       55      regulation of alpha-beta T cell activation
GO:0002819      2.28410014652837e-06    13.4270161290323        0.602034461282956
7       87      regulation of adaptive immune response
GO:0042035      3.0933376075761e-06     12.7840501792115        0.629714206629299
7       91      regulation of cytokine biosynthetic process
GO:0001911      3.18327162209952e-06    221.89175257732 0.0345996816829285      3
5       negative regulation of leukocyte mediated cytotoxicity
GO:0033077      3.85292758948487e-06    16.5911025145068        0.422116116531728
6       61      T cell differentiation in thymus
GO:0045621      4.2420269848367e-06     16.2936930091185        0.429036052868314
6       62      positive regulation of lymphocyte differentiation
GO:0002699      4.42872181967054e-06    12.0616165277274        0.664313888312227
7       96      positive regulation of immune effector process
GO:0031341      4.5622148997105e-06     24.3123938879457        0.249117708117085
5       36      regulation of cell killing
GO:0042089      5.81529802683322e-06    11.5395999537519        0.69199363365857
7       100     cytokine biosynthetic process
GO:0046640      6.1315496243756e-06     42.6696428571429        0.124558854058543
4       18      regulation of alpha-beta T cell proliferation
GO:0043900      6.21326030865359e-06    11.4160375200183        0.698913569995156
7       101     regulation of multi-organism process
GO:0031342      6.33450389734255e-06    147.917525773196        0.0415196180195142
3       6       negative regulation of cell killing
GO:0042107      6.63361502968287e-06    11.2950764006791        0.705833506331742
7       102     cytokine metabolic process
GO:0001817      6.77334646325785e-06    5.50327482315955        2.48425714483427
12      359     regulation of cytokine production
GO:0045076      7.72543885785311e-06    39.8222222222222        0.131478790395128
4       19      regulation of interleukin-2 biosynthetic process
GO:0001906      7.95559633014956e-06    14.4761904761905        0.477475607224414
6       69      cell killing
GO:0046635      1.12109039081268e-05    19.8240997229917        0.297557262473185
5       43      positive regulation of alpha-beta T cell activation
GO:0042094      1.18028222758029e-05    35.1323529411765        0.1453186630683 4
21      interleukin-2 biosynthetic process
GO:0046633      1.18028222758029e-05    35.1323529411765        0.1453186630683 4
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21      alpha-beta T cell proliferation
GO:0051607      1.30398546158758e-05    10.1151349158044        0.781952806034184
7       113     defense response to virus
GO:0002831      1.39536464786824e-05    13.022188449848 0.525915161580513       6
76      regulation of response to biotic stimulus
GO:0002698      1.57045022338153e-05    18.3697047496791        0.318317071482942
5       46      negative regulation of immune effector process
GO:0050777      1.74781816011287e-05    17.9310776942356        0.325237007819528
5       47      negative regulation of immune response
GO:0001816      1.7671017577208e-05     4.97317825777356        2.73337485295135
12      395     cytokine production
Tissue: Heart_Left_Ventricle=>Nerve_Tibial      Type:   asymmetric
SourceGene:     RP11-598F7.6(ENSG00000256540.1)
TargetGeneSet:  DFFB    SNHG3   RPS8    RPL5    RTCD1   NBPF12  RPS27   LHX4
ANGEL2  TP53BP2 LTBP1   PRKD3   PMS1    RPE     CXCR2P1 STRA13  RPL29   ARHGAP31
IFT122  DNAJC19 RP11    CRYGS   EEF1A1P9        RPS3A   BRD9    ADAMTS16        CTD
SERINC5 NDST1   RPL15P3 RPS10   RPL10A  RP3     CREB5   CTB     FASTK   FDFT1
SULF1   COL14A1 SHARPIN DNAJB5  NR4A3   DPP7    SSNA1   FAM35B  ASAH2B  MICU1
RPS3AP5 MGEA5   OAT     FAM160A2        ZBED5   TUT1    ARF3    LETMD1  RPL18AP3
PPTC7   RPLP0   RPSAP54 PARP4-AS1       HNRNPA1L2       C14orf28        POLR2M
RASL12  NUBP2   RPS2    TNRC6A  ZNF23   RPL13   TMUB2   CDK5RAP3        EPX     HGS
RP13    MAPRE2  RPL17   ZNF44   LPAR2   RPSAP58 HAMP    HAUS5   U2AF1L4 PHLDB3
RPL18   RPL13A  NAPSA   ZNF761  RPS5    RPL41P1 RPL12P4 LINC00478       YDJC
FAM3C2
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      4.06302085636613e-18    49.0806174957118        0.42190851844163
14      91      translational termination
GO:0006414      3.32537700549594e-17    41.489114658926 0.486817521278804       14
105     translational elongation
GO:0006614      3.32537700549594e-17    41.489114658926 0.486817521278804       14
105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      3.81822569968961e-17    41.0352748154225        0.491453878624317
14      106     cotranslational protein targeting to membrane
GO:0045047      3.81822569968961e-17    41.0352748154225        0.491453878624317
14      106     protein targeting to ER
GO:0072599      3.81822569968961e-17    41.0352748154225        0.491453878624317
14      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      1.80813913102758e-16    36.2699564586357        0.547090166770466
14      118     protein localization to endoplasmic reticulum
GO:0000184      2.04216684217347e-16    35.9220125786164        0.551726524115978
14      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006612      2.52622870824264e-16    29.7784280936455        0.7093626738634 15
153     protein targeting to membrane
GO:0043241      4.11738341002713e-16    28.727138246369 0.732544460590963       15
158     protein complex disassembly
GO:0032984      2.70651444135387e-15    25.0117260787992        0.829907964846723
15      179     macromolecular complex disassembly
GO:0019080      6.10466740217526e-15    27.4697700041317        0.700089959172376
14      151     viral genome expression
GO:0019083      6.10466740217526e-15    27.4697700041317        0.700089959172376
14      151     viral transcription
GO:0006413      6.70078678434336e-15    27.2687995624829        0.704726316517888
14      152     translational initiation
GO:0043624      7.35024214253945e-15    27.0707207818651        0.7093626738634 14
153     cellular protein complex disassembly
GO:0022411      1.06073992363403e-14    17.7063468634686        1.33527091550758
17      288     cellular component disassembly
GO:0072594      1.90503835490424e-14    21.6651404151404        0.945816898484534
15      204     establishment of protein localization to organelle
GO:0000956      2.97119394913301e-14    24.2490566037736        0.783544391391599
14      169     nuclear-transcribed mRNA catabolic process
GO:0034623      4.46468179576022e-14    23.4830188679245        0.806726178119161
14      174     cellular macromolecular complex disassembly
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GO:0006402      6.12847100379525e-14    22.9038196042338        0.825271607501211
14      178     mRNA catabolic process
GO:0071845      1.48462342162118e-13    16.5244366403278        1.31672548612553
16      284     cellular component disassembly at cellular level
GO:0006401      4.32642861684128e-13    19.6287661760348        0.950453255830046
14      205     RNA catabolic process
GO:0019058      2.21635904397534e-12    17.2452830188679        1.07099854681337
14      231     viral infectious cycle
GO:0022415      1.09848634987544e-11    15.1811627550238        1.20545290983323
14      260     viral reproductive process
GO:0006605      3.36150423800675e-10    9.53917287438993        2.19763338177289
16      474     protein targeting
GO:0033365      3.07755665728302e-09    8.77099428955324        2.19299702442738
15      473     protein localization to organelle
GO:0016032      1.46677606973516e-08    8.43046500582876        2.0909971628261 14
451     viral reproduction
Tissue: Nerve_Tibial=>Heart_Left_Ventricle      Type:   asymmetric
SourceGene:     U2AF1L4(ENSG00000161265.6)
TargetGeneSet:  MRPL20  UBR4    USP24   WARS2   RPS7    UBC     TXNDC9  SEC13
HIGD1A  RPL24   FAM162A BCL6    HMGB2   RP11    ROPN1L  SUB1    TBCA    APC
HINT1   NDFIP1  IP6K3   RPL10A  MRPL32  HMGN3   C6orf225        RP1     SEC61G
DNAJB9  RPS20   RPL30   C9orf131        PHF2    RC3H2   ASB6    POLR3A  RPL13AP5
PRDM11  CELF1   C11orf10        AHNAK   MTA2    OTUB1   IGSF9B  RPL18AP3
C12orf45        ARPC3   RPL6    MED13L  MED4    DAD1    SCFD1   CDC42BPB
RPS3AP6 RPL4    SEC11A  RPS15A  CYB5B   RPS7P1  KIAA0100        COPZ2   RPL17
RPL18A  COPE    COX6B1  PAK4    AP2S1   ATP5E   MRPL40  TCF20   PRDX4   UXT
MORF4L2 MCTS1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006614      3.60079167193237e-16    42.0910326086956        0.443221922358314
13      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      4.09140166898113e-16    41.6355286738351        0.447443083523632
13      106     cotranslational protein targeting to membrane
GO:0045047      4.09140166898113e-16    41.6355286738351        0.447443083523632
13      106     protein targeting to ER
GO:0072599      4.09140166898113e-16    41.6355286738351        0.447443083523632
13      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      1.72313424537865e-15    36.8462301587302        0.498097017507439
13      118     protein localization to endoplasmic reticulum
GO:0006612      5.31689166446401e-14    27.5669642857143        0.645837658293544
13      153     protein targeting to membrane
GO:0006415      1.07069485258902e-13    39.3525 0.384125666043872       11      91
translational termination
GO:0006414      5.39047585870216e-13    33.4587234042553        0.443221922358314
11      105     translational elongation
GO:0043624      1.43091558368718e-12    24.748588797221 0.645837658293544       12
153     cellular protein complex disassembly
GO:0043241      2.10175972426795e-12    23.8926474699469        0.66694346412013
12      158     protein complex disassembly
GO:0000184      2.18133588763371e-12    29.092962962963 0.502318178672756       11
119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0072594      2.18258509004625e-12    20.133835078534 0.861116877724725       13
204     establishment of protein localization to organelle
GO:0034623      6.61961889197239e-12    21.5086923658352        0.734482042765207
12      174     cellular macromolecular complex disassembly
GO:0032984      9.2560710604677e-12     20.8573872662838        0.755587848591793
12      179     macromolecular complex disassembly
GO:0019080      2.99890731462083e-11    22.3928571428571        0.637395335962909
11      151     viral genome expression
GO:0019083      2.99890731462083e-11    22.3928571428571        0.637395335962909
11      151     viral transcription
GO:0006413      3.2225444616925e-11     22.2324822695035        0.641616497128226
11      152     translational initiation
GO:0000956      1.01763794507333e-10    19.8167088607595        0.71337623693862
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11      169     nuclear-transcribed mRNA catabolic process
GO:0071845      1.40210960078767e-10    14.1103167281673        1.19880977095011
13      284     cellular component disassembly at cellular level
GO:0022411      1.66728785202561e-10    13.9011363636364        1.21569441561138
13      288     cellular component disassembly
GO:0006402      1.77991700667082e-10    18.7368862275449        0.751366687426476
11      178     mRNA catabolic process
GO:0006401      8.0514033024519e-10     16.0985567010309        0.865338038890042
11      205     RNA catabolic process
GO:0019058      2.84226767064228e-09    14.17   0.975088229188292       11      231
viral infectious cycle
GO:0033365      7.35475100774916e-09    9.04065266768646        1.99660923119507
14      473     protein localization to organelle
GO:0006605      7.5550260948262e-09     9.02035152636448        2.00083039236039
14      474     protein targeting
GO:0022415      9.77451514386162e-09    12.4940562248996        1.09750190298249
11      260     viral reproductive process
GO:0016032      3.20819743699977e-07    7.78262284412626        1.90374368555809
12      451     viral reproduction
Tissue: Nerve_Tibial=>Heart_Left_Ventricle      Type:   asymmetric
SourceGene:     U6(ENSG00000206712.1)
TargetGeneSet:  MRPL20  CAMTA1  SZT2    CMPK1   RP4     BRP44   RPS7    UBC
BOLA3   UBE2E3  HIGD1A  CHMP2B  NDUFB4  RP11    RPL35A  RPL34   NDUFC1  NDUFS6
NDUFAF2 GEMIN5  RN5S201 HCP5    C4B     ABCC10  RAB23   HMGN3   MMS22L  MRPS12
ZC2HC1B CYCS    MRPS24  INTS4L2 BRI3    RPS20   EEF1D   RPL8    NDUFB6  RPL35
RPL27A  MYBPC3  FAU     NDUFS8  RPL18AP3        MRP63   ABCD4   NPC2    GTF2A2
RPLP1   CTD     IFT140  CTA     CLN3    MINK1   FAM106A ANAPC11 RAB12   GPX4
RPS15   MAP2K2  RPL36   GLTSCR2 SEPW1   RPL18   DGCR6L  ARFGAP3 PNPLA4  SYAP1
DYNLT3  MED12
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      3.63490671144248e-18    50.006993006993 0.421424122898069       14
105     translational elongation
GO:0006415      2.51969853306545e-17    53.0185185185185        0.365234239844993
13      91      translational termination
GO:0006614      1.76159372811462e-16    44.9065217391304        0.421424122898069
13      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      2.00200048842737e-16    44.4205495818399        0.425437685973289
13      106     cotranslational protein targeting to membrane
GO:0045047      2.00200048842737e-16    44.4205495818399        0.425437685973289
13      106     protein targeting to ER
GO:0072599      2.00200048842737e-16    44.4205495818399        0.425437685973289
13      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      8.4512898968713e-16     39.3108994708995        0.473600442875926
13      118     protein localization to endoplasmic reticulum
GO:0000184      9.46016673155329e-16    38.9373165618449        0.477614005951145
13      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      2.20982379957687e-14    29.841384863124 0.606048024358176       13
151     viral genome expression
GO:0019083      2.20982379957687e-14    29.841384863124 0.606048024358176       13
151     viral transcription
GO:0006413      2.40945640094878e-14    29.624620303757 0.610061587433396       13
152     translational initiation
GO:0006612      2.62551825901736e-14    29.4109523809524        0.614075150508615
13      153     protein targeting to membrane
GO:0043624      2.62551825901736e-14    29.4109523809524        0.614075150508615
13      153     cellular protein complex disassembly
GO:0043241      3.99794444238319e-14    28.3868199233716        0.634142965884714
13      158     protein complex disassembly
GO:0000956      9.60689568646353e-14    26.3648148148148        0.678292159712131
13      169     nuclear-transcribed mRNA catabolic process
GO:0034623      1.40252027061988e-13    25.5370600414079        0.698359975088229
13      174     cellular macromolecular complex disassembly
GO:0006402      1.88255282837985e-13    24.9109764309764        0.714414227389108
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13      178     mRNA catabolic process
GO:0032984      2.0240585564025e-13     24.7591700133869        0.718427790464328
13      179     macromolecular complex disassembly
GO:0072594      1.0885229075839e-12     21.4806282722513        0.81876686734482
13      204     establishment of protein localization to organelle
GO:0006401      1.15882951268592e-12    21.3672453703704        0.82278043042004
13      205     RNA catabolic process
GO:0071845      4.35509721910966e-12    16.643265993266 1.1398519133624 14      284
cellular component disassembly at cellular level
GO:0022411      5.26033126274226e-12    16.3956536164565        1.15590616566328
14      288     cellular component disassembly
GO:0019058      5.30225772852097e-12    18.7844036697248        0.927133070375753
13      231     viral infectious cycle
GO:0022415      2.35598091127924e-11    16.5450292397661        1.04352639955712
13      260     viral reproductive process
GO:0016032      1.96566610969025e-09    10.1614312460994        1.81011694692409
14      451     viral reproduction
GO:0033365      3.45228616168807e-08    8.75019323671498        1.89841533457892
13      473     protein localization to organelle
GO:0006605      3.53913412529147e-08    8.73058568329718        1.90242889765414
13      474     protein targeting
GO:0006120      2.993531095236e-07      43.7066342057212        0.144488270707909
5       36      mitochondrial electron transport, NADH to ubiquinone
GO:0042773      1.17773404871539e-06    32.2349505840072        0.188637464535326
5       47      ATP synthesis coupled electron transport
GO:0042775      1.17773404871539e-06    32.2349505840072        0.188637464535326
5       47      mitochondrial ATP synthesis coupled electron transport
GO:0022904      2.24867507836758e-06    18.3371794871795        0.385302055221092
6       96      respiratory electron transport chain
GO:0006119      3.40171389065233e-06    25.5250978996084        0.232786658362743
5       58      oxidative phosphorylation
GO:0022900      1.54832871168784e-05    12.8590745192308        0.537817452079441
6       134     electron transport chain
Tissue: Nerve_Tibial=>Heart_Left_Ventricle      Type:   asymmetric
SourceGene:     ZNF681(ENSG00000196172.8)
TargetGeneSet:  KLHL17  ZBTB48  HNRNPR  RPL11   RP4     RP1     CCDC23  TAL1    JUN
COG2    TFB2M   PFN4    EMILIN1 LBX2    COX5B   RPL31   RPL37A  GMPPA   GORASP1 RP11
KBTBD5  SCAP    TNNC1   OSBPL11 ACPL2   EIF2B5  MB21D2  RPL35A  ATP5I   ALPK1
BBS12   NDUFS6  RPL37   ANKRD32 PGGT1B  BRD8    RPS14   TMEM14B CCND3   UBR2
RPL39P3 MICAL1  MRPS12  TCF21   FNDC1   AGPAT4  SGCE    CLDN15  ATP6V1F TNPO3   PTN
C8orf59 RPL30   COX6C   AZIN1   EEF1D   RPL8    LINC00475       CDK5RAP2
ITIH2   RPLP2   TAF10   RPL27A  CTD     VEGFB   MEN1    FAU     ALDH3B2 C11orf65
RPS25   PKNOX2  C12orf23        RPS2P5  ADPRHL1 AP1G2   RPS29   ZFYVE26 SLIRP
NDUFB1  PPP1R13B        FAN1    ATPBD4  PLDN    RPS3AP6 RPLP1   RBL2    CDK10
RPL23A  LRRC37B RPL19   RPL27   NMT1    TRIM37  RPL38   ALYREF  CABYR   TRAPPC8
RPS15   RPL36   DNM2    JUND    ATP13A1 USF2    POLR2I  COX7A1  TMEM91  GLTSCR2
KCNJ14  ZNF137P SAMHD1  NCOA3   NRIP1   CHCHD10 PNPLA4  GAGE10  COX7B   KIAA1210
MTM1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      1.51549713154803e-25    45.7307692307692        0.719327382188084
21      105     translational elongation
GO:0006415      3.01870293711272e-25    50.9217329292209        0.623417064563006
20      91      translational termination
GO:0019080      4.77951986072147e-25    33.6299342105263        1.0344612829562 23
151     viral genome expression
GO:0019083      4.77951986072147e-25    33.6299342105263        1.0344612829562 23
151     viral transcription
GO:0006614      6.77286508437162e-24    42.4929262844378        0.719327382188084
20      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      8.30422633248145e-24    41.9958787165146        0.726178119161304
20      106     cotranslational protein targeting to membrane
GO:0045047      8.30422633248145e-24    41.9958787165146        0.726178119161304
20      106     protein targeting to ER
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GO:0072599      8.30422633248145e-24    41.9958787165146        0.726178119161304
20      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      8.18896918089433e-23    36.822526478946 0.808386962839942       20
118     protein localization to endoplasmic reticulum
GO:0000184      9.79171447939428e-23    36.4480245492904        0.815237699813162
20      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006413      5.62966617062338e-22    29.2269524368761        1.04131201992942
21      152     translational initiation
GO:0043624      6.49138132258503e-22    29.0034965034965        1.04816275690264
21      153     cellular protein complex disassembly
GO:0043241      1.30317942730842e-21    27.935148792813 1.08241644176874        21
158     protein complex disassembly
GO:0022415      8.33452138219346e-21    19.1403389830508        1.78119161303716
24      260     viral reproductive process
GO:0034623      1.03851872134011e-20    24.9856711915535        1.19202823334025
21      174     cellular macromolecular complex disassembly
GO:0019058      1.05514302782179e-20    20.5789473684211        1.58252024081378
23      231     viral infectious cycle
GO:0006612      1.84924729330284e-20    27.0657656800228        1.04816275690264
20      153     protein targeting to membrane
GO:0032984      1.90259994217449e-20    24.1864654333009        1.22628191820635
21      179     macromolecular complex disassembly
GO:0000956      1.41224709153608e-19    24.1321892787359        1.15777454847415
20      169     nuclear-transcribed mRNA catabolic process
GO:0006402      4.04282799305268e-19    22.7431501361961        1.21943118123313
20      178     mRNA catabolic process
GO:0072594      6.23418712364457e-18    19.493670886076 1.39755034253685        20
204     establishment of protein localization to organelle
GO:0006401      6.87177814556804e-18    19.3869312350325        1.40440107951007
20      205     RNA catabolic process
GO:0016032      2.20165744349223e-17    11.6712973408541        3.08968237492215
26      451     viral reproduction
GO:0071845      2.82792175904935e-16    14.4227844398947        1.94560930039444
21      284     cellular component disassembly at cellular level
GO:0022411      3.75483763168943e-16    14.2026793431288        1.97301224828732
21      288     cellular component disassembly
GO:0033365      7.29247973035502e-13    8.80646183085207        3.24039858833299
22      473     protein localization to organelle
GO:0006605      7.60738743476219e-13    8.78634639696587        3.24724932530621
22      474     protein targeting
Tissue: Skin_Sun_Exposed_Lower_leg=>Heart_Left_Ventricle        Type:   asymmetric
SourceGene:     7SK(ENSG00000201600.1)
TargetGeneSet:  WASH7P  ATPAF1  SCP2    ACADM   GCLM    ACTG1P4 ATP5F1  KDM5B   RP11
TOMM20  FH      CNST    MDH1    C1D     NFU1    SUCLG1  SNRNP200        ATP5G3  PASK
VPRBP   CHMP2B  NDUFB4  RNF7    PIK3CA  HTT     ISOC1   SKP1    TMEM14C TMEM14B AIG1
BRP44L  GBAS    JHDM1D  AGK     C7orf34 VDAC3   MSC     ATAD2   FAM49B  NDUFB6
FAM108B1        HSDL2   NUP214  PHYH    RAB18   NDUFB8  PRDM11  TMEM126B        PTS
SLC25A3 C12orf23        ARL6IP4 FKBP3   PLEKHH1 ZFYVE26 PPP1R13B        DUT
COX5A   ETFA    UQCRC2  RNF40   RBL2    ANKFY1  TNRC6C  CTD     NDUFV2  VAPA
CDH20   NDUFS7  NDUFA13 UQCRFS1 RPL13A  CRLS1   C20orf94        TTLL9   ZHX3
TNRC6B  TCF20   FAM19A5 CDK16
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0045333      2.04011661884743e-15    29.9876802884615        0.648536433464812
14      142     cellular respiration
GO:0022904      4.90972084106769e-13    33.6470588235294        0.43844716628607
11      96      respiratory electron transport chain
GO:0006091      5.02898241236289e-12    11.7959183673469        1.95474361635873
17      428     generation of precursor metabolites and energy
GO:0015980      5.82989536677808e-12    14.1952054794521        1.402117500519  15
307     energy derivation by oxidation of organic compounds
GO:0022900      2.00256500788561e-11    23.190243902439 0.61199916960764        11
134     electron transport chain
GO:0006119      7.48133722625455e-09    33.345962113659 0.264895162964501       7
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58      oxidative phosphorylation
GO:0006120      5.75552198565753e-07    37.95346377578  0.164417687357276       5
36      mitochondrial electron transport, NADH to ubiquinone
GO:0042773      2.25292599187876e-06    27.9918032786885        0.214656425160889
5       47      ATP synthesis coupled electron transport
GO:0042775      2.25292599187876e-06    27.9918032786885        0.214656425160889
5       47      mitochondrial ATP synthesis coupled electron transport
Tissue: Skin_Sun_Exposed_Lower_leg=>Heart_Left_Ventricle        Type:   cluster
SourceGene:     7SK(ENSG00000201600.1)
TargetGeneSet:  WASH7P  ATPAF1  SCP2    ACADM   GCLM    ACTG1P4 ATP5F1  KDM5B   RP11
TOMM20  FH      CNST    MDH1    C1D     NFU1    SUCLG1  SNRNP200        ATP5G3  PASK
VPRBP   CHMP2B  NDUFB4  RNF7    PIK3CA  HTT     ISOC1   SKP1    TMEM14C TMEM14B AIG1
BRP44L  GBAS    JHDM1D  AGK     C7orf34 VDAC3   MSC     ATAD2   FAM49B  NDUFB6
FAM108B1        HSDL2   NUP214  PHYH    RAB18   NDUFB8  PRDM11  TMEM126B        PTS
SLC25A3 C12orf23        ARL6IP4 FKBP3   PLEKHH1 ZFYVE26 PPP1R13B        DUT
COX5A   ETFA    UQCRC2  RNF40   RBL2    ANKFY1  TNRC6C  CTD     NDUFV2  VAPA
CDH20   NDUFS7  NDUFA13 UQCRFS1 RPL13A  CRLS1   C20orf94        TTLL9   ZHX3
TNRC6B  TCF20   FAM19A5 CDK16
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0045333      2.04011661884743e-15    29.9876802884615        0.648536433464812
14      142     cellular respiration
GO:0022904      4.90972084106769e-13    33.6470588235294        0.43844716628607
11      96      respiratory electron transport chain
GO:0006091      5.02898241236289e-12    11.7959183673469        1.95474361635873
17      428     generation of precursor metabolites and energy
GO:0015980      5.82989536677808e-12    14.1952054794521        1.402117500519  15
307     energy derivation by oxidation of organic compounds
GO:0022900      2.00256500788561e-11    23.190243902439 0.61199916960764        11
134     electron transport chain
GO:0006119      7.48133722625455e-09    33.345962113659 0.264895162964501       7
58      oxidative phosphorylation
GO:0006120      5.75552198565753e-07    37.95346377578  0.164417687357276       5
36      mitochondrial electron transport, NADH to ubiquinone
GO:0042773      2.25292599187876e-06    27.9918032786885        0.214656425160889
5       47      ATP synthesis coupled electron transport
GO:0042775      2.25292599187876e-06    27.9918032786885        0.214656425160889
5       47      mitochondrial ATP synthesis coupled electron transport
Tissue: Heart_Left_Ventricle=>Skin_Sun_Exposed_Lower_leg        Type:   asymmetric
SourceGene:     C1DP1(ENSG00000231245.2)
TargetGeneSet:  RPL11   RPS8    RP11    RPL5    MAEL    FAM89A  RPS7    UBC
RPL31   GLS     EEF1B2  C3orf19 RPL24   CSTA    CNBP    RPL34   RPL37   RIOK2
RPL26L1 CDC40   BUD31   NSMCE2  ZDHHC21 RPS6    ZNF658  C9orf78 ADK     RPS24
CCDC90B RPS25   SETD8   SFSWAP  ARF4P4  EAPP    COX16   RPS27L  LRRK1   MAP1LC3B
RPS4XP17        LINC00324       RPL26   TMEM11  RPL19   SMARCE1 BECN1   RPL27
RPS7P11 CEP112  ICT1    NFKBIB  MED29   ZNF230  PIH1D1  ZNF350  SNRPB2  ZNRF3
PHF5A
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      1.87027438692148e-26    109.734234234234        0.295965677115771
17      91      translational termination
GO:0006414      2.5951120880528e-25     92.1863636363636        0.341498858210504
17      105     translational elongation
GO:0006614      2.29167751868088e-23    83.0155853570134        0.341498858210504
16      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      2.69360292890147e-23    82.0874551971326        0.3447512282887 16
106     cotranslational protein targeting to membrane
GO:0045047      2.69360292890147e-23    82.0874551971326        0.3447512282887 16
106     protein targeting to ER
GO:0072599      2.69360292890147e-23    82.0874551971326        0.3447512282887 16
106     establishment of protein localization to endoplasmic reticulum
GO:0034623      3.89985821497553e-23    56.6896551724138        0.565912393605979
18      174     cellular macromolecular complex disassembly
GO:0032984      6.60341824934804e-23    54.9098307988863        0.582174243996955
18      179     macromolecular complex disassembly
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GO:0070972      1.66002805142341e-22    72.3693864642631        0.383779669227043
16      118     protein localization to endoplasmic reticulum
GO:0000184      1.91399679581293e-22    71.6617601002192        0.387032039305238
16      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0043624      2.21961866314831e-22    59.45   0.497612621963878       17      153
cellular protein complex disassembly
GO:0043241      3.91334845523995e-22    57.3217494089835        0.513874472354854
17      158     protein complex disassembly
GO:0019080      1.02145400016613e-20    54.5529271206691        0.491107881807487
16      151     viral genome expression
GO:0019083      1.02145400016613e-20    54.5529271206691        0.491107881807487
16      151     viral transcription
GO:0006413      1.13929928685966e-20    54.1480075901328        0.494360251885683
16      152     translational initiation
GO:0006612      1.26976388250673e-20    53.748999293619 0.497612621963878       16
153     protein targeting to membrane
GO:0000956      6.53363370348099e-20    48.0742146320894        0.549650543215002
16      169     nuclear-transcribed mRNA catabolic process
GO:0006402      1.52860245164895e-19    45.3747510951812        0.57892187391876
16      178     mRNA catabolic process
GO:0071845      3.05587798645251e-19    32.9898885143894        0.92367310220746
18      284     cellular component disassembly at cellular level
GO:0022411      3.93092665671937e-19    32.4919540229885        0.936682582520241
18      288     cellular component disassembly
GO:0072594      1.40621880723957e-18    39.0281400137268        0.663483495951837
16      204     establishment of protein localization to organelle
GO:0006401      1.52214678734768e-18    38.8189110769756        0.666735866030033
16      205     RNA catabolic process
GO:0019058      1.04501178139908e-17    34.0621155288822        0.75129748806311
16      231     viral infectious cycle
GO:0022415      6.93995669532707e-17    29.9524061343205        0.845616220330773
16      260     viral reproductive process
GO:0033365      4.73789041113529e-14    17.3330409356725        1.53837104698637
17      473     protein localization to organelle
GO:0006605      4.90422245348897e-14    17.2938730853392        1.54162341706456
17      474     protein targeting
GO:0016032      3.84640051771802e-13    16.5742677048572        1.46681890526607
16      451     viral reproduction
GO:0022613      1.08689794804515e-10    20.2609034267913        0.731783267593938
11      225     ribonucleoprotein complex biogenesis
GO:0071843      2.07450223779525e-10    18.9980506822612        0.777316448688672
11      239     cellular component biogenesis at cellular level
GO:0042274      2.42652791495935e-09    131.785714285714        0.0585426614075151
5       18      ribosomal small subunit biogenesis
GO:0042254      2.36707126530468e-08    20.7499545371886        0.484603141651097
8       149     ribosome biogenesis
GO:0006364      4.0483575735676e-08     25.8115979381443        0.338246488132309
7       104     rRNA processing
GO:0016072      5.97647474353613e-08    24.2978155339806        0.357760708601481
7       110     rRNA metabolic process
GO:0034660      3.34660909614529e-06    10.4615384615385        0.926925472285655
8       285     ncRNA metabolic process
GO:0034470      3.44565047883556e-06    12.885621761658 0.650474015639056       7
200     ncRNA processing
GO:0042273      6.94949201671952e-06    109.05303030303 0.0390284409383434      3
12      ribosomal large subunit biogenesis
GO:0022618      1.36149834757131e-05    18.9338624338624        0.308975157428552
5       95      ribonucleoprotein complex assembly
GO:0071826      1.74781816011287e-05    17.9310776942356        0.325237007819528
5       100     ribonucleoprotein complex subunit organization
Tissue: Heart_Left_Ventricle=>Skin_Sun_Exposed_Lower_leg        Type:   asymmetric
SourceGene:     ENSG00000214754.3
TargetGeneSet:  RP4     KCNAB2  CDCA8   IQGAP3  NCAPH   CKAP2L  SPC25   POC1A
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NCAPG   RP11    NUDT6   NEIL3   CCNB1   NR2F2   CDC25C  HMMR    USP49   PMS2P9
IMMP2L-IT1      BAAT    ZWINT   KIF11   MKI67   MPP2    E2F7    DLGAP5  PAPOLA
BUB1B   C15orf42        PRC1    PKMYT1  SNX29P2 FAM64A  SPAG5   TOP2A   KIF18B
PALM3   UBE2C   CA5BP1  HTATSF1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0000280      5.86836681853956e-15    32.599537037037 0.775032869697599       14
350     nuclear division
GO:0007067      5.86836681853956e-15    32.599537037037 0.775032869697599       14
350     mitosis
GO:0000087      8.66675876103026e-15    31.6348747591522        0.797176665974673
14      360     M phase of mitotic cell cycle
GO:0048285      1.2656791333764e-14     30.7244069912609        0.819320462251747
14      370     organelle fission
GO:0051301      1.98055752977858e-13    24.8267376966007        1.00089959172376
14      452     cell division
GO:0007051      5.82160862710856e-12    66.4212962962963        0.177150370216594
8       80      spindle organization
GO:0000819      1.61299677968602e-11    89.4382222222222        0.115147740640786
7       52      sister chromatid segregation
GO:0007059      5.48522525331172e-10    36.0782828282828        0.310013147879039
8       140     chromosome segregation
GO:0000070      9.38407128529748e-10    77.1520572450805        0.108504601757664
6       49      mitotic sister chromatid segregation
GO:0007017      7.46425377494542e-09    16.6579634464752        0.870251193689018
10      393     microtubule-based process
GO:0010564      1.22667010602256e-08    15.7684518451845        0.916753165870874
10      414     regulation of cell cycle process
GO:0007346      1.2775245293167e-08     18.7999112688554        0.67095702719535
9       303     regulation of mitotic cell cycle
GO:0071156      8.02928498929883e-08    18.44140625     0.58459622171476        8
264     regulation of cell cycle arrest
GO:0000226      9.27877212936575e-08    18.0817369093231        0.595668119853297
8       269     microtubule cytoskeleton organization
GO:0030261      5.21110494056672e-07    79.0824175824176        0.0664313888312228
4       30      chromosome condensation
GO:0007093      5.24238690105645e-07    24.7877385772123        0.307798768251332
6       139     mitotic cell cycle checkpoint
GO:0000086      6.45536442742863e-07    23.88127090301  0.318870666389869       6
144     G2/M transition of mitotic cell cycle
GO:0007052      7.74487414122206e-07    70.8866995073892        0.073074527714345
4       33      mitotic spindle organization
GO:0000075      7.97570394176808e-07    16.900085106383 0.535879869905197       7
242     cell cycle checkpoint
GO:0007050      1.030563893515e-06      12.9806094182825        0.81710608262404
8       369     cell cycle arrest
GO:0000236      1.11098295158155e-06    33.1921296296296        0.188222268355131
5       85      mitotic prometaphase
GO:0007088      1.32068018549993e-06    31.9857206604195        0.194865407238253
5       88      regulation of mitosis
GO:0051783      1.32068018549993e-06    31.9857206604195        0.194865407238253
5       88      regulation of nuclear division
GO:0045786      3.64344177840547e-06    10.8702408702409        0.967683897308145
8       437     negative regulation of cell cycle
GO:0048015      7.75901084799842e-06    21.8824609733701        0.279011833091136
5       126     phosphatidylinositol-mediated signaling
GO:0048017      7.75901084799842e-06    21.8824609733701        0.279011833091136
5       126     inositol lipid-mediated signaling
GO:0051329      1.54238193478613e-05    10.5730107526882        0.839249878901114
7       379     interphase of mitotic cell cycle
GO:0051325      1.76546950891511e-05    10.3445263157895        0.856964915922773
7       387     interphase
Tissue: Skin_Sun_Exposed_Lower_leg=>Heart_Left_Ventricle        Type:   cluster
SourceGene:     ENSG00000214897.3
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TargetGeneSet: SLC35E2 CAPZB ASAP3 GNAI3 RP11 PMF1 PTRHD1 FAM161A RABL2A MYL3 RHOA MAP3K13 FGF12 NOP14 FAM184B SLAIN2 ENPEP NDUFC1 CTD ISOC1 PCDHB9 DHX16 IBTK UBE2J1 TRIM73 ANKIB1 ECD ATP5J2 UQCRB COX6C NOL8 CAMSAP1 DLG5 EIF5AL1 RPL13AP5 NDUFB8 RPLP2 C11orf10 PRDX5 FAU EFEMP2 RPS25 AVIL C12orf51 TESC ARL6IP4 RFC3 DHRS12 PSME2 LGALS3 NDUFB1 SRP14 ZFP106 POLR2M PSMA4 NDUFB10 HCFC1R1 TMEM219 RANBP10 CLEC18B PSMB6 KIAA0753 LRRC48 RPL27 EFTUD2 RPL38 C17orf89 SIRT7 IER3IP1 PIN1 GADD45GIP1 C19orf53 TPM4 COMP ZNF461 SEPW1 KCNJ14 RPS11 NDUFA3 ZNF471 RPS21 URB1 PI4KA NDUFB11 HUWE1 TAF1 UPRT COX7B CXorf57 NUP62CL NDUFA1

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0022904	1.33732100616129e-12	30.3247830279653	0.478305999584804	11	96	respiratory electron transport chain
GO:0022900	5.37588670989758e-11	20.9004398240704	0.667635457753789	11	134	electron transport chain
GO:0045333	1.01044201491657e-10	19.613064697785	0.707494291052522	11	142	cellular respiration
GO:0006414	2.31969129398839e-09	21.2544642857143	0.523147187045879	9	105	translational elongation
GO:0042773	3.03436326636512e-09	38.605	0.23417064563006	7	47	ATP synthesis coupled electron transport
GO:0042775	3.03436326636512e-09	38.605	0.23417064563006	7	47	mitochondrial ATP synthesis coupled electron transport
GO:0043624	4.02512454765841e-09	16.056846379427	0.762300186838281	10	153	cellular protein complex disassembly
GO:0043241	5.49696234036314e-09	15.5089363557105	0.78721195764999	10	158	protein complex disassembly
GO:0006119	1.38907487019764e-08	30.2552036199095	0.288976541415819	7	58	oxidative phosphorylation
GO:0034623	1.39179631874333e-08	13.9801337529504	0.866929624247457	10	174	cellular macromolecular complex disassembly
GO:0006415	1.55689248791091e-08	21.5301204819277	0.453394228773095	8	91	translational termination
GO:0032984	1.82530494398229e-08	13.561748425272	0.891841395059165	10	179	macromolecular complex disassembly
GO:0006120	2.14101005549352e-08	43.4818181818182	0.179364749844301	6	36	mitochondrial electron transport, NADH to ubiquinone
GO:0006614	4.83291413978044e-08	18.4046391752577	0.523147187045879	8	105	SRP-dependent cotranslational protein targeting to membrane
GO:0006613	5.20682592711374e-08	18.2155612244898	0.528129541208221	8	106	cotranslational protein targeting to membrane
GO:0045047	5.20682592711374e-08	18.2155612244898	0.528129541208221	8	106	protein targeting to ER
GO:0072599	5.20682592711374e-08	18.2155612244898	0.528129541208221	8	106	establishment of protein localization to endoplasmic reticulum
GO:0006612	6.3634435923876e-08	14.1220238095238	0.762300186838281	9	153	protein targeting to membrane
GO:0070972	1.20450250923153e-07	16.2147727272727	0.587917791156321	8	118	protein localization to endoplasmic reticulum
GO:0015980	3.17379971457975e-07	8.57958573327426	1.5295827278389	11	307	energy derivation by oxidation of organic compounds
GO:0071845	1.34311920586872e-06	8.3029197080292	1.41498858210504	10	284	cellular component disassembly at cellular level
GO:0022411	1.52401164617413e-06	8.18113251334416	1.43491799875441	10	288	cellular component disassembly
GO:0000184	2.03452396418553e-06	13.7182692307692	0.592900145318663	7	119	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0072594	7.58802498178715e-06	9.0452806122449	1.01640024911771	8	204	establishment of protein localization to organelle
GO:0006091	8.03621405590083e-06	6.03774029956363	2.13244758148225	11	428	generation of precursor metabolites and energy
GO:0019080	9.8734089327833e-06	10.6458333333333	0.752335478513598	7	151	viral genome expression

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GO:0019083      9.8734089327833e-06     10.6458333333333        0.752335478513598
7       151     viral transcription
GO:0006413      1.0309333582479e-05     10.5716710875332        0.757317832675939
7       152     translational initiation
GO:0016032      1.31432848272601e-05    5.71270491803279        2.24704172721611
11      451     viral reproduction
Tissue: Heart_Left_Ventricle=>Skin_Sun_Exposed_Lower_leg        Type:   cluster
SourceGene:     ENSG00000224505.1
TargetGeneSet:  RPL22   RPL11   RP1     TMEM222 SNRNP40 MFSD2A  ST7L    RBM8A   MCL1
CHTOP   CLK2    DDX59   ARL8A   ADCK3   OXER1   PPP3R1  RPIA    IL1RL2  CCDC115
WDR75   FAM117B FAM134A 7SK     CIDECP  SLC6A11 RPL32   C3orf19 ZNF501  FAM212A
C3orf14 RYBP    IFT57   QTRTD1  RAB41   MSL2    YTHDC1  DCK     RCHY1   CDKN2AIP
RP11    CARD6   ZNF131  RIOK2   RPS14   BOD1    BTN2A1  SRPK1   FRS3    TJAP1   RPF2
PPIL4   LATS1   AP5Z1   PMS2CL  TRA2A   RP9     RALA    URGCP   NUDCD3  COBL
CCT6P1  SBDSP1  MTERF   PON1    ZNF3    EPO     THAP5   ZC3HC1  TMEM209 TBXAS1
SLC37A3 C7orf34 ZNF212  NEIL2   R3HCC1  SGK3    TERF1   RPL30   EBAG9   UTP23   RPL8
KLHL9   C9orf156        EPB41L4B        ZFAND4  SIRT1   SLC25A16        SUPV3L1
TYSND1  DNAJB12 SMC3    RPLP2   RRP8    ARFGAP2 FAM111B MS4A7   VPS37C  ZBTB3
TRMT112 FAU     C11orf68        SF3B2   PITPNM1 ZNF259  RPS25   VPS11   NECAP1
MIR614  RPL14P1 PARPBP  C12orf73        SART3   RSRC2   USP12   KBTBD7  ARL11   TTC5
RBM23   NGDN    IFT43   NDNL2   FAM82A2 RPL4    WHAMM   VPS33B  TBC1D24 ZNF205
TFAP4   CCDC101 HIRIP3  VPS4A   GLOD4   DVL2    SNORA48 PLD6    FLCN    ZNF286B
TLK2P1  ZNF830  RPL19   MED1    PGAP3   SNX11   FAM117A SMG8    RPS6KB1 APPBP2
SNORA76 NOL11   KPNA2   SAP30BP L3MBTL4 GREB1L  SERPINB13       TMX3    SAFB    XAB2
NR2C2AP SUGP1   TSSK6   ZNF430  ZNF461  ZNF569  ZNF571  RPS16   CCDC97  ZNF574
ZNF180  SNRPD2  GLTSCR2 RPL18   RPS11   ZNF649  ZNF766  CHMP2A  ZCCHC3  RSPO4
PSMF1   MRPS26  FLRT3   DTD1    CRNKL1  PDRG1   CDK5RAP1        PCIF1   NCOA5
ZFP64   LSM14B  PRPF6   ICOSLG  C22orf39        SF3A1   LIMK2   IL2RB   RPL3    TEF
ARAF    TIMM17B GPKOW   DKC1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0000184      1.47353697992736e-14    16.537296037296 1.31755587848592        17
119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006415      6.29387212451571e-14    19.3489110707804        1.00754273060688
15      91      translational termination
GO:0006414      5.59455896737114e-13    16.3229885057471        1.1625493045464 15
105     translational elongation
GO:0006614      5.59455896737114e-13    16.3229885057471        1.1625493045464 15
105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      6.45523066346816e-13    16.1424782114437        1.17362120268494
15      106     cotranslational protein targeting to membrane
GO:0045047      6.45523066346816e-13    16.1424782114437        1.17362120268494
15      106     protein targeting to ER
GO:0072599      6.45523066346816e-13    16.1424782114437        1.17362120268494
15      106     establishment of protein localization to endoplasmic reticulum
GO:0006402      1.07553284885558e-12    11.1953345070423        1.97079786865961
18      178     mRNA catabolic process
GO:0070972      3.21418506412267e-12    14.2497489119518        1.30648398034738
15      118     protein localization to endoplasmic reticulum
GO:0000956      5.16016841499698e-12    11.0582903938167        1.87115078541277
17      169     nuclear-transcribed mRNA catabolic process
GO:0019080      1.01293782346996e-11    11.6510288065844        1.67185661891911
16      151     viral genome expression
GO:0019083      1.01293782346996e-11    11.6510288065844        1.67185661891911
16      151     viral transcription
GO:0006413      1.12143467704931e-11    11.5645424836601        1.68292851705764
16      152     translational initiation
GO:0006401      1.195397214553e-11      9.56059350756948        2.26973911840011
18      205     RNA catabolic process
GO:0019058      8.7700419798809e-11     8.37809958341599        2.55760847000208
18      231     viral infectious cycle
GO:0072594      1.05287618598566e-10    8.96630642085188        2.25866722026157
17      204     establishment of protein localization to organelle
GO:0006612      1.4136980983579e-10     10.6094452773613        1.69400041519618
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15      153     protein targeting to membrane
GO:0043624      1.4136980983579e-10     10.6094452773613        1.69400041519618
15      153     cellular protein complex disassembly
GO:0043241      2.23505409197828e-10    10.2348685796962        1.74935990588887
15      158     protein complex disassembly
GO:0022415      6.05733383335712e-10    7.35892212780817        2.87869351601965
18      260     viral reproductive process
GO:0034623      8.70727292601652e-10    9.19453480806766        1.92651027610546
15      174     cellular macromolecular complex disassembly
GO:0032984      1.29289078788587e-09    8.91105971404542        1.98186976679815
15      179     macromolecular complex disassembly
GO:0033365      2.7716193002126e-07     4.36392305266477        5.23700781952806
20      473     protein localization to organelle
GO:0000377      4.28867801478446e-07    6.52847526445133        2.25866722026157
13      204     RNA splicing, via transesterification reactions with bulged
adenosine as nucleophile
GO:0000398      4.28867801478446e-07    6.52847526445133        2.25866722026157
13      204     nuclear mRNA splicing, via spliceosome
GO:0000375      5.65602294868465e-07    6.35967652367069        2.31402671095426
13      209     RNA splicing, via transesterification reactions
GO:0016032      5.95962511640301e-07    4.32297412660888        4.99342606048024
19      451     viral reproduction
GO:0071845      6.07494944339125e-07    5.39238559159082        3.14441907134454
15      284     cellular component disassembly at cellular level
GO:0022411      7.25158637153665e-07    5.31186055323986        3.18870666389869
15      288     cellular component disassembly
GO:0006605      1.25658739599681e-06    4.09763853168108        5.2480797176666 19
474     protein targeting
GO:0022613      1.30272075961984e-06    5.87302656911821        2.49117708117085
13      225     ribonucleoprotein complex biogenesis
GO:0071843      2.55238701816115e-06    5.5037324664379 2.64618365511037        13
239     cellular component biogenesis at cellular level
GO:0008380      3.02433911209088e-06    4.69648454993283        3.57622309874749
15      323     RNA splicing
Tissue: Skin_Sun_Exposed_Lower_leg=>Heart_Left_Ventricle        Type:   asymmetric
SourceGene:     ENSG00000250699.1
TargetGeneSet:  RPL11   C1orf212        UBC     R3HDM1  RPL32   RPL14   ANTXR2
RPL15P3 RPS10   WDR11   CASP8AP2        PNPLA8  TAS2R5  MLL3    RPS20   RP11
DEPTOR  PRPF4   UCK1    RPL27A  RPS13   MRGPRX2 RPL14P1 RPL18AP3        HMGB3P4
MAPK1IP1L       FAN1    RPS3AP6 RPL4    RPS2    CTA     CLN3    SPAG7   RPL23A
RPL19   RPL27   UBA52   GLTSCR2 RPS5    RPS4X
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      4.24193765571411e-28    204.017777777778        0.195211404055083
16      91      translational termination
GO:0006414      5.02934023179459e-27    171.757303370787        0.225243927755865
16      105     translational elongation
GO:0006614      5.02934023179459e-27    171.757303370787        0.225243927755865
16      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      5.91761980235816e-27    169.837037037037        0.227389108020206
16      106     cotranslational protein targeting to membrane
GO:0045047      5.91761980235816e-27    169.837037037037        0.227389108020206
16      106     protein targeting to ER
GO:0072599      5.91761980235816e-27    169.837037037037        0.227389108020206
16      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      3.69319741403028e-26    149.730718954248        0.253131271192305
16      118     protein localization to endoplasmic reticulum
GO:0000184      4.26269833892774e-26    148.266666666667        0.255276451456647
16      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      2.35275647218531e-24    112.869135802469        0.323922219915577
16      151     viral genome expression
GO:0019083      2.35275647218531e-24    112.869135802469        0.323922219915577
16      151     viral transcription
GO:0006413      2.62695791137595e-24    112.03137254902 0.326067400179918       16
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152     translational initiation
GO:0006612      2.93086226808131e-24    111.205839416058        0.32821258044426
16      153     protein targeting to membrane
GO:0043624      2.93086226808131e-24    111.205839416058        0.32821258044426
16      153     cellular protein complex disassembly
GO:0043241      5.01021707818843e-24    107.252582159624        0.338938481765968
16      158     protein complex disassembly
GO:0000956      1.53371637953331e-23    99.4649237472767        0.362535464673725
16      169     nuclear-transcribed mRNA catabolic process
GO:0034623      2.48676496348234e-23    96.2835443037975        0.373261365995433
16      174     cellular macromolecular complex disassembly
GO:0006402      3.62246278899431e-23    93.8798353909465        0.381842087052799
16      178     mRNA catabolic process
GO:0032984      3.97411192101242e-23    93.2973415132924        0.383987267317141
16      179     macromolecular complex disassembly
GO:0072594      3.42510091437734e-22    80.7489361702128        0.43761677392568
16      204     establishment of protein localization to organelle
GO:0006401      3.71138034536168e-22    80.316049382716 0.439761954190021       16
205     RNA catabolic process
GO:0019058      2.61896002440318e-21    70.4744186046512        0.495536641062902
16      231     viral infectious cycle
GO:0022415      1.79345168034597e-20    61.9715846994536        0.557746868728808
16      260     viral reproductive process
GO:0071845      7.48960941953688e-20    56.326368159204 0.609231195073005       16
284     cellular component disassembly at cellular level
GO:0022411      9.38775022166801e-20    55.4823529411765        0.617811916130372
16      288     cellular component disassembly
GO:0033365      7.43915310463247e-18    37.1848370927318        1.01467026503356
17      473     protein localization to organelle
GO:0006605      7.70860707812217e-18    37.1008127539856        1.0168154452979 17
474     protein targeting
GO:0016032      1.21809364465966e-16    34.2927203065134        0.967476299218047
16      451     viral reproduction
Tissue: Skin_Sun_Exposed_Lower_leg=>Heart_Left_Ventricle        Type:   asymmetric
SourceGene:     ENSG00000258513.1
TargetGeneSet:  RP4     RPS7    RPL24   RP11    MECOM   CTD     RPL39P3 SNHG6
RPL35   RPLP2   RPL27A  U6      TRAC    RPS29   RPL7AP6 RPS7P1  RPS15   RPL36
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      8.75466515106586e-16    345.927710843374        0.0755657047955159
8       91      translational termination
GO:0006414      2.86223155543203e-15    295.711340206186        0.0871911978409799
8       105     translational elongation
GO:0006614      2.86223155543203e-15    295.711340206186        0.0871911978409799
8       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      3.09511656806613e-15    292.673469387755        0.0880215902013702
8       106     cotranslational protein targeting to membrane
GO:0045047      3.09511656806613e-15    292.673469387755        0.0880215902013702
8       106     protein targeting to ER
GO:0072599      3.09511656806613e-15    292.673469387755        0.0880215902013702
8       106     establishment of protein localization to endoplasmic reticulum
GO:0070972      7.48533940788438e-15    260.527272727273        0.0979862985260536
8       118     protein localization to endoplasmic reticulum
GO:0000184      8.02283483790861e-15    258.162162162162        0.0988166908864438
8       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      5.63410912080144e-14    199.944055944056        0.125389246418933
8       151     viral genome expression
GO:0019083      5.63410912080144e-14    199.944055944056        0.125389246418933
8       151     viral transcription
GO:0006413      5.94563862927435e-14    198.541666666667        0.126219638779323
8       152     translational initiation
GO:0006612      6.27211613900626e-14    197.158620689655        0.127050031139714
8       153     protein targeting to membrane
GO:0043624      6.27211613900626e-14    197.158620689655        0.127050031139714
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8       153     cellular protein complex disassembly
GO:0043241      8.15077837252388e-14    190.52  0.131201992941665       8       158
protein complex disassembly
GO:0000956      1.40934469304936e-13    177.366459627329        0.140336308905958
8       169     nuclear-transcribed mRNA catabolic process
GO:0034623      1.78610797332018e-13    171.963855421687        0.144488270707909
8       174     cellular macromolecular complex disassembly
GO:0006402      2.14811893079371e-13    167.870588235294        0.147809840149471
8       178     mRNA catabolic process
GO:0032984      2.2480565338914e-13     166.877192982456        0.148640232509861
8       179     macromolecular complex disassembly
GO:0072594      6.48443399499177e-13    145.336734693878        0.169400041519618
8       204     establishment of protein localization to organelle
GO:0006401      6.74608060895868e-13    144.58883248731 0.170230433880008       8
205     RNA catabolic process
GO:0019058      1.76984701078215e-12    127.497757847534        0.191820635250156
8       231     viral infectious cycle
GO:0022415      4.58855624840892e-12    112.595238095238        0.215902013701474
8       260     viral reproductive process
GO:0071845      9.32944532399793e-12    102.630434782609        0.235831430350841
8       284     cellular component disassembly at cellular level
GO:0022411      1.04380518630009e-11    101.135714285714        0.239152999792402
8       288     cellular component disassembly
GO:0016032      3.75459422710082e-10    63.1873589164786        0.374506954536018
8       451     viral reproduction
GO:0033365      5.48138591881141e-10    60.1032258064516        0.392775586464605
8       473     protein localization to organelle
GO:0006605      5.57407557789227e-10    59.9699570815451        0.393605978824995
8       474     protein targeting
Tissue: Heart_Left_Ventricle=>Skin_Sun_Exposed_Lower_leg        Type:   asymmetric
SourceGene:     KCTD9P1(ENSG00000225014.1)
TargetGeneSet:  FAM132A CTNNBIP1        CROCC   RPL11   C1orf135        SH3BGRL3
PPP1R8  YRDC    RPS8    UQCRH   TTC39A  KTI12   RP4     RPL5    DNTTIP2 HIAT1   RP11
HBXIP   ATP5F1  B3GALT2 TIMM17A TMEM183A        TFB2M   SH3YL1  RPS7    SPDYA
SNORA67 UBC     TPRKB   ANKRD36C        RPL31   GLI2    DAPL1   SENP2   NBEAL1
EEF1B2  MRPL44  MYEOV2  RPL15   CBX5P1  ZNF90P1 RPL24   MRPL47  SDHAP2  RPL35A  HOPX
FAM190A RPL34   OSTC    RPS3A   FBXO8   CDKN2AIP        SLC38A9 NDUFAF2 ADAMTS6
ZFYVE16 CAMLG   RPL26L1 TMEM14C TMEM14B TBCC    RP13    EEF1A1  RP1     TOMM7   GBAS
MIR1255B1       RPS3AP26        HBP1    TRIM35  EFCAB1  RDH10   TCEB1   PAF1
POLR2K  EIF3E   TTC35   EIF3H   RPS6    LINC00032       NDUFB6  ZNF658  KLF9
NCBP1   ATP6V1G1        ASB6    ANAPC16 CHCHD1  RPS24   MARK2P9 C10orf12
C11orf58        RPS13   EIF3M   VWCE    MALAT1  PAK1    CCDC90B RPS25   U6
TAS2R18 PFDN5   ANKS1B  PSMD9   TPT1    EBPL    THSD1   COMMD6  CLYBL-AS2       NGDN
EAPP    PSMA6   KLHDC2  PSMA3   MOAP1   BAG5    RSL24D1 RPS3AP6 RPS27L  WDR61
MORF4L1 MRPL46  SPSB3   RPS15A  LYRM1   TMED6   MAP1LC3B        RPL26   ZNF286B
RPS7P1  RPL17   RPL19   RPL27   HIGD1B  CTD     ICT1    ZFP161  WDR7    PQLC1
HSBP1L1 CAPS    WDR83   ZNF350  ZNF460  GCNT1P1 PSMA7   SNRPD3  PHF5A   EEF1B2P3
COX7B
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      7.00108156243048e-28    46.5087918321044        0.791986713722234
23      105     translational elongation
GO:0006415      9.9573812581339e-28     52.3081792437115        0.686388485225936
22      91      translational termination
GO:0006413      6.13779952928328e-27    33.3122422197225        1.14649505224552
25      152     translational initiation
GO:0000184      1.59603668113705e-26    39.687257751938 0.897584942218532       23
119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      1.70098294364476e-25    31.6035201482168        1.13895232163864
24      151     viral genome expression
GO:0019083      1.70098294364476e-25    31.6035201482168        1.13895232163864
24      151     viral transcription
GO:0006614      1.35355223956287e-24    40.5056818181818        0.791986713722234
21      105     SRP-dependent cotranslational protein targeting to membrane
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GO:0006613      1.67808866830512e-24    40.0263368983957        0.799529444329112
21      106     cotranslational protein targeting to membrane
GO:0045047      1.67808866830512e-24    40.0263368983957        0.799529444329112
21      106     protein targeting to ER
GO:0072599      1.67808866830512e-24    40.0263368983957        0.799529444329112
21      106     establishment of protein localization to endoplasmic reticulum
GO:0072594      1.2479011519117e-23     23.5484836392658        1.5387170438032 25
204     establishment of protein localization to organelle
GO:0019058      1.35404133555629e-23    21.6022333235381        1.74237077018891
26      231     viral infectious cycle
GO:0070972      1.8718659352694e-23     35.0451030927835        0.890042211611653
21      118     protein localization to endoplasmic reticulum
GO:0000956      7.73126774786728e-23    26.0041414463205        1.27472147256245
23      169     nuclear-transcribed mRNA catabolic process
GO:0043624      2.08118992313669e-22    27.4319557778363        1.1540377828524 22
153     cellular protein complex disassembly
GO:0006402      2.63003009516724e-22    24.4786946736684        1.34260604802436
23      178     mRNA catabolic process
GO:0022415      2.94732327295664e-22    18.8862115127175        1.96110995778839
26      260     viral reproductive process
GO:0006401      3.26019612331964e-22    22.0906077348066        1.54625977441008
24      205     RNA catabolic process
GO:0043241      4.32304443474305e-22    26.4141311697093        1.19175143588679
22      158     protein complex disassembly
GO:0034623      3.80972730832128e-21    23.6070780399274        1.31243512559684
22      174     cellular macromolecular complex disassembly
GO:0006612      5.61471104620423e-21    25.6895661157025        1.1540377828524 21
153     protein targeting to membrane
GO:0032984      7.18547446031269e-21    22.8472069697635        1.35014877863124
22      179     macromolecular complex disassembly
GO:0016032      1.63195272019299e-20    12.5569018912174        3.40177150370217
30      451     viral reproduction
GO:0071845      1.16772050414388e-17    14.4285396061659        2.14213549235347
23      284     cellular component disassembly at cellular level
GO:0022411      1.59447401062236e-17    14.2067134708205        2.17230641478098
23      288     cellular component disassembly
GO:0033365      8.80019870315439e-15    9.23017644557823        3.56771157705349
25      473     protein localization to organelle
GO:0006605      9.23680250813398e-15    9.20895641107222        3.57525430766037
25      474     protein targeting
GO:0022613      1.39770626050915e-08    9.02564858490566        1.69711438654764
13      225     ribonucleoprotein complex biogenesis
GO:0071843      2.8672468897145e-08     8.45814896755162        1.80271261504394
13      239     cellular component biogenesis at cellular level
GO:0042274      1.76388272266686e-07    52.9918639053254        0.135769150923812
5       18      ribosomal small subunit biogenesis
GO:0042254      1.7878479343382e-07     10.3211975873846        1.12386686042488
10      149     ribosome biogenesis
GO:0006364      1.14295904297322e-06    11.7541254125413        0.784443983115355
8       104     rRNA processing
GO:0042273      1.44706157301348e-06    68.2571428571429        0.090512767282541
4       12      ribosomal large subunit biogenesis
GO:0016072      1.75139242922031e-06    11.0580469811687        0.829700366756626
8       110     rRNA metabolic process
GO:0051352      1.67224777408421e-05    12.6001765225066        0.543076603695246
6       72      negative regulation of ligase activity
GO:0051444      1.67224777408421e-05    12.6001765225066        0.543076603695246
6       72      negative regulation of ubiquitin-protein ligase activity
GO:0031571      1.81091961104918e-05    12.4112447471381        0.550619334302124
6       73      mitotic cell cycle G1/S transition DNA damage checkpoint
Tissue: Heart_Left_Ventricle=>Skin_Sun_Exposed_Lower_leg        Type:   cluster
SourceGene:     KCTD9P1(ENSG00000225014.1)
TargetGeneSet:  FAM132A CTNNBIP1        CROCC   RPL11   C1orf135        SH3BGRL3
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PPP1R8  YRDC    RPS8    UQCRH   TTC39A  KTI12   RP4     RPL5    DNTTIP2 HIAT1   RP11
HBXIP   ATP5F1  B3GALT2 TIMM17A TMEM183A        TFB2M   SH3YL1  RPS7    SPDYA
SNORA67 UBC     TPRKB   ANKRD36C        RPL31   GLI2    DAPL1   SENP2   NBEAL1
EEF1B2  MRPL44  MYEOV2  RPL15   CBX5P1  ZNF90P1 RPL24   MRPL47  SDHAP2  RPL35A  HOPX
FAM190A RPL34   OSTC    RPS3A   FBXO8   CDKN2AIP        SLC38A9 NDUFAF2 ADAMTS6
ZFYVE16 CAMLG   RPL26L1 TMEM14C TMEM14B TBCC    RP13    EEF1A1  RP1     TOMM7   GBAS
MIR1255B1       RPS3AP26        HBP1    TRIM35  EFCAB1  RDH10   TCEB1   PAF1
POLR2K  EIF3E   TTC35   EIF3H   RPS6    LINC00032       NDUFB6  ZNF658  KLF9
NCBP1   ATP6V1G1        ASB6    ANAPC16 CHCHD1  RPS24   MARK2P9 C10orf12
C11orf58        RPS13   EIF3M   VWCE    MALAT1  PAK1    CCDC90B RPS25   U6
TAS2R18 PFDN5   ANKS1B  PSMD9   TPT1    EBPL    THSD1   COMMD6  CLYBL-AS2       NGDN
EAPP    PSMA6   KLHDC2  PSMA3   MOAP1   BAG5    RSL24D1 RPS3AP6 RPS27L  WDR61
MORF4L1 MRPL46  SPSB3   RPS15A  LYRM1   TMED6   MAP1LC3B        RPL26   ZNF286B
RPS7P1  RPL17   RPL19   RPL27   HIGD1B  CTD     ICT1    ZFP161  WDR7    PQLC1
HSBP1L1 CAPS    WDR83   ZNF350  ZNF460  GCNT1P1 PSMA7   SNRPD3  PHF5A   EEF1B2P3
COX7B
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      7.00108156243048e-28    46.5087918321044        0.791986713722234
23      105     translational elongation
GO:0006415      9.9573812581339e-28     52.3081792437115        0.686388485225936
22      91      translational termination
GO:0006413      6.13779952928328e-27    33.3122422197225        1.14649505224552
25      152     translational initiation
GO:0000184      1.59603668113705e-26    39.687257751938 0.897584942218532       23
119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      1.70098294364476e-25    31.6035201482168        1.13895232163864
24      151     viral genome expression
GO:0019083      1.70098294364476e-25    31.6035201482168        1.13895232163864
24      151     viral transcription
GO:0006614      1.35355223956287e-24    40.5056818181818        0.791986713722234
21      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.67808866830512e-24    40.0263368983957        0.799529444329112
21      106     cotranslational protein targeting to membrane
GO:0045047      1.67808866830512e-24    40.0263368983957        0.799529444329112
21      106     protein targeting to ER
GO:0072599      1.67808866830512e-24    40.0263368983957        0.799529444329112
21      106     establishment of protein localization to endoplasmic reticulum
GO:0072594      1.2479011519117e-23     23.5484836392658        1.5387170438032 25
204     establishment of protein localization to organelle
GO:0019058      1.35404133555629e-23    21.6022333235381        1.74237077018891
26      231     viral infectious cycle
GO:0070972      1.8718659352694e-23     35.0451030927835        0.890042211611653
21      118     protein localization to endoplasmic reticulum
GO:0000956      7.73126774786728e-23    26.0041414463205        1.27472147256245
23      169     nuclear-transcribed mRNA catabolic process
GO:0043624      2.08118992313669e-22    27.4319557778363        1.1540377828524 22
153     cellular protein complex disassembly
GO:0006402      2.63003009516724e-22    24.4786946736684        1.34260604802436
23      178     mRNA catabolic process
GO:0022415      2.94732327295664e-22    18.8862115127175        1.96110995778839
26      260     viral reproductive process
GO:0006401      3.26019612331964e-22    22.0906077348066        1.54625977441008
24      205     RNA catabolic process
GO:0043241      4.32304443474305e-22    26.4141311697093        1.19175143588679
22      158     protein complex disassembly
GO:0034623      3.80972730832128e-21    23.6070780399274        1.31243512559684
22      174     cellular macromolecular complex disassembly
GO:0006612      5.61471104620423e-21    25.6895661157025        1.1540377828524 21
153     protein targeting to membrane
GO:0032984      7.18547446031269e-21    22.8472069697635        1.35014877863124
22      179     macromolecular complex disassembly
GO:0016032      1.63195272019299e-20    12.5569018912174        3.40177150370217
30      451     viral reproduction
```

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GO:0071845      1.16772050414388e-17    14.4285396061659        2.14213549235347
23      284     cellular component disassembly at cellular level
GO:0022411      1.59447401062236e-17    14.2067134708205        2.17230641478098
23      288     cellular component disassembly
GO:0033365      8.80019870315439e-15    9.23017644557823        3.56771157705349
25      473     protein localization to organelle
GO:0006605      9.23680250813398e-15    9.20895641107222        3.57525430766037
25      474     protein targeting
GO:0022613      1.39770626050915e-08    9.02564858490566        1.69711438654764
13      225     ribonucleoprotein complex biogenesis
GO:0071843      2.8672468897145e-08     8.45814896755162        1.80271261504394
13      239     cellular component biogenesis at cellular level
GO:0042274      1.76388272266686e-07    52.9918639053254        0.135769150923812
5       18      ribosomal small subunit biogenesis
GO:0042254      1.7878479343382e-07     10.3211975873846        1.12386686042488
10      149     ribosome biogenesis
GO:0006364      1.14295904297322e-06    11.7541254125413        0.784443983115355
8       104     rRNA processing
GO:0042273      1.44706157301348e-06    68.2571428571429        0.090512767282541
4       12      ribosomal large subunit biogenesis
GO:0016072      1.75139242922031e-06    11.0580469811687        0.829700366756626
8       110     rRNA metabolic process
GO:0051352      1.67224777408421e-05    12.6001765225066        0.543076603695246
6       72      negative regulation of ligase activity
GO:0051444      1.67224777408421e-05    12.6001765225066        0.543076603695246
6       72      negative regulation of ubiquitin-protein ligase activity
GO:0031571      1.81091961104918e-05    12.4112447471381        0.550619334302124
6       73      mitotic cell cycle G1/S transition DNA damage checkpoint
Tissue: Heart_Left_Ventricle=>Skin_Sun_Exposed_Lower_leg        Type:   asymmetric
SourceGene:     MYADM(ENSG00000179820.10)
TargetGeneSet:  PRPF38A PFDN2   TFB2M   RPS7    PEX13   SNRPG   RPL31   PSMD14
EEF1B2  MYEOV2  RP11    LARS2   CCDC72  RPL35A  ATP5I   BRIP1   C5orf44 RPL26L1
HIST1H2BL       EEF1A1  LYRM2   RP1     GET4    SEC61G  CTB     HBP1    ARMC1
C9orf123        RPS6    CHMP5   YME1L1  NRBF2   CCDC90B U6      TRIAP1  MRP63
MTMR6   MOAP1   RPS3AP6 FAM96B  ZNHIT3  RPL27   MBD1    LONP1   PSMA7   RPS21
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      5.44827067695416e-12    46.2834051724138        0.27610545982977
9       105     translational elongation
GO:0006614      2.42015652695186e-10    39.3567010309278        0.27610545982977
8       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      2.61286891729163e-10    38.9523809523809        0.278735035637672
8       106     cotranslational protein targeting to membrane
GO:0045047      2.61286891729163e-10    38.9523809523809        0.278735035637672
8       106     protein targeting to ER
GO:0072599      2.61286891729163e-10    38.9523809523809        0.278735035637672
8       106     establishment of protein localization to endoplasmic reticulum
GO:0070972      6.19830965847345e-10    34.6739393939394        0.310289945332503
8       118     protein localization to endoplasmic reticulum
GO:0072594      2.13459292520077e-09    22.6281167108753        0.536433464812124
9       204     establishment of protein localization to organelle
GO:0006415      3.3446054642188e-09     38.5188172043011        0.239291398519134
7       91      translational termination
GO:0006612      4.90927691750099e-09    26.24   0.402325098609093       8       153
protein targeting to membrane
GO:0000184      2.19572843448776e-08    28.8326612903226        0.312919521140405
7       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      1.13802818805091e-07    22.3752240143369        0.397065946993288
7       151     viral genome expression
GO:0019083      1.13802818805091e-07    22.3752240143369        0.397065946993288
7       151     viral transcription
GO:0006413      1.1907172276201e-07     22.2193548387097        0.39969552280119
7       152     translational initiation
GO:0043624      1.24545264686063e-07    22.0656208572691        0.402325098609093
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7       153     cellular protein complex disassembly
GO:0043241      1.55212654087642e-07    21.3274941251869        0.415472977648606
7       158     protein complex disassembly
GO:0000956      2.45680923715139e-07    19.8639984070092        0.444398311535534
7       169     nuclear-transcribed mRNA catabolic process
GO:0033365      2.6624087110527e-07     10.7605677260105        1.24378935713791
10      473     protein localization to organelle
GO:0034623      2.99569810090014e-07    19.2625072435774        0.457546190575047
7       174     cellular macromolecular complex disassembly
GO:0006402      3.49557611814805e-07    18.8066402565554        0.468064493806657
7       178     mRNA catabolic process
GO:0032984      3.63097054203649e-07    18.6959864966242        0.47069406961456
7       179     macromolecular complex disassembly
GO:0071845      5.91091697188702e-07    13.6589371980676        0.746799529444329
8       284     cellular component disassembly at cellular level
GO:0022411      6.57065928879444e-07    13.46   0.757317832675939       8       288
cellular component disassembly
GO:0006401      9.06977118532895e-07    16.2113066145324        0.539063040620026
7       205     RNA catabolic process
GO:0016032      1.88937321413605e-06    9.80956467467624        1.18593868936406
9       451     viral reproduction
GO:0019058      2.01535733254347e-06    14.3034274193548        0.607432011625493
7       231     viral infectious cycle
GO:0006605      2.84452989698194e-06    9.30901001112347        1.24641893294582
9       474     protein targeting
GO:0022415      4.41083526082151e-06    12.6380211653704        0.683689710054667
7       260     viral reproductive process
GO:0042274      1.33208946821051e-05    82.2742857142857        0.0473323645422462
3       18      ribosomal small subunit biogenesis
Tissue: Heart_Left_Ventricle=>Skin_Sun_Exposed_Lower_leg        Type:   cluster
SourceGene:     NUDT12(ENSG00000112874.5)
TargetGeneSet:  MTND2P28        RPL22   PLOD1   DMAP1   RPS8    FGGY    RPL5    GAS5
DPYSL5  UBC     MYO3B   NGEF    HDLBP   RPL15   ZBTB20  RYK     GOLIM4  EXOSC9
RPS3A   NPY1R   C4orf27 CDKN2AIP        VDAC1   EEF1A1  RP11    MESTP1  STX7
CCT6P1  SBDSP1  RPS3AP26        DDHD2   C8orf40 HOOK3   VPS28   RPS6    EEF1A1P5
NRG3    PRG2    C11orf31        FAM55D  TAS2R18 RPL6    RIMBP2  KIAA1704
PCDH9   SNX6    AP5M1   IFT43   SPSB3   GPT2    SPG7    RPL26   RPL19   FAM195B CTD
RPL17   TNFRSF11A       CCDC130 KXD1    ZNF208  RPL13A  ZNF350  OLIG1   EIF3D
TMPRSS6 TBC1D22A        RBM3    RP3     TBC1D8B MT
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      4.83871524356167e-17    50.5375 0.385094457130994       13      105
translational elongation
GO:0006415      3.96725263306637e-16    53.0497066995986        0.333748529513528
12      91      translational termination
GO:0006614      2.36517683263292e-15    45.0196695515342        0.385094457130994
12      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      2.66009195205438e-15    44.5376232485729        0.388762023389385
12      106     cotranslational protein targeting to membrane
GO:0045047      2.66009195205438e-15    44.5376232485729        0.388762023389385
12      106     protein targeting to ER
GO:0072599      2.66009195205438e-15    44.5376232485729        0.388762023389385
12      106     establishment of protein localization to endoplasmic reticulum
GO:0006413      6.71973677287656e-15    33.3393884892086        0.557470071275344
13      152     translational initiation
GO:0070972      9.99107432151821e-15    39.462494247584 0.43277281849007        12
118     protein localization to endoplasmic reticulum
GO:0000184      1.10822942350723e-14    39.0909505356736        0.43644038474846
12      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0000956      2.69407286782552e-14    29.6708333333333        0.619818697667981
13      169     nuclear-transcribed mRNA catabolic process
GO:0006402      5.29469460127444e-14    28.034696969697 0.652826793993495       13
178     mRNA catabolic process
GO:0019080      2.01042907346556e-13    30.0242147745218        0.553802505016954
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12      151     viral genome expression
GO:0019083      2.01042907346556e-13    30.0242147745218        0.553802505016954
12      151     viral transcription
GO:0006612      2.35603391360195e-13    29.5941878567722        0.561137637533735
12      153     protein targeting to membrane
GO:0043624      2.35603391360195e-13    29.5941878567722        0.561137637533735
12      153     cellular protein complex disassembly
GO:0006401      3.28789564667675e-13    24.0466145833333        0.751851082970037
13      205     RNA catabolic process
GO:0043241      3.46951584994278e-13    28.570664884731 0.579475468825687       12
158     protein complex disassembly
GO:0034623      1.1017886676168e-12     25.7199638663053        0.638156528959934
12      174     cellular macromolecular complex disassembly
GO:0019058      1.51714240944642e-12    21.1399082568807        0.847207805688188
13      231     viral infectious cycle
GO:0032984      1.54458173719597e-12    24.9411421060318        0.656494360251886
12      179     macromolecular complex disassembly
GO:0022415      6.80504659985568e-12    18.6197368421053        0.95356722718151
13      260     viral reproductive process
GO:0072594      7.27518368965008e-12    21.655487804878 0.748183516711646       12
204     establishment of protein localization to organelle
GO:0071845      3.42610342688023e-10    15.200143472023 1.04158881738288        12
284     cellular component disassembly at cellular level
GO:0022411      4.02264026677077e-10    14.9756097560976        1.05625908241644
12      288     cellular component disassembly
GO:0033365      9.9851388680155e-10     10.9014021563041        1.73475884021867
14      473     protein localization to organelle
GO:0016032      6.04874592179812e-09    10.3584474885845        1.65407238253408
13      451     viral reproduction
GO:0006605      1.09617153304727e-08    9.82543383947939        1.73842640647706
13      474     protein targeting
GO:0016197      9.12150819894347e-06    14.2320478723404        0.491453878624317
6       134     endosomal transport
GO:0022613      1.69430301796759e-05    9.89828480255285        0.825202408137845
7       225     ribonucleoprotein complex biogenesis
Tissue: Skin_Sun_Exposed_Lower_leg=>Heart_Left_Ventricle        Type:   asymmetric
SourceGene:     PGRMC1(ENSG00000101856.8)
TargetGeneSet:  TRAPPC12        TCEB1P21        RPL37A  KLHL30  RPL32   RPL29   ERC2
RP11    LYSMD3  RPS14   RPS10   MRPS12  RP3     ELP3    TMEM65  RPL8    DNLZ    CST6
SETP17  C11orf75        MRPS36P4        CACNA1C RILPL1  RPL13   OR3A3   CCL2
RPS15   RPL36   RPL18   RPS11   RPS5    RPS21
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      2.36525599733211e-23    217.409090909091        0.151131409591032
13      91      translational termination
GO:0006414      1.70532207841082e-22    184.145256916996        0.17438239568196
13      105     translational elongation
GO:0006614      1.70532207841082e-22    184.145256916996        0.17438239568196
13      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.94231758806374e-22    182.152492668622        0.17604318040274
13      106     cotranslational protein targeting to membrane
GO:0045047      1.94231758806374e-22    182.152492668622        0.17604318040274
13      106     protein targeting to ER
GO:0072599      1.94231758806374e-22    182.152492668622        0.17604318040274
13      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      8.41874403674507e-22    161.2   0.195972597052107       13      118
protein localization to endoplasmic reticulum
GO:0000184      9.44450207397793e-22    159.668096054889        0.197633381772888
13      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      2.36729203985515e-20    122.369565217391        0.250778492837866
13      151     viral genome expression
GO:0019083      2.36729203985515e-20    122.369565217391        0.250778492837866
13      151     viral transcription
GO:0006413      2.58684652205297e-20    121.480706344016        0.252439277558646
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13      152     translational initiation
GO:0006612      2.82503658286128e-20    120.604545454545        0.254100062279427
13      153     protein targeting to membrane
GO:0043624      2.82503658286128e-20    120.604545454545        0.254100062279427
13      153     cellular protein complex disassembly
GO:0043241      4.34944305560692e-20    116.405015673981        0.26240398588333
13      158     protein complex disassembly
GO:0019058      8.15435952605171e-20    91.6774193548387        0.383641270500311
14      231     viral infectious cycle
GO:0000956      1.07082145951018e-19    108.113636363636        0.280672617811916
13      169     nuclear-transcribed mRNA catabolic process
GO:0034623      1.58064540448204e-19    104.719367588933        0.288976541415819
13      174     cellular macromolecular complex disassembly
GO:0006402      2.14045600967934e-19    102.152066115702        0.295619680298941
13      178     mRNA catabolic process
GO:0032984      2.30643262079744e-19    101.529572836802        0.297280465019722
13      179     macromolecular complex disassembly
GO:0022415      4.38531556145992e-19    80.7048780487805        0.431804027402948
14      260     viral reproductive process
GO:0072594      1.3107907802754e-18     88.0856734888148        0.338800083039236
13      204     establishment of protein localization to organelle
GO:0006401      1.39854045986023e-18    87.6207386363636        0.340460867760017
13      205     RNA catabolic process
GO:0071845      1.02100164815464e-16    61.7336464273734        0.471662860701682
13      284     cellular component disassembly at cellular level
GO:0022411      1.22587654717886e-16    60.8185123966942        0.478305999584804
13      288     cellular component disassembly
GO:0016032      1.00514907255067e-15    44.8192219679634        0.749013909072037
14      451     viral reproduction
GO:0033365      7.55931581953024e-14    35.8835968379447        0.785551172929209
13      473     protein localization to organelle
GO:0006605      7.76682818723057e-14    35.8031946361664        0.78721195764999
13      474     protein targeting
GO:0042274      3.23105168313163e-06    137.257142857143        0.0298941249740502
3       18      ribosomal small subunit biogenesis
Tissue: Skin_Sun_Exposed_Lower_leg=>Heart_Left_Ventricle        Type:   cluster
SourceGene:     RP11-16C18.3(ENSG00000237027.1)
TargetGeneSet:  CEP104  RP13    RPL11   RPL5    ACBD6   BCL11A  LRRTM4  COX5B
RPL31   RPL15   RPL24   RP11    BCL6    RPL35A  BRIX1   CTD     SOX9    ARHGEF37
SSR1    C6orf106        MRPL2   MRPS12  SEC61B  CTSL1P7 LCOR    FAM160B1
RPLP2   EIF3F   RPS13   FAU     RPS25   ZBTB44  RAPGEF3 RPL14P1 SNRPF   RPS2P5
LINC00427       UCHL3   MRPL52  AP1G2   SCFD1   RPS29   SLIRP   LINC00521       RPL4
AKAP13  HN1L    U6      WWOX    RPL26   NT5M    SLC47A1 RPL23A  RPL17   RPL19
ALYREF  RPL36   UBA52   PDCD2L  RPL18   HSPA13  EP300   SMS     EEF1B2P3
PHF16   RPS4X   UTP14A
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006614      3.29506663625902e-34    122.397979012826        0.385094457130994
22      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      4.14947076419811e-34    120.932411674347        0.388762023389385
22      106     cotranslational protein targeting to membrane
GO:0045047      4.14947076419811e-34    120.932411674347        0.388762023389385
22      106     protein targeting to ER
GO:0072599      4.14947076419811e-34    120.932411674347        0.388762023389385
22      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      5.52840024039884e-33    105.727150537634        0.43277281849007
22      118     protein localization to endoplasmic reticulum
GO:0006415      1.76933814408103e-31    122.296201451131        0.333748529513528
20      91      translational termination
GO:0006612      2.57782576196683e-30    77.2898300911106        0.561137637533735
22      153     protein targeting to membrane
GO:0006414      4.14342998131729e-30    102.053475935829        0.385094457130994
20      105     translational elongation
GO:0000184      6.25253485109073e-29    87.5359657177839        0.43644038474846
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20      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      1.43194412988401e-28    72.0259615384615        0.553802505016954
21      151     viral genome expression
GO:0019083      1.43194412988401e-28    72.0259615384615        0.553802505016954
21      151     viral transcription
GO:0006413      1.65794688744108e-28    71.4711354961832        0.557470071275344
21      152     translational initiation
GO:0072594      1.9617378947663e-27     55.4328252392769        0.748183516711646
22      204     establishment of protein localization to organelle
GO:0043624      1.31050972554044e-26    65.0034176349966        0.561137637533735
20      153     cellular protein complex disassembly
GO:0043241      2.57408670569871e-26    62.6262626262626        0.579475468825687
20      158     protein complex disassembly
GO:0000956      1.05117443232579e-25    57.9581045352857        0.619818697667981
20      169     nuclear-transcribed mRNA catabolic process
GO:0034623      1.92904013762762e-25    56.0566706021251        0.638156528959934
20      174     cellular macromolecular complex disassembly
GO:0006402      3.09348793557785e-25    54.6221710778673        0.652826793993495
20      178     mRNA catabolic process
GO:0032984      3.47494743442156e-25    54.274823708786 0.656494360251886       20
179     macromolecular complex disassembly
GO:0022415      4.70508112989575e-25    42.2228246137165        0.95356722718151
22      260     viral reproductive process
GO:0019058      1.53164327185711e-24    44.3375 0.847207805688188       21      231
viral infectious cycle
GO:0006401      5.71295170166455e-24    46.5618345618346        0.751851082970037
20      205     RNA catabolic process
GO:0033365      4.16162608129544e-22    25.7104677060134        1.73475884021867
24      473     protein localization to organelle
GO:0006605      4.37487273719778e-22    25.6514942528736        1.73842640647706
24      474     protein targeting
GO:0071845      4.27362753063403e-21    32.4471992653811        1.04158881738288
20      284     cellular component disassembly at cellular level
GO:0022411      5.65794276077651e-21    31.9538670284939        1.05625908241644
20      288     cellular component disassembly
GO:0016032      8.54399763582425e-20    23.1083540115798        1.65407238253408
22      451     viral reproduction
GO:0042273      7.80863562374655e-08    146.836734693878        0.0440107951006851
4       12      ribosomal large subunit biogenesis
GO:0022613      1.12022401523491e-07    13.4299242424242        0.825202408137845
9       225     ribonucleoprotein complex biogenesis
GO:0071843      1.87325294137031e-07    12.6    0.876548335755311       9       239
cellular component biogenesis at cellular level
GO:0042254      1.11473650659671e-06    15.2774035517453        0.546467372500173
7       149     ribosome biogenesis
Tissue: Heart_Left_Ventricle=>Skin_Sun_Exposed_Lower_leg        Type:   cluster
SourceGene:     RP11-332L8.1(ENSG00000237861.1)
TargetGeneSet:  RP11    RP4     RBM8A   MIR4426 ST13P19 ZC3H11B YPEL5   DPY30
RPL31   PSMD14  RPL37A  CRBN    RPL32   ATG3    RPL35A  PRSS12  CTD     RPL37   NSA2
PHAX    DCTN4   TTC1    RPL24P4 ZBTB2   BCL7B   NYAP1   WASL    SORBS3  RPL30
UTP23   C9orf78 UCK1    SRP9P1  RPL13AP5        NAV2-AS1        TAS2R20 RPL14P1
RILPL2  RPS7P10 RNF6    UPF3A   NDNL2   SELS    EIF3C   CD2BP2  AMFR    RPS2P46
RPL19   ORMDL3  DHX40   RPS16   EID2    RPS11   EEF1B2P3        GPKOW   ARMCX1  RP3
RP13    DAZ3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0000184      1.89169548238353e-14    48.5561728395062        0.337623693862016
11      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0000956      9.40718587582297e-13    33.0742616033755        0.479482388762023
11      169     nuclear-transcribed mRNA catabolic process
GO:0006402      1.66441886117584e-12    31.2720558882236        0.505016953844025
11      178     mRNA catabolic process
GO:0006415      3.0848556803244e-12     49.1432926829268        0.258182824718013
9       91      translational termination
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GO:0006401      7.79345903785994e-12    26.8687285223368        0.581620649090028
11      205     RNA catabolic process
GO:0006413      1.0429104271136e-11     32.412539754657 0.431250432496021       10
152     translational initiation
GO:0006612      1.11364910838922e-11    32.1836228287841        0.434087606394021
10      153     protein targeting to membrane
GO:0006414      1.1500479901178e-11     41.935546875    0.297903259290015       9
105     translational elongation
GO:0006614      1.1500479901178e-11     41.935546875    0.297903259290015       9
105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.25423704941304e-11    41.5003221649485        0.300740433188015
9       106     cotranslational protein targeting to membrane
GO:0045047      1.25423704941304e-11    41.5003221649485        0.300740433188015
9       106     protein targeting to ER
GO:0072599      1.25423704941304e-11    41.5003221649485        0.300740433188015
9       106     establishment of protein localization to endoplasmic reticulum
GO:0070972      3.33367514143575e-11    36.9005160550459        0.334786519964016
9       118     protein localization to endoplasmic reticulum
GO:0019080      3.0780454364018e-10     28.2596830985915        0.428413258598021
9       151     viral genome expression
GO:0019083      3.0780454364018e-10     28.2596830985915        0.428413258598021
9       151     viral transcription
GO:0043624      3.46231979714923e-10    27.86328125     0.434087606394021       9
153     cellular protein complex disassembly
GO:0043241      4.61374173750134e-10    26.9188338926174        0.448273475884022
9       158     protein complex disassembly
GO:0034623      1.08778441201842e-09    24.28125        0.493668258252024       9
174     cellular macromolecular complex disassembly
GO:0032984      1.39799328206266e-09    23.5588235294118        0.507854127742025
9       179     macromolecular complex disassembly
GO:0072594      4.4227488584892e-09     20.5024038461538        0.578783475192028
9       204     establishment of protein localization to organelle
GO:0019058      1.30952947058241e-08    17.9746621621622        0.655387170438032
9       231     viral infectious cycle
GO:0022415      3.6450655186889e-08     15.8654133466135        0.737665213480036
9       260     viral reproductive process
GO:0071845      7.7797305744964e-08     14.45625        0.805757387032039       9
284     cellular component disassembly at cellular level
GO:0022411      8.76806949627709e-08    14.2449596774194        0.81710608262404
9       288     cellular component disassembly
GO:0016032      3.73388083111285e-07    10.2179796649843        1.27956542799806
10      451     viral reproduction
GO:0006605      5.89368934217687e-07    9.69549499443827        1.34482042765207
10      474     protein targeting
GO:0022613      2.89559201436361e-06    13.4031300593632        0.638364127050031
7       225     ribonucleoprotein complex biogenesis
GO:0071843      4.31571459631471e-06    12.5818965517241        0.678084561622033
7       239     cellular component biogenesis at cellular level
GO:0033365      5.50598763044479e-06    8.45325969827586        1.34198325375407
9       473     protein localization to organelle
Tissue: Skin_Sun_Exposed_Lower_leg=>Heart_Left_Ventricle        Type:   asymmetric
SourceGene:     RP11-697K23.1(ENSG00000230530.1)
TargetGeneSet:  RPL11   RP4     HSPB11  RP11    ISG20L2 SNRPE   LINC00467
RPL31   UBE2V1  RPL37A  MRPS36P1        CCDC72  RPL35A  FGFBP1  RPL37   CTD
ZMAT2   CTB     HMGN3   HOXA10  PPIA    ECD     SNHG6   RPL7    C8orf59 RPL30
EIF5AL1 LGI1    RPL13AP5        RPS13   RPS25   PFDN5   NDUFA12 RPS7P10 RPL7AP6
SLIRP   SLC9A5  RPL26   RPL17   RPL38   ZNF446  ZNF788  C19orf43        CHMP4B
ZFP64   ZNF280B EEF1B2P3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      1.3235913401609e-20     108.621212121212        0.220399972320255
13      91      translational termination
GO:0006414      9.4483628916079e-20     92.001976284585 0.254307660369525       13
105     translational elongation
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GO:0006614      8.23690392874817e-18    80.3534361851332        0.254307660369525
12      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      9.2746953447363e-18     79.4930619796485        0.25672963808733
12      106     cotranslational protein targeting to membrane
GO:0045047      9.2746953447363e-18     79.4930619796485        0.25672963808733
12      106     protein targeting to ER
GO:0072599      9.2746953447363e-18     79.4930619796485        0.25672963808733
12      106     establishment of protein localization to endoplasmic reticulum
GO:0043624      1.51258162845701e-17    60.2558441558442        0.370562590824164
13      153     cellular protein complex disassembly
GO:0043241      2.32048493093861e-17    58.1576802507837        0.382672479413189
13      158     protein complex disassembly
GO:0070972      3.53222326000842e-17    70.4347826086957        0.28579337070099
12      118     protein localization to endoplasmic reticulum
GO:0000184      3.92255015796649e-17    69.7716375457131        0.288215348418795
12      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0034623      8.33715556476071e-17    52.3193111236589        0.421424122898069
13      174     cellular macromolecular complex disassembly
GO:0032984      1.21219596404493e-16    50.7256297918949        0.433534011487094
13      179     macromolecular complex disassembly
GO:0019080      7.38464718823052e-16    53.588989677823 0.365718635388554       12
151     viral genome expression
GO:0019083      7.38464718823052e-16    53.588989677823 0.365718635388554       12
151     viral transcription
GO:0006413      8.00573661742737e-16    53.2024844720497        0.368140613106359
12      152     translational initiation
GO:0006612      8.67420286888113e-16    52.8214616096207        0.370562590824164
12      153     protein targeting to membrane
GO:0000956      2.9167203549835e-15     47.3852118526724        0.409314234309044
12      169     nuclear-transcribed mRNA catabolic process
GO:0019058      3.43206911950644e-15    38.4849874895746        0.559476852812954
13      231     viral infectious cycle
GO:0006402      5.47603091337228e-15    44.7878470403353        0.431112033769289
12      178     mRNA catabolic process
GO:0022415      1.59263847671525e-14    33.8971291866029        0.629714206629299
13      260     viral reproductive process
GO:0072594      2.84182596419508e-14    38.6521739130435        0.494083454432219
12      204     establishment of protein localization to organelle
GO:0006401      3.01403382904676e-14    38.4492002703312        0.496505432150024
12      205     RNA catabolic process
GO:0071845      4.97717584360643e-14    30.8428379738343        0.687841671856619
13      284     cellular component disassembly at cellular level
GO:0022411      5.95874574839357e-14    30.3856198347107        0.697529582727839
13      288     cellular component disassembly
GO:0016032      8.67784210839148e-13    21.3257055682685        1.09231195073005
14      451     viral reproduction
GO:0033365      5.53917792190179e-10    15.7936433084976        1.14559546052176
12      473     protein localization to organelle
GO:0006605      5.67447946559664e-10    15.7583286278938        1.14801743823957
12      474     protein targeting
GO:0042273      1.40745924811973e-08    232.387096774194        0.02906373261366
4       12      ribosomal large subunit biogenesis
GO:0022613      4.99760970587808e-08    19.3876088069636        0.544944986506124
8       225     ribonucleoprotein complex biogenesis
GO:0071843      7.97107515811943e-08    18.1946448613115        0.578852674555394
8       239     cellular component biogenesis at cellular level
GO:0042254      1.37762246487303e-06    20.6505907885218        0.360874679952944
6       149     ribosome biogenesis
Tissue: Whole_Blood=>Heart_Left_Ventricle       Type:   asymmetric
```

SourceGene: CAMK1D(ENSG00000183049.8) calcium/calmodulin-dependent protein kinase ID

TargetGeneSet: ATP6V0B RP11 HFE2 RNF115 NES CCL15 ASPM CENPF
EIF2AK3 BUB1 EXOG ZNF595 CD38 NADKD1 RHOBTB3 HSPA9 ARHGAP26
SH3PXD2B LRRC16A TNFRSF21 UBE3D EGFR GATSL2 GNRH1 PBK
COBRA1 IL2RA CDK1 PBLD PDLIM1 NT5C2 C11orf92 C11orf93
VPS26B TROAP MIS18BP1 DLGAP5 VRK1 ARHGAP11A BUB1B CASC5 PRC1
VPS35 CRISPLD2 MIR22HG TOP2A CCDC40 TPX2

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0000280	4.14E-09	14.26613201	1.041450419	11	350	nuclear division
GO:0007067	4.14E-09	14.26613201	1.041450419	11	350	mitosis
GO:0000087	5.55E-09	13.84751074	1.071206145	11	360	M phase of mitotic cell cycle
GO:0048285	7.38E-09	13.452211	1.100961871	11	370	organelle fission
GO:0051301	5.78E-08	10.88697562	1.344958826	11	452	cell division
GO:0071173	2.95E-06	49.15555556	0.101169469	4	34	spindle assembly checkpoint
GO:0031577	7.01E-06	38.7854251	0.12497405	4	42	spindle checkpoint

GO:0030071 7.71E-06 37.78829717 0.127949623 4 43
regulation of mitotic metaphase/anaphase transition

GO:0007091 9.27E-06 35.93996248 0.133900768 4 45
mitotic metaphase/anaphase transition

Tissue: Whole_Blood=>Heart_Left_Ventricle Type: cluster

SourceGene: CCDC144A(ENSG00000170160.10) coiled-coil domain containing 144A

TargetGeneSet: KHDRBS1 GNG5 HBXIP MDM4 MOGS SUCLG1 TSPO NDUFB3
RPL32 KIAA2018 UBXN7 NDUFC1 NDUFS6 JMY RPL39P3 COQ3 REV3L RP11
RNASET2 RBAK SRI RBM48 GIGYF1 DOCK5 RPL30 CYC1 NDUFB6 RPL35 U8
ZNF22 POLR3A RPL13AP5 RPL27A NDUFS3 TRMT112 FAU NUMA1 C11orf67
USP35 C11orf1 FOXRED1 DHX37 RPS29 PROX2 SLIRP C15orf57 ANP32A
GOLGA6L4 SLC9A5 C1QBP LSMD1 CCDC144A FAM106A SRP68P2 FBXL20 GJC1
SNRPD1 RPS15 RPL36 MRPL4 C19orf43 MAU2 PDCD2L MYH7B RPL28
RPS21 IFNGR2 ATP5O COX7B IDH3G

GOBPID Pvalue OddsRatio ExpCount Count Size Term

GO:0006415 7.52E-13 42.08700764 0.327451387 10 91
translational termination

GO:0006414 3.25E-12 35.84962406 0.377828524 10 105

translational elongation

GO:0006614	3.25E-12	35.84962406	0.377828524	10	105
SRP-dependent cotranslational protein targeting to membrane

GO:0006613	3.58E-12	35.47371032	0.381426891	10	106
cotranslational protein targeting to membrane

GO:0045047	3.58E-12	35.47371032	0.381426891	10	106
protein targeting to ER

GO:0072599	3.58E-12	35.47371032	0.381426891	10	106
establishment of protein localization to endoplasmic reticulum

GO:0070972	1.06E-11	31.50573192	0.424607294	10	118
protein localization to endoplasmic reticulum

GO:0000184	1.16E-11	31.21450415	0.428205661	10	119
"nuclear-transcribed mRNA catabolic process, nonsense-mediated decay"

GO:0045333	6.78E-11	25.73412698	0.510968099	10	142

cellular respiration

GO:0072594 1.23E-10 19.7480096 0.734066847 11 204
establishment of protein localization to organelle

GO:0019080 1.25E-10 24.07632557 0.543353401 10 151
viral genome expression

GO:0019083 1.25E-10 24.07632557 0.543353401 10 151
viral transcription

GO:0006401 1.30E-10 19.64483279 0.737665213 11 205 RNA
catabolic process

GO:0006413 1.33E-10 23.90509725 0.546951768 10 152
translational initiation

GO:0006612 1.42E-10 23.73626374 0.550550135 10 153
protein targeting to membrane

GO:0043624 1.42E-10 23.73626374 0.550550135 10 153

						cellular protein complex disassembly
GO:0043241	1.96E-10	22.92631918	0.568541969	10	158	protein complex disassembly
GO:0000956	3.79E-10	21.32374963	0.608124005	10	169	nuclear-transcribed mRNA catabolic process
GO:0019058	4.66E-10	17.29146341	0.831222753	11	231	viral infectious cycle
GO:0034623	5.05E-10	20.66637631	0.62611584	10	174	cellular macromolecular complex disassembly
GO:0006402	6.31E-10	20.16865079	0.640509307	10	178	mRNA catabolic process
GO:0032984	6.67E-10	20.04790082	0.644107674	10	179	macromolecular complex disassembly
GO:0022415	1.63E-09	15.24635126	0.935575393	11	260	

viral reproductive process

GO:0022904 1.67E-09 29.56818182 0.345443222 8 96
respiratory electron transport chain

GO:0015980 9.26E-09 12.78287739 1.104698637 11 307
energy derivation by oxidation of organic compounds

GO:0022900 2.37E-08 20.5959596 0.482181164 8 134
electron transport chain

GO:0071845 5.60E-08 12.27407021 1.021936198 10 284
cellular component disassembly at cellular level

GO:0022411 6.39E-08 12.09403905 1.036329666 10 288
cellular component disassembly

GO:0006120 1.72E-07 49.30679478 0.129541208 5 36
"mitochondrial electron transport, NADH to ubiquinone"

GO:0006091 2.74E-07 8.995847225 1.540101031 11 428

generation of precursor metabolites and energy

GO:0016032	4.61E-07	8.511585366	1.62286347	11	451	viral reproduction
GO:0042773	6.78E-07	36.36524823	0.169123244	5	47	ATP synthesis coupled electron transport
GO:0042775	6.78E-07	36.36524823	0.169123244	5	47	mitochondrial ATP synthesis coupled electron transport
GO:0033365	7.38E-07	8.093495935	1.702027541	11	473	protein localization to organelle
GO:0006605	7.54E-07	8.075435916	1.705625908	11	474	protein targeting
GO:0006119	1.97E-06	28.79566439	0.20870528	5	58	oxidative phosphorylation

Tissue: Whole_Blood=>Heart_Left_Ventricle Type: asymmetric

SourceGene: CLEC5A(ENSG00000258227.2) "C-type lectin domain family 5, member A"

TargetGeneSet: WRAP73 THAP3 H6PD ZBTB17 KIF2C NOTCH2NL JTB IQGAP3 CCDC19 ASPM KIF14 GALNT3 ILKAP FANCD2 CD38 GLRB KIF20A CDC25C ARHGAP26 ZNF193 KIFC1 RP11 NDUFAF4 VIP CCT6A SND1 PBK GINS4 GKAP1 CDK1 PBLD MKI67 U6 CDCA5 SIDT2 ZNF202 TROAP PLBD2 DLGAP5 GSTZ1 ALKBH1 ARHGAP11A FMN1 BUB1B RAD51 NUSAP1 FANCI PRC1 SULT1A2 WWOX ATP6V0CP1 AURKB C17orf108 TOP2A KIF18B PRR11 BRIP1 QRICH2 BIRC5 THOC1 ATP9B PIAS4 ZGLP1 IRF2BP1 TPX2 RP3 GTSE1 RBM3 KIF4A

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0000087	1.16E-12	14.51782946	1.51961802	16	360	M phase of mitotic cell cycle
GO:0000280	1.10E-11	13.68105127	1.477406408	15	350	nuclear division
GO:0007067	1.10E-11	13.68105127	1.477406408	15	350	mitosis
GO:0048285	2.43E-11	12.89191672	1.561829631	15	370	organelle fission

GO:0051301	3.59E-11	11.37940877	1.907964847	16	452	cell division
GO:0007017	6.77E-10	11.01184528	1.658916338	14	393	microtubule-based process
GO:0007059	1.21E-07	16.30417381	0.590962563	8	140	chromosome segregation
GO:0010564	1.28E-07	8.521474261	1.747560722	12	414	regulation of cell cycle process
GO:0007346	4.96E-07	9.433848625	1.279011833	10	303	regulation of mitotic cell cycle
GO:0034501	1.42E-06	248.0517241	0.025326967	3	6	protein localization to kinetochore
GO:0007018	2.14E-06	13.68792867	0.599404885	7	142	microtubule-based movement

GO:0034502	2.40E-06	53.07848569	0.097086707	4	23
protein localization to chromosome					
GO:0000819	2.53E-06	27.24734043	0.219500381	5	52
sister chromatid segregation					
GO:0000910	2.68E-06	17.72975207	0.39678915	6	94
cytokinesis					
GO:0030261	7.25E-06	38.76923077	0.126634835	4	30
chromosome condensation					
GO:0000226	1.63E-05	8.171184848	1.135492353	8	269
microtubule cytoskeleton organization					

Tissue: Heart_Left_Ventricle=>Whole_Blood Type: cluster

SourceGene: DPP4(ENSG00000197635.5) dipeptidyl-peptidase 4

TargetGeneSet: RP11 CDCA8 KIF2C TNFSF13B CENPF NCAPH SMPD4 SPC25 FANCD2 CXCL3 CCNA2 CDC25C GFPT2 MCM7 EZH2 CDCA2 ESCO2 MCM4 DSCC1 ATAD2 TONSL ANP32B SMC2 ATP6V1G1 WDR34 MCM10 ZWINT CDK1

KIF11 HELLS SMC3 FEN1 CDCA5 H2AFX CHEK1 NCAPD3 MPP2 RACGAP1 RFC3
WDHD1 DLGAP5 CASC5 WDR76 KIF23 FANCI C15orf42 RCCD1 KIF22
HIRIP3 CDT1 HSPB9 PSMC3IP TK1 BIRC5 TYMS SKA1 UHRF1 SPC24
RNASEH2A FKBP1A-SDCBP2 TPX2 AURKA C21orf128 CDC45

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0000280	1.54E-30	42.19490255	1.380527299	28	350	nuclear division
GO:0007067	1.54E-30	42.19490255	1.380527299	28	350	mitosis
GO:0000087	3.44E-30	40.8948899	1.419970936	28	360	M phase of mitotic cell cycle
GO:0048285	7.48E-30	39.67090139	1.459414573	28	370	organelle fission
GO:0010564	1.52E-22	26.11468531	1.632966577	24	414	regulation of cell cycle process
GO:0051301	1.22E-21	23.73152082	1.782852398	24	452	cell division
GO:0006260	2.23E-19	28.40361446	1.057089475	19	268	DNA replication

GO:0007059	4.51E-18	40.76857143	0.55221092	15	140	chromosome segregation
GO:0071156	1.22E-16	24.34200405	1.04131202	17	264	regulation of cell cycle arrest
GO:0000075	7.32E-16	24.46449385	0.954536018	16	242	cell cycle checkpoint
GO:0007050	3.18E-14	16.95411932	1.45547021	17	369	cell cycle arrest
GO:0051329	4.93E-14	16.47403315	1.494913847	17	379	interphase of mitotic cell cycle
GO:0051325	6.94E-14	16.10864865	1.526468756	17	387	interphase
GO:0045786	4.99E-13	14.14035714	1.723686942	17	437	negative regulation of cell cycle
GO:0006281	9.33E-13	14.91539842	1.510691302	16	383	DNA

repair

GO:0000236	9.91E-13	40.6212766	0.335270916	10	85	mitotic prometaphase
GO:0007017	1.97E-11	13.24263039	1.550134939	15	393	microtubule-based process
GO:0000226	2.85E-11	16.31693892	1.061033838	13	269	microtubule cytoskeleton organization
GO:0006261	8.90E-11	31.94196429	0.366825825	9	93	DNA-dependent DNA replication
GO:0007346	1.25E-10	14.369279	1.195142205	13	303	regulation of mitotic cell cycle
GO:0000086	2.04E-10	22.64210861	0.567988375	10	144	G2/M transition of mitotic cell cycle
GO:0000070	7.67E-10	47.84	0.193273822	7	49	mitotic sister chromatid segregation

GO:0007051	8.18E-10	32.47619048	0.315549097	8	80	spindle organization
GO:0000819	1.18E-09	44.64133333	0.205106913	7	52	sister chromatid segregation
GO:0010389	1.59E-09	70.44117647	0.118330911	6	30	regulation of G2/M transition of mitotic cell cycle
GO:0007052	2.93E-09	62.60130719	0.130164002	6	33	mitotic spindle organization
GO:0051052	4.22E-08	15.06038136	0.73365165	9	186	regulation of DNA metabolic process
GO:0071103	4.85E-08	14.80625	0.745484742	9	189	DNA conformation change
GO:0006270	7.32E-08	60.07943144	0.110442184	5	28	DNA-dependent DNA replication initiation
GO:0030261	1.05E-07	55.26538462	0.118330911	5	30	chromosome condensation

GO:0006323	1.40E-07	16.04391274	0.603487648	8	153	DNA packaging
GO:0007076	1.51E-07	120.6289308	0.051276728	4	13	mitotic chromosome condensation
GO:0006271	2.03E-07	47.62931034	0.134108366	5	34	DNA strand elongation involved in DNA replication
GO:0022616	3.16E-07	43.15504808	0.145941457	5	37	DNA strand elongation
GO:0000082	6.25E-07	13.03921119	0.73365165	8	186	G1/S transition of mitotic cell cycle
GO:0031570	1.00E-06	15.48139535	0.536433465	7	136	DNA integrity checkpoint
GO:0050000	1.24E-06	63.82685905	0.082831638	4	21	chromosome localization
GO:0051303	1.24E-06	63.82685905	0.082831638	4	21	establishment of chromosome localization

GO:0051320	1.40E-06	14.67735294	0.564044011	7	143	S phase
GO:0000083	1.51E-06	60.27672956	0.086776002	4	22	regulation of transcription involved in G1/S phase of mitotic cell cycle
GO:0006275	1.58E-06	19.57318741	0.362881461	6	92	regulation of DNA replication
GO:0010948	2.03E-06	18.69803922	0.378658916	6	96	negative regulation of cell cycle process
GO:0006302	2.89E-06	17.52205882	0.402325099	6	102	double-strand break repair
GO:0000076	6.85E-06	114.1825397	0.039443637	3	10	DNA replication checkpoint
GO:0007062	7.20E-06	38.72237197	0.126219639	4	32	sister chromatid cohesion
GO:0070507	1.19E-05	19.39734561	0.299771642	5	76	regulation of microtubule cytoskeleton organization

GO:0010972	1.25E-05	88.7962963	0.047332365	3	12	negative regulation of G2/M transition of mitotic cell cycle
GO:0000084	1.40E-05	13.11213235	0.528544737	6	134	S phase of mitotic cell cycle
GO:0000216	1.44E-05	18.60706861	0.311604733	5	79	M/G1 transition of mitotic cell cycle
GO:0090307	1.62E-05	79.91111111	0.051276728	3	13	spindle assembly involved in mitosis
GO:0006310	1.71E-05	9.836039604	0.824372016	7	209	DNA recombination
GO:0031576	1.79E-05	30.10062893	0.157774548	4	40	G2/M transition checkpoint
GO:0007018	1.95E-05	12.33391003	0.560099647	6	142	microtubule-based movement
GO:0007098	1.98E-05	29.28505864	0.161718912	4	41	centrosome cycle

Tissue: Heart_Left_Ventricle=>Whole_Blood Type: cluster

SourceGene: ENSG00000237298.1

TargetGeneSet: CDCA8 CDC20 KIF2C RWDD3 IQGAP3 TNFSF13B RRM2
IGKJ5 IGKC IGKJ4 IGKJ1 IGKV1-5 IGKV1-9 IGKV1-17 IGKV2-28
NCAPH BUB1 ITM2C HJURP KIF15 CDC25A CCNB1 RP11 MCM7 EZH2
MYOM2 MCM4 WDR34 MCM10 CDK1 ART5 CDCA5 POU2AF1 ABCB9 RFC3
DLGAP5 IFI27L2 IGHA2 IGHG2 IGHGP IGHA1 IGHV6-1 BUB1B CASC5 NUSAP1
FANCI PKMYT1 PLK1 GINS2 AURKB SPAG5 CDC6 TYMS SKA1 PCNA TPX2
MYBL2 CDC45 IGLV4-69 IGLV1-51 IGLV7-46 IGLV7-43
IGLV2-23 IGLV3-19 IGLV2-14 IGLV2-8 IGLL5 IGLJ1 IGLC1
DERL3

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0000280	7.03E-23	33.7114547	1.210988859	22	350	nuclear division
GO:0007067	7.03E-23	33.7114547	1.210988859	22	350	mitosis
GO:0000087	1.31E-22	32.6908284	1.245588541	22	360	M phase of mitotic cell cycle

GO:0048285	2.38E-22	31.72885878	1.280188222	22	370	organelle fission
GO:0010564	1.88E-18	23.70050761	1.432426822	20	414	regulation of cell cycle process
GO:0007059	9.82E-16	39.48967866	0.484395544	13	140	chromosome segregation
GO:0000082	1.31E-15	32.17151163	0.643554079	14	186	G1/S transition of mitotic cell cycle
GO:0051329	4.12E-15	19.97848652	1.311327936	17	379	interphase of mitotic cell cycle
GO:0051301	4.22E-15	18.10239055	1.563905612	18	452	cell division
GO:0051325	5.81E-15	19.53538084	1.339007681	17	387	interphase

GO:0000075	5.14E-14	24.17422027	0.837312297	14	242	cell cycle checkpoint
GO:0071156	1.71E-13	22.01266667	0.913431596	14	264	regulation of cell cycle arrest
GO:0000236	2.44E-13	47.75333333	0.294097294	10	85	mitotic prometaphase
GO:0051983	1.27E-12	137.7400821	0.083039236	7	24	regulation of chromosome segregation
GO:0007050	1.60E-11	15.38685446	1.276728254	14	369	cell cycle arrest
GO:0007017	3.70E-11	14.3878628	1.35976749	14	393	microtubule-based process
GO:0006260	8.40E-11	17.44860197	0.927271469	12	268	DNA replication
GO:0000226	8.77E-11	17.37947983	0.930731437	12	269	microtubule cytoskeleton organization

GO:0000083	9.00E-11	122.5994318	0.0761193	6	22	regulation of transcription involved in G1/S phase of mitotic cell cycle
GO:0045786	1.51E-10	12.85080116	1.51200609	14	437	negative regulation of cell cycle
GO:0007346	3.46E-10	15.31199132	1.048370355	12	303	regulation of mitotic cell cycle
GO:0007088	5.96E-10	34.09761905	0.304477199	8	88	regulation of mitosis
GO:0051783	5.96E-10	34.09761905	0.304477199	8	88	regulation of nuclear division
GO:0006271	1.57E-09	69.99837662	0.117638918	6	34	DNA strand elongation involved in DNA replication
GO:0033043	2.12E-09	11.47063652	1.525845962	13	441	regulation of organelle organization

GO:0022616	2.70E-09	63.2111437	0.128018822	6	37	DNA strand elongation
GO:0034502	1.30E-08	88.78395062	0.079579268	5	23	protein localization to chromosome
GO:0000070	1.57E-08	45.53276956	0.16953844	6	49	mitotic sister chromatid segregation
GO:0000084	1.71E-08	21.57974301	0.463635735	8	134	S phase of mitotic cell cycle
GO:0000819	2.27E-08	42.55434783	0.179918345	6	52	sister chromatid segregation
GO:0051320	2.86E-08	20.12839506	0.494775448	8	143	S phase
GO:0030261	5.39E-08	63.89333333	0.103799045	5	30	chromosome condensation

GO:0000090	6.15E-08	156.4456522	0.041519618	4	12	mitotic anaphase
GO:0051322	1.24E-07	125.1391304	0.048439554	4	14	anaphase
GO:0071103	2.48E-07	14.96448303	0.653933984	8	189	DNA conformation change
GO:0008608	2.92E-07	96.24080268	0.058819459	4	17	attachment of spindle microtubules to kinetochore
GO:0007051	3.11E-07	26.40110565	0.276797453	6	80	spindle organization
GO:0031577	3.12E-07	43.13513514	0.145318663	5	42	spindle checkpoint
GO:0030071	3.52E-07	41.99707602	0.148778631	5	43	regulation of mitotic metaphase/anaphase transition

GO:0031145	3.88E-07	25.36717828	0.287177358	6	83	anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process
GO:0007091	4.45E-07	39.89166667	0.155698568	5	45	mitotic metaphase/anaphase transition
GO:0051313	4.73E-07	83.39710145	0.065739395	4	19	attachment of spindle microtubules to chromosome
GO:0000086	5.88E-07	16.94924461	0.498235416	7	144	G2/M transition of mitotic cell cycle
GO:0006958	7.61E-07	35.44691358	0.172998408	5	50	"complement activation, classical pathway"
GO:0006261	7.64E-07	22.43573668	0.32177704	6	93	DNA-dependent DNA replication
GO:0034501	7.74E-07	306.3404255	0.020759809	3	6	protein localization to kinetochore

GO:0006323	8.86E-07	15.89439312	0.52937513	7	153	DNA packaging
GO:0006956	2.44E-06	27.47701149	0.217977995	5	63	complement activation
GO:0002460	2.73E-06	13.31047848	0.626254238	7	181	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains
GO:0033205	2.83E-06	50.00347826	0.100339077	4	29	cell cycle cytokinesis
GO:0002455	2.85E-06	26.55740741	0.224897931	5	65	humoral immune response mediated by circulating immunoglobulin
GO:0006959	3.75E-06	16.7927116	0.422116117	6	122	humoral immune response
GO:0007052	4.82E-06	43.09445277	0.11417895	4	33	mitotic spindle organization

GO:0002250	4.95E-06	12.11128698	0.685073697	7	198	adaptive immune response
GO:0071173	5.45E-06	41.65507246	0.117638918	4	34	spindle assembly checkpoint
GO:0034453	6.13E-06	40.3085554	0.121098886	4	35	microtubule anchoring
GO:0071174	6.88E-06	39.04619565	0.124558854	4	36	mitotic cell cycle spindle checkpoint
GO:0051439	7.05E-06	21.80821918	0.269877517	5	78	regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
GO:0043161	7.06E-06	11.44289662	0.723133347	7	209	proteasomal ubiquitin-dependent protein catabolic process
GO:0000216	7.51E-06	21.51201201	0.273337485	5	79	M/G1 transition of mitotic cell cycle

GO:0010498	8.75E-06	11.05418938	0.747353124	7	216	proteasomal protein catabolic process
GO:0072376	9.02E-06	20.66955267	0.28371739	5	82	protein activation cascade
GO:0000079	9.57E-06	20.4031339	0.287177358	5	83	regulation of cyclin-dependent protein kinase activity
GO:0007076	1.09E-05	91.85744681	0.044979586	3	13	mitotic chromosome condensation
GO:0010948	1.95E-05	17.47252747	0.332156944	5	96	negative regulation of cell cycle process
GO:0051438	1.95E-05	17.47252747	0.332156944	5	96	regulation of ubiquitin-protein ligase activity

Tissue: Heart_Left_Ventricle=>Whole_Blood Type: cluster
SourceGene: ENSG00000260964.1
TargetGeneSet: CDC20 KIF2C RP11 DEPDC1 IQGAP3 APOA1BP CENPF NCAPH

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CKAP2L  DNAJC10 PID1    CAMK1   KIF15   CD86    PLK4    MARCH1  CLCN3   CCNB1
PTTG1   HLA-DPA1        KIFC1   EZH2    CDCA2   FBXO43  ENG     ESPL1   IKBIP
GPR183  CEBPE   DLGAP5  BUB1B   TLN2    RCCD1   NME4    HN1L    ABI3    BRIP1   SKA1
CTD     SUGP1   WDR62   ARHGAP35        GINS1   KCTD17  ATXN10  RP13
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0000280      1.07074260135991e-11    18.7185101811112        1.0172306414781 13
350     nuclear division
GO:0007067      1.07074260135991e-11    18.7185101811112        1.0172306414781 13
350     mitosis
GO:0000087      1.5248419935658e-11     18.1661532346219        1.04629437409176
13      360     M phase of mitotic cell cycle
GO:0048285      2.14907455434004e-11    17.6447406548826        1.07535810670542
13      370     organelle fission
GO:0007059      1.97213566160475e-10    29.7251908396947        0.406892256591239
9       140     chromosome segregation
GO:0051301      4.42700214233742e-08    11.2389730085583        1.31368071413743
11      452     cell division
GO:0030071      1.4385899176527e-07     51.1059743954481        0.124974050238738
5       43      regulation of mitotic metaphase/anaphase transition
GO:0000236      1.53329632772209e-07    30.2320675105485        0.24704172721611
6       85      mitotic prometaphase
GO:0007091      1.81811730010386e-07    48.5439189189189        0.13078679676147
5       45      mitotic metaphase/anaphase transition
GO:0000070      2.81351512788933e-07    44.1185503685504        0.142412289806934
5       49      mitotic sister chromatid segregation
GO:0000819      3.81014127946705e-07    41.2938470385279        0.151131409591032
5       52      sister chromatid segregation
GO:0007017      1.49505621429259e-06    9.9609375       1.14220469171684        9
393     microtubule-based process
GO:0071174      3.39342499763601e-06    47.2927631578947        0.104629437409176
4       36      mitotic cell cycle spindle checkpoint
GO:0033043      3.85331021273676e-06    8.82386363636364        1.2817106082624 9
441     regulation of organelle organization
GO:0007088      5.31813666563279e-06    23.324649951156 0.255760847000208       5
88      regulation of mitosis
GO:0051783      5.31813666563279e-06    23.324649951156 0.255760847000208       5
88      regulation of nuclear division
GO:0031577      6.36721579592055e-06    39.808864265928 0.122067676977372       4
42      spindle checkpoint
Tissue: Whole_Blood=>Heart_Left_Ventricle       Type:   asymmetric



SourceGene:     FTH1P25(ENSG00000232792.1)      "ferritin, heavy polypeptide 1
pseudogene 25"



TargetGeneSet:  LAPTM5  CD53    CTSS    LCP2    DOK3    DEFA6   CARD9   SPI1
MS4A7   FERMT3  PTPN6   RP11    SELPLG  KIAA1737        PLCB2   CORO1A  SCIMP
ACAP1   HMHA1   VAV1    STXBP2  IFI30   TYROBP  CD37    LILRB1  HCK     CYTH4
SASH3

GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term



GO:0002252      3.90E-06        13.65393695     0.694484811     7       386
immune effector process
```

GO:0050870	1.18E-05	20.45180723	0.30766037	5	171	positive regulation of T cell activation
GO:0002694	1.81E-05	13.43809524	0.577537887	6	321	regulation of leukocyte activation

Tissue: Whole_Blood=>Heart_Left_Ventricle Type: asymmetric

SourceGene: NF1(ENSG00000196712.10) neurofibromin 1

TargetGeneSet: RP4 FLG2 CRCT1 LCE1A IVL NPR1 SHE RAB25 MALL
SPC25 RNU5B-3P DKK2 RP11 BAG2 INTS10 SLURP1 ZCCHC7 SH2D3C
EMILIN3 TRIM29 ESAM KRT5 KRT2 KRT1 KRT77 DCD MUCL1 SCEL
CLEC14A PRKCH IFI27 CHST14 FES TNS4 KRT10 KRT15 TK1 DSC2
SERPINB5 SBSN RASIP1 KLK5 SMOX FAM83C

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0008544	3.30E-10	22.94574899	0.622448273	10	257	epidermis development
GO:0030216	8.99E-08	33.68652038	0.227665905	6	94	keratinocyte differentiation
GO:0009913	2.30E-07	28.47214854	0.266417549	6	110	epidermal cell differentiation

Tissue: Whole_Blood=>Heart_Left_Ventricle Type: asymmetric

SourceGene: OSBP2(ENSG00000184792.11) oxysterol binding protein 2

TargetGeneSet: THAP3 ATP6V0B IQGAP3 RP11 AUP1 ILKAP FANCD2 ARHGAP31-AS1
ZCCHC9 GTF2H4 HCG22 ZNHIT1 FAM115B TM2D2 ARMC1 WDR67 CD72 TLN1 MELK
MRPS2 C9orf142 C10orf71 MKI67 IGF2 ACER3 TROAP DDIT3
SLC7A7 BRMS1L SAMD4A BUB1B RAD51 KIF23 STARD5 FANCI CCDC78 NARFL E4F1
COX4NB SPATA2L DERL2 SCO1 TOP2A KIF18B BRIP1 ABHD8 LGALS4 BCAT2 CTB
FKBP1A-SDCBP2 SLMO2 APOBEC3B SGSM3 GTSE1

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term

Tissue: Heart_Left_Ventricle=>Whole_Blood Type: asymmetric

SourceGene: PIK3R2(ENSG00000105647.8) "phosphoinositide-3-kinase, regulatory subunit 2"

TargetGeneSet: CDCA8 KIF2C PKLR LZTFL1 PHF7 BMP2K TRIP13 CTD
CDC25C HLA-DRB5 HLA-DRB1 HLA-DQB1 KIFC1 NDUFAF4 CD164 PKIB
PCMT1 WIPI2 RP11 MRPL50 ZNF32-AS2 SIGIRR CDCA3 ESPL1 CHST11 RFC3
SLAIN1 CLYBL PCID2 GSTZ1 HMGN2P5 KIAA0101 CLN6 BLM CCDC101
ITGAM PITPNM3 BRIP1 TK1 TYMS CIRBP SPC24 TNPO2 RASAL3 JAK3
PRR24 FUZ ZNF446 CDC45 RP4 RIBC1 CETN2

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0051301	3.80E-06	8.867310948	1.282402602	9	452	cell division
GO:0000280	5.20E-06	9.972000709	0.993010864	8	350	nuclear division
GO:0007067	5.20E-06	9.972000709	0.993010864	8	350	mitosis

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GO:0000087      6.39E-06        9.681818182     1.021382603     8       360     M
phase of mitotic cell cycle




GO:0048285      7.81E-06        9.407667839     1.049754342     8       370
organelle fission




Tissue: Heart_Left_Ventricle=>Whole_Blood       Type:   asymmetric



SourceGene:     RCAN3(ENSG00000117602.6)        RCAN family member 3



TargetGeneSet:  FCRL5   RP11    SH2D6   SULT1C2 BANK1   GALNTL6 RSPH9   BLK     PAX5
ACTR1A  GYLTL1B MS4A1   CD27    DTX1    TCL1B   KIAA0125        IGHV1-2 IGHV1-24
PLA2G4B CD19    SPDYE4  HDAC5   CD79B   FCER2   RHPN2   CD79A   SPIB    IGLC5
TNFRSF13C       TCEAL6

GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term



GO:0042113      8.28E-08        36.43367347     0.232925057     6       153     B
cell activation



GO:0046649      2.39E-06        15.33974961     0.659193135     7       433
lymphocyte activation



Tissue: Whole_Blood=>Heart_Left_Ventricle       Type:   asymmetric
SourceGene:     RP11-1033H12.3(ENSG00000258440.1)
TargetGeneSet:  RPL22   RPL11   AK2     RPL5    RP11    PSMA5   ACP1    SLC4A1AP
UBC     RNF181  RPL15   C3orf26 RPL24   RPL35A  BTF3    PCDHGA1 CTB     RPS14
MRPS12  ATP6V1F UBE3C   PPP2CB  RPS20   RPL7    ENY2    GLRX3   RPS13   CRYAB
STRAP   PSMC6   PSMC1   AHNAK2  RPL26   KCNJ12  PSMB3   RPL17   DNAJC7  SLMO1
C18orf21        RPL18   SNRPB   EEF1B2P3        RPS23P8
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      1.13024861698362e-22    124.147186147186        0.220399972320255
14      91      translational termination
GO:0006414      9.52400953644563e-22    104.945054945055        0.254307660369525
14      105     translational elongation
GO:0006614      9.52400953644563e-22    104.945054945055        0.254307660369525
14      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.0958337582712e-21     103.797101449275        0.25672963808733
14      106     cotranslational protein targeting to membrane
GO:0045047      1.0958337582712e-21     103.797101449275        0.25672963808733
14      106     protein targeting to ER
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GO:0072599      1.0958337582712e-21     103.797101449275        0.25672963808733
14      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      5.32068668405306e-21    91.7435897435897        0.28579337070099
14      118     protein localization to endoplasmic reticulum
GO:0000184      6.02187460500713e-21    90.8634920634921        0.288215348418795
14      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      1.92429404839666e-19    69.4841849148418        0.365718635388554
14      151     viral genome expression
GO:0019083      1.92429404839666e-19    69.4841849148418        0.365718635388554
14      151     viral transcription
GO:0006413      2.11661143776567e-19    68.975845410628 0.368140613106359       14
152     translational initiation
GO:0006612      2.32660648605977e-19    68.4748201438849        0.370562590824164
14      153     protein targeting to membrane
GO:0043624      2.32660648605977e-19    68.4748201438849        0.370562590824164
14      153     cellular protein complex disassembly
GO:0043241      3.6978387346578e-19     66.0740740740741        0.382672479413189
14      158     protein complex disassembly
GO:0000956      9.72417227373162e-19    61.3376344086021        0.409314234309044
14      169     nuclear-transcribed mRNA catabolic process
GO:0034623      1.47654099777653e-18    59.4    0.421424122898069       14      174
cellular macromolecular complex disassembly
GO:0016032      1.57149853098814e-18    34.1929085722049        1.09231195073005
18      451     viral reproduction
GO:0006402      2.04378168080614e-18    57.9349593495935        0.431112033769289
14      178     mRNA catabolic process
GO:0032984      2.21415407274473e-18    57.579797979798 0.433534011487094       14
179     macromolecular complex disassembly
GO:0072594      1.42425792613121e-17    49.9157894736842        0.494083454432219
14      204     establishment of protein localization to organelle
GO:0006401      1.52655504908356e-17    49.6509598603839        0.496505432150024
14      205     RNA catabolic process
GO:0019058      8.25737690205258e-17    43.6221198156682        0.559476852812954
14      231     viral infectious cycle
GO:0022415      4.34881362463966e-16    38.4010840108401        0.629714206629299
14      260     viral reproductive process
GO:0071845      1.49317566910718e-15    34.9283950617284        0.687841671856619
14      284     cellular component disassembly at cellular level
GO:0022411      1.81445639266429e-15    34.4087591240876        0.697529582727839
14      288     cellular component disassembly
GO:0033365      1.65509849938895e-12    20.2716049382716        1.14559546052176
14      473     protein localization to organelle
GO:0006605      1.70309181669195e-12    20.2260869565217        1.14801743823957
14      474     protein targeting
GO:0042273      4.83997390650977e-11    343.071428571429        0.02906373261366
5       12      ribosomal large subunit biogenesis
GO:0022613      4.99760970587808e-08    19.3876088069636        0.544944986506124
8       225     ribonucleoprotein complex biogenesis
GO:0071843      7.97107515811943e-08    18.1946448613115        0.578852674555394
8       239     cellular component biogenesis at cellular level
GO:0006364      1.64612882806908e-07    30.2280084447572        0.25188568265172
6       104     rRNA processing
GO:0016072      2.29963934403525e-07    28.4721485411141        0.26641754895855
6       110     rRNA metabolic process
GO:0006977      4.97362279991076e-07    39.2213114754098        0.15985052937513
5       66      DNA damage response, signal transduction by p53 class mediator
resulting in cell cycle arrest
GO:0072413      4.97362279991076e-07    39.2213114754098        0.15985052937513
5       66      signal transduction involved in mitotic cell cycle checkpoint
GO:0072431      4.97362279991076e-07    39.2213114754098        0.15985052937513
5       66      signal transduction involved in mitotic cell cycle G1/S transition
DNA damage checkpoint
GO:0072474      4.97362279991076e-07    39.2213114754098        0.15985052937513
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5       66      signal transduction involved in mitotic cell cycle G1/S checkpoint
GO:0051436      5.36541489798949e-07    38.5860215053763        0.162272507092935
5       67      negative regulation of ubiquitin-protein ligase activity involved in
mitotic cell cycle
GO:0072401      5.36541489798949e-07    38.5860215053763        0.162272507092935
5       67      signal transduction involved in DNA integrity checkpoint
GO:0072404      5.36541489798949e-07    38.5860215053763        0.162272507092935
5       67      signal transduction involved in G1/S transition checkpoint
GO:0072422      5.36541489798949e-07    38.5860215053763        0.162272507092935
5       67      signal transduction involved in DNA damage checkpoint
GO:0072395      5.78121366136425e-07    37.9708994708995        0.16469448481074
5       68      signal transduction involved in cell cycle checkpoint
GO:0051352      7.70609308533534e-07    35.6940298507463        0.17438239568196
5       72      negative regulation of ligase activity
GO:0051437      7.70609308533534e-07    35.6940298507463        0.17438239568196
5       72      positive regulation of ubiquitin-protein ligase activity involved in
mitotic cell cycle
GO:0051444      7.70609308533534e-07    35.6940298507463        0.17438239568196
5       72      negative regulation of ubiquitin-protein ligase activity
GO:0031571      8.25839238324015e-07    35.1666666666667        0.176804373399765
5       73      mitotic cell cycle G1/S transition DNA damage checkpoint
GO:0002479      9.45662089990647e-07    34.1571428571429        0.181648328835375
5       75      antigen processing and presentation of exogenous peptide antigen via
MHC class I, TAP-dependent
GO:0051439      1.15070253195326e-06    32.7465753424658        0.18891426198879
5       78      regulation of ubiquitin-protein ligase activity involved in mitotic
cell cycle
GO:0000216      1.22632538943352e-06    32.3018018018018        0.191336239706595
5       79      M/G1 transition of mitotic cell cycle
GO:0042590      1.22632538943352e-06    32.3018018018018        0.191336239706595
5       79      antigen processing and presentation of exogenous peptide antigen via
MHC class I
GO:0071158      1.3058151925104e-06     31.8688888888889        0.1937582174244 5
80      positive regulation of cell cycle arrest
GO:0042254      1.37762246487303e-06    20.6505907885218        0.360874679952944
6       149     ribosome biogenesis
GO:0031575      1.47696702907015e-06    31.0367965367965        0.19860217286001
5       82      mitotic cell cycle G1/S transition checkpoint
GO:0051443      1.47696702907015e-06    31.0367965367965        0.19860217286001
5       82      positive regulation of ubiquitin-protein ligase activity
GO:0002478      1.56892269816487e-06    30.6367521367521        0.201024150577815
5       83      antigen processing and presentation of exogenous peptide antigen
GO:0031145      1.56892269816487e-06    30.6367521367521        0.201024150577815
5       83      anaphase-promoting complex-dependent proteasomal ubiquitin-dependent
protein catabolic process
GO:0019884      1.76635167310192e-06    29.8666666666667        0.205868106013425
5       85      antigen processing and presentation of exogenous antigen
GO:0051351      1.87213794113529e-06    29.4958847736626        0.20829008373123
5       86      positive regulation of ligase activity
GO:0071779      1.87213794113529e-06    29.4958847736626        0.20829008373123
5       86      G1/S transition checkpoint
GO:0000209      2.16420693584304e-06    19.0358175750834        0.389938412566604
6       161     protein polyubiquitination
GO:0031397      2.61623622572555e-06    27.4501915708812        0.22282195003806
5       92      negative regulation of protein ubiquitination
GO:0051438      3.22934745288586e-06    26.2362637362637        0.23250986090928
5       96      regulation of ubiquitin-protein ligase activity
GO:0002474      3.7591586958813e-06     25.3936170212766        0.239775794062695
5       99      antigen processing and presentation of peptide antigen via MHC class
I
GO:2000045      3.7591586958813e-06     25.3936170212766        0.239775794062695
5       99      regulation of G1/S transition of mitotic cell cycle
GO:0051340      3.95015569920992e-06    25.1245614035088        0.2421977717805 5
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100     regulation of ligase activity
GO:0034660      4.51600848980766e-06    12.7140287769784        0.690263649574424
7       285     ncRNA metabolic process
GO:0048002      5.76797129387682e-06    23.1601941747573        0.26157359352294
5       108     antigen processing and presentation of peptide antigen
GO:0034470      7.57338935750658e-06    15.1674369001066        0.484395543560999
6       200     ncRNA processing
GO:0030330      8.53563514448506e-06    21.2857142857143        0.283371392983185
5       117     DNA damage response, signal transduction by p53 class mediator
GO:0043161      9.74212639797436e-06    14.4858162051979        0.506193343021244
6       209     proteasomal ubiquitin-dependent protein catabolic process
GO:0006521      1.03962421825924e-05    34.9677419354839        0.138052729914885
4       57      regulation of cellular amino acid metabolic process
GO:0072331      1.08936063853011e-05    20.1949152542373        0.297903259290015
5       123     signal transduction by p53 class mediator
GO:0010498      1.17561679581293e-05    13.9960591133005        0.523147187045879
6       216     proteasomal protein catabolic process
GO:0031398      1.27289428155871e-05    19.5273224043716        0.307591170161234
5       127     positive regulation of protein ubiquitination
GO:0000077      1.42573752894829e-05    19.0546666666667        0.31485710331465
5       130     DNA damage checkpoint
GO:0000084      1.65141134739317e-05    18.4586563307494        0.32454501418587
5       134     S phase of mitotic cell cycle
GO:0031570      1.77421908200658e-05    18.1743002544529        0.329388969621479
5       136     DNA integrity checkpoint
GO:0007093      1.97166089152038e-05    17.7636815920398        0.336654902774894
5       139     mitotic cell cycle checkpoint
Tissue: Whole_Blood=>Heart_Left_Ventricle       Type:   asymmetric
SourceGene:     RP11-166P13.3(ENSG00000263004.1)
TargetGeneSet:  CTNNBIP1        RSG1    WBP1    FUCA1   PPIE    UROD    RP11
ZFYVE9  ZRANB2  MTF2    PSMA5   CERS2   PSMB4   C1orf61 SMG7    GS1     RBBP5
KIF3C   GCFC2   RNF181  POU3F3  PSMD14  PSMD6   PSMC1P1 C3orf17 GK5     NMD3
YEATS2  GRIA2   GPM6A   BRD9    WDR70   PAPD4   YTHDC2  CTB     PDLIM7  UFL1
PSMB1   AMPH    CDK13   UBE3C   PYCRL   KIAA2026        NFIB    XPA     FPGS    COQ4
NOXA1   TAF3    DLG5    BTAF1   PSMD13  OR52E8  ZNF143  YIF1A   C12orf5 AKAP3
STRAP   PSG1    ATF7    MVK     IFT81   VPS29   PABPC3  EXOSC8  UCHL3   FBXL3
PSMC6   PSMC1   VRK1    RPL4    COMMD4  SNX33   WDR61   FBXL16  CREBBP  MAZ
SULT1A3 SALL1   TMEM208 CTCF    ZFHX3   ZBTB4   C17orf39        RPL17P43
KCNJ12  WIPF2   G6PC3   GFAP    ANKRD40 TUBD1   MAP3K3  CHMP6   MIR133A1
C19orf6 ZBTB7A  NCAN    ZNF461  CTU1    ZNF580  SNRPB   ITPA    PYGB    SLPI
ZNF512B CBS     TCF20   RBM3    MAGED1  PABPC1P3        BCORL1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006521      2.53435722653352e-09    27.8134110787172        0.362881461490554
8       57      regulation of cellular amino acid metabolic process
GO:0031397      6.49469187792333e-09    18.6506024096386        0.585703411528614
9       92      negative regulation of protein ubiquitination
GO:0006977      8.40770360980823e-09    23.4827586206897        0.420178534357484
8       66      DNA damage response, signal transduction by p53 class mediator
resulting in cell cycle arrest
GO:0072413      8.40770360980823e-09    23.4827586206897        0.420178534357484
8       66      signal transduction involved in mitotic cell cycle checkpoint
GO:0072431      8.40770360980823e-09    23.4827586206897        0.420178534357484
8       66      signal transduction involved in mitotic cell cycle G1/S transition
DNA damage checkpoint
GO:0072474      8.40770360980823e-09    23.4827586206897        0.420178534357484
8       66      signal transduction involved in mitotic cell cycle G1/S checkpoint
GO:0051436      9.49838521246666e-09    23.0831315577078        0.426544875787143
8       67      negative regulation of ubiquitin-protein ligase activity involved in
mitotic cell cycle
GO:0072401      9.49838521246666e-09    23.0831315577078        0.426544875787143
8       67      signal transduction involved in DNA integrity checkpoint
GO:0072404      9.49838521246666e-09    23.0831315577078        0.426544875787143
8       67      signal transduction involved in G1/S transition checkpoint
```

GO:0072422	9.49838521246666e-09	23.0831315577078	0.426544875787143	8	67	signal transduction involved in DNA damage checkpoint
GO:0072395	1.07092005205718e-08	22.6968253968254	0.432911217216802	8	68	signal transduction involved in cell cycle checkpoint
GO:0033238	1.69844533038307e-08	21.2723214285714	0.458376582935437	8	72	regulation of cellular amine metabolic process
GO:0051352	1.69844533038307e-08	21.2723214285714	0.458376582935437	8	72	negative regulation of ligase activity
GO:0051437	1.69844533038307e-08	21.2723214285714	0.458376582935437	8	72	positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
GO:0051444	1.69844533038307e-08	21.2723214285714	0.458376582935437	8	72	negative regulation of ubiquitin-protein ligase activity
GO:0031571	1.8976266206716e-08	20.9435897435897	0.464742924365096	8	73	mitotic cell cycle G1/S transition DNA damage checkpoint
GO:0002479	2.35713488196993e-08	20.3155650319829	0.477475607224414	8	75	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent
GO:0051439	3.22534796497062e-08	19.4408163265306	0.49657463151339	8	78	regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
GO:0000216	3.57022105002875e-08	19.1656606304494	0.502940972943049	8	79	M/G1 transition of mitotic cell cycle
GO:0042590	3.57022105002875e-08	19.1656606304494	0.502940972943049	8	79	antigen processing and presentation of exogenous peptide antigen via MHC class I
GO:0071158	3.94641181496668e-08	18.8981481481481	0.509307314372708	8	80	positive regulation of cell cycle arrest
GO:0031575	4.80226761571519e-08	18.3848133848134	0.522039997232025	8	82	mitotic cell cycle G1/S transition checkpoint
GO:0051443	4.80226761571519e-08	18.3848133848134	0.522039997232025	8	82	positive regulation of ubiquitin-protein ligase activity
GO:0002478	5.2870454764339e-08	18.1384126984127	0.528406338661684	8	83	antigen processing and presentation of exogenous peptide antigen
GO:0031145	5.2870454764339e-08	18.1384126984127	0.528406338661684	8	83	anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process
GO:0019884	6.38420335084693e-08	17.6648113790971	0.541139021521002	8	85	antigen processing and presentation of exogenous antigen
GO:0051351	7.00261860721298e-08	17.4371184371184	0.547505362950661	8	86	positive regulation of ligase activity
GO:0071779	7.00261860721298e-08	17.4371184371184	0.547505362950661	8	86	G1/S transition checkpoint
GO:0051438	1.66164145842762e-07	15.4448051948052	0.611168777247249	8	96	regulation of ubiquitin-protein ligase activity
GO:0002474	2.11225746466807e-07	14.9324960753532	0.630267801536226	8	99	antigen processing and presentation of peptide antigen via MHC class I
GO:2000045	2.11225746466807e-07	14.9324960753532	0.630267801536226	8	99	regulation of G1/S transition of mitotic cell cycle
GO:0051340	2.28406896786785e-07	14.7691511387164	0.636634142965885	8	100	regulation of ligase activity
GO:0042770	2.55183165295285e-07	11.7770624482663	0.891287800152239	9	140	signal transduction in response to DNA damage
GO:0051320	3.05775335256105e-07	11.5109692501349	0.910386824441215	9	143	S phase
GO:0048002	4.14541140637089e-07	13.58	0.687564874403156	8	108	antigen processing and presentation of peptide antigen
GO:0030330	7.66453401281928e-07	12.4508519003932	0.744861947270085	8	117	DNA damage response, signal transduction by p53 class mediator
GO:0000209	8.3355571864438e-07	10.1349873176918	1.02498097017507	9	161	protein polyubiquitination
GO:0072331	1.12210981268672e-06	11.7962732919255	0.783059995848038			

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8       123     signal transduction by p53 class mediator
GO:0031396      1.19040865829112e-06    9.68401909524892        1.06954536018269
9       168     regulation of protein ubiquitination
GO:0031398      1.43044643452998e-06    11.3965586234494        0.808525361566674
8       127     positive regulation of protein ubiquitination
GO:0000077      1.7066354953522e-06     11.1139734582358        0.82762438585565
8       130     DNA damage checkpoint
GO:0000084      2.1445634729058e-06     10.7581254724112        0.853089751574286
8       134     S phase of mitotic cell cycle
GO:0031570      2.39717622022303e-06    10.5885416666667        0.865822434433603
8       136     DNA integrity checkpoint
GO:0007093      2.82334120209182e-06    10.343874954562 0.88492145872258        8
139     mitotic cell cycle checkpoint
GO:2000602      4.28674983908019e-06    9.74306269270298        0.935852190159851
8       147     regulation of interphase of mitotic cell cycle
GO:0090068      5.23212999626783e-06    9.46786546786547        0.961317555878486
8       151     positive regulation of cell cycle process
GO:0019882      5.49428429262543e-06    9.40145502645503        0.967683897308145
8       152     antigen processing and presentation
GO:0010565      6.05209203002869e-06    9.27136333985649        0.980416580167462
8       154     regulation of cellular ketone metabolic process
GO:0043161      7.17183441957019e-06    7.67656626506024        1.3305653587987 9
209     proteasomal ubiquitin-dependent protein catabolic process
GO:0010498      9.35637758101783e-06    7.41330539549502        1.37512974880631
9       216     proteasomal protein catabolic process
GO:0006511      1.92912918139558e-05    5.38824187738258        2.31734828039582
11      364     ubiquitin-dependent protein catabolic process
Tissue: Whole_Blood=>Heart_Left_Ventricle       Type:   cluster
SourceGene:     RP11-166P13.3(ENSG00000263004.1)
TargetGeneSet:  CTNNBIP1        RSG1    WBP1    FUCA1   PPIE    UROD    RP11
ZFYVE9  ZRANB2  MTF2    PSMA5   CERS2   PSMB4   C1orf61 SMG7    GS1     RBBP5
KIF3C   GCFC2   RNF181  POU3F3  PSMD14  PSMD6   PSMC1P1 C3orf17 GK5     NMD3
YEATS2  GRIA2   GPM6A   BRD9    WDR70   PAPD4   YTHDC2  CTB     PDLIM7  UFL1
PSMB1   AMPH    CDK13   UBE3C   PYCRL   KIAA2026        NFIB    XPA     FPGS    COQ4
NOXA1   TAF3    DLG5    BTAF1   PSMD13  OR52E8  ZNF143  YIF1A   C12orf5 AKAP3
STRAP   PSG1    ATF7    MVK     IFT81   VPS29   PABPC3  EXOSC8  UCHL3   FBXL3
PSMC6   PSMC1   VRK1    RPL4    COMMD4  SNX33   WDR61   FBXL16  CREBBP  MAZ
SULT1A3 SALL1   TMEM208 CTCF    ZFHX3   ZBTB4   C17orf39        RPL17P43
KCNJ12  WIPF2   G6PC3   GFAP    ANKRD40 TUBD1   MAP3K3  CHMP6   MIR133A1
C19orf6 ZBTB7A  NCAN    ZNF461  CTU1    ZNF580  SNRPB   ITPA    PYGB    SLPI
ZNF512B CBS     TCF20   RBM3    MAGED1  PABPC1P3        BCORL1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006521      2.53435722653352e-09    27.8134110787172        0.362881461490554
8       57      regulation of cellular amino acid metabolic process
GO:0031397      6.49469187792333e-09    18.6506024096386        0.585703411528614
9       92      negative regulation of protein ubiquitination
GO:0006977      8.40770360980823e-09    23.4827586206897        0.420178534357484
8       66      DNA damage response, signal transduction by p53 class mediator
resulting in cell cycle arrest
GO:0072413      8.40770360980823e-09    23.4827586206897        0.420178534357484
8       66      signal transduction involved in mitotic cell cycle checkpoint
GO:0072431      8.40770360980823e-09    23.4827586206897        0.420178534357484
8       66      signal transduction involved in mitotic cell cycle G1/S transition
DNA damage checkpoint
GO:0072474      8.40770360980823e-09    23.4827586206897        0.420178534357484
8       66      signal transduction involved in mitotic cell cycle G1/S checkpoint
GO:0051436      9.49838521246666e-09    23.0831315577078        0.426544875787143
8       67      negative regulation of ubiquitin-protein ligase activity involved in
mitotic cell cycle
GO:0072401      9.49838521246666e-09    23.0831315577078        0.426544875787143
8       67      signal transduction involved in DNA integrity checkpoint
GO:0072404      9.49838521246666e-09    23.0831315577078        0.426544875787143
8       67      signal transduction involved in G1/S transition checkpoint
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GO:0072422      9.49838521246666e-09    23.0831315577078        0.426544875787143
8       67      signal transduction involved in DNA damage checkpoint
GO:0072395      1.07092005205718e-08    22.6968253968254        0.432911217216802
8       68      signal transduction involved in cell cycle checkpoint
GO:0033238      1.69844533038307e-08    21.2723214285714        0.458376582935437
8       72      regulation of cellular amine metabolic process
GO:0051352      1.69844533038307e-08    21.2723214285714        0.458376582935437
8       72      negative regulation of ligase activity
GO:0051437      1.69844533038307e-08    21.2723214285714        0.458376582935437
8       72      positive regulation of ubiquitin-protein ligase activity involved in
mitotic cell cycle
GO:0051444      1.69844533038307e-08    21.2723214285714        0.458376582935437
8       72      negative regulation of ubiquitin-protein ligase activity
GO:0031571      1.8976266206716e-08     20.9435897435897        0.464742924365096
8       73      mitotic cell cycle G1/S transition DNA damage checkpoint
GO:0002479      2.35713488196993e-08    20.3155650319829        0.477475607224414
8       75      antigen processing and presentation of exogenous peptide antigen via
MHC class I, TAP-dependent
GO:0051439      3.22534796497062e-08    19.4408163265306        0.49657463151339
8       78      regulation of ubiquitin-protein ligase activity involved in mitotic
cell cycle
GO:0000216      3.57022105002875e-08    19.1656606304494        0.502940972943049
8       79      M/G1 transition of mitotic cell cycle
GO:0042590      3.57022105002875e-08    19.1656606304494        0.502940972943049
8       79      antigen processing and presentation of exogenous peptide antigen via
MHC class I
GO:0071158      3.94641181496668e-08    18.8981481481481        0.509307314372708
8       80      positive regulation of cell cycle arrest
GO:0031575      4.80226761571519e-08    18.3848133848134        0.522039997232025
8       82      mitotic cell cycle G1/S transition checkpoint
GO:0051443      4.80226761571519e-08    18.3848133848134        0.522039997232025
8       82      positive regulation of ubiquitin-protein ligase activity
GO:0002478      5.2870454764339e-08     18.1384126984127        0.528406338661684
8       83      antigen processing and presentation of exogenous peptide antigen
GO:0031145      5.2870454764339e-08     18.1384126984127        0.528406338661684
8       83      anaphase-promoting complex-dependent proteasomal ubiquitin-dependent
protein catabolic process
GO:0019884      6.38420335084693e-08    17.6648113790971        0.541139021521002
8       85      antigen processing and presentation of exogenous antigen
GO:0051351      7.00261860721298e-08    17.4371184371184        0.547505362950661
8       86      positive regulation of ligase activity
GO:0071779      7.00261860721298e-08    17.4371184371184        0.547505362950661
8       86      G1/S transition checkpoint
GO:0051438      1.66164145842762e-07    15.4448051948052        0.611168777247249
8       96      regulation of ubiquitin-protein ligase activity
GO:0002474      2.11225746466807e-07    14.9324960753532        0.630267801536226
8       99      antigen processing and presentation of peptide antigen via MHC class
I
GO:2000045      2.11225746466807e-07    14.9324960753532        0.630267801536226
8       99      regulation of G1/S transition of mitotic cell cycle
GO:0051340      2.28406896786785e-07    14.7691511387164        0.636634142965885
8       100     regulation of ligase activity
GO:0042770      2.55183165295285e-07    11.7770624482663        0.891287800152239
9       140     signal transduction in response to DNA damage
GO:0051320      3.05775335256105e-07    11.5109692501349        0.910386824441215
9       143     S phase
GO:0048002      4.14541140637089e-07    13.58   0.687564874403156       8       108
antigen processing and presentation of peptide antigen
GO:0030330      7.66453401281928e-07    12.4508519003932        0.744861947270085
8       117     DNA damage response, signal transduction by p53 class mediator
GO:0000209      8.3355571864438e-07     10.1349873176918        1.02498097017507
9       161     protein polyubiquitination
GO:0072331      1.12210981268672e-06    11.7962732919255        0.783059995848038
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8       123     signal transduction by p53 class mediator
GO:0031396      1.19040865829112e-06    9.68401909524892        1.06954536018269
9       168     regulation of protein ubiquitination
GO:0031398      1.43044643452998e-06    11.3965586234494        0.808525361566674
8       127     positive regulation of protein ubiquitination
GO:0000077      1.7066354953522e-06     11.1139734582358        0.82762438585565
8       130     DNA damage checkpoint
GO:0000084      2.1445634729058e-06     10.7581254724112        0.853089751574286
8       134     S phase of mitotic cell cycle
GO:0031570      2.39717622022303e-06    10.5885416666667        0.865822434433603
8       136     DNA integrity checkpoint
GO:0007093      2.82334120209182e-06    10.343874954562 0.88492145872258        8
139     mitotic cell cycle checkpoint
GO:2000602      4.28674983908019e-06    9.74306269270298        0.935852190159851
8       147     regulation of interphase of mitotic cell cycle
GO:0090068      5.23212999626783e-06    9.46786546786547        0.961317555878486
8       151     positive regulation of cell cycle process
GO:0019882      5.49428429262543e-06    9.40145502645503        0.967683897308145
8       152     antigen processing and presentation
GO:0010565      6.05209203002869e-06    9.27136333985649        0.980416580167462
8       154     regulation of cellular ketone metabolic process
GO:0043161      7.17183441957019e-06    7.67656626506024        1.3305653587987 9
209     proteasomal ubiquitin-dependent protein catabolic process
GO:0010498      9.35637758101783e-06    7.41330539549502        1.37512974880631
9       216     proteasomal protein catabolic process
GO:0006511      1.92912918139558e-05    5.38824187738258        2.31734828039582
11      364     ubiquitin-dependent protein catabolic process
Tissue: Heart_Left_Ventricle=>Whole_Blood       Type:   asymmetric
SourceGene:     RP11-29H23.6(ENSG00000223503.1)
TargetGeneSet:  RP11    TNFSF13B        AKT3    STK25   STEAP2  XRCC2   SMC3    FEN1
KNTC1   RFC3    CACNA1H PKMYT1  CDH11   CDT1    CDK5R1  CDC6    EME1    TYMS
RNASEH2A        CDC45
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006260      1.30978487834235e-09    36.3358974358974        0.370908587640994
8       268     DNA replication
GO:0000083      1.92033805358757e-08    200.180555555556        0.0304477198809771
4       22      regulation of transcription involved in G1/S phase of mitotic cell
cycle
GO:0006261      1.42254481950831e-07    54.3295454545455        0.128710815860494
5       93      DNA-dependent DNA replication
GO:0000076      2.70364629542563e-07    363.63025210084 0.0138398726731714      3
10      DNA replication checkpoint
GO:0051329      4.66216865145218e-07    20.3500827129859        0.524531174313196
7       379     interphase of mitotic cell cycle
GO:0010972      4.94794066892285e-07    282.78431372549 0.0166078472078057      3
12      negative regulation of G2/M transition of mitotic cell cycle
GO:0051325      5.36791290777933e-07    19.9103238866397        0.535603072451733
7       387     interphase
GO:0010564      8.45215652260883e-07    18.5537705537706        0.572970728669296
7       414     regulation of cell cycle process
GO:0000084      8.81850629341559e-07    36.9560723514212        0.185454293820497
5       134     S phase of mitotic cell cycle
GO:0051320      1.21685080455504e-06    34.524154589372 0.197910179226351       5
143     S phase
GO:0000082      4.43631168046153e-06    26.2430939226519        0.257421631720988
5       186     G1/S transition of mitotic cell cycle
GO:0010948      8.1665664208113e-06     38.9646739130435        0.13286277662446
4       96      negative regulation of cell cycle process
GO:0010389      8.98724677238467e-06    94.1437908496732        0.0415196180195142
3       30      regulation of G2/M transition of mitotic cell cycle
GO:0006281      9.42699119265486e-06    15.9765062523683        0.530067123382465
6       383     DNA repair
GO:0046683      1.0900525832417e-05     801.611111111111        0.00553594906926856
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2       4       response to organophosphorus
GO:0006271      1.31995368287061e-05    81.9734345351044        0.0470555670887828
3       34      DNA strand elongation involved in DNA replication
GO:0000075      1.5951907560306e-05     19.9634317862166        0.334924918690748
5       242     cell cycle checkpoint
GO:0022616      1.7093775598175e-05     74.7249134948097        0.0512075288907342
3       37      DNA strand elongation
Tissue: Heart_Left_Ventricle=>Whole_Blood       Type:   asymmetric
SourceGene:     RP3-434O14.8(ENSG00000232222.1)
TargetGeneSet:  MPL     RP11    PEAR1   SELP    C1orf198        C2orf88 VIL1
KLF15   PPBP    ARHGAP21        CTD     SH3TC2  F13A1   LY6G6F  C6orf25 TREML1  DAO
EDF1    TSPAN15 CTTN    PDE2A   NRGN    ESAM    ARG2    C14orf133       LGMN
PCSK6   ITGB3   C17orf109       KXD1    SYTL4
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0007596      2.57611964243697e-07    17.5070643642072        0.723686942080133
8       498     blood coagulation
GO:0030168      4.80947826801868e-07    26.9554502369668        0.315341498858211
6       217     platelet activation
GO:0002576      5.62061770647382e-06    42.7431124348474        0.120614490346689
4       83      platelet degranulation
Tissue: Whole_Blood=>Heart_Left_Ventricle       Type:   asymmetric




SourceGene:     ZUFSP(ENSG00000153975.5)        zinc finger with UFM1-specific
peptidase domain




TargetGeneSet:  MRPL20  WBP1    ZBTB40  MRPL37  HBXIP   ATP5F1  HAX1    MRPL24
LINC00467       MSH6    EIF3FP3 COMMD1  SNRNP200        CHCHD5  ATP5G3  UBE2E3
WDR48   FYCO1   MYL3    PBRM1   SPCS1   THOC7   GTPBP8  FBXO40  SRPRB   TRA2B
OCIAD1  NDUFC1  SMARCA5 KIAA0922        KIAA0947        SUB1    NDUFS4  PCBD2
SLC35A4 TBC1D9B TMEM14B CUL9    GABRR2  GTF3C6  HDDC2   BAZ1B   FIS1    TNPO3   RP4
DCTN6   MRPL15  RPS20   ARFGEF1 KLHL38  NDUFB9  CTD     CYC1    C9orf46 ERP44
NIPSNAP3B       RABGAP1 PSMB7   AK1     RP11    METTL11A        FCN2    KIAA0913
SMC3    NUDT22  RELA    YIF1A   PPP6R3  NUMA1   LAMTOR1 SPCS2   ERC1    MRPL51
SMARCC2 ANKRD52 GLIPR1L1        NDUFA12 SLC25A3 ALDH1L2 TCP11L2 ISCU    KDM2B   MED4
MED4-AS1        SALL2   CEBPE   C14orf182       CDC42BPB        HERC2   TPM1
DENND4A UBL7    COX5A   SIN3A   MRPS11  ITFG3   MRPL28  ZNF598  CREBBP  SETD1A  RBL2
COX4I1  PSMB6   DVL2    CTC1    POLDIP2 SYNRG   SOCS7   C17orf53        NPEPPS
TBKBP1  SNF8    SLC35B1 ICT1    RNF213  C18orf32        HAUS8   POP4    COX6B1
PPP6R1  CHMP2A  CBFA2T2 CEP250  ATP5O   MRPL40  LDOC1L  PRDX4   SAT1    HSD17B10
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COX7B FAM127A MT

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0022904	7.46E-11	20.06304348	0.684243305	11	96	respiratory electron transport chain
GO:0022900	2.78E-09	13.827766	0.955089613	11	134	electron transport chain
GO:0045333	5.15E-09	12.97602058	1.012109889	11	142	cellular respiration
GO:0015980	2.69E-07	6.904837491	2.188153069	13	307	energy derivation by oxidation of organic compounds

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GO:0006091      2.01E-06        5.29436031      3.050584735     14      428
generation of precursor metabolites and energy
```

```
Tissue: Whole_Blood=>Heart_Left_Ventricle       Type:   cluster
SourceGene:     ZUFSP(ENSG00000153975.5)
TargetGeneSet:  MRPL20  WBP1    ZBTB40  MRPL37  HBXIP   ATP5F1  HAX1    MRPL24
LINC00467       MSH6    EIF3FP3 COMMD1  SNRNP200        CHCHD5  ATP5G3  UBE2E3
WDR48   FYCO1   MYL3    PBRM1   SPCS1   THOC7   GTPBP8  FBXO40  SRPRB   TRA2B
OCIAD1  NDUFC1  SMARCA5 KIAA0922        KIAA0947        SUB1    NDUFS4  PCBD2
SLC35A4 TBC1D9B TMEM14B CUL9    GABRR2  GTF3C6  HDDC2   BAZ1B   FIS1    TNPO3   RP4
DCTN6   MRPL15  RPS20   ARFGEF1 KLHL38  NDUFB9  CTD     CYC1    C9orf46 ERP44
NIPSNAP3B       RABGAP1 PSMB7   AK1     RP11    METTL11A        FCN2    KIAA0913
SMC3    NUDT22  RELA    YIF1A   PPP6R3  NUMA1   LAMTOR1 SPCS2   ERC1    MRPL51
SMARCC2 ANKRD52 GLIPR1L1        NDUFA12 SLC25A3 ALDH1L2 TCP11L2 ISCU    KDM2B   MED4
MED4-AS1        SALL2   CEBPE   C14orf182       CDC42BPB        HERC2   TPM1
DENND4A UBL7    COX5A   SIN3A   MRPS11  ITFG3   MRPL28  ZNF598  CREBBP  SETD1A  RBL2
COX4I1  PSMB6   DVL2    CTC1    POLDIP2 SYNRG   SOCS7   C17orf53        NPEPPS
TBKBP1  SNF8    SLC35B1 ICT1    RNF213  C18orf32        HAUS8   POP4    COX6B1
PPP6R1  CHMP2A  CBFA2T2 CEP250  ATP5O   MRPL40  LDOC1L  PRDX4   SAT1    HSD17B10
COX7B   FAM127A MT
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      7.46040687237286e-11    20.0630434782609        0.684243304961594
11      96      respiratory electron transport chain
GO:0022900      2.78209342845419e-09    13.8277659950513        0.955089613175559
11      134     electron transport chain
GO:0045333      5.14719971426576e-09    12.9760205774975        1.01210988858902
11      142     cellular respiration
GO:0015980      2.68791510830652e-07    6.90483749055178        2.18815306899177
13      307     energy derivation by oxidation of organic compounds
GO:0006091      2.0110456640133e-06     5.29436031048146        3.05058473462044
14      428     generation of precursor metabolites and energy
Tissue: Lung=>Adipose_Subcutaneous      Type:   asymmetric
SourceGene:     CHPF(ENSG00000123989.9)
TargetGeneSet:  RP4     C1QC    RPS6KA1 MTMR9LP PPP1R8P1        VAV3    ADORA3  RHOC
SLAMF8  PEA15   CD84    ARHGAP30        MR1     PTPRC   PTPN7   PLEK    VAMP8
HCLS1   CD86    RBM47   TXK     RP13    RP11    DOCK2   AIF1    DEFA6   AOAH
PKD1L1  IRF5    TSPAN33 TBXAS1  SYK     FGD3    CARD9   C1DP3   PIK3AP1 MS4A6A
MS4A7   FOLR2   SLCO2B1 PTPN6   BIN2    NCKAP1L ARHGAP9 SELPLG  STX2    GPR65
PLCB2   MCTP2   PRKCB   CORO1A  CD68    CD209   MYO1F   IFI30   LRRC25  HCST    CD37
SIGLEC7 CD33    LILRB4  HCK     PLTP    CYTH4   WAS     BTK
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0002757      6.11223291950693e-11    17.7365731567421        0.894401771503702
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12      235     immune response-activating signal transduction
GO:0002253      6.54365716990887e-11    15.2705627705628        1.13798353055152
13      299     activation of immune response
GO:0002764      1.14208734396507e-10    16.7441860465116        0.94387931631029
12      248     immune response-regulating signaling pathway
GO:0046649      5.41088583227107e-10    11.3905349554689        1.64798283855789
14      433     lymphocyte activation
GO:0050778      7.40609348814129e-10    12.3853615520282        1.38537125458446
13      364     positive regulation of immune response
GO:0050853      1.01921517828083e-09    76.5199645075421        0.110372984568542
6       29      B cell receptor signaling pathway
GO:0050867      1.32569903754072e-09    15.4661572052402        0.913431596429313
11      240     positive regulation of cell activation
GO:0050865      4.63022740892164e-09    11.8583573385794        1.30544598989689
12      343     regulation of cell activation
GO:0050851      1.90796505601299e-08    21.1374653098982        0.468133693170023
8       123     antigen receptor-mediated signaling pathway
GO:0042110      2.57057938060402e-08    11.4350649350649        1.21410283025396
11      319     T cell activation
GO:0002429      3.52583829389788e-08    19.4328510638298        0.506193343021244
8       133     immune response-activating cell surface receptor signaling pathway
GO:0002768      6.55712897074683e-08    17.8473091364205        0.548058957857588
8       144     immune response-regulating cell surface receptor signaling pathway
GO:0051249      9.51426925376304e-08    11.4961334961335        1.07708809078956
10      283     regulation of lymphocyte activation
GO:0051251      1.06145383596951e-07    13.4772055719713        0.818282471801259
9       215     positive regulation of lymphocyte activation
GO:0008154      1.7226534053312e-07     20.4366830065359        0.414850183378313
7       109     actin polymerization or depolymerization
GO:0030036      1.92858143964797e-07    9.27116402116402        1.48052037921251
11      389     actin cytoskeleton organization
GO:0002696      2.10535661092062e-07    12.3784937888199        0.886789841533458
9       233     positive regulation of leukocyte activation
GO:0046651      2.58755171194995e-07    14.7711468604048        0.654625977441008
8       172     lymphocyte proliferation
GO:0032943      2.8272629926242e-07     14.5911304793643        0.662237907411252
8       174     mononuclear cell proliferation
GO:0042098      2.96909936061453e-07    18.7678303303303        0.449103868244412
7       118     T cell proliferation
GO:0002694      3.06600623033077e-07    10.064308681672 1.22171476022421        10
321     regulation of leukocyte activation
GO:0070661      3.98656356977441e-07    13.9124480313035        0.692685627292229
8       182     leukocyte proliferation
GO:0030029      5.48532531646207e-07    8.29869358669834        1.64417687357276
11      432     actin filament-based process
GO:0007015      6.73682319805254e-07    12.9334395266811        0.742163172098817
8       195     actin filament organization
GO:0030041      7.97214287029456e-07    22.1911650736244        0.323507023735382
6       85      actin filament polymerization
GO:0051495      9.79249704460455e-07    21.3748133399701        0.334924918690748
6       88      positive regulation of cytoskeleton organization
GO:0030097      1.08560817286059e-06    7.71238938053097        1.76216178811155
11      463     hemopoiesis
GO:0050670      1.14681197787023e-06    15.1783759124088        0.548058957857588
7       144     regulation of lymphocyte proliferation
GO:0032944      1.20147351317198e-06    15.0673309178744        0.55186492284271
7       145     regulation of mononuclear cell proliferation
GO:0071346      1.44578315745954e-06    19.9090909090909        0.357760708601481
6       94      cellular response to interferon-gamma
GO:0070663      1.50869838822367e-06    14.5354020979021        0.57089474776832
7       150     regulation of leukocyte proliferation
GO:0050671      1.6365783844003e-06     19.4639455782313        0.365372638571725
6       96      positive regulation of lymphocyte proliferation
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GO:0002252      1.64707071475623e-06    8.28605200945626        1.46910248425714
10      386     immune effector process
GO:0042113      1.72278053118714e-06    14.2337328767123        0.582312642723687
7       153     B cell activation
GO:0050863      1.72969697843863e-06    11.3339326740585        0.841118261711992
8       221     regulation of T cell activation
GO:0032946      1.73941345316669e-06    19.2487104732003        0.369178603556847
6       97      positive regulation of mononuclear cell proliferation
GO:0050871      1.81977169383397e-06    29.2795918367347        0.205522109196595
5       54      positive regulation of B cell activation
GO:0002521      1.84552895574968e-06    9.41734678735718        1.14940142550689
9       302     leukocyte differentiation
GO:0070665      2.08004396836927e-06    18.6304819800261        0.380596498512214
6       100     positive regulation of leukocyte proliferation
GO:0048534      2.08294024346492e-06    7.18595041322314        1.88395266763546
11      495     hemopoietic or lymphoid organ development
GO:0042129      2.20498672155191e-06    18.4330827067669        0.384402463497336
6       101     regulation of T cell proliferation
GO:0032956      2.52346204665754e-06    13.3987903225806        0.616566327589786
7       162     regulation of actin cytoskeleton organization
GO:0050900      3.29870176098336e-06    10.3464523787782        0.917237561414435
8       241     leukocyte migration
GO:0050870      3.61411491160361e-06    12.655487804878 0.650820012455885       7
171     positive regulation of T cell activation
GO:0034341      3.82642501010807e-06    16.665889212828 0.422462113348557       6
111     response to interferon-gamma
GO:0032970      3.90346141969277e-06    12.5012550200803        0.65843194242613
7       173     regulation of actin filament-based process
GO:0045579      4.31188258041909e-06    138.365384615385        0.0342536848660992
3       9       positive regulation of B cell differentiation
GO:0042102      4.96753059948155e-06    23.5    0.251193689018061       5       66
positive regulation of T cell proliferation
GO:0030838      6.23852637015201e-06    40.2464985994398        0.121790879523908
4       32      positive regulation of actin filament polymerization
GO:0002697      1.04599573534299e-05    10.6759020618557        0.76499896200955
7       201     regulation of immune effector process
GO:0030098      1.15198716201983e-05    10.5111040609137        0.776416856964916
7       204     lymphocyte differentiation
GO:0060333      1.20664215297118e-05    19.3540540540541        0.300671233824649
5       79      interferon-gamma-mediated signaling pathway
GO:0050864      1.36387504586515e-05    18.8421052631579        0.308283163794893
5       81      regulation of B cell activation
GO:0046631      1.44825732697815e-05    18.5961038961039        0.312089128780015
5       82      alpha-beta T cell activation
GO:0051258      1.45711156481009e-05    13.0325921413341        0.532835097917099
6       140     protein polymerization
GO:0045088      1.61993107460472e-05    9.94751602564103        0.818282471801259
7       215     regulation of innate immune response
GO:0008064      1.72605505608459e-05    17.895  0.323507023735382       5       85
regulation of actin polymerization or depolymerization
GO:0006909      1.82732688707784e-05    17.6728395061728        0.327312988720504
5       86      phagocytosis
GO:0030832      1.82732688707784e-05    17.6728395061728        0.327312988720504
5       86      regulation of actin filament length
GO:0031347      1.9042756689007e-05     6.95310086073714        1.53380388900422
9       403     regulation of defense response
GO:0031334      1.93316911744593e-05    17.4560975609756        0.331118953705626
5       87      positive regulation of protein complex assembly
Tissue: Lung=>Adipose_Subcutaneous      Type:   asymmetric
SourceGene:     DSC1(ENSG00000134765.5)
TargetGeneSet:  FBXO2   RPL11   KHDRBS1 ANKRD13C        RP4     RPL5    RP11
SNRPE   RCOR3   TTC32   UBC     C1D     TPRKB   DGUOK   PTCD3   RPL31   MMADHC
PPIL3   EEF1B2  CNOT10  TRANK1  RPL29   H1FX    COMMD2  RPL22L1 RPL35A  NUP54
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ENOPH1  RPL34   TAF9    BTF3    RPS10   RPL10A  RP1     TRMT11  BZW2    C7orf44
ABHD11  SYPL1   NUDT18  SNHG6   RPL30   RPS6    DCTN3   PSMB7   RPL35   RPL7A
NSMCE4A C10orf137       ZBED5   EIF3M   RPS25   PHB2    EMG1    COPZ1   RPL18AP3
RPL6    OXA1L   GOLGA8J TMEM85  TMOD2   RPS15A  RPL26   RPL23A  RPL17   RPL19
VPS25   RPL27   RPS15   RPL36   NDUFA11 RPS16   RPL18   C19orf48        NLRP9
ZNF805  RPS5    SOGA1   DPM1    H1F0    RPL9P7  UXT     IDH3G
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      6.8517814376163e-41     115.140429338104        0.508615320739049
27      105     translational elongation
GO:0006415      1.07660031965565e-40    130.145454545455        0.440799944640509
26      91      translational termination
GO:0070972      2.39429347011336e-39    98.6020955788398        0.571586741401979
27      118     protein localization to endoplasmic reticulum
GO:0006614      7.61708551753886e-39    106.976985040276        0.508615320739049
26      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.00628456576097e-38    105.632386363636        0.513459276174659
26      106     cotranslational protein targeting to membrane
GO:0045047      1.00628456576097e-38    105.632386363636        0.513459276174659
26      106     protein targeting to ER
GO:0072599      1.00628456576097e-38    105.632386363636        0.513459276174659
26      106     establishment of protein localization to endoplasmic reticulum
GO:0000184      2.91356155036349e-37    90.7839687194526        0.576430696837589
26      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006413      4.36141351998054e-36    71.6115348837209        0.736281226212719
27      152     translational initiation
GO:0000956      9.43996005117733e-35    62.9631509990174        0.818628468618089
27      169     nuclear-transcribed mRNA catabolic process
GO:0019080      2.5199545712287e-34     67.392  0.731437270777109       26      151
viral genome expression
GO:0019083      2.5199545712287e-34     67.392  0.731437270777109       26      151
viral transcription
GO:0006612      3.64064317998685e-34    66.3214030064424        0.741125181648329
26      153     protein targeting to membrane
GO:0043624      3.64064317998685e-34    66.3214030064424        0.741125181648329
26      153     cellular protein complex disassembly
GO:0006402      4.19636154062652e-34    59.1729554905283        0.862224067538579
27      178     mRNA catabolic process
GO:0043241      8.92655360355916e-34    63.7868457300276        0.765344958826379
26      158     protein complex disassembly
GO:0034623      1.29106482638928e-32    56.8270884520885        0.842848245796139
26      174     cellular macromolecular complex disassembly
GO:0006401      2.34022159727951e-32    50.1020381499869        0.993010864300048
27      205     RNA catabolic process
GO:0032984      2.8151867905633e-32     54.9506833036245        0.867068022974189
26      179     macromolecular complex disassembly
GO:0072594      9.99212004379702e-31    47.149897854954 0.988166908864438       26
204     establishment of protein localization to organelle
GO:0019058      2.85830184933422e-29    40.8620842572062        1.11895370562591
26      231     viral infectious cycle
GO:0071845      2.06522322414906e-28    34.5080083250385        1.37568334371324
27      284     cellular component disassembly at cellular level
GO:0022411      3.03273804619751e-28    33.9695268644747        1.39505916545568
27      288     cellular component disassembly
GO:0022415      6.71787336382133e-28    35.7247474747475        1.2594284132586 26
260     viral reproductive process
GO:0016032      1.10406752191663e-25    23.3967749393134        2.18462390146011
29      451     viral reproduction
GO:0033365      1.90883405523007e-22    19.6185733653144        2.29119092104353
27      473     protein localization to organelle
GO:0006605      2.01814587967951e-22    19.5732792258467        2.29603487647914
27      474     protein targeting
GO:0071843      6.65226882536092e-12    15.7288888888889        1.15770534911079
14      239     cellular component biogenesis at cellular level
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GO:0022613      4.84441706346201e-11    15.2430486593843        1.08988997301225
13      225     ribonucleoprotein complex biogenesis
GO:0042254      1.23986568456352e-10    19.2425693932695        0.721749359905889
11      149     ribosome biogenesis
GO:0006364      1.64635398508183e-09    22.1870578084556        0.503771365303439
9       104     rRNA processing
GO:0016072      2.71939754178963e-09    20.8602499594222        0.532835097917099
9       110     rRNA metabolic process
GO:0042274      1.88175089364032e-08    85.0177514792899        0.0871911978409799
5       18      ribosomal small subunit biogenesis
GO:0034470      3.96892570148744e-08    12.4482456140351        0.968791087121998
10      200     ncRNA processing
GO:0034660      1.11608774414704e-07    9.59897315353211        1.38052729914885
11      285     ncRNA metabolic process
GO:0042273      2.42665430939766e-07    108.886363636364        0.0581274652273199
4       12      ribosomal large subunit biogenesis
Tissue: Lung=>Adipose_Subcutaneous      Type:   cluster
SourceGene:     DSC1(ENSG00000134765.5)
TargetGeneSet:  FBXO2   RPL11   KHDRBS1 ANKRD13C        RP4     RPL5    RP11
SNRPE   RCOR3   TTC32   UBC     C1D     TPRKB   DGUOK   PTCD3   RPL31   MMADHC
PPIL3   EEF1B2  CNOT10  TRANK1  RPL29   H1FX    COMMD2  RPL22L1 RPL35A  NUP54
ENOPH1  RPL34   TAF9    BTF3    RPS10   RPL10A  RP1     TRMT11  BZW2    C7orf44
ABHD11  SYPL1   NUDT18  SNHG6   RPL30   RPS6    DCTN3   PSMB7   RPL35   RPL7A
NSMCE4A C10orf137       ZBED5   EIF3M   RPS25   PHB2    EMG1    COPZ1   RPL18AP3
RPL6    OXA1L   GOLGA8J TMEM85  TMOD2   RPS15A  RPL26   RPL23A  RPL17   RPL19
VPS25   RPL27   RPS15   RPL36   NDUFA11 RPS16   RPL18   C19orf48        NLRP9
ZNF805  RPS5    SOGA1   DPM1    H1F0    RPL9P7  UXT     IDH3G
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      6.8517814376163e-41     115.140429338104        0.508615320739049
27      105     translational elongation
GO:0006415      1.07660031965565e-40    130.145454545455        0.440799944640509
26      91      translational termination
GO:0070972      2.39429347011336e-39    98.6020955788398        0.571586741401979
27      118     protein localization to endoplasmic reticulum
GO:0006614      7.61708551753886e-39    106.976985040276        0.508615320739049
26      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.00628456576097e-38    105.632386363636        0.513459276174659
26      106     cotranslational protein targeting to membrane
GO:0045047      1.00628456576097e-38    105.632386363636        0.513459276174659
26      106     protein targeting to ER
GO:0072599      1.00628456576097e-38    105.632386363636        0.513459276174659
26      106     establishment of protein localization to endoplasmic reticulum
GO:0000184      2.91356155036349e-37    90.7839687194526        0.576430696837589
26      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006413      4.36141351998054e-36    71.6115348837209        0.736281226212719
27      152     translational initiation
GO:0000956      9.43996005117733e-35    62.9631509990174        0.818628468618089
27      169     nuclear-transcribed mRNA catabolic process
GO:0019080      2.5199545712287e-34     67.392  0.731437270777109       26      151
viral genome expression
GO:0019083      2.5199545712287e-34     67.392  0.731437270777109       26      151
viral transcription
GO:0006612      3.64064317998685e-34    66.3214030064424        0.741125181648329
26      153     protein targeting to membrane
GO:0043624      3.64064317998685e-34    66.3214030064424        0.741125181648329
26      153     cellular protein complex disassembly
GO:0006402      4.19636154062652e-34    59.1729554905283        0.862224067538579
27      178     mRNA catabolic process
GO:0043241      8.92655360355916e-34    63.7868457300276        0.765344958826379
26      158     protein complex disassembly
GO:0034623      1.29106482638928e-32    56.8270884520885        0.842848245796139
26      174     cellular macromolecular complex disassembly
GO:0006401      2.34022159727951e-32    50.1020381499869        0.993010864300048
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27      205     RNA catabolic process
GO:0032984      2.8151867905633e-32     54.9506833036245        0.867068022974189
26      179     macromolecular complex disassembly
GO:0072594      9.99212004379702e-31    47.149897854954 0.988166908864438       26
204     establishment of protein localization to organelle
GO:0019058      2.85830184933422e-29    40.8620842572062        1.11895370562591
26      231     viral infectious cycle
GO:0071845      2.06522322414906e-28    34.5080083250385        1.37568334371324
27      284     cellular component disassembly at cellular level
GO:0022411      3.03273804619751e-28    33.9695268644747        1.39505916545568
27      288     cellular component disassembly
GO:0022415      6.71787336382133e-28    35.7247474747475        1.2594284132586 26
260     viral reproductive process
GO:0016032      1.10406752191663e-25    23.3967749393134        2.18462390146011
29      451     viral reproduction
GO:0033365      1.90883405523007e-22    19.6185733653144        2.29119092104353
27      473     protein localization to organelle
GO:0006605      2.01814587967951e-22    19.5732792258467        2.29603487647914
27      474     protein targeting
GO:0071843      6.65226882536092e-12    15.7288888888889        1.15770534911079
14      239     cellular component biogenesis at cellular level
GO:0022613      4.84441706346201e-11    15.2430486593843        1.08988997301225
13      225     ribonucleoprotein complex biogenesis
GO:0042254      1.23986568456352e-10    19.2425693932695        0.721749359905889
11      149     ribosome biogenesis
GO:0006364      1.64635398508183e-09    22.1870578084556        0.503771365303439
9       104     rRNA processing
GO:0016072      2.71939754178963e-09    20.8602499594222        0.532835097917099
9       110     rRNA metabolic process
GO:0042274      1.88175089364032e-08    85.0177514792899        0.0871911978409799
5       18      ribosomal small subunit biogenesis
GO:0034470      3.96892570148744e-08    12.4482456140351        0.968791087121998
10      200     ncRNA processing
GO:0034660      1.11608774414704e-07    9.59897315353211        1.38052729914885
11      285     ncRNA metabolic process
GO:0042273      2.42665430939766e-07    108.886363636364        0.0581274652273199
4       12      ribosomal large subunit biogenesis
Tissue: Lung=>Adipose_Subcutaneous      Type:   cluster
SourceGene:     ENSG00000229344.1
TargetGeneSet:  RP11    DDI2    SDHB    HSPG2   RPL11   RP1     MEAF6   PPCS    RPS8
RPS15AP10       RNF11   JAK1    RPL5    HBXIP   ATP5F1  RAP1A   SETDB1  LCE1C
RPS27   ELL2P1  COPA    CEP350  ARPC5   RPS7    NBAS    BIRC6   SOS1-IT1
CALM2   UBC     GMCL1   DGUOK-AS1       EIF5B   MZT2B   H3F3AP4 COL4A4  MFF
EFHD1   GIGYF2  SNED1   HDLBP   BRK1    RAD54L2 TMF1    PCNP    RPL24   NDUFB4  RYK
PDCD10  DNAJC19 PPP1R2  HTT     BOD1L   OCIAD2  PPM1K   RPL34   NDUFC1  NIPBL   CTD
MRPS36  TAF9    COX7C   ERAP1   SKP1    MTND5P11        SIL1    NDFIP1  TMEM14C RP3
WDR11   RWDD1   IGF2R   ANKRD61 STARD3NL        TRGV5   ZNF117  TRIM56  RPL19P12
NDUFA5  DCTN6   HOOK3   ARFGEF1 POLR2K  EIF3H   TG      RPL8    CLTA    RFK
ATP6V1G1        RPL35   UBAC1   DNLZ    SEC16A  C10orf31        PRINS   ADRA2A
RPS24   RPL27A  RPS13   CKAP5   BTBD18  DDB1    RNASEH2C        SPCS2   TMEM126B
C11orf73        ATM     SDHD    BACE1   UBE4A   ATP5L   DDX6    SCAF11  MLL4
PFDN5   NACA    LRP1    GNS     RBMS1P1 EEA1    APAF1   VPS29   KNTC1   N6AMT2
MRP63   ESD     MED4    RPL13AP25       COMMD6  CCNB1IP1        C14orf21
CGRRF1  YLPM1   CCNK    VPS39   DUT     SEC11A  MPG     NME3    NDUFB10 RPS15A
VPS53   TLCD2   WDR81   RPL26   ZSWIM7  TOM1L2  RPS7P1  SUPT6H  RFFL    RPL19
RPL27   TNRC6C  ROCK1P1 C18orf32        RPS15   PTPRS   NDUFA11 ZNF121  NDUFB7
SLC35E1 ZNF429  KRTDAP  EIF3K   ZNF587  TMEM230 MKKS    CHD6    RP4     TSHZ2
ATP5J   LINC00310       DDT     TTC28   SLC5A1  APOBEC3C        DYNLT3  USP9X
WDR45   GNL3L   COX7B   G6PD    FUNDC2
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006614      3.26207169581812e-20    26.1360294117647        1.07535810670542
20      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      3.98659510008024e-20    25.8303052325581        1.08559961248357
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20      106     cotranslational protein targeting to membrane
GO:0045047      3.98659510008024e-20    25.8303052325581        1.08559961248357
20      106     protein targeting to ER
GO:0072599      3.98659510008024e-20    25.8303052325581        1.08559961248357
20      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      3.78016822177201e-19    22.6482780612245        1.20849768182133
20      118     protein localization to endoplasmic reticulum
GO:0006415      1.33530892782906e-18    26.9905163329821        0.931977025811363
18      91      translational termination
GO:0006413      3.77607043734472e-18    17.8885616397187        1.55670887827832
21      152     translational initiation
GO:0006414      2.00822316971168e-17    22.6249336870027        1.07535810670542
18      105     translational elongation
GO:0006612      7.61369365212001e-17    16.6470864661654        1.56695038405647
20      153     protein targeting to membrane
GO:0072594      1.2786141947727e-16     13.5470957613815        2.08926717874196
22      204     establishment of protein localization to organelle
GO:0000184      2.05224819323133e-16    19.4696115765423        1.21873918759947
18      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0000956      5.51800123988594e-16    14.8427013422819        1.73081447650682
20      169     nuclear-transcribed mRNA catabolic process
GO:0019080      9.77020477086083e-16    15.8121329574818        1.54646737250017
19      151     viral genome expression
GO:0019083      9.77020477086083e-16    15.8121329574818        1.54646737250017
19      151     viral transcription
GO:0006402      1.53379161530991e-15    13.9883306962025        1.82298802851014
20      178     mRNA catabolic process
GO:0006401      1.89653849367975e-15    12.6882488873673        2.0995086845201 21
205     RNA catabolic process
GO:0043624      1.93095066362258e-14    14.5312820512821        1.56695038405647
18      153     cellular protein complex disassembly
GO:0043241      3.41437332424465e-14    14.0073626373626        1.6181579129472 18
158     protein complex disassembly
GO:0034623      1.85821896107544e-13    12.5565088757396        1.78202200539755
18      174     cellular macromolecular complex disassembly
GO:0019058      2.32531915226996e-13    10.4354265402844        2.36578783475192
20      231     viral infectious cycle
GO:0032984      3.04275127705642e-13    12.1622551361682        1.83322953428828
18      179     macromolecular complex disassembly
GO:0033365      1.97347455481443e-12    6.60608061026149        4.84423223306346
26      473     protein localization to organelle
GO:0022415      2.12750949238825e-12    9.15559895833333        2.66279150231818
20      260     viral reproductive process
GO:0006605      1.36183104177285e-11    6.27138899451355        4.8544737388416 25
474     protein targeting
GO:0022904      1.55909165751853e-11    16.4979919678715        0.983184554702097
13      96      respiratory electron transport chain
GO:0071845      6.95920595890273e-10    7.30670908039329        2.9085876409937 18
284     cellular component disassembly at cellular level
GO:0022411      8.7144524615395e-10     7.19641025641026        2.94955366410629
18      288     cellular component disassembly
GO:0022900      1.09587499561989e-09    11.2865625956535        1.37236177427168
13      134     electron transport chain
GO:0016032      1.14150660593146e-09    5.64672364672365        4.61891910594422
22      451     viral reproduction
GO:0045333      2.24881783961179e-09    10.5806488659202        1.45429382049685
13      142     cellular respiration
GO:0015980      2.41573730619789e-09    6.71418685121107        3.14414227389108
18      307     energy derivation by oxidation of organic compounds
GO:0006091      3.86827183404706e-07    4.69181988742964        4.38336447304685
18      428     generation of precursor metabolites and energy
GO:0042773      7.91887131465248e-06    14.6980419099966        0.481350771572902
6       47      ATP synthesis coupled electron transport
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GO:0042775      7.91887131465248e-06    14.6980419099966        0.481350771572902
6       47      mitochondrial ATP synthesis coupled electron transport
Tissue: Adipose_Subcutaneous=>Lung      Type:   asymmetric
SourceGene:     ENSG00000232098.1
TargetGeneSet:  RPL22   SPEN    KIAA0090        RPL11   CSF3R   RPS8    UQCRH   RP4
CSRP3   RPL5    CDC14A  RPS27   RAB4A   RPS7    TCEB1P21        RPL31   MIR1302-3
ILKAP   RPL32   RPL15   RPL29   CNBP    ANAPC13 RP11    RPL35A  RPL34   ACSL1   BTF3
TBCA    HINT1   CTB     ZNF300  HIGD2A  TMEM14C MDC1    CUTA    USP49   RWDD1
TNFAIP3 HAUS6P1 NAMPT   DOCK5   TCEA1   KIAA1429        RPL30   MRPL41  POLR3A
RPS24   RPS3AP5 IFITM2  EIF3F   RPL27A  RPS13   C11orf31        UBXN1   PRDX5   FAU
AIP     ATP5L   RPS25   C12orf57        IRAK4   NACA    IRAK3   ISCU    C12orf47
USP12   MTIF3   TPT1    CHD8    TRAV41  RPL36A  RPL7AP6 C14orf142       FAN1
RPAP1   LYSMD2  RPL4    SEC11A  NDUFB10 ECI1    RPS15A  PRSS53  GPR97   SPAG7
LSMD1   RPL26   C17orf48        RPS7P1  RPL17   RPL19   MYL12B  GPX4    RPS15   AES
C19orf43        C19orf55        RPL18   RPS11   FPR2    C22orf32        TBC1D22A
IGBP1   RPS4X
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006614      1.30157353101289e-40    96.2424242424242        0.595806518580029
28      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006415      1.42773035295904e-40    109.725852272727        0.516365649436025
27      91      translational termination
GO:0006613      1.76237998532743e-40    95.0018993352327        0.601480866376029
28      106     cotranslational protein targeting to membrane
GO:0045047      1.76237998532743e-40    95.0018993352327        0.601480866376029
28      106     protein targeting to ER
GO:0072599      1.76237998532743e-40    95.0018993352327        0.601480866376029
28      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      5.25504361418136e-39    82.2658436213992        0.669573039928033
28      118     protein localization to endoplasmic reticulum
GO:0006414      1.21496653414584e-38    89.9433566433566        0.595806518580029
27      105     translational elongation
GO:0006413      2.07569771424529e-37    63.373830342077 0.862500864992042       29
152     translational initiation
GO:0000184      5.41404405242449e-37    76.1816205533597        0.675247387724033
27      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      1.04959904748575e-35    60.0554049984944        0.856826517196042
28      151     viral genome expression
GO:0019083      1.04959904748575e-35    60.0554049984944        0.856826517196042
28      151     viral transcription
GO:0006612      1.56335148583073e-35    59.0862222222222        0.868175212788042
28      153     protein targeting to membrane
GO:0032984      3.40885401343939e-35    51.8680503144654        1.01570825548405
29      179     macromolecular complex disassembly
GO:0043241      4.12806040857741e-35    56.7937321937322        0.896546951768044
28      158     protein complex disassembly
GO:0034623      7.42987953103547e-34    50.5129375951294        0.987336516504048
28      174     cellular macromolecular complex disassembly
GO:0043624      9.00678986623874e-34    55.4922077922078        0.868175212788042
27      153     cellular protein complex disassembly
GO:0072594      1.88099283904718e-33    44.3801617250674        1.15756695038406
29      204     establishment of protein localization to organelle
GO:0000956      1.58933499772773e-32    49.1842509603073        0.958964777524047
27      169     nuclear-transcribed mRNA catabolic process
GO:0006402      7.01366727036605e-32    46.2234798314269        1.01003390768805
27      178     mRNA catabolic process
GO:0019058      3.04048001079587e-30    36.183908045977 1.31077434087606        28
231     viral infectious cycle
GO:0006401      3.82648578122869e-30    39.1375893769152        1.16324129818006
27      205     RNA catabolic process
GO:0022411      5.75479917681415e-29    29.8091352808334        1.63421216524808
29      288     cellular component disassembly
GO:0022415      9.13227108067185e-29    31.5961047254151        1.47533042696007
28      260     viral reproductive process
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GO:0071845      1.13022894149101e-27    28.5853587962963        1.61151477406408
28      284     cellular component disassembly at cellular level
GO:0033365      9.31581315988051e-23    17.1606748257692        2.68396650750813
29      473     protein localization to organelle
GO:0006605      9.88664938193443e-23    17.1208819164723        2.68964085530413
29      474     protein targeting
GO:0016032      4.31396126097778e-22    17.0951755538044        2.55913085599612
28      451     viral reproduction
GO:0042274      4.20414596204079e-08    71.7082917082917        0.102138260328005
5       18      ribosomal small subunit biogenesis
GO:0006364      1.25804355440942e-07    16.0731981981982        0.590132170784029
8       104     rRNA processing
GO:0042254      1.59632331877313e-07    12.5304305283757        0.845477821604041
9       149     ribosome biogenesis
GO:0016072      1.94699862244784e-07    15.1213566507684        0.62417825756003
8       110     rRNA metabolic process
GO:0042273      4.6044454228744e-07     92.0576923076923        0.0680921735520033
4       12      ribosomal large subunit biogenesis
GO:0022613      5.50957393660927e-07    9.14341085271318        1.27672825410006
10      225     ribonucleoprotein complex biogenesis
GO:0071843      9.56637484526541e-07    8.57593401261524        1.35616912324407
10      239     cellular component biogenesis at cellular level
GO:0034470      1.73618969894452e-05    7.98254504504505        1.13486955920006
8       200     ncRNA processing
Tissue: Adipose_Subcutaneous=>Lung      Type:   cluster
SourceGene:     HBE1(ENSG00000213931.1)
TargetGeneSet:  DDX11L1 RP11    RPL22   PIK3CD  RPL11   RP4     UQCRH   LRP8    RPL5
NENF    MFSD2B  UBC     CCDC104 RPL31   DDX11L2 CXCR2P1 RPL24   KLHL6-AS1
RPL35A  HTT     RPL34   CDC20B  BTF3    RFESD   EPB41L4A-AS1    U6      TRIM40
LY6G6F  C6orf25 RPL10A  RPL24P4 TOMM7   CTD     RPL30   TLN1    EDF1    PTGDS
RPL27A  RPS13   PTPRJ   UBXN1   SYT12   ARAP1-AS2       RPS25   C12orf57
KCTD4   TPT1    HS6ST3  HERC1   RPS15A  C16orf74        GP1BA   SLC46A1 CCR10
ITGA2B  PRKCA   GLTSCR2 RPS11   SNORD88B        LINC00493       WFDC12  PPPDE2  UXT
IGBP1   RPL39
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      5.51818513167869e-25    109.19619047619 0.277074250916892       16
91      translational termination
GO:0006414      6.46485337105153e-24    91.9293739967897        0.31970105875026
16      105     translational elongation
GO:0006614      6.46485337105153e-24    91.9293739967897        0.31970105875026
16      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      7.60018665220828e-24    90.9015873015873        0.322745830738357
16      106     cotranslational protein targeting to membrane
GO:0045047      7.60018665220828e-24    90.9015873015873        0.322745830738357
16      106     protein targeting to ER
GO:0072599      7.60018665220828e-24    90.9015873015873        0.322745830738357
16      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      4.69496705520481e-23    80.140056022409 0.35928309459553        16
118     protein localization to endoplasmic reticulum
GO:0000184      5.41431967622629e-23    79.3564493758668        0.362327866583627
16      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      2.90778262073247e-21    60.410582010582 0.459760570202754       16
151     viral genome expression
GO:0019083      2.90778262073247e-21    60.410582010582 0.459760570202754       16
151     viral transcription
GO:0006413      3.24389404359499e-21    59.9621848739496        0.462805342190852
16      152     translational initiation
GO:0006612      3.61607575891177e-21    59.5203336809176        0.46585011417895
16      153     protein targeting to membrane
GO:0043624      3.61607575891177e-21    59.5203336809176        0.46585011417895
16      153     cellular protein complex disassembly
GO:0043241      6.15518583250217e-21    57.4044265593561        0.481073974119438
16      158     protein complex disassembly
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GO:0072594      8.79035658425368e-21    47.8787878787879        0.621133485571933
17      204     establishment of protein localization to organelle
GO:0000956      1.86655759439021e-20    53.2362278244631        0.514566465988513
16      169     nuclear-transcribed mRNA catabolic process
GO:0034623      3.01350515566819e-20    51.5334538878843        0.529790325929001
16      174     cellular macromolecular complex disassembly
GO:0006402      4.3747520852651e-20     50.2469135802469        0.541969413881392
16      178     mRNA catabolic process
GO:0032984      4.79532045155869e-20    49.9351446099912        0.54501418586949
16      179     macromolecular complex disassembly
GO:0006401      4.37959984370942e-19    42.9871504157218        0.62417825756003
16      205     RNA catabolic process
GO:0019058      3.02228381570828e-18    37.7196013289037        0.703342329250571
16      231     viral infectious cycle
GO:0022415      2.01868487634857e-17    33.1686182669789        0.791640716905404
16      260     viral reproductive process
GO:0071845      8.2577947910492e-17     30.1471215351812        0.864715244619749
16      284     cellular component disassembly at cellular level
GO:0022411      1.03150092486073e-16    29.6953781512605        0.87689433257214
16      288     cellular component disassembly
GO:0033365      6.33950229792127e-16    21.228740490279 1.44017715037022        18
473     protein localization to organelle
GO:0006605      6.57817992612401e-16    21.1806680161943        1.44322192235831
18      474     protein targeting
GO:0016032      1.16227648846917e-13    18.3540229885057        1.37319216663207
16      451     viral reproduction
GO:0042273      5.68413960043026e-06    117.056910569106        0.0365372638571725
3       12      ribosomal large subunit biogenesis
Tissue: Lung=>Adipose_Subcutaneous      Type:   cluster
SourceGene:     HSPB1P2(ENSG00000230216.1)
TargetGeneSet:  RPS6KA1 SYTL1   C1orf38 CSF3R   VAV3    CD53    RSBN1   CTSS    CD84
ARHGAP30        PTPRC   ADIPOR1 MERTK   CXXC11  NUP210  PP2D1   HCLS1   CD86
P2RY13  RPL7L1P8        TLR1    TXK     EMB     GZMK    MAP3K1  IQGAP2  CD14
DOCK2   GRK6    DOK3    DEFA6   OSBPL3  IKZF1   TFEC    TBXAS1  LYN     KIF24   PAX5
SYK     CARD9   MRC1    FAM21C  TNKS2   TM9SF3  PIK3AP1 FRAT1   SNORA19 KCNQ1
KCNQ1OT1        MS4A6A  MS4A4E  MS4A7   LGALS12 CCDC88B TBC1D10C        SLCO2B1 CTSC
CRTAM   PTPN6   CD163   C3AR1   SELPLG  ELF1    LCP1    CLCN7   C16orf54
ADCY7   RNF166  CXCL16  PIK3R5  EVI2B   FMNL1   BTBD17  HMHA1   DENND1C VAV1
MAN2B1  LRRC25  GMIP    HCST    SPINT2  CEACAM4 CD37    CTD     CD33    SIGLEC5
LILRA2  LILRB1  LILRB4  CASS4   ZBP1    SH3BP1  WAS     API5P1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0002764      2.83025612685634e-10    13.0396453900709        1.25278527437548
13      248     immune response-regulating signaling pathway
GO:0002757      1.9787310374037e-09     12.4869514077777        1.18711507854128
12      235     immune response-activating signal transduction
GO:0050778      2.9229016976017e-08     8.65864197530864        1.83876548335755
13      364     positive regulation of immune response
GO:0002253      2.94324989621189e-08    9.65853658536585        1.51041450418656
12      299     activation of immune response
GO:0042110      5.99918653887682e-08    9.01650024029476        1.61144557470071
12      319     T cell activation
GO:0045088      1.18297775136088e-07    10.9740611691831        1.08608400802713
10      215     regulation of innate immune response
GO:0001817      2.1639261029611e-07     7.95445741011953        1.81350771572902
12      359     regulation of cytokine production
GO:0046649      2.20399140272921e-07    7.20055555555556        2.18732267663137
13      433     lymphocyte activation
GO:0050867      3.28882310531892e-07    9.7639751552795 1.21237284616982        10
240     positive regulation of cell activation
GO:0002252      4.70331852634171e-07    7.36600333128781        1.94989966092312
12      386     immune effector process
GO:0001816      6.00831906475875e-07    7.18828917519154        1.99536364265449
12      395     cytokine production
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GO:0002768      6.22527330396889e-07    12.8886877828054        0.727423707701889
8       144     immune response-regulating cell surface receptor signaling pathway
GO:0051251      1.28561864970946e-06    9.67445388349515        1.08608400802713
9       215     positive regulation of lymphocyte activation
GO:0050870      2.28002046053706e-06    10.7333647947145        0.863815652895993
8       171     positive regulation of T cell activation
GO:0002696      2.49899579738861e-06    8.8857421875    1.1770197148986         9
233     positive regulation of leukocyte activation
GO:0050851      2.78889692962869e-06    13.0399686520376        0.62134108366203
7       123     antigen receptor-mediated signaling pathway
GO:0046631      3.48609898204514e-06    16.8523173605656        0.41422738910802
6       82      alpha-beta T cell activation
GO:0002429      4.69291948171638e-06    11.996632996633 0.671856618919106       7
133     immune response-activating cell surface receptor signaling pathway
GO:0031347      5.20921106174128e-06    6.33006912442396        2.03577607086015
11      403     regulation of defense response
GO:0042035      6.4028684164143e-06     15.0584723441615        0.459691370839388
6       91      regulation of cytokine biosynthetic process
GO:0002697      7.55348514979535e-06    9.04583499402152        1.01536225866722
8       201     regulation of immune effector process
GO:0050865      8.19942858096007e-06    6.69479002812336        1.73268285931769
10      343     regulation of cell activation
GO:0002699      8.72980708353583e-06    14.2169154228856        0.484949138467926
6       96      positive regulation of immune effector process
GO:0042089      1.10482670915257e-05    13.6081295649413        0.505155352570756
6       100     cytokine biosynthetic process
GO:0051249      1.20945271920179e-05    7.23859489051095        1.42958964777524
9       283     regulation of lymphocyte activation
GO:0042107      1.23813915098647e-05    13.3227611940299        0.515258459622171
6       102     cytokine metabolic process
GO:0050853      1.29351108289805e-05    33.2823188405797        0.146495052245519
4       29      B cell receptor signaling pathway
GO:0045089      1.3959425733553e-05     10.060202020202 0.793093903536087       7
157     positive regulation of innate immune response
GO:0050863      1.50818786243891e-05    8.18490429758035        1.11639332918137
8       221     regulation of T cell activation
Tissue: Lung=>Adipose_Subcutaneous      Type:   asymmetric
SourceGene:     MARCH10(ENSG00000173838.6)
TargetGeneSet:  TNFRSF4 C1QC    RPS6KA1 C1orf38 LAPTM5  CSF3R   MCOLN2  CD53
ADORA3  ARHGEF11        MNDA    SLAMF8  CD84    ARHGAP30        FCGR2A  FCGR3A
POU2F1  SELL    RP11    PTPRC   CR1     WDR26   GJC2    NLRC4   PLEK    VAMP8
MERTK   TFCP2L1 SLC11A1 CAB39   CDCP1   HCLS1   CD86    P2RY1   PHC3    ATP11B  TFRC
HTT     TLR1    RBM47   WDFY3   SNCA    DAPP1   C4orf21 FAM105A FYB     GM2A
HAVCR2  DOCK2   DOK3    ZNF192  AIF1    GPSM3   DEFA6   TTYH3   AOAH    AKAP9
PILRA   TFEC    IRF5    TBXAS1  MSR1    DOK2    DOCK5   CTD     VPS13B  UBR5    SLA
HEATR7A SYK     FBP1    FKBP15  CARD9   C10orf31        MRC1    WDFY4   PIK3AP1
PTPRE   MUC6    RP13    COMMD9  PTPRJ   MS4A6A  MS4A7   MS4A6E  CCDC88B UNC93B5
SLCO2B1 MYO7A   IL10RA  IFT46   C11orf45        PTPN6   CD163   M6PR    CLEC7A  BIN2
NCKAP1L ARHGAP9 MAPKAPK5        GLT1D1  LCP1    PLCB2   DMXL2   AQP9    DENND4A
FANCI   PRKCB   APOBR   C16orf54        CORO1A  ATP6V0D1        ZZEF1   ARRB2
SNORA48 CD68    PIK3R5  LGALS9  CD300A  HMHA1   C19orf59        CD209   PRAM1
MYO1F   MAN2B1  KLF2    IFI30   LRRC25  GMIP    ZNF714  SPINT2  RASGRP4 PLD3
CEACAM4 CD37    SIGLEC7 FPR2    LILRB2  LILRB1  ZIM2    SIGLEC1 HCK     MMP9
CRYBB1  CYTH4   SH3BP1  TLR8    OFD1    CYBB    WAS     VSIG4   BTK     RP4
ARHGAP4
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0002764      3.17525917561392e-12    10.5078260869565        2.1108573801121 18
248     immune response-regulating signaling pathway
GO:0050778      3.5639430893975e-12     8.39435774309724        3.09819389661615
21      364     positive regulation of immune response
GO:0002253      7.88480122848184e-12    9.16593406593407        2.54494498650612
19      299     activation of immune response
GO:0050865      8.50416276958404e-11    7.89636752136752        2.91945194104214
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19      343     regulation of cell activation
GO:0002252      8.5223353516287e-11     7.40728951137991        3.28544737388416
20      386     immune effector process
GO:0002757      1.45183016632472e-10    9.6335936499808 2.0002075980901 16      235
immune response-activating signal transduction
GO:0042098      3.34398676056419e-10    14.5048444671086        1.00435955989205
12      118     T cell proliferation
GO:0046649      6.46625481834432e-10    6.54223183431674        3.68548889350218
20      433     lymphocyte activation
GO:0042110      1.64901707330439e-09    7.44851930526053        2.71517542038613
17      319     T cell activation
GO:0002694      1.8131862504206e-09     7.39846077457795        2.73219846377413
17      321     regulation of leukocyte activation
GO:0046651      2.40778009111816e-09    10.5315608919383        1.46398173136807
13      172     lymphocyte proliferation
GO:0032943      2.77379799910712e-09    10.3992659514399        1.48100477475607
13      174     mononuclear cell proliferation
GO:0002768      3.37344018686564e-09    11.6265356265356        1.22565912393606
12      144     immune response-regulating cell surface receptor signaling pathway
GO:0070661      4.79816032963925e-09    9.9013986013986 1.54909694830808        13
182     leukocyte proliferation
GO:0006897      5.3768325469158e-09     6.84537505752416        2.93647498443014
17      345     endocytosis
GO:0050670      3.89120289605634e-08    10.4823442534909        1.22565912393606
11      144     regulation of lymphocyte proliferation
GO:0032944      4.18065378295491e-08    10.4033848614072        1.23417064563006
11      145     regulation of mononuclear cell proliferation
GO:0070663      5.93542564562744e-08    10.0256294964029        1.27672825410006
11      150     regulation of leukocyte proliferation
GO:0006954      6.94440190076239e-08    5.36061776061776        3.93232302262819
18      462     inflammatory response
GO:0051249      1.26540204035743e-07    6.71279969987381        2.40876063940212
14      283     regulation of lymphocyte activation
GO:0050867      1.28847622001187e-07    7.34132959551462        2.0427652065601 13
240     positive regulation of cell activation
GO:0050853      1.36117103737063e-07    31.8952062430323        0.246834129126012
6       29      B cell receptor signaling pathway
GO:0002697      1.40749861590465e-07    8.08751608751609        1.71081586049408
12      201     regulation of immune effector process
GO:0042129      1.88840355589208e-07    12.2162471395881        0.859663691094042
9       101     regulation of T cell proliferation
GO:0002429      1.92794548484794e-07    10.2201597237211        1.13203238530206
10      133     immune response-activating cell surface receptor signaling pathway
GO:0001816      2.35237047731635e-07    5.50351392005524        3.36205106913016
16      395     cytokine production
GO:0045088      2.92116919480973e-07    7.5223006257489 1.82997716421009        12
215     regulation of innate immune response
GO:0001817      3.89407282254098e-07    5.64599483204134        3.05563628814615
15      359     regulation of cytokine production
GO:0006909      6.674296027887e-07      12.7090301003344        0.731990865684036
8       86      phagocytosis
GO:0050764      7.43106896175798e-07    22.9102564102564        0.323437824372016
6       38      regulation of phagocytosis
GO:0050851      1.01746170274446e-06    9.84349030470914        1.04691716836205
9       123     antigen receptor-mediated signaling pathway
GO:0002443      1.82900287747965e-06    6.93785714285714        1.79593107743409
11      211     leukocyte mediated immunity
GO:0051251      2.19631347999062e-06    6.79989495798319        1.82997716421009
11      215     positive regulation of lymphocyte activation
GO:0050863      2.86867805888058e-06    6.60280612244898        1.88104629437409
11      221     regulation of T cell activation
GO:0002274      3.5334009097762e-06     9.99841897233201        0.910732821258044
8       107     myeloid leukocyte activation
```

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GO:0002696      4.77291829778004e-06    6.2405888030888 1.9831845547021 11      233
positive regulation of leukocyte activation
GO:0001911      5.94319790784005e-06    179.075 0.0425576084700021      3       5
negative regulation of leukocyte mediated cytotoxicity
GO:0030100      7.33596052824878e-06    8.99162055335968        1.00435955989205
8       118     regulation of endocytosis
GO:0031347      8.362296822036e-06      4.60239145303177        3.43014324268217
14      403     regulation of defense response
GO:0030097      9.01559837148166e-06    4.3030753968254 3.94083454432219        15
463     hemopoiesis
GO:0002263      9.96894014034679e-06    8.59765595463138        1.04691716836205
8       123     cell activation involved in immune response
GO:0002366      9.96894014034679e-06    8.59765595463138        1.04691716836205
8       123     leukocyte activation involved in immune response
GO:0031342      1.18124064034452e-05    119.375 0.0510691301640025      3       6
negative regulation of cell killing
GO:0002703      1.31223329447269e-05    10.1116632860041        0.783059995848038
7       92      regulation of leukocyte mediated immunity
GO:0050870      1.52829267162052e-05    6.90350877192982        1.45547020967407
9       171     positive regulation of T cell activation
GO:0032675      1.53764606366223e-05    12.8394062078273        0.536225866722026
6       63      regulation of interleukin-6 production
GO:0042116      1.65034237097815e-05    18.3551617873652        0.323437824372016
5       38      macrophage activation
GO:0050671      1.73595233003197e-05    9.65449438202247        0.81710608262404
7       96      positive regulation of lymphocyte proliferation
GO:0032635      1.84353107544292e-05    12.4024337244676        0.553248910110027
6       65      interleukin-6 production
GO:0032946      1.85789172614029e-05    9.54655172413793        0.82561760431804
7       97      positive regulation of mononuclear cell proliferation
GO:0048534      1.98443236597909e-05    4.00694444444444        4.21320323853021
15      495     hemopoietic or lymphoid organ development
Tissue: Lung=>Adipose_Subcutaneous      Type:   cluster
SourceGene:     MARCH10(ENSG00000173838.6)
TargetGeneSet:  TNFRSF4 C1QC    RPS6KA1 C1orf38 LAPTM5  CSF3R   MCOLN2  CD53
ADORA3  ARHGEF11        MNDA    SLAMF8  CD84    ARHGAP30        FCGR2A  FCGR3A
POU2F1  SELL    RP11    PTPRC   CR1     WDR26   GJC2    NLRC4   PLEK    VAMP8
MERTK   TFCP2L1 SLC11A1 CAB39   CDCP1   HCLS1   CD86    P2RY1   PHC3    ATP11B  TFRC
HTT     TLR1    RBM47   WDFY3   SNCA    DAPP1   C4orf21 FAM105A FYB     GM2A
HAVCR2  DOCK2   DOK3    ZNF192  AIF1    GPSM3   DEFA6   TTYH3   AOAH    AKAP9
PILRA   TFEC    IRF5    TBXAS1  MSR1    DOK2    DOCK5   CTD     VPS13B  UBR5    SLA
HEATR7A SYK     FBP1    FKBP15  CARD9   C10orf31        MRC1    WDFY4   PIK3AP1
PTPRE   MUC6    RP13    COMMD9  PTPRJ   MS4A6A  MS4A7   MS4A6E  CCDC88B UNC93B5
SLCO2B1 MYO7A   IL10RA  IFT46   C11orf45        PTPN6   CD163   M6PR    CLEC7A  BIN2
NCKAP1L ARHGAP9 MAPKAPK5        GLT1D1  LCP1    PLCB2   DMXL2   AQP9    DENND4A
FANCI   PRKCB   APOBR   C16orf54        CORO1A  ATP6V0D1        ZZEF1   ARRB2
SNORA48 CD68    PIK3R5  LGALS9  CD300A  HMHA1   C19orf59        CD209   PRAM1
MYO1F   MAN2B1  KLF2    IFI30   LRRC25  GMIP    ZNF714  SPINT2  RASGRP4 PLD3
CEACAM4 CD37    SIGLEC7 FPR2    LILRB2  LILRB1  ZIM2    SIGLEC1 HCK     MMP9
CRYBB1  CYTH4   SH3BP1  TLR8    OFD1    CYBB    WAS     VSIG4   BTK     RP4
ARHGAP4
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0002764      3.17525917561392e-12    10.5078260869565        2.1108573801121 18
248     immune response-regulating signaling pathway
GO:0050778      3.5639430893975e-12     8.39435774309724        3.09819389661615
21      364     positive regulation of immune response
GO:0002253      7.88480122848184e-12    9.16593406593407        2.54494498650612
19      299     activation of immune response
GO:0050865      8.50416276958404e-11    7.89636752136752        2.91945194104214
19      343     regulation of cell activation
GO:0002252      8.5223353516287e-11     7.40728951137991        3.28544737388416
20      386     immune effector process
GO:0002757      1.45183016632472e-10    9.6335936499808 2.0002075980901 16      235
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immune response-activating signal transduction
GO:0042098	3.34398676056419e-10	14.5048444671086	1.00435955989205
12	118	T cell proliferation
GO:0046649	6.46625481834432e-10	6.54223183431674	3.68548889350218
20	433	lymphocyte activation
GO:0042110	1.64901707330439e-09	7.44851930526053	2.71517542038613
17	319	T cell activation
GO:0002694	1.8131862504206e-09	7.39846077457795	2.73219846377413
17	321	regulation of leukocyte activation
GO:0046651	2.40778009111816e-09	10.5315608919383	1.46398173136807
13	172	lymphocyte proliferation
GO:0032943	2.77379799910712e-09	10.3992659514399	1.48100477475607
13	174	mononuclear cell proliferation
GO:0002768	3.37344018686564e-09	11.6265356265356	1.22565912393606
12	144	immune response-regulating cell surface receptor signaling pathway
GO:0070661	4.79816032963925e-09	9.9013986013986 1.54909694830808	13
182	leukocyte proliferation
GO:0006897	5.3768325469158e-09	6.84537505752416	2.93647498443014
17	345	endocytosis
GO:0050670	3.89120289605634e-08	10.4823442534909	1.22565912393606
11	144	regulation of lymphocyte proliferation
GO:0032944	4.18065378295491e-08	10.4033848614072	1.23417064563006
11	145	regulation of mononuclear cell proliferation
GO:0070663	5.93542564562744e-08	10.0256294964029	1.27672825410006
11	150	regulation of leukocyte proliferation
GO:0006954	6.94440190076239e-08	5.36061776061776	3.93232302262819
18	462	inflammatory response
GO:0051249	1.26540204035743e-07	6.71279969987381	2.40876063940212
14	283	regulation of lymphocyte activation
GO:0050867	1.28847622001187e-07	7.34132959551462	2.0427652065601 13
240	positive regulation of cell activation
GO:0050853	1.36117103737063e-07	31.8952062430323	0.246834129126012
6	29	B cell receptor signaling pathway
GO:0002697	1.40749861590465e-07	8.08751608751609	1.71081586049408
12	201	regulation of immune effector process
GO:0042129	1.88840355589208e-07	12.2162471395881	0.859663691094042
9	101	regulation of T cell proliferation
GO:0002429	1.92794548484794e-07	10.2201597237211	1.13203238530206
10	133	immune response-activating cell surface receptor signaling pathway
GO:0001816	2.35237047731635e-07	5.50351392005524	3.36205106913016
16	395	cytokine production
GO:0045088	2.92116919480973e-07	7.5223006257489 1.82997716421009	12
215	regulation of innate immune response
GO:0001817	3.89407282254098e-07	5.64599483204134	3.05563628814615
15	359	regulation of cytokine production
GO:0006909	6.674296027887e-07	12.7090301003344	0.731990865684036
8	86	phagocytosis
GO:0050764	7.43106896175798e-07	22.9102564102564	0.323437824372016
6	38	regulation of phagocytosis
GO:0050851	1.01746170274446e-06	9.84349030470914	1.04691716836205
9	123	antigen receptor-mediated signaling pathway
GO:0002443	1.82900287747965e-06	6.93785714285714	1.79593107743409
11	211	leukocyte mediated immunity
GO:0051251	2.19631347999062e-06	6.79989495798319	1.82997716421009
11	215	positive regulation of lymphocyte activation
GO:0050863	2.86867805888058e-06	6.60280612244898	1.88104629437409
11	221	regulation of T cell activation
GO:0002274	3.5334009097762e-06	9.99841897233201	0.910732821258044
8	107	myeloid leukocyte activation
GO:0002696	4.77291829778004e-06	6.2405888030888 1.9831845547021 11	233
positive regulation of leukocyte activation
GO:0001911	5.94319790784005e-06	179.075 0.0425576084700021	3	5
negative regulation of leukocyte mediated cytotoxicity
```

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GO:0030100      7.33596052824878e-06    8.99162055335968        1.00435955989205
8       118     regulation of endocytosis
GO:0031347      8.362296822036e-06      4.60239145303177        3.43014324268217
14      403     regulation of defense response
GO:0030097      9.01559837148166e-06    4.3030753968254 3.94083454432219        15
463     hemopoiesis
GO:0002263      9.96894014034679e-06    8.59765595463138        1.04691716836205
8       123     cell activation involved in immune response
GO:0002366      9.96894014034679e-06    8.59765595463138        1.04691716836205
8       123     leukocyte activation involved in immune response
GO:0031342      1.18124064034452e-05    119.375 0.0510691301640025      3       6
negative regulation of cell killing
GO:0002703      1.31223329447269e-05    10.1116632860041        0.783059995848038
7       92      regulation of leukocyte mediated immunity
GO:0050870      1.52829267162052e-05    6.90350877192982        1.45547020967407
9       171     positive regulation of T cell activation
GO:0032675      1.53764606366223e-05    12.8394062078273        0.536225866722026
6       63      regulation of interleukin-6 production
GO:0042116      1.65034237097815e-05    18.3551617873652        0.323437824372016
5       38      macrophage activation
GO:0050671      1.73595233003197e-05    9.65449438202247        0.81710608262404
7       96      positive regulation of lymphocyte proliferation
GO:0032635      1.84353107544292e-05    12.4024337244676        0.553248910110027
6       65      interleukin-6 production
GO:0032946      1.85789172614029e-05    9.54655172413793        0.82561760431804
7       97      positive regulation of mononuclear cell proliferation
GO:0048534      1.98443236597909e-05    4.00694444444444        4.21320323853021
15      495     hemopoietic or lymphoid organ development
Tissue: Lung=>Adipose_Subcutaneous      Type:   asymmetric
SourceGene:     RP11-131H24.4(ENSG00000258987.1)
TargetGeneSet:  GNL2    WDR65   RPS8    RPL5    RP11    FAM46C  S100A6  EEF1B2
C2orf57 ZNF502  GRM2    ACTL6A  SLC30A9 EXOC7   BRD9    CTD     AGGF1   SNX24
ZNF300  TDP2    RARS2   DNAJC2  NAA38   ARF5    RPS20   SNHG6   DCAF13  RPL8    RPS6
NFX1    TXN     RPL12   CDNF    SLC39A13        SLC35E3 RPL18AP3        RPLP0
PRHOXNB CCDC122 GMFB    WDHD1   LGALS3  TRMT5   RPS3AP6 RPLP1   RPS17L  ABCC6
LCMT1   DDX19B  RAC3    RPS15   RPL36   DPY19L3 RPS19   C19orf48        RPS9    DTD1
DMC1    EEF1B2P3        IGBP1-AS1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      4.47492340187973e-20    73.4153846153846        0.31970105875026
14      105     translational elongation
GO:0006415      4.44824292612228e-19    77.0376344086021        0.277074250916892
13      91      translational termination
GO:0006614      3.1495736053317e-18     65.2507012622721        0.31970105875026
13      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      3.58264347410442e-18    64.5445716267777        0.322745830738357
13      106     cotranslational protein targeting to membrane
GO:0045047      3.58264347410442e-18    64.5445716267777        0.322745830738357
13      106     protein targeting to ER
GO:0072599      3.58264347410442e-18    64.5445716267777        0.322745830738357
13      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      1.52891891748631e-17    57.1201228878648        0.35928309459553
13      118     protein localization to endoplasmic reticulum
GO:0000184      1.71298613237649e-17    56.5772976262934        0.362327866583627
13      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      4.11922810399803e-16    43.3606825619448        0.459760570202754
13      151     viral genome expression
GO:0019083      4.11922810399803e-16    43.3606825619448        0.459760570202754
13      151     viral transcription
GO:0006413      4.49543126155085e-16    43.0457182640984        0.462805342190852
13      152     translational initiation
GO:0006612      4.90299489292293e-16    42.7352534562212        0.46585011417895
13      153     protein targeting to membrane
GO:0043624      4.90299489292293e-16    42.7352534562212        0.46585011417895
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13      153     cellular protein complex disassembly
GO:0043241      7.49987316382628e-16    41.2471635150167        0.481073974119438
13      158     protein complex disassembly
GO:0000956      1.82027593177232e-15    38.3091397849462        0.51456646598851З
13      169     nuclear-transcribed mRNA catabolic process
GO:0034623      2.66953271065401e-15    37.1063915047085        0.529790325929001
13      174     cellular macromolecular complex disassembly
GO:0006402      3.59626010982814e-15    36.1966764418377        0.541969413881392
13      178     mRNA catabolic process
GO:0032984      3.87009377822261e-15    35.9760979401477        0.54501418586949
13      179     macromolecular complex disassembly
GO:0072594      2.12913434551424e-14    31.212295220402 0.621133485571933       13
204     establishment of protein localization to organelle
GO:0006401      2.26871484396848e-14    31.0475470430108        0.62417825756003
13      205     RNA catabolic process
GO:0019058      1.06290140406222e-13    27.2946137910624        0.703342329250571
13      231     viral infectious cycle
GO:0022415      4.84922544983523e-13    24.0407470288625        0.791640716905404
13      260     viral reproductive process
GO:0071845      1.49424458973798e-12    21.8745387453875        0.864715244619749
13      284     cellular component disassembly at cellular level
GO:0022411      1.78473401619954e-12    21.5502639296188        0.87689433257214
13      288     cellular component disassembly
GO:0033365      6.25701820180238e-11    14.1809731299927        1.44017715037022
14      473     protein localization to organelle
GO:0006605      6.43461749299724e-11    14.1491304347826        1.44322192235831
14      474     protein targeting
GO:0016032      4.82255836927957e-10    13.3743555751952        1.37319216663207
13      451     viral reproduction
GO:0042254      5.38470278183566e-10    26.204693877551 0.453671026226559       9
149     ribosome biogenesis
GO:0022613      1.07083822534352e-09    19.4145006839945        0.685073697321985
10      225     ribonucleoprotein complex biogenesis
GO:0042274      1.72182548076821e-09    141.952662721893        0.0548058957857588
5       18      ribosomal small subunit biogenesis
GO:0071843      1.922874683998e-09      18.2096069868996        0.727700505155353
10      239     cellular component biogenesis at cellular level
GO:0006364      2.51065623580698e-08    27.9102814154361        0.316656286762162
7       104     rRNA processing
GO:0016072      3.71045693642895e-08    26.2734190501181        0.334924918690748
7       110     rRNA metabolic process
GO:0034660      1.98540881113008e-06    11.3357400722022        0.867760016607847
8       285     ncRNA metabolic process
GO:0034470      2.17447811327912e-06    13.933342669094 0.608954397619542       7
200     ncRNA processing
Tissue: Lung=>Adipose_Subcutaneous      Type:   cluster
SourceGene:     RP11-131H24.4(ENSG00000258987.1)
TargetGeneSet:  GNL2    WDR65   RPS8    RPL5    RP11    FAM46C  S100A6  EEF1B2
C2orf57 ZNF502  GRM2    ACTL6A  SLC30A9 EXOC7   BRD9    CTD     AGGF1   SNX24
ZNF300  TDP2    RARS2   DNAJC2  NAA38   ARF5    RPS20   SNHG6   DCAF13  RPL8    RPS6
NFX1    TXN     RPL12   CDNF    SLC39A13        SLC35E3 RPL18AP3        RPLP0
PRHOXNB CCDC122 GMFB    WDHD1   LGALS3  TRMT5   RPS3AP6 RPLP1   RPS17L  ABCC6
LCMT1   DDX19B  RAC3    RPS15   RPL36   DPY19L3 RPS19   C19orf48        RPS9    DTD1
DMC1    EEF1B2P3        IGBP1-AS1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      4.47492340187973e-20    73.4153846153846        0.31970105875026
14      105     translational elongation
GO:0006415      4.44824292612228e-19    77.0376344086021        0.277074250916892
13      91      translational termination
GO:0006614      3.1495736053317e-18     65.2507012622721        0.31970105875026
13      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      3.58264347410442e-18    64.5445716267777        0.322745830738357
13      106     cotranslational protein targeting to membrane
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GO:0045047      3.58264347410442e-18    64.5445716267777        0.322745830738357
13      106     protein targeting to ER
GO:0072599      3.58264347410442e-18    64.5445716267777        0.322745830738357
13      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      1.52891891748631e-17    57.1201228878648        0.35928309459553
13      118     protein localization to endoplasmic reticulum
GO:0000184      1.71298613237649e-17    56.5772976262934        0.362327866583627
13      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      4.11922810399803e-16    43.3606825619448        0.459760570202754
13      151     viral genome expression
GO:0019083      4.11922810399803e-16    43.3606825619448        0.459760570202754
13      151     viral transcription
GO:0006413      4.49543126155085e-16    43.0457182640984        0.462805342190852
13      152     translational initiation
GO:0006612      4.90299489292293e-16    42.7352534562212        0.46585011417895
13      153     protein targeting to membrane
GO:0043624      4.90299489292293e-16    42.7352534562212        0.46585011417895
13      153     cellular protein complex disassembly
GO:0043241      7.49987316382628e-16    41.2471635150167        0.481073974119438
13      158     protein complex disassembly
GO:0000956      1.82027593177232e-15    38.3091397849462        0.514566465988513
13      169     nuclear-transcribed mRNA catabolic process
GO:0034623      2.66953271065401e-15    37.1063915047085        0.529790325929001
13      174     cellular macromolecular complex disassembly
GO:0006402      3.59626010982814e-15    36.1966764418377        0.541969413881392
13      178     mRNA catabolic process
GO:0032984      3.87009377822261e-15    35.9760979401477        0.54501418586949
13      179     macromolecular complex disassembly
GO:0072594      2.12913434551424e-14    31.212295220402 0.621133485571933       13
204     establishment of protein localization to organelle
GO:0006401      2.26871484396848e-14    31.0475470430108        0.62417825756003
13      205     RNA catabolic process
GO:0019058      1.06290140406222e-13    27.2946137910624        0.703342329250571
13      231     viral infectious cycle
GO:0022415      4.84922544983523e-13    24.0407470288625        0.791640716905404
13      260     viral reproductive process
GO:0071845      1.49424458973798e-12    21.8745387453875        0.864715244619749
13      284     cellular component disassembly at cellular level
GO:0022411      1.78473401619954e-12    21.5502639296188        0.87689433257214
13      288     cellular component disassembly
GO:0033365      6.25701820180238e-11    14.1809731299927        1.44017715037022
14      473     protein localization to organelle
GO:0006605      6.43461749299724e-11    14.1491304347826        1.44322192235831
14      474     protein targeting
GO:0016032      4.82255836927957e-10    13.3743555751952        1.37319216663207
13      451     viral reproduction
GO:0042254      5.38470278183566e-10    26.204693877551 0.453671026226559       9
149     ribosome biogenesis
GO:0022613      1.07083822534352e-09    19.4145006839945        0.685073697321985
10      225     ribonucleoprotein complex biogenesis
GO:0042274      1.72182548076821e-09    141.952662721893        0.0548058957857588
5       18      ribosomal small subunit biogenesis
GO:0071843      1.922874683998e-09      18.2096069868996        0.727700505155353
10      239     cellular component biogenesis at cellular level
GO:0006364      2.51065623580698e-08    27.9102814154361        0.316656286762162
7       104     rRNA processing
GO:0016072      3.71045693642895e-08    26.2734190501181        0.334924918690748
7       110     rRNA metabolic process
GO:0034660      1.98540881113008e-06    11.3357400722022        0.867760016607847
8       285     ncRNA metabolic process
GO:0034470      2.17447811327912e-06    13.933342669094 0.608954397619542       7
200     ncRNA processing
Tissue: Lung=>Adipose_Subcutaneous      Type:   asymmetric
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SourceGene:     RP11-156P1.1(ENSG00000263142.1)
TargetGeneSet:  SDHB    DNAJC8  PRDX3P2 ZMYM4   MEAF6   NFYC    RPL5    ATP5F1
LCE1C   ELL2P1  COPA    MGST3   CEP350  CICP13  RPS7    BIRC6   SOS1-IT1
CALM2   COX5B   UGGT1   H3F3AP4 FTH1P20 COL4A4  EFHD1   SNED1   HDLBP   RP11
RPL24   NDUFB4  CNBP    RYK     NME9    DNAJC19 PSAPL1  BOD1L   CD38    TXK
ANKRD17 PPM1K   NDUFC1  CTD     TBCA    ELL2    ISOC1   SKP1    MTND5P11
TRIM41  RPL15P3 AGPAT1  RP3     COX7A2  RWDD1   CYCS    SEPT7   RP4     SYPL1
NDUFA5  FSCN3   CHCHD3  DCTN6   VDAC3   HOOK3   ARFGEF1 OXR1    EIF3E   ATP6V1G1
RPL7A   SEC16A  ATP5C1  C10orf31        VDAC2   C10orf99        NDUFB8  FAM196A
RPL27A  CKAP5   NDUFS3  ZBTB3   C11orf73        SDHD    UBE4A   ATP5L   DDX6
NCKAP5L PFDN5   NACA    LRP1    GNS     CPM     CCDC59  RPL6    GOLGA3  MRP63   ESD
CGRRF1  VPS39   SEC11A  MPG     NDUFB10 ECI1    RPS15A  SMG1    MT1X    VPS53
TLCD2   WDR81   RPL26   CCDC144B        RPS7P1  RFFL    RPL19   SUMO2   TNRC6C  EPG5
LINGO3  PTPRS   CTB     ZNF121  ZNF490  BRD4    ZNF429  KRTDAP  EIF3K   ZNF587
SAMHD1  LBP     CHD6    FAM65C  ATP5J   ATP5O   SNRPD3  TNRC6B  DYNLT3  USP9X
GNL3L   COX7B
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      1.9149620777185e-17     30.0210526315789        0.737388416026573
16      96      respiratory electron transport chain
GO:0022900      4.63841446181159e-15    20.2990187332739        1.02927133070376
16      134     electron transport chain
GO:0045333      1.17844961179359e-14    18.9994987468672        1.09072036537264
16      142     cellular respiration
GO:0015980      1.89261166250888e-11    9.41020203147673        2.35810670541831
18      307     energy derivation by oxidation of organic compounds
GO:0000184      1.74980904851174e-09    14.4955555555556        0.914054390699606
11      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006091      4.08077617690187e-09    6.57592446892211        3.28752335478514
18      428     generation of precursor metabolites and energy
GO:0000956      6.40356036300852e-09    10.9500096506466        1.29811085738011
12      169     nuclear-transcribed mRNA catabolic process
GO:0006614      7.43270873231137e-09    14.8462741010943        0.806518580029064
10      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      8.15473212166693e-09    14.6905940594059        0.814199709362674
10      106     cotranslational protein targeting to membrane
GO:0045047      8.15473212166693e-09    14.6905940594059        0.814199709362674
10      106     protein targeting to ER
GO:0072599      8.15473212166693e-09    14.6905940594059        0.814199709362674
10      106     establishment of protein localization to endoplasmic reticulum
GO:0006402      1.15049751333791e-08    10.3497626871121        1.3672410213826 12
178     mRNA catabolic process
GO:0006119      1.3082411512096e-08     22.1980582524272        0.445505501349388
8       58      oxidative phosphorylation
GO:0070972      2.31095331448848e-08    13.047304730473 0.906373261365995       10
118     protein localization to endoplasmic reticulum
GO:0006413      2.32705898368316e-08    11.0772340425532        1.16753165870874
11      152     translational initiation
GO:0042776      2.99252715655819e-08    84.5047169811321        0.0998546813369317
5       13      mitochondrial ATP synthesis coupled proton transport
GO:0006415      3.10777257931095e-08    15.3421807747489        0.698982769358522
9       91      translational termination
GO:0006401      5.54930093184093e-08    8.88491128905637        1.57463151339008
12      205     RNA catabolic process
GO:0042773      6.3632460322739e-08     24.0625 0.361013078679676       7       47
ATP synthesis coupled electron transport
GO:0042775      6.3632460322739e-08     24.0625 0.361013078679676       7       47
mitochondrial ATP synthesis coupled electron transport
GO:0006414      1.08983174846975e-07    13.0919117647059        0.806518580029064
9       105     translational elongation
GO:0015985      1.93212855523158e-07    51.9847605224964        0.138260328004982
5       18      energy coupled proton transport, down electrochemical gradient
GO:0015986      1.93212855523158e-07    51.9847605224964        0.138260328004982
5       18      ATP synthesis coupled proton transport
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GO:0006612      2.7204775674273e-07     9.82967527521983        1.17521278804235
10      153     protein targeting to membrane
GO:0006120      2.89411785563967e-07    27.2571428571429        0.276520656009965
6       36      mitochondrial electron transport, NADH to ubiquinone
GO:0072594      4.6775763684049e-07     8.06305699481865        1.56695038405647
11      204     establishment of protein localization to organelle
GO:0019080      2.38618692897094e-06    8.82228666114333        1.15985052937513
9       151     viral genome expression
GO:0019083      2.38618692897094e-06    8.82228666114333        1.15985052937513
9       151     viral transcription
GO:0043624      2.66077457554848e-06    8.69852941176471        1.17521278804235
9       153     cellular protein complex disassembly
GO:0043241      3.46915865338344e-06    8.40367153572839        1.2136184347104 9
158     protein complex disassembly
GO:0009206      6.40552059862489e-06    15.1174603174603        0.460867760016608
6       60      purine ribonucleoside triphosphate biosynthetic process
GO:0009145      7.06022074628325e-06    14.8415584415584        0.468548889350218
6       61      purine nucleoside triphosphate biosynthetic process
GO:0034623      7.62820847741854e-06    7.58021390374332        1.33651650404816
9       174     cellular macromolecular complex disassembly
GO:0032984      9.59230485512941e-06    7.35467128027682        1.37492215071621
9       179     macromolecular complex disassembly
GO:0009201      1.0244481206526e-05     13.8314769975787        0.499273406684659
6       65      ribonucleoside triphosphate biosynthetic process
GO:0009142      1.45026023931333e-05    12.9496598639456        0.529997924019099
6       69      nucleoside triphosphate biosynthetic process
Tissue: Lung=>Adipose_Subcutaneous      Type:   cluster
SourceGene:     RP11-160E2.11(ENSG00000262292.1)
TargetGeneSet:  RPL22   SDHB    KIAA0090        RPL11   RP1     WASF2   DNAJC8  PPCS
RPS8    UQCRH   RPL5    RP11    HBXIP   RPS27   ELL2P1  GAS5    CEP350  RPS7
BIRC6   UBC     TGOLN2  MGAT4A  RPL31   CBWD2   H3F3AP4 BRK1    SLC26A6 RPL24
MRPS22  DNAJC19 MRFAP1  MRFAP1L1        CD38    PPM1K   GPRIN3  RPL34   RPS3A   TAF9
BTF3    TBCA    COX7C   ISOC1   MTND5P11        CTB     RPS14   RPL15P3 AGPAT1
SYNGAP1 WDR11   FOXK1   MPLKIP  RPS3AP26        POLR2J  MLL3    DRP2    HMBOX1  CTD
DCTN6   HOOK3   RPS20   ARFGEF1 ESRP1   RPL30   EIF3E   EIF3H   RPS6    RPL35
RPL7A   SEC16A  RPS24   SFR1    NSMCE4A FAM53B  RPL27A  RPS13   TSG101  ZBTB3
TMEM151A        MED17   CWC15   ATM     UBE4A   ATP5L   DDX6    RPS25   PFDN5   NACA
GNS     CPM     RPL6    GOLGA3  SLC35E1P1       N6AMT2  ESD     COMMD6  TEP1
OXA1L   MED6    CCNDBP1 SEC11A  NDUFB10 RPS15A  VPS53   WDR81   GABARAP RPL26   STX8
RPS7P1  RPL23A  ZNHIT3  RPL17   RPL19   RPL27   RPS7P11 RNF213  RPTOR   DSG4
RPS15   ZNF121  NACC1   UBA52   KRTDAP  EIF3K   KLK7    ZNF587  TMEM230 RP4
NCOA3   RPL12P4 DNAJC5  ATP5O   DDT     EIF3D   EIF3L   TNRC6B  USP9X   HCFC1   EMD
FUNDC2
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006413      2.59532108432318e-42    52.5092328796033        1.22012317486679
35      152     translational initiation
GO:0006415      1.62419912617089e-41    81.6279069767442        0.730468479689987
30      91      translational termination
GO:0006614      3.57187374446435e-41    70.2847376788553        0.842848245796139
31      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      5.01928893781292e-41    69.3427450980392        0.850875371946578
31      106     cotranslational protein targeting to membrane
GO:0045047      5.01928893781292e-41    69.3427450980392        0.850875371946578
31      106     protein targeting to ER
GO:0072599      5.01928893781292e-41    69.3427450980392        0.850875371946578
31      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      2.25327351345254e-39    59.7279242731575        0.947200885751851
31      118     protein localization to endoplasmic reticulum
GO:0006414      2.45020924486043e-39    66.3255813953488        0.842848245796139
30      105     translational elongation
GO:0000184      3.02954693644464e-39    59.0450534759358        0.95522801190229
31      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0000956      2.94901928077747e-37    41.5101878100638        1.35658431942426
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33      169     nuclear-transcribed mRNA catabolic process
GO:0006402      1.86114498252538e-36    38.9090153718322        1.42882845477822
33      178     mRNA catabolic process
GO:0019080      1.08105197935443e-35    43.2024509803922        1.21209604871635
31      151     viral genome expression
GO:0019083      1.08105197935443e-35    43.2024509803922        1.21209604871635
31      151     viral transcription
GO:0006612      1.68354596780378e-35    42.4882352941176        1.22815030101723
31      153     protein targeting to membrane
GO:0006401      2.62585967334747e-34    32.7387923788176        1.64556086084008
33      205     RNA catabolic process
GO:0043624      7.0210990329592e-34     40.3062960862167        1.22815030101723
30      153     cellular protein complex disassembly
GO:0043241      1.98407448707917e-33    38.7182049418605        1.26828593176943
30      158     protein complex disassembly
GO:0072594      7.17861863174953e-33    31.3687707641196        1.63753373468964
32      204     establishment of protein localization to organelle
GO:0019058      1.6093317035152e-32     28.3875502008032        1.85426614075151
33      231     viral infectious cycle
GO:0022415      3.50768024999193e-32    25.885279516512 2.08705279911425        34
260     viral reproductive process
GO:0034623      4.35322273150039e-32    34.3774224806202        1.39671995017646
30      174     cellular macromolecular complex disassembly
GO:0032984      1.0701396096537e-31     33.212117527704         1.43685558092866
30      179     macromolecular complex disassembly
GO:0071845      1.60462062487861e-25    19.3384911188427        2.27970382672479
30      284     cellular component disassembly at cellular level
GO:0022411      2.43955813941746e-25    19.0332612222823        2.31181233132655
30      288     cellular component disassembly
GO:0016032      3.0186688141698e-25     14.4576507597341        3.62023389384818
35      451     viral reproduction
GO:0033365      1.50678394882498e-24    13.7097637972828        3.79683066915784
35      473     protein localization to organelle
GO:0006605      1.617776013179e-24      13.677549987345 3.80485779530828        35
474     protein targeting
GO:0042274      5.29092247522081e-11    83.6263552960801        0.144488270707909
7       18      ribosomal small subunit biogenesis
GO:0071843      7.63415018523914e-10    9.35577263083451        1.91848314995502
15      239     cellular component biogenesis at cellular level
GO:0022613      3.26822337374959e-09    9.18762196821857        1.80610338384887
14      225     ribonucleoprotein complex biogenesis
GO:0042254      3.00501739088863e-08    10.7775707384403        1.19604179641547
11      149     ribosome biogenesis
GO:0006364      1.46867009016005e-07    12.6079685194294        0.834821119645699
9       104     rRNA processing
GO:0016072      2.38452828197917e-07    11.853983529194 0.882983876548336       9
110     rRNA metabolic process
GO:0000028      9.90432079028175e-06    126.83185840708 0.0481627569026365      3
6       ribosomal small subunit assembly
GO:0030490      1.72309942510636e-05    95.1172566371681        0.0561898830530759
3       7       maturation of SSU-rRNA
Tissue: Lung=>Adipose_Subcutaneous      Type:   asymmetric
SourceGene:     RP11-407G23.3(ENSG00000260946.1)
TargetGeneSet:  RPL22   IGSF21  C1QC    RPL11   C1orf38 DNAJC8  THRAP3  MEAF6   RPS8
RPL5    RP11    KCNA2   PTPN22  BOLA1   MRPL9   LCE1C   SPRR2G  FCGR2A  NCF2
TSEN15  PTPRC   RPS7    REL     GMCL1   VAMP5   MMADHC  HOXD8   SLC11A1 RPL32
RPL15   RPL24   NR1I2   HCLS1   CD86    RYK     DNAJC19 HTT     ENOPH1  DAPP1
RPL34   RPS3A   TLR2    MARCH1  FYB     SLC30A5 BTF3    SKP1    CTB     RPS14   TTC1
DOCK2   GNB2L1  RPL15P3 RPS18   WDR11   REV3L   RWDD1   IGF2R   RNASET2 ZNF117
CACNA2D1        GNG11   RPS3AP26        TBXAS1  MLL3    MSR1    CTD     THAP1
HOOK3   RPL30   VPS13B  UBR5    SLA     TRAPPC9 EEF1D   RPL8    RPS6    RPL35
RPL7A   C10orf31        ALOX5   DDX50   RPS24   RPS3AP5 BCCIP   CHID1   KCNQ1
BTBD10  RPS13   TSG101  LRRC55  TRPT1   KRT17   AIP     SPCS2   SLCO2B1 TMEM126B
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DDX6    C12orf57        CD163   ITPR2   MCRS1   C12orf44        PFDN5   NACA    LRP1
ARHGAP9 U6      TMBIM4  ACTR6   RPL18AP3        SELPLG  RPL6    RP1     TPT1    ESD
MED4    COMMD6  TEP1    RIN3    IFI27L1 C15orf41        PLCB2   RPS3AP6 AKAP13  MPG
MEFV    RPS15A  ADCY7   RPL26   RPS7P1  RPL17   RPL19   RPL27   RPS7P11 SUMO2
ACOX1   RP13    LINGO3  PTPRS   MYO1F   BRD4    KRTDAP  CEACAM4 C5AR1   GPR77
RPL18   RPL13A  LENG1   LILRB3  LAIR1   RPS5    PCNA    CTSA    ATP5O   THAP7
EIF3L   RPL3    TNRC6B  ST13    C22orf32        NCAPH2  TLR8    WAS     RPS4X   NXF3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      8.90260066887873e-39    63.7108792846498        0.881599889281019
30      91      translational termination
GO:0006414      2.45146164253578e-38    54.7169600793454        1.0172306414781 31
105     translational elongation
GO:0006614      2.45146164253578e-38    54.7169600793454        1.0172306414781 31
105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      3.43924825166242e-38    53.9836085626911        1.02691855234932
31      106     cotranslational protein targeting to membrane
GO:0045047      3.43924825166242e-38    53.9836085626911        1.02691855234932
31      106     protein targeting to ER
GO:0072599      3.43924825166242e-38    53.9836085626911        1.02691855234932
31      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      1.51404976931951e-36    46.498365496151 1.14317348280396        31
118     protein localization to endoplasmic reticulum
GO:0000184      9.16360688403386e-35    43.5812053115424        1.15286139367518
30      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006413      8.58274082744216e-33    33.3527939949958        1.47256245242544
31      152     translational initiation
GO:0006612      1.06842080691773e-32    33.0770792600391        1.48225036329666
31      153     protein targeting to membrane
GO:0072594      2.1385152007553e-31     25.5025414002295        1.97633381772888
33      204     establishment of protein localization to organelle
GO:0019080      2.27838923299197e-31    31.9834710743802        1.46287454155422
30      151     viral genome expression
GO:0019083      2.27838923299197e-31    31.9834710743802        1.46287454155422
30      151     viral transcription
GO:0000956      2.88251403007626e-31    29.2090812391969        1.63725693723618
31      169     nuclear-transcribed mRNA catabolic process
GO:0043624      3.47869053599559e-31    31.4589800443459        1.48225036329666
30      153     cellular protein complex disassembly
GO:0043241      9.75045185487522e-31    30.2194602272727        1.53068991765276
30      158     protein complex disassembly
GO:0006402      1.57733266169576e-30    27.4033576733446        1.72444813507716
31      178     mRNA catabolic process
GO:0006401      6.33025622993196e-30    24.2140869192892        1.9860217286001 32
205     RNA catabolic process
GO:0034623      2.08415886227826e-29    26.8314393939394        1.68569649159228
30      174     cellular macromolecular complex disassembly
GO:0032984      5.08174098584053e-29    25.921903599756 1.73413604594838        30
179     macromolecular complex disassembly
GO:0019058      6.69876711852795e-27    20.0661009174312        2.23790741125182
31      231     viral infectious cycle
GO:0033365      6.8736100075274e-27     12.8203233256351        4.58238184208705
40      473     protein localization to organelle
GO:0006605      9.44776718180015e-26    12.317377944691 4.59206975295827        39
474     protein targeting
GO:0022415      2.69705410457792e-25    17.4889627819398        2.5188568265172 31
260     viral reproductive process
GO:0071845      6.41542633135444e-23    15.0934144595562        2.75136668742648
30      284     cellular component disassembly at cellular level
GO:0022411      9.68968918339025e-23    14.8551797040169        2.79011833091136
30      288     cellular component disassembly
GO:0016032      3.78840189522482e-20    10.2506148548942        4.36924780292021
33      451     viral reproduction
GO:0042274      6.15001974211389e-07    40.7350427350427        0.17438239568196
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5       18      ribosomal small subunit biogenesis
GO:0042254      1.83285082907639e-06    7.84283342556724        1.44349871981178
10      149     ribosome biogenesis
GO:0022613      1.91185981805711e-06    6.20510563380282        2.1797799460245 12
225     ribonucleoprotein complex biogenesis
GO:0071843      3.57861456959509e-06    5.81662995594714        2.31541069822158
12      239     cellular component biogenesis at cellular level
GO:0006364      7.47797117621961e-06    8.97411616161616        1.00754273060688
8       104     rRNA processing
GO:0016072      1.13291539428615e-05    8.44266191325015        1.0656701958342 8
110     rRNA metabolic process
Tissue: Lung=>Adipose_Subcutaneous      Type:   cluster
SourceGene:     RP11-407G23.3(ENSG00000260946.1)
TargetGeneSet:  RPL22   IGSF21  C1QC    RPL11   C1orf38 DNAJC8  THRAP3  MEAF6   RPS8
RPL5    RP11    KCNA2   PTPN22  BOLA1   MRPL9   LCE1C   SPRR2G  FCGR2A  NCF2
TSEN15  PTPRC   RPS7    REL     GMCL1   VAMP5   MMADHC  HOXD8   SLC11A1 RPL32
RPL15   RPL24   NR1I2   HCLS1   CD86    RYK     DNAJC19 HTT     ENOPH1  DAPP1
RPL34   RPS3A   TLR2    MARCH1  FYB     SLC30A5 BTF3    SKP1    CTB     RPS14   TTC1
DOCK2   GNB2L1  RPL15P3 RPS18   WDR11   REV3L   RWDD1   IGF2R   RNASET2 ZNF117
CACNA2D1        GNG11   RPS3AP26        TBXAS1  MLL3    MSR1    CTD     THAP1
HOOK3   RPL30   VPS13B  UBR5    SLA     TRAPPC9 EEF1D   RPL8    RPS6    RPL35
RPL7A   C10orf31        ALOX5   DDX50   RPS24   RPS3AP5 BCCIP   CHID1   KCNQ1
BTBD10  RPS13   TSG101  LRRC55  TRPT1   KRT17   AIP     SPCS2   SLCO2B1 TMEM126B
DDX6    C12orf57        CD163   ITPR2   MCRS1   C12orf44        PFDN5   NACA    LRP1
ARHGAP9 U6      TMBIM4  ACTR6   RPL18AP3        SELPLG  RPL6    RP1     TPT1    ESD
MED4    COMMD6  TEP1    RIN3    IFI27L1 C15orf41        PLCB2   RPS3AP6 AKAP13  MPG
MEFV    RPS15A  ADCY7   RPL26   RPS7P1  RPL17   RPL19   RPL27   RPS7P11 SUMO2
ACOX1   RP13    LINGO3  PTPRS   MYO1F   BRD4    KRTDAP  CEACAM4 C5AR1   GPR77
RPL18   RPL13A  LENG1   LILRB3  LAIR1   RPS5    PCNA    CTSA    ATP5O   THAP7
EIF3L   RPL3    TNRC6B  ST13    C22orf32        NCAPH2  TLR8    WAS     RPS4X   NXF3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      8.90260066887873e-39    63.7108792846498        0.881599889281019
30      91      translational termination
GO:0006414      2.45146164253578e-38    54.7169600793454        1.0172306414781 31
105     translational elongation
GO:0006614      2.45146164253578e-38    54.7169600793454        1.0172306414781 31
105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      3.43924825166242e-38    53.9836085626911        1.02691855234932
31      106     cotranslational protein targeting to membrane
GO:0045047      3.43924825166242e-38    53.9836085626911        1.02691855234932
31      106     protein targeting to ER
GO:0072599      3.43924825166242e-38    53.9836085626911        1.02691855234932
31      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      1.51404976931951e-36    46.498365496151 1.14317348280396        31
118     protein localization to endoplasmic reticulum
GO:0000184      9.16360688403386e-35    43.5812053115424        1.15286139367518
30      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006413      8.58274082744216e-33    33.3527939949958        1.47256245242544
31      152     translational initiation
GO:0006612      1.06842080691773e-32    33.0770792600391        1.48225036329666
31      153     protein targeting to membrane
GO:0072594      2.1385152007553e-31     25.5025414002295        1.97633381772888
33      204     establishment of protein localization to organelle
GO:0019080      2.27838923299197e-31    31.9834710743802        1.46287454155422
30      151     viral genome expression
GO:0019083      2.27838923299197e-31    31.9834710743802        1.46287454155422
30      151     viral transcription
GO:0000956      2.88251403007626e-31    29.2090812391969        1.63725693723618
31      169     nuclear-transcribed mRNA catabolic process
GO:0043624      3.47869053599559e-31    31.4589800443459        1.48225036329666
30      153     cellular protein complex disassembly
GO:0043241      9.75045185487522e-31    30.2194602272727        1.53068991765276
30      158     protein complex disassembly
```

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GO:0006402      1.57733266169576e-30    27.4033576733446        1.72444813507716
31      178     mRNA catabolic process
GO:0006401      6.33025622993196e-30    24.2140869192892        1.9860217286001 32
205     RNA catabolic process
GO:0034623      2.08415886227826e-29    26.8314393939394        1.68569649159228
30      174     cellular macromolecular complex disassembly
GO:0032984      5.08174098584053e-29    25.921903599756 1.73413604594838        30
179     macromolecular complex disassembly
GO:0019058      6.69876711852795e-27    20.0661009174312        2.23790741125182
31      231     viral infectious cycle
GO:0033365      6.8736100075274e-27     12.8203233256351        4.58238184208705
40      473     protein localization to organelle
GO:0006605      9.44776718180015e-26    12.317377944691 4.59206975295827        39
474     protein targeting
GO:0022415      2.69705410457792e-25    17.4889627819398        2.5188568265172 31
260     viral reproductive process
GO:0071845      6.41542633135444e-23    15.0934144595562        2.75136668742648
30      284     cellular component disassembly at cellular level
GO:0022411      9.68968918339025e-23    14.8551797040169        2.79011833091136
30      288     cellular component disassembly
GO:0016032      3.78840189522482e-20    10.2506148548942        4.36924780292021
33      451     viral reproduction
GO:0042274      6.15001974211389e-07    40.7350427350427        0.17438239568196
5       18      ribosomal small subunit biogenesis
GO:0042254      1.83285082907639e-06    7.84283342556724        1.44349871981178
10      149     ribosome biogenesis
GO:0022613      1.91185981805711e-06    6.20510563380282        2.1797799460245 12
225     ribonucleoprotein complex biogenesis
GO:0071843      3.57861456959509e-06    5.81662995594714        2.31541069822158
12      239     cellular component biogenesis at cellular level
GO:0006364      7.47797117621961e-06    8.97411616161616        1.00754273060688
8       104     rRNA processing
GO:0016072      1.13291539428615e-05    8.44266191325015        1.0656701958342 8
110     rRNA metabolic process
Tissue: Lung=>Adipose_Subcutaneous      Type:   asymmetric
SourceGene:     SIT1(ENSG00000137078.4)
TargetGeneSet:  MRPL20  RPL22   DNAJC8  TAF12   MAGOH   JTB     RPS27   RP11
RAB4A   ILKAP   RPL24   GRPEL1  RPS3A   GPBP1   RPS10   CHCHD2  RPS3AP26        CUX1
RPL12   RPS3AP5 RPL27A  ARHGAP1 ZNHIT2  MED17   CWC15   RPS25   RPL6    MED6    DLK1
SIVA1   RPS15A  KAT8    RNASEK  ALOX12B ZNHIT3  RPL17   RNF126  DOHH    C19orf43
AXL     GPR77   RPL18   DDT
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0000184      1.23316123375953e-18    73.1147798742138        0.304684796899869
13      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006415      2.98749533634624e-18    87.0987341772152        0.232994256452841
12      91      translational termination
GO:0006414      1.80689935585985e-17    73.9148387096774        0.268839526676355
12      105     translational elongation
GO:0006614      1.80689935585985e-17    73.9148387096774        0.268839526676355
12      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      2.03429421514149e-17    73.1234042553191        0.271399903120891
12      106     cotranslational protein targeting to membrane
GO:0045047      2.03429421514149e-17    73.1234042553191        0.271399903120891
12      106     protein targeting to ER
GO:0072599      2.03429421514149e-17    73.1234042553191        0.271399903120891
12      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      7.73556153387231e-17    64.7909433962264        0.302124420455332
12      118     protein localization to endoplasmic reticulum
GO:0000956      1.34046564043452e-16    49.5069444444444        0.432703619126704
13      169     nuclear-transcribed mRNA catabolic process
GO:0006402      2.65916559860613e-16    46.7770202020202        0.455747007127534
13      178     mRNA catabolic process
GO:0072594      1.59305806352616e-15    40.3357329842932        0.522316794685489
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13      204     establishment of protein localization to organelle
GO:0019080      1.61037838056575e-15    49.294964028777 0.386616843125043       12
151     viral genome expression
GO:0019083      1.61037838056575e-15    49.294964028777 0.386616843125043       12
151     viral transcription
GO:0006401      1.69826728764919e-15    40.1228298611111        0.524877171130026
13      205     RNA catabolic process
GO:0006413      1.74559508534522e-15    48.9394285714286        0.38917721956958
12      152     translational initiation
GO:0006612      1.89110575840793e-15    48.5889361702128        0.391737596014117
12      153     protein targeting to membrane
GO:0043624      1.89110575840793e-15    48.5889361702128        0.391737596014117
12      153     cellular protein complex disassembly
GO:0043241      2.79924691482103e-15    46.9084931506849        0.4045394782368 12
158     protein complex disassembly
GO:0034623      9.03722727194804e-15    42.2281481481482        0.445505501349388
12      174     cellular macromolecular complex disassembly
GO:0032984      1.27346671987408e-14    40.9494610778443        0.458307383572071
12      179     macromolecular complex disassembly
GO:0019058      2.72312793902935e-13    31.1123287671233        0.59144695868798
12      231     viral infectious cycle
GO:0022415      1.10991614205457e-12    27.418064516129 0.665697875579545       12
260     viral reproductive process
GO:0071845      3.14852810412604e-12    24.9564705882353        0.727146910248426
12      284     cellular component disassembly at cellular level
GO:0022411      3.71207946366908e-12    24.5878260869565        0.737388416026573
12      288     cellular component disassembly
GO:0016032      4.03999074838108e-11    17.2838660578387        1.15472977648606
13      451     viral reproduction
GO:0033365      7.3062961268106e-11     16.4313405797101        1.21105805826586
13      473     protein localization to organelle
GO:0006605      7.50042751609051e-11    16.3945227765727        1.2136184347104 13
474     protein targeting
Tissue: Adipose_Subcutaneous=>Lung      Type:   asymmetric
SourceGene:     WDFY3(ENSG00000163625.11)
TargetGeneSet:  RPL22   RPL11   CSMD2   RPS27   SHE     EIF3FP3 RPL31   KRT18P17
RP11    RPL34   RPL37   EEF1A1P19       EEF1A1  POT1    RPL30   PLIN2   ZFAND5
RPS13   NACA    POP5    RPL4    TMCO7   DNAAF1  FAM108A7P       RPL19   MARCH10
RPS11
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      1.35985670371787e-21    231.258064516129        0.1453186630683 12
105     translational elongation
GO:0006415      5.30064694715127e-20    219.251388888889        0.12594284132586
11      91      translational termination
GO:0006614      2.76818952993206e-19    186.414893617021        0.1453186630683 11
105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      3.08694207198322e-19    184.439766081871        0.146702650335617
11      106     cotranslational protein targeting to membrane
GO:0045047      3.08694207198322e-19    184.439766081871        0.146702650335617
11      106     protein targeting to ER
GO:0072599      3.08694207198322e-19    184.439766081871        0.146702650335617
11      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      1.05519204053085e-18    163.617860851506        0.163310497543423
11      118     protein localization to endoplasmic reticulum
GO:0000184      1.1619967546663e-18     162.091563786008        0.16469448481074
11      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      1.73719940600089e-17    124.762698412698        0.208982077364888
11      151     viral genome expression
GO:0019083      1.73719940600089e-17    124.762698412698        0.208982077364888
11      151     viral transcription
GO:0006413      1.87164661224655e-17    123.869188337273        0.210366064632205
11      152     translational initiation
GO:0006612      2.01547134919857e-17    122.988262910798        0.211750051899523
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11      153     protein targeting to membrane
GO:0043624      2.01547134919857e-17    122.988262910798        0.211750051899523
11      153     cellular protein complex disassembly
GO:0043241      2.89682250741231e-17    118.763416477702        0.218669988236108
11      158     protein complex disassembly
GO:0000956      6.17981707707572e-17    110.409985935302        0.233893848176597
11      169     nuclear-transcribed mRNA catabolic process
GO:0034623      8.57523165633006e-17    106.985685071575        0.240813784513182
11      174     cellular macromolecular complex disassembly
GO:0006402      1.10671254440759e-16    104.393878908849        0.246349733582451
11      178     mRNA catabolic process
GO:0032984      1.17849536408632e-16    103.765211640212        0.247733720849768
11      179     macromolecular complex disassembly
GO:0072594      5.08842463871518e-16    90.1658031088083        0.282333402532697
11      204     establishment of protein localization to organelle
GO:0006401      5.37383564971277e-16    89.6947308132875        0.283717389800014
11      205     RNA catabolic process
GO:0019058      2.03115432450918e-15    78.95   0.31970105875026        11      231
viral infectious cycle
GO:0022415      7.53863094679851e-15    69.6126729138777        0.359836689502457
11      260     viral reproductive process
GO:0071845      1.99989030693318e-14    63.3854293854294        0.393052383918068
11      284     cellular component disassembly at cellular level
GO:0022411      2.33351167860072e-14    62.4524669073406        0.398588332987337
11      288     cellular component disassembly
GO:0016032      3.16139853576349e-12    38.8638888888889        0.62417825756003
11      451     viral reproduction
GO:0033365      5.30029164637227e-12    36.9550264550265        0.654625977441008
11      473     protein localization to organelle
GO:0006605      5.423028319588e-12      36.8725701943845        0.656009964708325
11      474     protein targeting
Tissue: Lung=>Artery_Tibial     Type:   asymmetric
SourceGene:     AGAP11(ENSG00000151303.10)
TargetGeneSet:  ARID1A  WASF2   PUM1    TMEM234 HIVEP3  PPCS    LRRC39  RP11
S100A6  S100A2  LINC00467       MIA3    ACP1    KIDINS220       KIF3C   MTA3
DCTN1   GCFC2   RNF181  COX5B   FAM134A INHA    GIGYF2  SETD2   CSPG5   IP6K1
WDR82   STAG1   PPP1R2  BOD1L   RFC1    WDFY3   WDFY3-AS1       NDUFC1  NIPBL
MAN2A1  YTHDC2  EHMT2   DAXX    BRPF3   KIAA0240        PHF3    ARID1B  IGF2R
PHF14   SEPT7P2 BAZ1B   TMEM168 ARF5    CPA1    AGK     WHSC1L1 CHCHD7  UBR5
SLC45A4 MPDZ    DENND1A MIR181A2HG      STXBP1  CALM2P2 C10orf131       FAM204A UROS
STIM1   PRKCDBP SBF2    ZDHHC5  INCENP  RSF1    DYNC2H1 MLL     ERC1    GOLT1B
LRRK2   PFKM    ATF7    CTDSP2  VSIG10  PDS5B   MED4    RP3     HERC2   SMAD3   CIB1
DNM1P46 FAM173A CREBBP  KIAA0430        CTCF    GLG1    GCSH    MBTPS1  RPS4XP17
ZBTB4   LSMD1   C17orf39        THRA    WIPF2   STAT5B  NMT1    USP32   BPTF    DYM
ATP8B1  CTB     SAMD4B  ARHGAP35        MAVS    RP1     NCOA6   CEP250  SOGA1   CHD6
SYS1    STAU1   ATP9A   ATP5E   CTD     MORC2   LGALS1  EP300   TCF20   PPEF1   TFE3
SMC1A   EIF4BP7 BCORL1  RAP2C
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0016568      1.99813512363887e-09    7.46901568108823        2.78347519202823
17      419     chromatin modification
GO:0016570      1.22838361857895e-06    7.30141176470588        1.73385924849491
11      261     histone modification
GO:0016569      1.53408747062912e-06    7.12725183823529        1.77371808179365
11      267     covalent chromatin modification
GO:0016571      2.48991183776502e-06    17.9899371069182        0.391945194104214
6       59      histone methylation
GO:0048096      5.60074418648522e-06    154.322580645161        0.0398588332987337
3       6       chromatin-mediated maintenance of transcription
GO:0006479      1.19020364805122e-05    13.41220657277  0.511521694000415       6
77      protein methylation
GO:0008213      1.19020364805122e-05    13.41220657277  0.511521694000415       6
77      protein alkylation
GO:0034968      1.4328298882083e-05     18.7244897959184        0.312227527506747
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5       47      histone lysine methylation
Tissue: Artery_Tibial=>Lung     Type:   cluster
SourceGene:     CKS1BP7(ENSG00000254331.1)
TargetGeneSet:  NADK    PIK3CD  ZDHHC18 WDTC1   RP11    HAX1    MNDA    CEP350
RGS18   PRKD3   RMND5A  IL1R2   GCC2    SPOPL   CXCR2   CXCR1   LTF     NICN1-AS1
PRKCD   ACOX2   EIF4E3  ABTB1   TLR1    KLHL8   TLR2    IRF2    FYB     PDF
CYFIP2  DOCK2   E2F3    FAM65B  GPSM3   VNN2    ARID1B  RPS6KA2 SNX13   TRGJP2
RPL13AP17       TSC22D4 HIPK2   TNFRSF10C       KAT6A   SGK196  UBXN2B  NECAB1
RAD21   ZCCHC6  SEMA4D  TRIM14  TNFSF8  TSPAN14 NAALAD2 SORL1   C3AR1   CLEC4D
CLEC4E  TAS2R30 PLXNC1  SLC9A7P1        APAF1   GLT1D1  ULK1    BAZ1A   TECPR2  AQP9
MEFV    UBN1    PRKCB   XPO6    C16orf54        CORO1A  ZNF267  CNOT1   ARRB2
PIK3R5  TRIM16  FMNL1   IL27RA  EMR2    MAST3   KLK5    ZNF765  FCAR    RNF24
OSBPL2  IL17RA  CYTH4   SH3BP1  NFAM1   NUP50   TLR8    CXorf38
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0001816      9.01575364855086e-08    7.80769890996481        2.022697391184  13
395     cytokine production
GO:0001817      1.96600952919472e-06    7.03881590950556        1.83835028717736
11      359     regulation of cytokine production
GO:0050778      2.24798288077245e-06    6.93664283465983        1.86395405162273
11      364     positive regulation of immune response
GO:0002757      3.00931514065176e-06    8.66977535738598        1.20337692893225
9       235     immune response-activating signal transduction
GO:0002764      4.67177874673838e-06    8.19066623752816        1.26994671649021
9       248     immune response-regulating signaling pathway
GO:0060326      5.96165913046696e-06    11.5395117436075        0.696422392913985
7       136     cell chemotaxis
GO:0042113      1.29158075474608e-05    10.183704763852 0.783475192028233       7
153     B cell activation
GO:0050853      1.36553311380717e-05    32.8045714285714        0.148501833783129
4       29      B cell receptor signaling pathway
Tissue: Lung=>Artery_Tibial     Type:   asymmetric
SourceGene:     CTD-2537O9.1(ENSG00000254787.1)
TargetGeneSet:  SDF4    GLTPD1  KLHL21  UBE4B   CASP9   OTUD3   GPATCH3 WDTC1   RP11
WASF2   PTAFR   COL16A1 MTMR9LP AK2     TMEM53  CYP4B1  CDKN2C  JUN     DBT
SORT1   TSPAN2  PEX11B  FAM63A  C1orf56 S100A10 ZBTB7B  LMNA    RRNAD1  CCDC19  RXRG
PRRX1   FMO2    PTGS2   LMOD1   ADIPOR1 ETNK2   TRIM11  RYR2    VSNL1   PPP1CB
PPM1B   ATOH8   RMND5A  CLASP1  TNFAIP6 CACNB4  GPR155  KANSL1L ACADL   CNPPD1
ATG9A   IRS1    GPC1    RNPEPL1 JAGN1   SLC25A38        SLC26A6 GPX1    IP6K1
TEX264  SEMA5B  ALDH1L1 ALDH1L1-AS2     KLF15   ZXDC    PPM1L   EGFEM1P NAALADL2
MCCC1   ABCF3   SNORA81 BDH1    FAM53A  WDR1    CD38    TAPT1   CXCL1   CXCL2   ADH5
ADH4    ADH1A   ADAMTS16        C1QTNF3 PTGER4  JMY     SSBP2   PDLIM4  IRF1
PHF15   KDM3B   PPP2R2B DPYSL3  GPX3    CTB     FGF18   TUBB    RP3     CDYL
PAK1IP1 GFOD1   LRRC16A HIST1H1C        DHX16   FKBPL   PRRT1   B3GALT4 CCND3   UBR2
KLHDC3  CDC5L   MUT     PGM3    CNR1    STXBP2  SESN1   CDK19   LAMA2   EPB41L2
KATNA1  SYNJ2   RPS6KA2 WIPI2   BZW2    IL6     HOXA6   CREB5   AQP1    PHKG1   ADSL
WBSCR16 HIP1    FGL2    HGF     ZNF789  C7orf58 HILPDA  FAM180A ZNF282  ZNF212
DDHD2   PPAPDC1B        FGFR1   SLCO5A1 GRIP1   PVT1    DENND3  ZC3H3   CYHR1
SLC35D2 MSANTD3 ZDHHC12 ZER1    TBC1D13 PHYHD1  ASB13   ITIH5   DHTKD1  CAMK1D  OLAH
ARL5B   PRTFDC1 KIAA1279        EIF4EBP2        ASCC1   DNAJB12 P4HA1   PLAU
FRAT1   ANKRD2  HOGA1   POLL    DUSP5   SMC3    SHOC2   TALDO1  TOLLIP  RRM1    CD44
RP1     PRDM11  PEX16   AMBRA1  ARFGAP2 TNKS1BP1        SLC43A1 ZBTB3   TAF6L
RAB1B   POLDIP2 CDK2AP2 SNORD5  VPS11   C2CD2L  CD9     H2AFJ   FGD4    METTL7A
TENC1   ELK3    TXNRD1  RAB35   PITPNM2 PXMP2   ELF1    FBXL3   ERCC5   IRS2
C14orf93        SLC7A8  PCK2    ARID4A  RHOJ    GALNTL1 ZFYVE1  ALDH6A1 DLST
TGFB3   DIO2    BAHD1   GCHFR   KBTBD13 STRA6   ANKRD34C        PEX11A  CHSY1
MSRB1   FAM100A CDIPT   RBL2    PDP2    C16orf70        MLYCD   CHMP1A  FAM57A
INPP5K  WDR81   KIF1C   TMEM102 SNORA48 FXR2    ALOX15B C17orf59        ABHD15  BLMH
CCL2    ERBB2   CSF3    THRA    GHDC    NMT1    KANSL1  CALCOCO2        PDK2    VMP1
PSMC5   SMARCD2 TEX2    SLC39A11        GPRC5C  ACOX1   SPHK1   CBX4    PCYT2
SIRT7   DCXR    C17orf101       HEXDC   APCDD1  C18orf8 VPS4B   PIAS4   UBXN6
RANBP3  ACSBG2  CLPP    INSR    MCOLN1  MAP2K7  SLC44A2 TMED1   ZNF490  WDR83   GCDH
ABHD8   MAP1S   KLHL26  NFKBIB  SHKBP1  RABAC1  PPP1R37 FBXO46  SIX5    HIF3A
SPHK2   BCAT2   SCAF1   AP2A1   MED25   TBC1D17 SIGLEC16        SIGLEC10        EPN1
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FKBP1A  MAVS    MACROD2 CRNKL1  ACSS2   ZHX3    SERINC3 ACOT8   LSM14B  STMN3
RCAN1   SLC25A18        PRODH   CLTCL1  YPEL1   GGT5    ZNRF3   MCM5    TST     MPST
SUN2    CBX6    SNORD83B        TAB1    PMM1    TTC38   ZBED1   GPX1P1  REPS2   MAOA
MIR221  ARAF    WDR13   VSIG4   TCEAL4  TCEAL3  TMEM164 ABCD1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0044282      2.06735142438574e-10    6.15278111244498        4.17867275621064
22      218     small molecule catabolic process
GO:0016054      1.85992761282614e-08    5.79398786541644        3.56528959933569
18      186     organic acid catabolic process
GO:0046395      1.85992761282614e-08    5.79398786541644        3.56528959933569
18      186     carboxylic acid catabolic process
GO:0030258      1.45692307301709e-07    6.09038861901457        2.81772887689433
15      147     lipid modification
GO:0072329      2.99830484500555e-07    8.57839451570102        1.51428966853505
11      79      monocarboxylic acid catabolic process
GO:0019395      8.11356084996354e-07    7.67105263157895        1.66763545775379
11      87      fatty acid oxidation
GO:0006635      1.05650632978825e-06    10.0939187043506        1.07342052453117
9       56      fatty acid beta-oxidation
GO:0034440      1.14562991314059e-06    7.37817645379271        1.72514012871082
11      90      lipid oxidation
GO:0032787      2.95377075405425e-06    3.30487855684706        7.6864576845893 23
401     monocarboxylic acid metabolic process
GO:0009062      5.62208561143766e-06    8.03408803440425        1.30343920835928
9       68      fatty acid catabolic process
Tissue: Lung=>Artery_Tibial     Type:   cluster
SourceGene:     CTD-2537O9.1(ENSG00000254787.1)
TargetGeneSet:  SDF4    GLTPD1  KLHL21  UBE4B   CASP9   OTUD3   GPATCH3 WDTC1   RP11
WASF2   PTAFR   COL16A1 MTMR9LP AK2     TMEM53  CYP4B1  CDKN2C  JUN     DBT
SORT1   TSPAN2  PEX11B  FAM63A  C1orf56 S100A10 ZBTB7B  LMNA    RRNAD1  CCDC19  RXRG
PRRX1   FMO2    PTGS2   LMOD1   ADIPOR1 ETNK2   TRIM11  RYR2    VSNL1   PPP1CB
PPM1B   ATOH8   RMND5A  CLASP1  TNFAIP6 CACNB4  GPR155  KANSL1L ACADL   CNPPD1
ATG9A   IRS1    GPC1    RNPEPL1 JAGN1   SLC25A38        SLC26A6 GPX1    IP6K1
TEX264  SEMA5B  ALDH1L1 ALDH1L1-AS2     KLF15   ZXDC    PPM1L   EGFEM1P NAALADL2
MCCC1   ABCF3   SNORA81 BDH1    FAM53A  WDR1    CD38    TAPT1   CXCL1   CXCL2   ADH5
ADH4    ADH1A   ADAMTS16        C1QTNF3 PTGER4  JMY     SSBP2   PDLIM4  IRF1
PHF15   KDM3B   PPP2R2B DPYSL3  GPX3    CTB     FGF18   TUBB    RP3     CDYL
PAK1IP1 GFOD1   LRRC16A HIST1H1C        DHX16   FKBPL   PRRT1   B3GALT4 CCND3   UBR2
KLHDC3  CDC5L   MUT     PGM3    CNR1    STXBP2  SESN1   CDK19   LAMA2   EPB41L2
KATNA1  SYNJ2   RPS6KA2 WIPI2   BZW2    IL6     HOXA6   CREB5   AQP1    PHKG1   ADSL
WBSCR16 HIP1    FGL2    HGF     ZNF789  C7orf58 HILPDA  FAM180A ZNF282  ZNF212
DDHD2   PPAPDC1B        FGFR1   SLCO5A1 GRIP1   PVT1    DENND3  ZC3H3   CYHR1
SLC35D2 MSANTD3 ZDHHC12 ZER1    TBC1D13 PHYHD1  ASB13   ITIH5   DHTKD1  CAMK1D  OLAH
ARL5B   PRTFDC1 KIAA1279        EIF4EBP2        ASCC1   DNAJB12 P4HA1   PLAU
FRAT1   ANKRD2  HOGA1   POLL    DUSP5   SMC3    SHOC2   TALDO1  TOLLIP  RRM1    CD44
RP1     PRDM11  PEX16   AMBRA1  ARFGAP2 TNKS1BP1        SLC43A1 ZBTB3   TAF6L
RAB1B   POLDIP2 CDK2AP2 SNORD5  VPS11   C2CD2L  CD9     H2AFJ   FGD4    METTL7A
TENC1   ELK3    TXNRD1  RAB35   PITPNM2 PXMP2   ELF1    FBXL3   ERCC5   IRS2
C14orf93        SLC7A8  PCK2    ARID4A  RHOJ    GALNTL1 ZFYVE1  ALDH6A1 DLST
TGFB3   DIO2    BAHD1   GCHFR   KBTBD13 STRA6   ANKRD34C        PEX11A  CHSY1
MSRB1   FAM100A CDIPT   RBL2    PDP2    C16orf70        MLYCD   CHMP1A  FAM57A
INPP5K  WDR81   KIF1C   TMEM102 SNORA48 FXR2    ALOX15B C17orf59        ABHD15  BLMH
CCL2    ERBB2   CSF3    THRA    GHDC    NMT1    KANSL1  CALCOCO2        PDK2    VMP1
PSMC5   SMARCD2 TEX2    SLC39A11        GPRC5C  ACOX1   SPHK1   CBX4    PCYT2
SIRT7   DCXR    C17orf101       HEXDC   APCDD1  C18orf8 VPS4B   PIAS4   UBXN6
RANBP3  ACSBG2  CLPP    INSR    MCOLN1  MAP2K7  SLC44A2 TMED1   ZNF490  WDR83   GCDH
ABHD8   MAP1S   KLHL26  NFKBIB  SHKBP1  RABAC1  PPP1R37 FBXO46  SIX5    HIF3A
SPHK2   BCAT2   SCAF1   AP2A1   MED25   TBC1D17 SIGLEC16        SIGLEC10        EPN1
FKBP1A  MAVS    MACROD2 CRNKL1  ACSS2   ZHX3    SERINC3 ACOT8   LSM14B  STMN3
RCAN1   SLC25A18        PRODH   CLTCL1  YPEL1   GGT5    ZNRF3   MCM5    TST     MPST
SUN2    CBX6    SNORD83B        TAB1    PMM1    TTC38   ZBED1   GPX1P1  REPS2   MAOA
MIR221  ARAF    WDR13   VSIG4   TCEAL4  TCEAL3  TMEM164 ABCD1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
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GO:0044282      2.06735142438574e-10    6.15278111244498        4.17867275621064
22      218     small molecule catabolic process
GO:0016054      1.85992761282614e-08    5.79398786541644        3.56528959933569
18      186     organic acid catabolic process
GO:0046395      1.85992761282614e-08    5.79398786541644        3.56528959933569
18      186     carboxylic acid catabolic process
GO:0030258      1.45692307301709e-07    6.09038861901457        2.81772887689433
15      147     lipid modification
GO:0072329      2.99830484500555e-07    8.57839451570102        1.51428966853505
11      79      monocarboxylic acid catabolic process
GO:0019395      8.11356084996354e-07    7.67105263157895        1.66763545775379
11      87      fatty acid oxidation
GO:0006635      1.05650632978825e-06    10.0939187043506        1.07342052453117
9       56      fatty acid beta-oxidation
GO:0034440      1.14562991314059e-06    7.37817645379271        1.72514012871082
11      90      lipid oxidation
GO:0032787      2.95377075405425e-06    3.30487855684706        7.6864576845893 23
401     monocarboxylic acid metabolic process
GO:0009062      5.62208561143766e-06    8.03408803440425        1.30343920835928
9       68      fatty acid catabolic process
Tissue: Lung=>Artery_Tibial     Type:   asymmetric
SourceGene:     E2F3(ENSG00000112242.9)
TargetGeneSet:  UQCRH   DNTTIP2 BCAS2   NOTCH2  RP11    ZBTB7B  PLXNA2  MIA3
HS1BP3-IT1      C2orf28 COX5B   NDUFB4  MRPS22  MBNL1   ATP11B  ATP5I   POLN
NDUFC1  WWC2    CTD     COX7C   FER     HINT1   UQCRQ   SPINK5  TBC1D9B SNORA40 RP3
MRPL2   PSMB1   NDUFA4  MALSU1  ECD     CKS1BP7 COX6C   HEMGN   INVS    LRRC8A
KIAA0913        NAV2-AS2        NDUFA12 MED4    SLIRP   C14orf2 ARHGAP11B
ZNF609  NDE1    SLC12A4 MINK1   ICT1    CTIF    C19orf70        NDUFB7  CYP2G1P
TBC1D20 SNRPB2  LPIN3   ATP5J   MIAT    TCF20   NDUFA1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      4.56552515661742e-18    62.2981927710843        0.325513805272992
13      96      respiratory electron transport chain
GO:0022900      4.09336789036212e-16    42.6200642791552        0.454363019860217
13      134     electron transport chain
GO:0045333      8.84150635104301e-16    39.9545650301464        0.481489170299633
13      142     cellular respiration
GO:0015980      1.84344044969469e-11    17.3284202569917        1.04096602311259
13      307     energy derivation by oxidation of organic compounds
GO:0006091      1.1205995440234e-09     12.170749665328 1.45124904850875        13
428     generation of precursor metabolites and energy
GO:0042773      1.07011493057609e-08    48.874645490641 0.159366133831569       6
47      ATP synthesis coupled electron transport
GO:0042775      1.07011493057609e-08    48.874645490641 0.159366133831569       6
47      mitochondrial ATP synthesis coupled electron transport
GO:0006119      3.92198943479283e-08    38.5062611806798        0.196664590685766
6       58      oxidative phosphorylation
GO:0006120      1.26601969064591e-07    52.6796187683284        0.122067676977372
5       36      mitochondrial electron transport, NADH to ubiquinone
Tissue: Lung=>Artery_Tibial     Type:   cluster
SourceGene:     FBXO18(ENSG00000134452.12)
TargetGeneSet:  MECR    ZCCHC17 KHDRBS1 PSMB2   OSCP1   RPS8    RP1     RP11
ALG14   RP4     SRGAP2P1        SRGAP2P2        MRPS21  SCNM1   PSMB4   DENND4B PMF1
MYOC    KLHDC8A SLC41A1 SRGAP3  LINC00467       TATDN3  KLHL29  C2orf28 RPLP0P6
SFXN5   RNF181  COX5B   CHCHD5  RPL37A  PPP1R7  LSM3    KRBOX1  ZNF852  KIF9    WDR6
SPCS1   CLCP1   BBX     CLDN18  GMPS    SMC4    OCIAD1-AS1      MRPL1   LARP7   WWC2
CTD     ARHGAP26        RPS14   MED7    WRNIP1  TMEM14B NOL7    HLA-F-AS1       MICD
RP3     COX6A1P2        MRPL2   EYS     C6orf57 RPL39P3 IMPG1   MRPS12  PEX7
SF3B5   PSMB1   ANKMY2  MALSU1  ECD     C7orf61 SSBP1   SLC4A2  AGAP3   KIF13B
CHCHD7  COX6C   UTP23   NDUFB9  SNAPC3  RPS6    DCTN3   FAM205A RC3H2   FAM129B
FAM208B FBXO18  CALM2P2 NHP2P1  NDUFB8  TCF7L2  FAM204A RPLP2   CARS    C11orf10
PLCB3   PPP2R5B FAU     SIPA1   MRPL11  KDM2A   C11orf1 PCSK7   ATP5L   SPA17
GALNT8  GPD1    ATP5G2  RBMS2   SLC35E3 NDUFA12 CHPT1   RPL18AP3        SSH1
MED13L  RPS11P5 SAP18   PDS5B   WDFY2   OR11H7  RPS29   SLIRP   U6      RCOR1
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C14orf2 NDN     MAPKBP1 TCF12   RPLP1   KIF7    RAB11FIP3       C16orf79        NDE1
SMG1    ATXN2L  DOC2A   NUDT21  SLC12A4 GAN     KIAA0513        TRAPPC2L
MINK1   ARHGAP44        FOXO3B  C17orf51        RPS7P1  USP32   RPL38   CDR2L   ICT1
NT5C    SLC16A3 FOXK2   ZNF532  PIP5K1C CCDC94  C19orf70        PNPLA6  C19orf53
NDUFA13 COX6B1  POLR2I  GGN     EIF3K   SMG9    SNRPD2  SYNGR4  VSIG10L ZNF8    RPS5
CHMP2A  TBC1D20 MCM8    SNRPB2  POLR3F  ITCH    MT1P3   ROMO1   ATP5J   SYNJ1
ZNF280B SAMM50  SBF1    PNPLA4  PSMA6P2 EEF1B2P3        GSPT2   ATRX    CXorf56
RPL10   MT
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      3.78849351354665e-12    18.6784776902887        0.881599889281019
13      91      translational termination
GO:0000184      8.24992733445461e-12    15.0328042328042        1.15286139367518
14      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0000956      8.63920865152007e-11    11.0314285714286        1.63725693723618
15      169     nuclear-transcribed mRNA catabolic process
GO:0006402      1.80682231573148e-10    10.4157055214724        1.72444813507716
15      178     mRNA catabolic process
GO:0043624      2.52635066746848e-10    11.3285371702638        1.48225036329666
14      153     cellular protein complex disassembly
GO:0006414      3.84141034299822e-10    14.3326612903226        1.0172306414781 12
105     translational elongation
GO:0006614      3.84141034299822e-10    14.3326612903226        1.0172306414781 12
105     SRP-dependent cotranslational protein targeting to membrane
GO:0043241      3.88033221363672e-10    10.9313271604938        1.53068991765276
14      158     protein complex disassembly
GO:0006613      4.29631560125202e-10    14.1791888297872        1.02691855234932
12      106     cotranslational protein targeting to membrane
GO:0045047      4.29631560125202e-10    14.1791888297872        1.02691855234932
12      106     protein targeting to ER
GO:0072599      4.29631560125202e-10    14.1791888297872        1.02691855234932
12      106     establishment of protein localization to endoplasmic reticulum
GO:0006401      1.30736137255254e-09    8.91852631578947        1.9860217286001 15
205     RNA catabolic process
GO:0034623      1.38880095640572e-09    9.82708333333333        1.68569649159228
14      174     cellular macromolecular complex disassembly
GO:0070972      1.50897771532649e-09    12.5633844339623        1.14317348280396
12      118     protein localization to endoplasmic reticulum
GO:0032984      2.0125567867469e-09     9.52592592592593        1.73413604594838
14      179     macromolecular complex disassembly
GO:0006612      2.84111606763006e-09    10.3612485939258        1.48225036329666
13      153     protein targeting to membrane
GO:0072594      1.09104705392107e-08    8.25789473684211        1.97633381772888
14      204     establishment of protein localization to organelle
GO:0019080      2.52507886289359e-08    9.55845323741007        1.46287454155422
12      151     viral genome expression
GO:0019083      2.52507886289359e-08    9.55845323741007        1.46287454155422
12      151     viral transcription
GO:0006413      2.71904693879787e-08    9.48950892857143        1.47256245242544
12      152     translational initiation
GO:0071845      1.0540381480096e-07     6.26408921933086        2.75136668742648
15      284     cellular component disassembly at cellular level
GO:0022411      1.26476224341199e-07    6.17054945054945        2.79011833091136
15      288     cellular component disassembly
GO:0022904      3.68580792010241e-07    11.2324295867334        0.930039443637119
9       96      respiratory electron transport chain
GO:0019058      3.79386595355862e-07    6.6173878494546 2.23790741125182        13
231     viral infectious cycle
GO:0022415      1.44555172918941e-06    5.82842934106921        2.5188568265172 13
260     viral reproductive process
GO:0006605      3.34412438836537e-06    4.18989165821636        4.59206975295827
17      474     protein targeting
GO:0022900      6.07869643150417e-06    7.79688549618321        1.29818005674348
9       134     electron transport chain
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GO:0016032      7.60754506047406e-06    4.11598071931776        4.36924780292021
16      451     viral reproduction
GO:0045333      9.74864465719486e-06    7.32376743385181        1.37568334371324
9       142     cellular respiration
Tissue: Artery_Tibial=>Lung     Type:   asymmetric
SourceGene:     HOXC-AS5(ENSG00000249641.2)
TargetGeneSet:  RPL22   UBR4    RPL11   SYF2    CEP85   WDTC1   PTAFR   KPNA7
KIAA1522        SLC2A1  ZCCHC11 MAGOH   ALG14   SNX27   TMCO1   UBC     USP34
MYEOV2  VHL     RPL32   LSM3    ZNF852  RPL24   RP11    PSMD2   RPL35A  HTT     UBA6
ANKRD17 RPL34   LARP7   NIPBL   RPL37   NDUFS4  BTF3    TBCA    ARAP3   FOXC1
HNRNPC  C6orf130        RPL24P4 RPL39P3 TOMM7   LSM5    SEC61G  CHCHD2  SBDS
BUD31   PMS2P1  SSBP1   PINX1   DCTN6   C8orf40 RPL30   POLR2K  ATP6V1C1        U6
KIAA1797        OR1K1   NR6A1   NUP188  ETFA    PTPRJ   FAU     KDM2A   C11orf30
RPS25   DPAGT1  ZCRB1   PFDN5   PSG1    DIABLO  SAP18   ESD     HEATR5A ERH
MAPKBP1 SRRM2   GSPT1   CNOT1   NFAT5   CAMTA2  COPS3   KIAA0100        CRLF3   NF1
WNT3    NPEPPS  MED13   GGA3    SPACA4  SNRPB2  DTD1    RPS21   EEF1B2P3
MIR98   MED12   ZMYM3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0000956      3.39701043801567e-17    25.2425856307435        0.935575392706387
17      169     nuclear-transcribed mRNA catabolic process
GO:0006401      4.18664409670476e-17    22.0210453682939        1.13486955920006
18      205     RNA catabolic process
GO:0006402      8.2558719796398e-17     23.8164251207729        0.985398934329804
17      178     mRNA catabolic process
GO:0000184      2.87997198583813e-15    28.820202020202 0.658777939242959       14
119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006614      1.54354116335653e-14    30.114698247891 0.581274652273199       13
105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.75169478408974e-14    29.7887979457551        0.586810601342468
13      106     cotranslational protein targeting to membrane
GO:0045047      1.75169478408974e-14    29.7887979457551        0.586810601342468
13      106     protein targeting to ER
GO:0072599      1.75169478408974e-14    29.7887979457551        0.586810601342468
13      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      7.26938441718237e-14    26.3621890547264        0.65324199017369
13      118     protein localization to endoplasmic reticulum
GO:0006415      7.81242114831192e-14    31.9255398361876        0.503771365303439
12      91      translational termination
GO:0006414      4.54578329727447e-13    27.0929791271347        0.581274652273199
12      105     translational elongation
GO:0019080      1.81349865949945e-12    20.0117888816786        0.835928309459553
13      151     viral genome expression
GO:0019083      1.81349865949945e-12    20.0117888816786        0.835928309459553
13      151     viral transcription
GO:0006612      2.14850737372985e-12    19.7231343283582        0.84700020759809
13      153     protein targeting to membrane
GO:0043624      2.14850737372985e-12    19.7231343283582        0.84700020759809
13      153     cellular protein complex disassembly
GO:0043241      3.24835767185265e-12    19.0363355635615        0.874679952944433
13      158     protein complex disassembly
GO:0072594      5.30806290630558e-12    15.8320574162679        1.12933361013079
14      204     establishment of protein localization to organelle
GO:0034623      1.11386038621489e-11    17.125243348475 0.96325513805273        13
174     cellular macromolecular complex disassembly
GO:0032984      1.59605733806533e-11    16.6035784930768        0.990934883399073
13      179     macromolecular complex disassembly
GO:0006413      3.85621560422897e-11    17.9382352941176        0.841464258528822
12      152     translational initiation
GO:0019058      3.88209261568777e-10    12.59680953033  1.27880423500104        13
231     viral infectious cycle
GO:0033365      6.46696766313897e-10    8.23430103035366        2.61850390976403
17      473     protein localization to organelle
GO:0006605      6.67922392713022e-10    8.21569240387621        2.6240398588333 17
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474     protein targeting
GO:0022415      1.65498000540588e-09    11.095051060487 1.43934675800983        13
260     viral reproductive process
GO:0071845      4.82115272069261e-09    10.0952800572782        1.57220953567227
13      284     cellular component disassembly at cellular level
GO:0022411      5.70474276916864e-09    9.94561736770692        1.59435333194935
13      288     cellular component disassembly
GO:0016032      2.12671550358649e-08    7.37561750176429        2.49671303024012
15      451     viral reproduction
GO:0008380      1.11510363562749e-05    6.41624828845276        1.78811154937375
10      323     RNA splicing
GO:0006397      1.17302553785348e-05    5.74529359031824        2.20884367863816
11      399     mRNA processing
GO:0000377      1.66882052411206e-05    8.03571428571429        1.12933361013079
8       204     RNA splicing, via transesterification reactions with bulged
adenosine as nucleophile
GO:0000398      1.66882052411206e-05    8.03571428571429        1.12933361013079
8       204     nuclear mRNA splicing, via spliceosome
GO:0000375      1.98771484760446e-05    7.83305693753455        1.15701335547713
8       209     RNA splicing, via transesterification reactions
Tissue: Artery_Tibial=>Lung     Type:   asymmetric
SourceGene:     IGHV3-7(ENSG00000211938.2)
TargetGeneSet:  AMYP1   RP11    IGKJ5   IGKC    IGKJ3   IGKJ2   IGKJ1   IGKV4-1
IGKV1-5 IGKV1-9 IGKV1-12        IGKV3-15        IGKV1-16        IGKV1-17
IGKV3-20        IGKV6-21        IGKV1-27        IGKV2-28        IGKV1-33
IGKV1D-39       IGKV1D-37       IGKV1D-33       IGKV2D-30       IGKV2D-28
IGKV3D-20       HOXD3   TWIST2  CCR10   FYTTD1  LRRC66  IGJ     PGRMC2  CTB
ZNF815  PCP2    MATN2   IGHV6-1 IGHV3-21        IGHV5-51        SPG11   UBE2Q2  TMC5
CTA     SIRT6   TPD52L2 IGLV5-48        IGLV5-45        IGLV1-40        IGLV2-14
IGLV3-9 IGLC6
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006958      6.56174599161319e-11    130.781818181818        0.0726593315341499
6       50      complement activation, classical pathway
GO:0006956      2.7733150750002e-10     100.863157894737        0.0915507577330289
6       63      complement activation
GO:0002455      3.3654040772284e-10     97.4305084745763        0.0944571309943949
6       65      humoral immune response mediated by circulating immunoglobulin
GO:0072376      1.40520274699429e-09    75.5473684210526        0.119161303716006
6       82      protein activation cascade
GO:0016064      8.85392507192161e-09    54.5714285714286        0.161303716005813
6       111     immunoglobulin mediated immune response
GO:0019724      1.04006006824943e-08    53.0444444444444        0.165663275897862
6       114     B cell mediated immunity
GO:0006959      1.5651210711786e-08     49.3586206896552        0.177288768943326
6       122     humoral immune response
GO:0002449      1.02319466325083e-07    35.4509316770186        0.242682167324061
6       167     lymphocyte mediated immunity
GO:0002460      1.64953366296707e-07    32.5828571428571        0.263026780153623
6       181     adaptive immune response based on somatic recombination of immune
receptors built from immunoglobulin superfamily domains
GO:0002250      2.80419069122154e-07    29.6625 0.287730952875234       6       198
adaptive immune response
GO:0002443      4.07855411949053e-07    27.7560975609756        0.306622379074112
6       211     leukocyte mediated immunity
GO:0002253      3.116569335006e-06      19.2996587030717        0.434502802574216
6       299     activation of immune response
GO:0050778      9.65416030917766e-06    15.722905027933 0.528959933568611       6
364     positive regulation of immune response
GO:0002252      1.34902972300728e-05    14.7894736842105        0.560930039443637
6       386     immune effector process
Tissue: Lung=>Artery_Tibial     Type:   cluster
SourceGene:     MALSU1(ENSG00000156928.4)
TargetGeneSet:  RERE    UBE4B   SPEN    ARID1A  WASF2   EYA3    PHACTR4 SRSF4   MECR
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PUM1    BSDC1   PPCS    ERI3    PCSK9   LRRC40  FPGT-TNNI3K     RP4     ARNT
SETDB1  GATAD2B DENND4B CRTC2   ARHGEF11        PCP4L1  PRRC2C  SLC41A1 RP11    ACP1
MORN2   MDH1    PRADC1  MTHFD2  SUCLG1  COX5B   BCL2L11 AMMECR1L        TANC1   MOB4
C2orf69 NELL2   KANSL1L SEC13   WDR48   ARF4    PDHB    UBA3    FOXP1   KALRN
PPP1R2  MIR570  SLC30A9 COMMD8  CCNI    SEC24B  TRAM1L1 NUDT6   NDUFC1  SUB1
NIPBL   C5orf28 ERCC8   C5orf44 MAN2A1  LSM11   UIMC1   PRL     DAXX    FANCE
BRPF3   PHF3    IRAK1BP1        IBTK    UBE2J1  UFL1    CDK19   ECHDC1  RP3
ARID1B  TCTE3   NDUFA4  TMEM106B        ETV1    SEPT7   GRB10   CHCHD2  DTX2
PSMC2   CAPZA2  BPGM    PPP1R3B RBPMS   LSM1    CTD     RAB2A   MRPS35  DECR1
RBM12B  COX6C   SLC45A4 NDUFB6  RUSC2   AKNA    CIZ1    IDI1    ERCC6   ADK
TCF7L2  FAM204A AKIP1   IMMP1L  MARK2   NDUFS8  C11orf51        FAT3    C11orf70
TAGLN   RNF214  MLL     SC5DL   SLC38A4 ZNF740  RARG    PSG1    ATF7    SMARCC2
R3HDM2  CTDSP2  C12orf61        ARL1    NUP37   ATXN2   MRPL52  PSMA3   BCRP2
BAHD1   ZNF609  CLK3    WDR61   CIB1    IGF1R   CREBBP  BFAR    KIAA0430
TMEM159 ATXN2L  TBC1D10B        GCSH    ZC3H18  GLOD4   LSMD1   CTC1    PEMT
FBXL20  HSD17B1P1       ATP5G1  NDC80   AFG3L2  ZNF397  KIAA1328        IER3IP1
ATP8B1  UQCR11  TICAM1  C19orf70        INSR    RAVER1  NDUFA13 KDELR1  CDS2
STAU1   SCAF4   HSF2BP  ZNF280B TTC28-AS1       MTMR3   MORC2   GTPBP1  STS
TBC1D25 COX7B   NDUFA1  BCORL1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0045333      9.26263010788783e-11    12.3116319444444        1.37568334371324
14      142     cellular respiration
GO:0015980      9.71131285330417e-10    7.15854557830847        2.97418863746454
18      307     energy derivation by oxidation of organic compounds
GO:0022904      2.0746907009595e-09     14.2714090287278        0.930039443637119
11      96      respiratory electron transport chain
GO:0006091      5.4481847749318e-09     5.67933006535948        4.14642585288215
20      428     generation of precursor metabolites and energy
GO:0022900      7.07465700228225e-08    9.83601184849058        1.29818005674348
11      134     electron transport chain
Tissue: Lung=>Artery_Tibial     Type:   cluster
SourceGene:     MED30(ENSG00000164758.3)
TargetGeneSet:  MRPL20  RPL22   SDHB    MECR    ZCCHC17 ZBTB8OS ERI3    UQCRH   RP4
PSMB4   DPM3    PMF1    ACBD6   NAV1    SNRPE   ARV1    ACP1    FAM150B KIDINS220
RP11    TET3    COX5B   UNC50   MZT2B   TANC1   MOB4    SLC23A3 FARSB   HDLBP   LSM3
OXSR1   EXOSC7  USP4    SPCS1   CHMP2B  STAG1   MRPS22  ATP11B  ST6GAL1 RGS12
MRPL1   MRPS18C GRID2   NDUFC1  WWC2    SUB1    BRIX1   MOCS2   NDUFAF2 COX7C
RIOK2   MAN2A1  HINT1   UQCRQ   SKP1    GFRA3   PDF     RPS14   MRPL22  UBLCP1  MSX2
TMEM14B NOL7    HNRNPC  SRPK1   BRPF3   MEA1    MRPL2   C6orf57 COX7A2  IMPG1
C6orf203        RP1     L3MBTL3 SF3B5   ARID1B  PSMB1   NDUFA4  MALSU1  LSM5
YAE1D1  CHCHD2  STAG3L4 PMS2P1  PSMC2   BRAF    SSBP1   CCDC25  GS1     VPS13B
COX6C   ZNF706  NDUFB9  CPSF1   C8orf33 GLIS3   KIAA2026        PLIN2   NDUFB6
DCTN3   INVS    FAM149B1        FAM204A TPP1    RPL27A  C11orf31        ARL2
CCDC85B NDUFS8  LAMTOR1 CWC15   MAML2   C11orf1 TMPRSS5 ATP5L   ERC1    ATF7
RPS26   RBMS2   R3HDM2  C12orf61        CHST11  ALKBH2  MED13L  COX6A1  TRAC    MED4
MBIP    C14orf101       PSMA3   ERH     ENTPD5  SLIRP   PSMC1   C14orf2 CDCA4
CYFIP1  NDN     SRP14   GALK2   RPLP1   MRPL28  C16orf42        NDE1    NDUFAB1
BCL7C   MIR4519 NUDT21  SLC12A4 GCSH    TRAPPC2L        PSMB6   MINK1   CCL13   RFFL
PSMB3   SMARCE1 KRT223P COPZ2   MRPS23  ICT1    ATP5H   NT5C    TNRC6C  KIAA1328
IER3IP1 ELAC1   ZNF532  CFD     UQCR11  MRPL54  DPP9    C19orf70        NDUFA11
SWSAP1  NDUFB7  CPAMD8  NDUFA13 PDCD2L  COX6B1  SIPA1L3 SNRPA   ZNF428  GEMIN7
SNRPD2  RPS5    SNRPB   SNORA51 MRPS26  SNRPB2  DYNLRB1 ROMO1   MYL9    ATP5E
ATP5J   RANBP1  ZNF280B DEPDC5  TCF20   RP6     TIMM17B COX7B   NDUFA1  VMA21
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      4.80768187824279e-26    33.8452380952381        1.08947477683205
24      96      respiratory electron transport chain
GO:0022900      2.60589388894084e-22    22.094025974026 1.52072520932807        24
134     electron transport chain
GO:0045333      1.10821348634874e-21    20.5845036319613        1.61151477406408
24      142     cellular respiration
GO:0015980      8.88607998440733e-15    8.93221592938415        3.48404954674417
25      307     energy derivation by oxidation of organic compounds
GO:0006091      2.35233740270025e-12    6.50749873819309        4.85724171337624
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26      428     generation of precursor metabolites and energy
GO:0042773      2.35984507743052e-09    21.7726655348048        0.533388692824026
9       47      ATP synthesis coupled electron transport
GO:0042775      2.35984507743052e-09    21.7726655348048        0.533388692824026
9       47      mitochondrial ATP synthesis coupled electron transport
GO:0006120      5.3550209187755e-09     26.1153846153846        0.40855304131202
8       36      mitochondrial electron transport, NADH to ubiquinone
GO:0006119      1.65772557638898e-08    16.8718894009217        0.658224344336032
9       58      oxidative phosphorylation
GO:0000377      8.22136912979041e-08    6.92484210526316        2.31513390076811
14      204     RNA splicing, via transesterification reactions with bulged
adenosine as nucleophile
GO:0000398      8.22136912979041e-08    6.92484210526316        2.31513390076811
14      204     nuclear mRNA splicing, via spliceosome
GO:0000375      1.11120510449526e-07    6.74488888888889        2.37187737872812
14      209     RNA splicing, via transesterification reactions
GO:0008380      8.29527736929109e-07    4.92296857117704        3.66562867621618
16      323     RNA splicing
GO:0051437      1.49815446664285e-06    11.3966346153846        0.81710608262404
8       72      positive regulation of ubiquitin-protein ligase activity involved in
mitotic cell cycle
GO:0006200      2.05175450682395e-06    10.8840413318025        0.851152169400042
8       75      ATP catabolic process
GO:0051439      2.77048720394003e-06    10.4153846153846        0.885198256176043
8       78      regulation of ubiquitin-protein ligase activity involved in mitotic
cell cycle
GO:0006521      3.5003022957087e-06     12.6954140127389        0.646875648744032
7       57      regulation of cellular amino acid metabolic process
GO:0051443      4.05273567851081e-06    9.84961884961885        0.930593038544045
8       82      positive regulation of ubiquitin-protein ligase activity
GO:0031145      4.44218161283476e-06    9.71760683760684        0.941941734136046
8       83      anaphase-promoting complex-dependent proteasomal ubiquitin-dependent
protein catabolic process
GO:0051351      5.80616794550596e-06    9.34188034188034        0.975987820912048
8       86      positive regulation of ligase activity
GO:0006977      9.46532592415997e-06    10.7520241822304        0.749013909072037
7       66      DNA damage response, signal transduction by p53 class mediator
resulting in cell cycle arrest
GO:0072413      9.46532592415997e-06    10.7520241822304        0.749013909072037
7       66      signal transduction involved in mitotic cell cycle checkpoint
GO:0072431      9.46532592415997e-06    10.7520241822304        0.749013909072037
7       66      signal transduction involved in mitotic cell cycle G1/S transition
DNA damage checkpoint
GO:0072474      9.46532592415997e-06    10.7520241822304        0.749013909072037
7       66      signal transduction involved in mitotic cell cycle G1/S checkpoint
GO:0046034      9.56129334288728e-06    7.34879032258065        1.37319216663207
9       121     ATP metabolic process
GO:0031397      9.6156759661805e-06     8.67094017094017        1.04407999446405
8       92      negative regulation of protein ubiquitination
GO:0051436      1.04696797282814e-05    10.5720806794055        0.760362604664037
7       67      negative regulation of ubiquitin-protein ligase activity involved in
mitotic cell cycle
GO:0072401      1.04696797282814e-05    10.5720806794055        0.760362604664037
7       67      signal transduction involved in DNA integrity checkpoint
GO:0072404      1.04696797282814e-05    10.5720806794055        0.760362604664037
7       67      signal transduction involved in G1/S transition checkpoint
GO:0072422      1.04696797282814e-05    10.5720806794055        0.760362604664037
7       67      signal transduction involved in DNA damage checkpoint
GO:0042776      1.05566600669119e-05    39.6611111111111        0.147533042696007
4       13      mitochondrial ATP synthesis coupled proton transport
GO:0072395      1.15607817328684e-05    10.3980369635585        0.771711300256038
7       68      signal transduction involved in cell cycle checkpoint
GO:0051438      1.31827508045277e-05    8.27447552447553        1.08947477683205
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8       96      regulation of ubiquitin-protein ligase activity
GO:0033238      1.69123168055106e-05    9.75541401273885        0.81710608262404
7       72      regulation of cellular amine metabolic process
GO:0051352      1.69123168055106e-05    9.75541401273885        0.81710608262404
7       72      negative regulation of ligase activity
GO:0051444      1.69123168055106e-05    9.75541401273885        0.81710608262404
7       72      negative regulation of ubiquitin-protein ligase activity
GO:0051340      1.78042045340318e-05    7.91248606465998        1.13486955920006
8       100     regulation of ligase activity
GO:0031571      1.85293019263661e-05    9.60692916425401        0.82845477821604
7       73      mitotic cell cycle G1/S transition DNA damage checkpoint
Tissue: Artery_Tibial=>Lung     Type:   asymmetric
SourceGene:     RFC1(ENSG00000035928.10)
TargetGeneSet:  MTND2P28        RPL22   DNAJC11 RPS8    RP4     SRP9    UBC     COA5
BRK1    RPL15   SCN5A   RP11    ANXA2R  KIAA0825        HINT1   PRDM1   CHCHD2
SYPL1   ATP6V1C1        AGAP11  RPL27A  C11orf31        ANGPTL5 STAT2   HECTD1
DACT1   ZFYVE26 SIVA1   VPS18   C15orf61        HIC1    RPL27   RPL17   ZNF236  MIF
RPL36
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      5.01697336459565e-13    63.9508928571429        0.21797799460245
9       105     translational elongation
GO:0006614      5.01697336459565e-13    63.9508928571429        0.21797799460245
9       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      5.47525666702937e-13    63.2871870397644        0.220053975503425
9       106     cotranslational protein targeting to membrane
GO:0045047      5.47525666702937e-13    63.2871870397644        0.220053975503425
9       106     protein targeting to ER
GO:0072599      5.47525666702937e-13    63.2871870397644        0.220053975503425
9       106     establishment of protein localization to endoplasmic reticulum
GO:0070972      1.46736138181706e-12    56.2726081258191        0.244965746315134
9       118     protein localization to endoplasmic reticulum
GO:0006415      9.44003889127307e-12    62.8170865279299        0.18891426198879
8       91      translational termination
GO:0006612      1.56118916760135e-11    42.4910714285714        0.317625077849284
9       153     protein targeting to membrane
GO:0000184      8.38542969311404e-11    46.8796068796069        0.24704172721611
8       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0072594      2.06567116178528e-10    31.2659340659341        0.423500103799045
9       204     establishment of protein localization to organelle
GO:0019080      5.68241249197198e-10    36.3076923076923        0.313473116047332
8       151     viral genome expression
GO:0019083      5.68241249197198e-10    36.3076923076923        0.313473116047332
8       151     viral transcription
GO:0006413      5.98992822114789e-10    36.0530303030303        0.315549096948308
8       152     translational initiation
GO:0043624      6.31179356207962e-10    35.8018808777429        0.317625077849284
8       153     cellular protein complex disassembly
GO:0043241      8.15671725087671e-10    34.5963636363636        0.328004982354162
8       158     protein complex disassembly
GO:0000956      1.39316502393249e-09    32.2077922077922        0.350840772264895
8       169     nuclear-transcribed mRNA catabolic process
GO:0034623      1.75577584099916e-09    31.2267250821468        0.361220676769774
8       174     cellular macromolecular complex disassembly
GO:0006402      2.102229557835e-09      30.483422459893 0.369524600373677       8
178     mRNA catabolic process
GO:0032984      2.19757703533489e-09    30.3030303030303        0.371600581274652
8       179     macromolecular complex disassembly
GO:0006401      6.40579489682571e-09    26.2556529764652        0.425576084700021
8       205     RNA catabolic process
GO:0019058      1.63240654798781e-08    23.1520587036282        0.479551588125389
8       231     viral infectious cycle
GO:0022415      4.09700665663054e-08    20.4458874458874        0.539755034253685
8       260     viral reproductive process
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GO:0071845      8.1089228630068e-08     18.6363636363636        0.589578575877102
8       284     cellular component disassembly at cellular level
GO:0022411      9.03188654516489e-08    18.3649350649351        0.597882499481005
8       288     cellular component disassembly
GO:0033365      3.09825975321922e-07    12.8913177339901        0.981938966161511
9       473     protein localization to organelle
GO:0006605      3.15399742993329e-07    12.8626728110599        0.984014947062487
9       474     protein targeting
GO:0016032      2.70433110559206e-06    11.4738354196593        0.936267386340046
8       451     viral reproduction
Tissue: Lung=>Artery_Tibial     Type:   asymmetric
SourceGene:     RP11-14I17.3(ENSG00000254362.1)
TargetGeneSet:  RPL22   RP11    AMY2A   FAHD2B  UBE2V1  RPL37A  RPL10AP6
COX7C   SEC24A  RPS10   TOMM7   GTF2I   SNHG6   FBXO43  EIF3H   PSCA    RPLP2   FAU
ATP5G2  ANKS1B  RPS29   RPL36A  MGAT2   RPLP1   C16orf55        RPL38   EIF3K
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006413      3.92646057137708e-15    91.4724711907811        0.220884367863816
10      152     translational initiation
GO:0006415      3.43684867188714e-13    106.372567191844        0.132239983392153
8       91      translational termination
GO:0006414      1.11491359288827e-12    90.9310071371927        0.152584596221715
8       105     translational elongation
GO:0006614      1.11491359288827e-12    90.9310071371927        0.152584596221715
8       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.2049572002447e-12     89.9968602825746        0.154037782852398
8       106     cotranslational protein targeting to membrane
GO:0045047      1.2049572002447e-12     89.9968602825746        0.154037782852398
8       106     protein targeting to ER
GO:0072599      1.2049572002447e-12     89.9968602825746        0.154037782852398
8       106     establishment of protein localization to endoplasmic reticulum
GO:0070972      2.89469742734692e-12    80.1118881118881        0.171476022420594
8       118     protein localization to endoplasmic reticulum
GO:0000184      3.10082702951292e-12    79.3846153846154        0.17292920905127
8       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0072594      4.73687877974069e-12    54.75   0.296450072659332       9       204
establishment of protein localization to organelle
GO:0019080      2.13907017560942e-11    61.4825174825175        0.219431181233133
8       151     viral genome expression
GO:0019083      2.13907017560942e-11    61.4825174825175        0.219431181233133
8       151     viral transcription
GO:0006612      2.37864207008614e-11    60.6259946949602        0.222337554494499
8       153     protein targeting to membrane
GO:0043624      2.37864207008614e-11    60.6259946949602        0.222337554494499
8       153     cellular protein complex disassembly
GO:0043241      3.08249190817365e-11    58.5846153846154        0.229603487647914
8       158     protein complex disassembly
GO:0000956      5.2972725883944e-11     54.539894887721 0.245588540585427       8
169     nuclear-transcribed mRNA catabolic process
GO:0034623      6.69467825914751e-11    52.8785912882298        0.252854473738842
8       174     cellular macromolecular complex disassembly
GO:0006402      8.03358941506834e-11    51.6199095022624        0.258667220261574
8       178     mRNA catabolic process
GO:0032984      8.40264151260377e-11    51.3144399460189        0.260120406892257
8       179     macromolecular complex disassembly
GO:0006401      2.48511036922702e-10    44.4607575165951        0.297903259290015
8       205     RNA catabolic process
GO:0019058      6.42550655272773e-10    39.205243187306 0.335686111687772       8
231     viral infectious cycle
GO:0022415      1.63902718783161e-09    34.6227106227106        0.377828523977579
8       260     viral reproductive process
GO:0071845      3.28786737084684e-09    31.5585284280936        0.412705003113971
8       284     cellular component disassembly at cellular level
GO:0022411      3.67030348448347e-09    31.0989010989011        0.418517749636703
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8       288     cellular component disassembly
GO:0033365      8.28002994255104e-09    22.5743534482759        0.687357276313058
9       473     protein localization to organelle
GO:0006605      8.43381150091961e-09    22.5241935483871        0.688810462943741
9       474     protein targeting
GO:0016032      1.20424027420166e-07    19.4297621114777        0.655387170438032
8       451     viral reproduction
Tissue: Lung=>Artery_Tibial     Type:   asymmetric
SourceGene:     RP11-469J4.3(ENSG00000242578.1)
TargetGeneSet:  NOTCH2  MRPS21  KIRREL  RP11    NAV1    RPL35P1 KIDINS220
EXOC6B  MZT2A   RPL37A  TBC1D5  ZNF852  PBRM1   STAG1   TM4SF19-AS1     OCIAD1-AS1
CLOCK   WWC2    COX7C   CTD     RPS14   MRPL2   RPL39P3 PSMB1   C7orf50 TOMM7
MALSU1  HIP1    TAF6    SSBP1   SLC4A2  UQCRB   ZNF706  HK1     RPLP2   FAU
ARHGEF17        YAP1    PFDN5   ATF7    RPL18AP3        MED13L  PSME2P2 RPS29
C14orf2 MAPKBP1 NR2F2   COX4I1  RPL13   CCT6B   RPL38   WDR7    RSL24D1P8
C19orf53        RPL18A  NDUFA13 FXYD1   ETFB    IFNGR2  SLC38A5 ATRX    RGAG1   MT
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      3.21955477760918e-10    37.3116248778899        0.283371392983185
8       91      translational termination
GO:0006414      1.02297167185496e-09    31.8952354416272        0.326966991903675
8       105     translational elongation
GO:0006614      1.02297167185496e-09    31.8952354416272        0.326966991903675
8       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.10395183700959e-09    31.5675675675676        0.330080963255138
8       106     cotranslational protein targeting to membrane
GO:0045047      1.10395183700959e-09    31.5675675675676        0.330080963255138
8       106     protein targeting to ER
GO:0072599      1.10395183700959e-09    31.5675675675676        0.330080963255138
8       106     establishment of protein localization to endoplasmic reticulum
GO:0070972      2.60527694582146e-09    28.1002457002457        0.367448619472701
8       118     protein localization to endoplasmic reticulum
GO:0000184      2.78666132651158e-09    27.845142439737 0.370562590824164       8
119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0072594      1.06541617984882e-08    18.2192307692308        0.635250155698568
9       204     establishment of protein localization to organelle
GO:0019080      1.83321836171405e-08    21.5656775656776        0.470209674070999
8       151     viral genome expression
GO:0019083      1.83321836171405e-08    21.5656775656776        0.470209674070999
8       151     viral transcription
GO:0006413      1.93063668823183e-08    21.4144144144144        0.473323645422462
8       152     translational initiation
GO:0006612      2.03249372007879e-08    21.2652376514445        0.476437616773926
8       153     protein targeting to membrane
GO:0043624      2.03249372007879e-08    21.2652376514445        0.476437616773926
8       153     cellular protein complex disassembly
GO:0043241      2.61444317343914e-08    20.5491891891892        0.492007473531244
8       158     protein complex disassembly
GO:0000956      4.42016157169263e-08    19.1304347826087        0.526261158397343
8       169     nuclear-transcribed mRNA catabolic process
GO:0034623      5.54487334207817e-08    18.5477043308369        0.541831015154661
8       174     cellular macromolecular complex disassembly
GO:0006402      6.6144265321733e-08     18.106200317965 0.554286900560515       8
178     mRNA catabolic process
GO:0032984      6.90801909820277e-08    17.9990516832622        0.557400871911978
8       179     macromolecular complex disassembly
GO:0071845      1.83687142817769e-07    12.8463636363636        0.884367863815653
9       284     cellular component disassembly at cellular level
GO:0006401      1.9656774814511e-07     15.5950061736864        0.638364127050031
8       205     RNA catabolic process
GO:0022411      2.06815135429612e-07    12.6586021505376        0.896823749221507
9       288     cellular component disassembly
GO:0019058      4.88983744313021e-07    13.7515452672403        0.719327382188084
8       231     viral infectious cycle
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GO:0016032      9.5001796262223e-07     9.04761904761905        1.40440107951007
10      451     viral reproduction
GO:0022415      1.19467009618048e-06    12.1441441441441        0.809632551380527
8       260     viral reproductive process
GO:0033365      1.46260855257869e-06    8.60413452638075        1.47290844924227
10      473     protein localization to organelle
GO:0006605      1.49077133793387e-06    8.58497536945813        1.47602242059373
10      474     protein targeting
GO:0022904      1.15325666764779e-05    19.6634615384615        0.298941249740502
5       96      respiratory electron transport chain
Tissue: Artery_Tibial=>Lung     Type:   asymmetric
SourceGene:     RP11-96L14.7(ENSG00000236782.1)
TargetGeneSet:  RPL22   RPL11   ZNF593  RP11    RPS8    RPL5    GGCX    RPL31
RPL32   RPL14   RPL24   RPL34   RPL37   RPS14   EEF1A1  MRPS12  TRBV24-1        CTSB
RPS20   RPL30   EIF3H   RPS6    RPL35   RPS24   RPLP2   RPL27A  RPS13   FAU
RPS25   NACA    TPT1    RPS29   RPS3AP6 RPLP1   RPL13   RPL17   RPL19   RPL27
RPL36   RPS16   RPL13A  RPS11   RPS9    RPS21   RPL3    UQCRBP1 RPL10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      1.97525674743371e-72    935.086956521739        0.31970105875026
36      105     translational elongation
GO:0006415      3.43864902203077e-72    996.597222222222        0.277074250916892
35      91      translational termination
GO:0006614      1.61864780111005e-69    796.5   0.31970105875026        35      105
SRP-dependent cotranslational protein targeting to membrane
GO:0006613      2.41509908595394e-69    785.226917057903        0.322745830738357
35      106     cotranslational protein targeting to membrane
GO:0045047      2.41509908595394e-69    785.226917057903        0.322745830738357
35      106     protein targeting to ER
GO:0072599      2.41509908595394e-69    785.226917057903        0.322745830738357
35      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      2.11197063344298e-67    671.137884872825        0.35928309459553
35      118     protein localization to endoplasmic reticulum
GO:0000184      2.99013222654803e-67    663.101851851852        0.362327866583627
35      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006413      1.17751969382613e-65    554.39224137931 0.462805342190852       36
152     translational initiation
GO:0019080      4.43240956748714e-63    479.104406130268        0.459760570202754
35      151     viral genome expression
GO:0019083      4.43240956748714e-63    479.104406130268        0.459760570202754
35      151     viral transcription
GO:0006612      7.45719533960017e-63    470.918079096045        0.46585011417895
35      153     protein targeting to membrane
GO:0043624      7.45719533960017e-63    470.918079096045        0.46585011417895
35      153     cellular protein complex disassembly
GO:0043241      2.64851024598509e-62    451.616982836495        0.481073974119438
35      158     protein complex disassembly
GO:0000956      3.69334038571315e-61    414.224709784411        0.514566465988513
35      169     nuclear-transcribed mRNA catabolic process
GO:0034623      1.14860445592635e-60    399.184652278177        0.529790325929001
35      174     cellular macromolecular complex disassembly
GO:0006402      2.77381950384788e-60    387.909867909868        0.541969413881392
35      178     mRNA catabolic process
GO:0032984      3.44589867297839e-60    385.189043209877        0.54501418586949
35      179     macromolecular complex disassembly
GO:0072594      5.24187975638026e-58    327.633136094675        0.621133485571933
35      204     establishment of protein localization to organelle
GO:0006401      6.31720966569355e-58    325.683006535948        0.62417825756003
35      205     RNA catabolic process
GO:0019058      5.85559460952628e-56    281.964285714286        0.703342329250571
35      231     viral infectious cycle
GO:0022415      4.95867185056708e-54    245.120987654321        0.791640716905404
35      260     viral reproductive process
GO:0071845      1.32699761335688e-52    221.120035698349        0.864715244619749
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35      284     cellular component disassembly at cellular level
GO:0022411      2.22919411718453e-52    217.562582345191        0.87689433257214
35      288     cellular component disassembly
GO:0016032      2.94340186076153e-45    130.791933760684        1.37319216663207
35      451     viral reproduction
GO:0033365      1.64019212160537e-44    124.027143581938        1.44017715037022
35      473     protein localization to organelle
GO:0006605      1.76985173622779e-44    123.73576309795 1.44322192235831        35
474     protein targeting
GO:0042274      4.56291058623043e-14    247.597051597052        0.0548058957857588
7       18      ribosomal small subunit biogenesis
GO:0042254      1.84125380903576e-11    30.1904358865849        0.453671026226559
10      149     ribosome biogenesis
GO:0006364      2.09431075921755e-11    38.7392481203008        0.316656286762162
9       104     rRNA processing
GO:0016072      3.49321364128278e-11    36.422630834512 0.334924918690748       9
110     rRNA metabolic process
GO:0022613      4.98619319428979e-11    22.107476635514 0.685073697321985       11
225     ribonucleoprotein complex biogenesis
GO:0071843      9.5425123723057e-11     20.7295321637427        0.727700505155353
11      239     cellular component biogenesis at cellular level
GO:0030490      2.59849612795674e-09    480.133333333333        0.021313403916684
4       7       maturation of SSU-rRNA
GO:0034470      7.25689103555196e-09    19.1389678384443        0.608954397619542
9       200     ncRNA processing
GO:0034660      1.54035450347411e-07    13.1655279503106        0.867760016607847
9       285     ncRNA metabolic process
GO:0000028      5.23384924917998e-07    351.317073170732        0.0182686319285863
3       6       ribosomal small subunit assembly
GO:0000462      5.23384924917998e-07    351.317073170732        0.0182686319285863
3       6       maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA,
5.8S rRNA, LSU-rRNA)
GO:0042273      5.68413960043026e-06    117.056910569106        0.0365372638571725
3       12      ribosomal large subunit biogenesis
GO:0042255      1.43460475172112e-05    81.0168855534709        0.0487163518095634
3       16      ribosome assembly
Tissue: Artery_Tibial=>Lung     Type:   asymmetric
SourceGene:     SPOCD1(ENSG00000134668.7)
TargetGeneSet:  RPL22   AKR7L   C1orf210        RPS8    RPL5    RP11    RPS7
ITGB1BP1        PEX13   GGCX    FHL2    HOXD8   MFF     RPL15   LIMD1   PRKCD
THOC7   YEATS2  RPL34   FAM160A1        BTF3    AP3S1   THG1L   FNDC1   LANCL2
TRIM50  RUNDC3B SLC25A13        RPL30   CHRAC1  TUSC1   ASPN    NR6A1   FAM35A
TRAF6   MSANTD4 TEX12   RPS25   SIAE    ZCRB1   RNASEH2B        RP4     RAP1AP
DICER1-AS1      DUOXA1  DUOX1   RPL4    RPS15A  RABEP2  RPL26   CDH2    RAB3D
ZNF737  ZNF428  SSC5D   PTPRA   SMARCB1 SEC14L4 OGT     RP6     KLHL4   PCDH19
BCORL1  IGSF1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      6.18283030552637e-15    53.2273648648649        0.302262819182064
11      91      translational termination
GO:0006414      3.14913099296321e-14    45.2556066705003        0.348764791363919
11      105     translational elongation
GO:0006614      3.14913099296321e-14    45.2556066705003        0.348764791363919
11      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      3.50547736857288e-14    44.7761024182077        0.352086360805481
11      106     cotranslational protein targeting to membrane
GO:0045047      3.50547736857288e-14    44.7761024182077        0.352086360805481
11      106     protein targeting to ER
GO:0072599      3.50547736857288e-14    44.7761024182077        0.352086360805481
11      106     establishment of protein localization to endoplasmic reticulum
GO:0019080      5.48979982789341e-14    34.2062350119904        0.501556985675732
12      151     viral genome expression
GO:0019083      5.48979982789341e-14    34.2062350119904        0.501556985675732
12      151     viral transcription
```

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GO:0072594      7.53061646116167e-14    27.637397157816 0.677600166078472       13
204     establishment of protein localization to organelle
GO:0070972      1.17282443718462e-13    39.7211417024501        0.391945194104214
11      118     protein localization to endoplasmic reticulum
GO:0000184      1.2892281125846e-13     39.3506006006006        0.395266763545775
11      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0034623      3.03097968682246e-13    29.3024691358025        0.577953082831638
12      174     cellular macromolecular complex disassembly
GO:0032984      4.25593784698778e-13    28.4151696606786        0.594560930039444
12      179     macromolecular complex disassembly
GO:0022415      1.69033341926163e-12    21.2872180451128        0.863608054805896
13      260     viral reproductive process
GO:0006413      1.95749546305293e-12    30.0713053479011        0.504878555117293
11      152     translational initiation
GO:0006612      2.10414550553252e-12    29.8574419489912        0.508200124558854
11      153     protein targeting to membrane
GO:0043624      2.10414550553252e-12    29.8574419489912        0.508200124558854
11      153     cellular protein complex disassembly
GO:0006401      2.14148223372021e-12    24.5423143350604        0.680921735520033
12      205     RNA catabolic process
GO:0043241      2.99731007256948e-12    28.8317705460563        0.52480797176666
11      158     protein complex disassembly
GO:0071845      5.17613432623823e-12    19.3691091196626        0.943325721403363
13      284     cellular component disassembly at cellular level
GO:0022411      6.17595894880333e-12    19.081974025974 0.956611999169608       13
288     cellular component disassembly
GO:0000956      6.2693993305163e-12     26.8037974683544        0.561345235623832
11      169     nuclear-transcribed mRNA catabolic process
GO:0019058      8.77082327890228e-12    21.5890410958904        0.767282541000623
12      231     viral infectious cycle
GO:0006402      1.1047880814047e-11     25.3432594270918        0.591239360597883
11      178     mRNA catabolic process
GO:0016032      1.59915347183911e-09    11.8424657534247        1.49802781814407
13      451     viral reproduction
GO:0033365      2.84643893940064e-09    11.2583229813665        1.57110234585842
13      473     protein localization to organelle
GO:0006605      2.91995796837528e-09    11.2330957545708        1.57442391529998
13      474     protein targeting
GO:0022613      8.64531046197235e-06    11.1093085701499        0.747353124351256
7       225     ribonucleoprotein complex biogenesis
GO:0071843      1.28092044106524e-05    10.4286164844407        0.793855096533112
7       239     cellular component biogenesis at cellular level
Tissue: Lung=>Artery_Tibial     Type:   cluster
SourceGene:     SYCN(ENSG00000179751.5)
TargetGeneSet:  HES2    CELA2A  CELA3B  CELA3A  RP1     RP11    CLCA4   AMY2A
SCARNA2 BCL9    CRNN    SPRR1B  SPRR2D  TKT     PPP1R12B        C4BPA   PRKD3
MAP4K3  REG1B   REG1A   REG3A   IGKV2-24        ITGA9   APPL1   CPB1    SCARNA7
C3orf70 CC2D2A  NR3C2   LRBA    SPINK1  PRL     HIST1H1E        MUC21   CLPS
SRPK1   PGC     7SK     NHSL1   JAZF1   CPA2    CPA1    PRSS1   PRSS3P1 PRSS3P2 RHEB
KBTBD11 EFHA2   FGL1    VPS28   RGP1    ORM1    RP11-88G17      MRPL41  WDR85
MAPK8   PNLIP   PNLIPRP2        PARVA   CD248   FAM168A CREBZF  TAF1D   RECQL
KRT6A   KRT4    MSRB3   PLA2G1B GJB2    HMGB1   EXOC5   DNAL1   C14orf45
TTLL5   HERC2P10        MAP1A   RHCG    C15orf38        CIB1    PCSK6   SPSB3   E4F1
GP2     CTRB2   CTRB1   TSR1    KRT33B  KRT13   AOC3    GH1     CEP112  SCARNA17
SCARNA18        SERPINB3        FGF22   GPX4    TMIGD2  ALKBH7  ZNF426  SYCN    KLK1
RP4     MAP1LC3A        CTD     C21orf119       PEX26   HIRA    RBFOX2  APOBEC3C
TRABD   FAM123B ZC4H2   TTC3P1  APOOL   MID2    MT
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0007586      7.64920615419947e-10    19.2148148148148        0.641132101584665
10      109     digestion
GO:0044241      1.44827079758011e-06    64.4444444444444        0.0882291882914677
4       15      lipid digestion
Tissue: Lung=>Artery_Tibial     Type:   cluster
```

```
SourceGene:     TMEM138(ENSG00000149483.6)
TargetGeneSet:  MRPL20  SDHB    UBR4    ATPIF1  MECR    PSMB2   UQCRH   MAGOH
ALG14   RP4     UFC1    SDHC    SNRPE   MORN2   COX5B   CCDC93  PKP4    MOB4
MYEOV2  HDLBP   LSM3    SLC6A6  KRBOX1  LZTFL1  SPCS1   CHMP2B  RP11    MRPL47
MRPL1   MRPS18C LAMTOR3 ANAPC10 FRG1    PDCD6   FASTKD3 SUB1    MRPS30  COX7C   SKP1
PDF     DIAPH1  ATOX1   MRPL22  UBLCP1  NUDCD2  TMEM14B HLA-F-AS1       HNRNPC
SRPK1   SLC29A1 ECHDC1  MRPS12  TAB2    RP1     MLLT4   PSMB1   C7orf50 NUDT1   RPA3
NDUFA4  LSM5    EPDR1   YAE1D1  PPIA    CHCHD2  SKP1P1  STAG3L4 KIAA1147
SSBP1   TAS2R5  NAT1    ZNF703  MRPS35  COX6C   UBR5    UTP23   NDUFB9  TUSC1
NDUFB6  DCTN3   ISCA1   ATP6V1G1        CDC123  OPTN    PLAC9   C10orf32
MRPL23  C11orf58        IMMP1L  INCENP  BAD     MRPL11  NDUFS8  LAMTOR1 DCUN1D5
C11orf1 ATP5L   CBL     ARHGEF12        C12orf69        PRR13   R3HDM2  UBE2N
CCDC53  COX6A1  RFXAP   MED4    COMMD6  A2LD1   C14orf126       MBIP    PSMA3   ERH
RP3     SLIRP   CDCA4   NDN     SRP14   PHGR1   CHST14  GTF2A2  WDR61   MAN2A2  CTD
NDUFAB1 TMEM219 PLD2    FAM106A TMEM132E        PSMB3   MRPS23  MAP2K6  ICT1
ELAC1   BSG     UQCR11  MRPL54  C19orf70        NDUFA11 ALKBH7  OR7D2   PIN1    DNM2
SWSAP1  WDR83OS C19orf53        GIPC1   NDUFB7  NDUFA13 ZNF726  COX6B1  ZNF428
AP2S1   C19orf63        MCM8    SNRPB2  C20orf4 ZNF334  DIP2A   MTMR3   PATZ1   TXN2
CXorf38 FUNDC1  GSPT2   PDZD11  PIN4    NGFRAP1 NXT2    NDUFA1  THOC2
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      2.28502963868585e-20    30.288961038961 0.896823749221507       19
96      respiratory electron transport chain
GO:0022900      7.964367203689e-19      21.6659038901602        1.25181648328835
20      134     electron transport chain
GO:0045333      2.60949951688323e-18    20.2337847469708        1.32655179572348
20      142     cellular respiration
GO:0015980      8.78165891987501e-13    9.03662127346338        2.86796761469794
21      307     energy derivation by oxidation of organic compounds
GO:0006091      9.6882034216554e-12     7.05363756613757        3.99833921527922
23      428     generation of precursor metabolites and energy
GO:0042773      1.08965520046757e-08    23.0599636583889        0.439069960556363
8       47      ATP synthesis coupled electron transport
GO:0042775      1.08965520046757e-08    23.0599636583889        0.439069960556363
8       47      mitochondrial ATP synthesis coupled electron transport
GO:0006120      3.53695208346047e-08    26.9420797413793        0.336308905958065
7       36      mitochondrial electron transport, NADH to ubiquinone
GO:0006119      6.09371845813226e-08    17.9729133858268        0.541831015154661
8       58      oxidative phosphorylation
GO:0051443      9.3903136075027e-07     12.1234305171313        0.766036952460037
8       82      positive regulation of ubiquitin-protein ligase activity
GO:0051351      1.35489818955297e-06    11.4984857662023        0.8034046086776 8
86      positive regulation of ligase activity
GO:0051438      3.13130240229175e-06    10.184681460272 0.896823749221507       8
96      regulation of ubiquitin-protein ligase activity
GO:0051340      4.259098915901e-06      9.73913043478261        0.93419140543907
8       100     regulation of ligase activity
Tissue: Lung=>Heart_Left_Ventricle      Type:   asymmetric
```

SourceGene: BCL6(ENSG00000113916.13) B-cell lymphoma 6 protein isoform 1

TargetGeneSet: KLHL17 s CAPZB PLA2G2A ASAP3 INPP5B UTP11L KIAA1107
ECM1 BNIPL LYSMD1 SNX27 ILF2 FAM189B LMNA PMF1 CRABP2 RGS5 DPT
CEP350 TGFB2 C2orf44 AFF3 GCC2 GALNT5 FRZB COL3A1 COL5A2 SATB2
KANSL1L FN1 ARPC2 SLC23A3 GALNTL2 TGFBR2 TRANK1 ROBO1 CCDC80 KLF15
ABTB1 TNIK BCL6 11-Sep AFF1 UNC5C ARSJ PDE5A BBS12 PHF17
EDNRA LPCAT1 RAI14 PTGER4 SLC38A9 GUSBP9 KLHL35 ARSK PPP2CA PHF15 BRD8
SOX9 SPARC CNOT8 ADAM19 ADRA1B PDLIM7 DTNBP1 IER3 CCND3 FBXO9
COL12A1 KIAA1009 RP11 LFNG 7-Sep COL1A2 ECD RP13 PCOLCE
NAMPT IMPDH1 CALU TNPO3 DCTN6 UBXN2B MSC SDC2 YWHAZ EXT1
COL14A1 CER1 FREM1 DNAJB5 OGN ASPN ECM2 C9orf3 PTCH1 COL15A1
MSANTD3 CDK5RAP2 PSMB7 RXRA COL5A1 WAC ZNF37BP CSGALNACT2
KIAA0913 FRAT2 AP2A2 HTATIP2 PRG2 CARNS1 DYNC2H1 KBTBD3 ZBTB16
SCN4B HINFP TSPAN9 NTN4 EMP1 C12orf35 TENC1 PSG1 ZC3H10 AVIL
CTDSP2 LUM GLT8D2 CMKLR1 TMEM119 MPHOSPH8 AP1G2 LRFN5 MLH3 DIO2
ACTC1 ANKDD1A CILP ZWILCH FEM1B LRRC49 COMMD4 WDR61 MRPL28 TNFRSF12A
PPL MT1M MT1X HSD11B2 AARS ZNRF1 CENPN KIAA1609 ACSF3
WDR81 SPAG7 CTC1 C17orf39 GHDC STAT3 EZH1 SCRN2 COPZ2
STXBP4 MRC2 PRKAR1A GGA3 LLGL2 RECQL5 RHBDF2 MYL12B CXXC1 MOB3A
DAPK3 CDC37 WDR83 C19orf44 LSM4 ZNF14 PSMC4 ADCK4 TMEM91
ZNF233 SNRPB MAVS PHF20 SAMHD1 PLCG1 PKIG ELMO2 APCDD1L SYNJ1
COL6A2 TFIP11 TPST2 TTLL12 NRK TSC22D3 KIAA1210 PGRMC1 HMGB3
PNMA6C GAB3

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term

GO:0030199	1.00E-10	33.4171875	0.385924849	9	33
collagen fibril organization					
GO:0030198	5.13E-08	7.958333333	1.882845478	13	161
extracellular matrix organization					
GO:0043062	5.53E-08	7.904362416	1.89454017	13	162
extracellular structure organization					

Tissue: Heart_Left_Ventricle=>Lung Type: asymmetric

SourceGene: C15orf40(ENSG00000169609.8) "Unknown protein (BLAST reveals a conserved domain of unknown function, DIF167 superfamily)"

TargetGeneSet: RPL5 RP11 ZEB2 RPL32 CTB RPL10A MRPS12 PDGFA AIMP2 ZDHHC4 RPS6 NFKBIA EXD1 RPL4 RANBP10 R3HDM4 TIMM44 LILRB4 CTA RPL3 RPL10

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0006415	9.34E-12	108.7045455	0.113348557	7	91	translational termination
GO:0006414	2.60E-11	93.08441558	0.130786797	7	105	translational elongation
GO:0006614	2.60E-11	93.08441558	0.130786797	7	105	SRP-dependent cotranslational protein targeting to membrane
GO:0006613	2.78E-11	92.13774105	0.132032385	7	106	cotranslational protein targeting to membrane
GO:0045047	2.78E-11	92.13774105	0.132032385	7	106	protein targeting to ER
GO:0072599	2.78E-11	92.13774105	0.132032385	7	106	establishment of protein localization to endoplasmic reticulum
GO:0072594	5.33E-11	58.11020408	0.254100062	8	204	establishment of protein localization to organelle
GO:0070972	5.97E-11	82.10810811	0.146979448	7	118	protein localization to endoplasmic reticulum
GO:0000184	6.34E-11	81.36931818	0.148225036	7	119	"nuclear-transcribed mRNA catabolic process, nonsense-mediated decay"
GO:0019080	3.42E-10	63.14583333	0.18808387	7	151	viral genome expression

GO:0019083	3.42E-10	63.14583333	0.18808387	7	151	viral transcription
GO:0006413	3.58E-10	62.70595611	0.189329458	7	152	translational initiation
GO:0006612	3.75E-10	62.27210461	0.190575047	7	153	protein targeting to membrane
GO:0043624	3.75E-10	62.27210461	0.190575047	7	153	cellular protein complex disassembly
GO:0043241	4.70E-10	60.18904275	0.196802989	7	158	protein complex disassembly
GO:0000956	7.54E-10	56.05892256	0.210504463	7	169	nuclear-transcribed mRNA catabolic process
GO:0034623	9.25E-10	54.3614589	0.216732406	7	174	cellular macromolecular complex disassembly
GO:0006402	1.09E-09	53.07496013	0.22171476	7	178	mRNA catabolic process
GO:0032984	1.13E-09	52.76268499	0.222960349	7	179	macromolecular complex disassembly
GO:0033365	1.50E-09	30.10560345	0.58916338	9	473	protein localization to organelle
GO:0006605	1.52E-09	30.03870968	0.590408968	9	474	protein targeting
GO:0006401	2.91E-09	45.75068871	0.255345651	7	205	RNA catabolic process
GO:0019058	6.67E-09	40.36647727	0.287730953	7	231	viral infectious cycle
GO:0022415	1.51E-08	35.66654689	0.323853021	7	260	viral reproductive process
GO:0071845	2.78E-08	32.52116836	0.353747146	7	284	cellular component disassembly at cellular level
GO:0022411	3.06E-08	32.04917502	0.3587295	7	288	cellular component disassembly

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GO:0016032      6.50E-07        20.0497543      0.561760432     7       451
viral reproduction


Tissue: Lung=>Heart_Left_Ventricle      Type:   asymmetric
SourceGene:     CTD-2224J9.8(ENSG00000213777.4)
TargetGeneSet:  KIF17   AK2     MRPL37  USP24   ATP5F1  FH      BOLA3   COX5B
UBE2F   HIGD1A  VPRBP   CHMP2B  RP11    TMEM14E RPL39L  NDUFS6  NDFIP1  RP1     COQ3
SEC61G  STAG3L4 PTK2B   CYC1    NDUFB6  ATP5C1  SEMA4G  GLRX3   MACROD1 SSSCA1  FIBP
NDUFS8  PTS     RAPGEF3 SMARCC2 RPL6    SALL2   COX16   ANGEL1  CDC42BPB
C15orf29        TPM1    RPL4    SIN3A   CTD     NDUFB10 DCTPP1  TXNDC17 RPL17P43
PCGF2   NDUFV2  NDUFS7  UQCR11  MRPL4   NDUFB7  TIMM50  ZNF765  YWHAB   NCOA3
FOXO4
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      7.75203118275651e-16    49.8745644599303        0.352086360805481
12      96      respiratory electron transport chain
GO:0045333      2.74000707798801e-15    35.9490310077519        0.52079440869144
13      142     cellular respiration
GO:0022900      4.72993834892767e-14    34.2487005197921        0.491453878624317
12      134     electron transport chain
GO:0015980      3.24049693201275e-12    17.2810011376564        1.12594284132586
14      307     energy derivation by oxidation of organic compounds
GO:0006119      3.14111757666897e-11    51.0151111111111        0.212718842986645
8       58      oxidative phosphorylation
GO:0006120      4.55106132982168e-11    75.3995502248876        0.132032385302055
7       36      mitochondrial electron transport, NADH to ubiquinone
GO:0006091      2.71045007873877e-10    12.1253561253561        1.5697183585911 14
428     generation of precursor metabolites and energy
GO:0042773      3.32506633580914e-10    54.6228260869565        0.17237561414435
7       47      ATP synthesis coupled electron transport
GO:0042775      3.32506633580914e-10    54.6228260869565        0.17237561414435
7       47      mitochondrial ATP synthesis coupled electron transport
Tissue: Heart_Left_Ventricle=>Lung      Type:   asymmetric




SourceGene:     GCC2(ENSG00000135968.13)        GRIP and coiled-coil domain
containing 2




TargetGeneSet:  7SK     BRD8    FCER1A  CEP350  TSEN15  PLB1    EHD3    IL1R2
EAF1-AS1        BCL6    RP11    SULT1B1 HSP90AB3P       EDNRA   TLR2    RNF175  NAIP
PCDHA3  SH3PXD2B        DRD1    C6orf1  FKBP5   ARMC12  RAB23   WASF1   GUCY2C
FBXO32  TLR4    SUPV3L1 CHST3   ABCC2   HRAS    TMEM223 ZBTB16  NNMT    RP1
IRAK3   UBE3A   ST20    MT1M    MT1JP   MT1A    MYO1C   CANT1   PSTPIP2 C19orf35
ITPKC   GRIK5   FPR2    VN1R1   SEC14L2 RP3     WNK3    PCDH11X TSC22D3

GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term




GO:0061082      9.06E-08        134.2377622     0.044633589     4       15
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myeloid leukocyte cytokine production

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GO:0010934      2.90E-06        154.2964286     0.029755726     3       10
macrophage cytokine production

GO:0010935      2.90E-06        154.2964286     0.029755726     3       10
regulation of macrophage cytokine production

GO:0002718      4.66E-06        43.36048265     0.11307176      4       38
regulation of cytokine production involved in immune response

GO:0002367      7.71E-06        37.78829717     0.127949623     4       43
cytokine production involved in immune response
```

Tissue: Lung=>Heart_Left_Ventricle   Type: asymmetric

SourceGene: GCKR(ENSG00000084734.4) "glucokinase (hexokinase 4) regulator (is expressed mainly in liver, but also in lung, funtion unknown)"

TargetGeneSet: CAPZB PLA2G2A CDA ASAP3 FGR COL16A1 CYR61 ST7L
PSMB4 SLC39A1 EFNA4 EFNA1 RP11 FAM189B LMNA CRABP2 PTGS2 CALM2
ANTXR1 STEAP3 TNFAIP6 PSMD14 LIPA FRZB COL3A1 COL5A2 KANSL1L FN1
PSMD1 COL6A3 MTMR14 TRANK1 PTH1R COL8A1 ABI3BP CCDC80 GAP43 KLF15 SKIL
SPON2 KIT 11-Sep UNC5C PDE5A LPCAT1 SUB1 RAI14 PTGER4 CTD
KLHL35 LHFPL2 PPP2CA PHF15 MATR3 SPARC CTB HK3 DTNBP1 RBM24
MOCS1 MTO1 USP45 TCF21 LFNG CYTH3 7-Sep SFRP4 YKT6 COL1A2 ECD
PDAP1 SLC12A9 ZNHIT1 NAMPT DYNLL1 TNFRSF10C EBF2 TRPA1 SDC2
YWHAZ COL14A1 FREM1 OGN OMD ASPN ECM2 PTCH1 PSMB7 COL5A1
ITIH5 FAM107B KAZALD1 ADAM12 NRXN2 RIN1 TEAD4 NTN4 EMP1 MGP
STK38L C12orf35 TENC1 LUM GLT8D2 CMKLR1 TMEM119 AP1G2 LRFN5
COX16 DIO2 CILP FEM1B ISLR SCAMP2 WDR61 FAM174B MRPL28 PPL CDR2
MMP2 PDP2 SLC9A5 WDR81 RASL10B CCR7 STAT3 NBR2 COPZ2 COL1A1
MTMR4 MRC2 RHBDF2 PRCD C17orf62 GALNT1 DSEL MOB3A KRI1 LSM4
U2AF1L4 PSMC4 CLEC11A ZNF766 ZNF600 ZNF845 ZNF525 CHMP2A MZF1 ZNF341
PTPRT HSPA13 CBS COL6A1 COL6A2 TPST2 MN1 MFNG ATP6AP2 TCEAL4 NRK
CAPN6 PLS3 PGRMC1

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0070208	1.32E-10	163.8549618	0.094803128	6	10	protein heterotrimerization
GO:0030198	3.73E-10	10.96941541	1.526330358	14	161	extracellular matrix organization

GO:0043062	4.05E-10	10.89452868	1.535810671	14	162
extracellular structure organization					
GO:0030199	2.05E-08	29.59053254	0.312850322	7	33
collagen fibril organization					
GO:0071230	3.18E-08	27.47307692	0.331810947	7	35
cellular response to amino acid stimulus					

GO:0051291	5.15E-08	18.43152455	0.530897516	8	56
protein heterooligomerization					
GO:0071229	1.01E-07	22.61538462	0.388692824	7	41
cellular response to acid					
GO:0071418	4.20E-07	17.8706619	0.474015639	7	50
cellular response to amine stimulus					
GO:0031589	4.84E-07	7.136336842	1.915023182	12	202
cell-substrate adhesion					

GO:0071417	5.53E-07	17.07401709	0.492976265	7	52	cellular response to organic nitrogen
GO:0070206	5.84E-07	24.23579304	0.312850322	6	33	protein trimerization
GO:0001101	1.38E-06	11.46642505	0.805826586	8	85	response to acid
GO:0001503	1.46E-06	5.826628841	2.5217632	13	266	ossification

GO:0001501	1.57E-06	4.993089973	3.403432288	15	359	skeletal system development
GO:0043200	2.60E-06	13.23501326	0.616220331	7	65	response to amino acid stimulus
GO:0010811	6.51E-06	15.20078111	0.464535326	6	49	positive regulation of cell-substrate adhesion
GO:0001957	1.63E-05	106.7985075	0.056881877	3	6	

intramembranous ossification

GO:0036072 1.63E-05 106.7985075 0.056881877 3 6 direct ossification

Tissue: Lung=>Heart_Left_Ventricle Type: asymmetric

SourceGene: HS3ST6(ENSG00000162040.5) heparan sulfate (glucosamine) 3-O-sulfotransferase 6

TargetGeneSet: CAPZB ZFYVE9 PSMA5 RPRD2 PSMB4 PMF1 SLC30A10 MIA3 FAM110C NBAS COMMD1 PSMD14 ARPC2 SNED1 GALNTL2 SLC12A8 PIK3CB PHF17 PHF15 SPARC DTNBP1 KIAA1009 ECD MEPCE ZNHIT1 ATXN7L1 ADCK2 MIR939 NFX1 ECM2 MSANTD3 ZFP37 CDK5RAP2 PSMB7 ST6GALNAC6 COL5A1 WAC TM9SF3 SLC43A1 DYNC2H1 NPAT SCN4B NTN4 MPHOSPH8 PSMB5 PSME2 C14orf149 CILP MRPL28 PPL HSD11B2 DEF8 EZH1 RPL27 LLGL2 SRSF2 MYL12B CDC37 PDCD5 PSMC4 ZNF615 ZNF766 ZNF845 ZNF525 ZNF329 CSRP2BP PHF20 EIF4ENIF1 RIPPLY1 KIAA1210 HMGB3

GOBPID Pvalue OddsRatio ExpCount Count Size Term

GO:0006521	2.95E-09	38.61307692	0.232717459	7	57	regulation of cellular amino acid metabolic process
GO:0006977	8.46E-09	32.70241199	0.269462321	7	66	"DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest"
GO:0072413	8.46E-09	32.70241199	0.269462321	7	66	signal transduction involved in mitotic cell cycle checkpoint
GO:0072431	8.46E-09	32.70241199	0.269462321	7	66	signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint
GO:0072474	8.46E-09	32.70241199	0.269462321	7	66	signal transduction involved in mitotic cell cycle G1/S checkpoint
GO:0051436	9.42E-09	32.15512821	0.273545083	7	67	negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
GO:0072401	9.42E-09	32.15512821	0.273545083	7	67	signal transduction involved in DNA integrity checkpoint

GO:0072404	9.42E-09	32.15512821	0.273545083	7	67	signal transduction involved in G1/S transition checkpoint
GO:0072422	9.42E-09	32.15512821	0.273545083	7	67	signal transduction involved in DNA damage checkpoint
GO:0072395	1.05E-08	31.62578815	0.277627846	7	68	signal transduction involved in cell cycle checkpoint
GO:0033238	1.57E-08	29.67130178	0.293958896	7	72	regulation of cellular amine metabolic process
GO:0051352	1.57E-08	29.67130178	0.293958896	7	72	negative regulation of ligase activity
GO:0051437	1.57E-08	29.67130178	0.293958896	7	72	positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
GO:0051444	1.57E-08	29.67130178	0.293958896	7	72	negative regulation of ubiquitin-protein ligase activity

GO:0031571	1.73E-08	29.21969697	0.298041658	7	73	mitotic cell cycle G1/S transition DNA damage checkpoint
GO:0002479	2.10E-08	28.35633484	0.306207183	7	75	"antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent"
GO:0051439	2.76E-08	27.15249187	0.31845547	7	78	regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
GO:0000216	3.02E-08	26.77350427	0.322538233	7	79	M/G1 transition of mitotic cell cycle
GO:0042590	3.02E-08	26.77350427	0.322538233	7	79	antigen processing and presentation of exogenous peptide antigen via MHC class I
GO:0071158	3.30E-08	26.40489989	0.326620995	7	80	positive regulation of cell cycle arrest
GO:0031575	3.93E-08	25.69717949	0.33478652	7	82	mitotic cell cycle G1/S transition checkpoint

GO:0051443	3.93E-08	25.69717949	0.33478652	7	82	positive regulation of ubiquitin-protein ligase activity
GO:0002478	4.27E-08	25.35728745	0.338869282	7	83	antigen processing and presentation of exogenous peptide antigen
GO:0031145	4.27E-08	25.35728745	0.338869282	7	83	anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process
GO:0031398	4.34E-08	18.81430219	0.51851083	8	127	positive regulation of protein ubiquitination
GO:0019884	5.05E-08	24.70364892	0.347034807	7	85	antigen processing and presentation of exogenous antigen
GO:0051351	5.48E-08	24.38924051	0.35111757	7	86	positive regulation of ligase activity
GO:0071779	5.48E-08	24.38924051	0.35111757	7	86	G1/S transition checkpoint

GO:0031397	8.76E-08	22.6581448	0.375614144	7	92	negative regulation of protein ubiquitination
GO:0051438	1.18E-07	21.63375108	0.391945194	7	96	regulation of ubiquitin-protein ligase activity
GO:0002474	1.46E-07	20.92391304	0.404193481	7	99	antigen processing and presentation of peptide antigen via MHC class I
GO:2000045	1.46E-07	20.92391304	0.404193481	7	99	regulation of G1/S transition of mitotic cell cycle
GO:0051340	1.56E-07	20.69747725	0.408276244	7	100	regulation of ligase activity
GO:0043161	1.57E-07	12.7728	0.85329735	9	209	proteasomal ubiquitin-dependent protein catabolic process
GO:0010498	2.07E-07	12.33478261	0.881876687	9	216	proteasomal protein catabolic process

GO:0048002	2.65E-07	19.04741051	0.440938343	7	108	antigen processing and presentation of peptide antigen
GO:0031396	3.78E-07	13.95294118	0.68590409	8	168	regulation of protein ubiquitination
GO:0030330	4.59E-07	17.47797203	0.477683205	7	117	"DNA damage response, signal transduction by p53 class mediator"
GO:0000075	5.41E-07	10.93828326	0.98802851	9	242	cell cycle checkpoint
GO:0072331	6.44E-07	16.56697613	0.50217978	7	123	signal transduction by p53 class mediator
GO:0000082	8.20E-07	12.52610707	0.759393814	8	186	G1/S transition of mitotic cell cycle
GO:0000077	9.37E-07	15.61647905	0.530759117	7	130	DNA damage checkpoint

GO:0071156	1.12E-06	9.979058824	1.077849284	9	264	regulation of cell cycle arrest
GO:0000084	1.15E-06	15.12038159	0.547090167	7	134	S phase of mitotic cell cycle
GO:0031570	1.27E-06	14.88387001	0.555255692	7	136	DNA integrity checkpoint
GO:0007093	1.47E-06	14.54254079	0.567503979	7	139	mitotic cell cycle checkpoint
GO:0042770	1.54E-06	14.43218623	0.571586741	7	140	signal transduction in response to DNA damage
GO:0051320	1.78E-06	14.11085973	0.583835029	7	143	S phase
GO:2000602	2.14E-06	13.70384615	0.600166078	7	147	regulation of interphase of mitotic cell cycle

GO:0090068	2.56E-06	13.31944444	0.616497128	7	151	positive regulation of cell cycle process
GO:0019882	2.68E-06	13.22665782	0.620579891	7	152	antigen processing and presentation
GO:0010565	2.92E-06	13.04487179	0.628745416	7	154	regulation of cellular ketone metabolic process
GO:0000209	3.92E-06	12.4458042	0.657324753	7	161	protein polyubiquitination
GO:0044106	9.11E-06	10.87325175	0.747145526	7	183	cellular amine metabolic process
GO:0006511	1.53E-05	7.117352113	1.486125528	9	364	ubiquitin-dependent protein catabolic process
GO:0009308	1.73E-05	9.800690335	0.824718013	7	202	amine metabolic process

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GO:0019941      1.78E-05        6.976243094     1.514704865     9       371
modification-dependent protein catabolic process

GO:0043632      1.89E-05        6.917424658     1.526953152     9       374
modification-dependent macromolecule catabolic process

Tissue: Heart_Left_Ventricle=>Lung      Type:   asymmetric

SourceGene:     KIAA1797(ENSG00000188352.7)     FOCAD focadhesin

TargetGeneSet:  RPL11   RP4     RP11    RPL5    U1      UBC     RPL31   EEF1A1P12
CYBRD1  TMEFF2  RPL37A  RPL32   RPL15   RPL24   RPL35A  RPL34   CTD     RPL37
EEF1A1P19       RPS14   RPL24P4 MRPS12  TRBV6-1 RPS20   RPL30   RPS6    STRA13  7SK
RPL13AP5        RPS13   FAU     C12orf57        AMHR2   NACA    RPL14P1 RPL3P4  U4
RPLP1   RPL26   MFAP4   RPL19   RPL27   RPS15   RPL18A  RPS16   FBL     ZNF574
RPL18   RPL13A  RPS9    KIR3DX1 RPL28   RPS5    INSM1   RPS21   H2BFS   RPL3
SLC25A6 EEF1B2P3        RPS23P8 RP3     RPL10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term

GO:0006415      1.75E-62        555.7772397     0.289668535     32      91
translational termination
```

GO:0006414	4.28E-60	448.7514677	0.334232925	32	105	translational elongation
GO:0006614	4.28E-60	448.7514677	0.334232925	32	105	SRP-dependent cotranslational protein targeting to membrane
GO:0006613	6.13E-60	442.6563707	0.337416096	32	106	cotranslational protein targeting to membrane
GO:0045047	6.13E-60	442.6563707	0.337416096	32	106	protein targeting to ER
GO:0072599	6.13E-60	442.6563707	0.337416096	32	106	establishment of protein localization to endoplasmic reticulum
GO:0070972	3.38E-58	380.5714286	0.375614144	32	118	protein localization to endoplasmic reticulum
GO:0000184	4.62E-58	376.1707718	0.378797315	32	119	"nuclear-transcribed mRNA catabolic process, nonsense-mediated decay"
GO:0019080	2.62E-54	274.4009604	0.480658778	32	151	viral genome expression

GO:0019083	2.62E-54	274.4009604	0.480658778	32	151
viral transcription					
GO:0006413	3.32E-54	272.0952381	0.483841949	32	152
translational initiation					
GO:0006612	4.19E-54	269.8276269	0.487025119	32	153
protein targeting to membrane					
GO:0043624	4.19E-54	269.8276269	0.487025119	32	153
cellular protein complex disassembly					
GO:0043241	1.32E-53	259.0294785	0.502940973	32	158
protein complex disassembly					
GO:0000956	1.42E-52	238.0479666	0.537955851	32	169
nuclear-transcribed mRNA catabolic process					
GO:0034623	3.95E-52	229.5855131	0.553871704	32	174
cellular macromolecular complex disassembly					
GO:0072594	5.13E-52	211.3009447	0.649366826	33	204
establishment of protein localization to organelle					

GO:0006402	8.77E-52	223.2328767	0.566604387	32	178	mRNA catabolic process
GO:0032984	1.07E-51	221.6987366	0.569787558	32	179	macromolecular complex disassembly
GO:0019058	4.24E-50	182.1410256	0.735312435	33	231	viral infectious cycle
GO:0006401	1.19E-49	188.0363336	0.652549997	32	205	RNA catabolic process
GO:0022415	2.71E-48	158.547611	0.827624386	33	260	viral reproductive process
GO:0071845	7.80E-45	128.3718821	0.904020483	32	284	cellular component disassembly at cellular level
GO:0022411	1.25E-44	126.3303571	0.916753166	32	288	cellular component disassembly
GO:0016032	4.49E-40	84.94129555	1.435609992	33	451	viral reproduction

GO:0033365	2.24E-39	80.56730769	1.505639748	33	473	protein localization to organelle
GO:0006605	2.41E-39	80.37885924	1.508822919	33	474	protein targeting
GO:0006364	7.88E-13	42.29018913	0.331049754	10	104	rRNA processing
GO:0016072	1.40E-12	39.73611111	0.350148779	10	110	rRNA metabolic process
GO:0042254	2.97E-11	28.50919265	0.474292437	10	149	ribosome biogenesis
GO:0022613	8.44E-11	20.84125501	0.716213411	11	225	ribonucleoprotein complex biogenesis
GO:0071843	1.61E-10	19.54223058	0.760777801	11	239	cellular component biogenesis at cellular level
GO:0034470	5.44E-10	20.78216374	0.636634143	10	200	ncRNA processing

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GO:0042274      2.17E-09        135.0093809     0.057297073     5       18
ribosomal small subunit biogenesis




GO:0034660      1.66E-08        14.27272727     0.907203654     10      285
ncRNA metabolic process




GO:0042273      4.37E-08        171.3928571     0.038198049     4       12
ribosomal large subunit biogenesis





Tissue: Heart_Left_Ventricle=>Lung      Type:   cluster
SourceGene:     RP11-110I1.11(ENSG00000254428.1)
TargetGeneSet:  FAM87B  TTC34   H6PD    PRDX3P2 LCK     CDC20   ATG4C   LEPROT
LRRC39  NRAS    GAPDHP32        JTB     PYGO2   IQGAP3  RP11    B4GALT3 POU2F1
C1orf106        SH3YL1  DHX57   STAMBP  PCGF1   IMMT    TMEM127 CKAP2L  TANC1
C2orf77 CCDC150 ALS2CR8 HJURP   MSL3P1  CRELD1  ATG7    GLYCTK  KCTD6   PDZRN3
KIAA1524        POLQ    CCNL1   SERP1   GFM1    CTA     ABCA11P PCDH7   HOPX
C4orf21 MAD2L1  OTUD4   TRIP13  NUP155  CENPH   ARSB    KIF20A  CTB     PCDHB6  RARS
TRIM27  TBCC    KLC4    SLC35B2 FAM184A SCAF8   CLDN20  TRA2A   STK17A  NPC1L1
LANCL2  STX1A   RBM48   SLC25A13        RINT1   MCM4    IMPAD1  MLLT3   PIP5K1B
C9orf85 SMC2    FKTN    FBXW2   FPGS    C9orf106        MAN1B1  RP1     CDC123
NSUN6   ZNF33A  ZWINT   CDK1    PBLD    PLA2G12B        KIF11   CEP55   ANO9    CTD
C11orf16        PARVA   PRMT3   ALKBH3  ARHGAP1 F2      DDB1    FEN1    GANAB
ZDHHC24 CDK2AP2 KDM4D   CHEK1   DSTNP2  FGFR1OP2        MED21   REP15   IPO8
TROAP   ESPL1   AVIL    NUP107  NEDD1   C12orf76        DYNLL1  RPL22P19        SKA3
FANCB   TUBGCP3 SUPT16H RNF31   FANCM   POLE2   BUB1B   CASC5   RTF1    CCNB2
KIF23   FANCI   C15orf42        PRC1    PLA2G10 FAM57B  ZNF629  CIAPIN1 DHX38
CFDP1   TMEM170A        SPG7    TMEM220 ELAC2   B9D1    ATAD5   CCT6B   GRB7
GSDMB   TOP2A   RAB5C   G6PC3   C17orf53        EFTUD2  KIF18B  TUBD1   BRIP1
GRIN2C  CHAF1A  PCP2    SPC24   TNPO2   DCAF15  ZNF493  WDR62   PPP1R13L        IRF3
CTU1    TMEM190 ZNF444  ZNF274  ZSCAN22 GINS1   TPX2    MYH7B   DHX35   RNF114
FAM207CP        UFD1L   DEPDC5  PRR5    CPT1B   MBTPS2  MED14   SUV39H1 KIF4A   ACRC
PGAM4   TMSB15B CD99L2  CLIC2
GOBPID  Pvalue  OddsRatio               ExpCount        Count   Size    Term
GO:0000087      3.41459242023721e-11    6.88313609467456        3.83641270500311
22      360     M phase of mitotic cell cycle
GO:0051301      7.54876927158181e-11    5.9823148813803 4.81682928517058        24
452     cell division
GO:0000280      1.39624192754594e-10    6.70356742921133        3.72984568541969
21      350     nuclear division
GO:0007067      1.39624192754594e-10    6.70356742921133        3.72984568541969
21      350     mitosis
GO:0048285      3.87675594808876e-10    6.31036042829136        3.94297972458653
21      370     organelle fission
GO:0007017      6.84997114978721e-09    5.57160577808011        4.1880838696284 20
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393     microtubule-based process
GO:0000226      1.8416091459656e-07     5.96626635699315        2.86665282679399
15      269     microtubule cytoskeleton organization
GO:0007059      2.9322238130853e-07     8.44841979725701        1.49193827416788
11      140     chromosome segregation
GO:0000075      3.08459887073844e-07    6.17061403508772        2.57892187391876
14      242     cell cycle checkpoint
GO:0010564      4.3275899288451e-07     4.64605614973262        4.41187461075358
18      414     regulation of cell cycle process
GO:0006261      6.290165268519e-07      10.5022167487685        0.991073282125804
9       93      DNA-dependent DNA replication
GO:0071156      8.81285201837645e-07    5.6188  2.81336931700228        14      264
regulation of cell cycle arrest
GO:0006260      1.054382882607e-06      5.52874015748031        2.85599612483565
14      268     DNA replication
GO:0051329      2.88979446412345e-06    4.45051303549327        4.03889004221161
16      379     interphase of mitotic cell cycle
GO:0006281      3.30705403402202e-06    4.40074240808751        4.08151685004498
16      383     DNA repair
GO:0000236      3.33212173069237e-06    10.1191958726205        0.905819666459069
8       85      mitotic prometaphase
GO:0051325      3.77768379451081e-06    4.35204500175788        4.12414365787835
16      387     interphase
GO:0007050      9.4456641151353e-06     4.25039629313498        3.93232302262819
15      369     cell cycle arrest
Tissue: Heart_Left_Ventricle=>Lung      Type:   asymmetric
SourceGene:     RP11-115C9.2(ENSG00000223582.1)
TargetGeneSet:  ALPL    STMN1   SDC3    CLSPN   RP11    OLFML3  PRCC    RNASEL
CSRP1   TNFSF13B        TLR5    CENPO   HAT1    TRAIP   NIT2    CCNL1   BCHE
SLIT2   CTD     SGCD    KIF13A  TCF19   RDBP    TBC1D22B        SAP25   DENND2A
ADAMDEC1        GGH     ZNF704  SMC2    CERCAM  MCM10   PARVA   FEN1    ME3
H2AFJ   DCTN2   FANCB   CAB39L  TRAV13-2        VRK1    KIF23   CHTF18  MPDU1
DUSP3   BRIP1   CDH2    CHAF1A  ZNF844  TPM4    CCNE1   GINS1   E2F1    LMF2
NCAPH2  ACOT9   SUV39H1 MAGED2  RP3     FHL1    HTATSF1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006260      4.92726359204836e-07    11.1662864162864        0.982907757248633
9       268     DNA replication
GO:0051329      9.75469589256103e-07    8.84162097434928        1.39000761192997
10      379     interphase of mitotic cell cycle
GO:0051325      1.17885522139013e-06    8.64906544938622        1.41934814199709
10      387     interphase
GO:0006323      1.33198077694893e-06    14.854675402025 0.561137637533735       7
153     DNA packaging
GO:0071103      5.43013306545825e-06    11.8862876254181        0.69317002283579
7       189     DNA conformation change
Tissue: Heart_Left_Ventricle=>Lung      Type:   asymmetric
SourceGene:     RP11-322F10.2(ENSG00000225782.1)
TargetGeneSet:  RP4     PYGO2   KRTCAP3 EPCAM   UBC     XYLB    RPL24   ALCAM   CD47
RPL35A  MRPS36  MARVELD2        RPL39P3 RP11    PPP1R35 RPS6    C9orf40 FOLR1
CARD16  SIRT4   MSI1    ENTPD5  RPS21   CLIC2
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      1.66530354802416e-07    52.1220930232558        0.132239983392153
5       91      translational termination
GO:0006414      3.41324614487545e-07    44.78125        0.152584596221715       5
105     translational elongation
GO:0006614      3.41324614487545e-07    44.78125        0.152584596221715       5
105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      3.57890162989507e-07    44.3347772277228        0.154037782852398
5       106     cotranslational protein targeting to membrane
GO:0045047      3.57890162989507e-07    44.3347772277228        0.154037782852398
5       106     protein targeting to ER
GO:0072599      3.57890162989507e-07    44.3347772277228        0.154037782852398
5       106     establishment of protein localization to endoplasmic reticulum
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GO:0070972      6.11059274672063e-07    39.5934734513274        0.171476022420594
5       118     protein localization to endoplasmic reticulum
GO:0000184      6.37269221328044e-07    39.2434210526316        0.17292920905127
5       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      2.07252023160669e-06    30.5736301369863        0.219431181233133
5       151     viral genome expression
GO:0019083      2.07252023160669e-06    30.5736301369863        0.219431181233133
5       151     viral transcription
GO:0006413      2.14102678163662e-06    30.3635204081633        0.220884367863816
5       152     translational initiation
GO:0006612      2.21130613221479e-06    30.15625        0.222337554494499       5
153     protein targeting to membrane
GO:0043624      2.21130613221479e-06    30.15625        0.222337554494499       5
153     cellular protein complex disassembly
GO:0043241      2.59046790562861e-06    29.1605392156863        0.229603487647914
5       158     protein complex disassembly
GO:0000956      3.60508079251103e-06    27.1836890243902        0.245588540585427
5       169     nuclear-transcribed mRNA catabolic process
GO:0034623      4.15875560962841e-06    26.3701923076923        0.252854473738842
5       174     cellular macromolecular complex disassembly
GO:0006402      4.64809310483942e-06    25.7532514450867        0.258667220261574
5       178     mRNA catabolic process
GO:0032984      4.77722089716488e-06    25.6034482758621        0.260120406892257
5       179     macromolecular complex disassembly
GO:0072594      9.03640818071238e-06    22.347675879397 0.296450072659332       5
204     establishment of protein localization to organelle
GO:0006401      9.25371449781464e-06    22.234375       0.297903259290015       5
205     RNA catabolic process
GO:0019058      1.65016098367336e-05    19.6404867256637        0.335686111687772
5       231     viral infectious cycle
Tissue: Heart_Left_Ventricle=>Lung      Type:   asymmetric
SourceGene:     RP11-469M7.1(ENSG00000260006.1)
TargetGeneSet:  EXOSC10 DHDDS   IPP     RP11    TMED5   NRAS    GAPDHP32        ECM1
BGLAP   POU2F1  TARBP1  DDX1    DHX57   ANKRD36 PSMD14  SPC25   THUMPD3 MAP4
TRAIP   FAM116A PSMC1P1 POLQ    KALRN   CCNL1   ACTG1P1 PSMD2   CTA     FAM200B
TRIP13  NUP155  AP3B1   CTB     ANXA6   RARS    MDC1    SLC35B2 MMS22L  RP1
LPAL2   BET1    SAP25   RINT1   U1      ZDHHC2  WRN     MAL2    VCP     FBXW2
ITGB1   ZNF33A  PBLD    SFTPA2  SMPD1   PARVA   FEN1    C11orf75        GUCY1A2
RPL23AP64       RNF26   CHEK1   RAD52   MED21   NUP107  NEDD1   UBL3    FANCB
FANCM   POLE2   PLEKHG3 LRRC57  TPM1    KBTBD13 KIAA1199        FANCI   PRC1
GDPD3   ZNF629  DHX38   TMEM170A        ELAC2   ATAD5   CCT6B   KIF18B  TUBD1
BRIP1   ATP5A1  HAUS1   DSEL    CHAF1A  S1PR2   SPC24   SLC7A9  ZNF615  CDK5RAP1
MYH9    MBTPS2  SUV39H1 LONRF3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006281      1.96003099635743e-09    8.91898777173913        2.09376513736074
15      383     DNA repair
GO:0006302      4.15365138271882e-09    19.7405529953917        0.557608470002076
9       102     double-strand break repair
GO:0006310      1.95112202809718e-07    10.3218993518316        1.14255068853367
10      209     DNA recombination
GO:0045005      3.96064953679518e-07    95.76   0.0656009964708325      4       12
maintenance of fidelity involved in DNA-dependent DNA replication
GO:0006261      7.23288120010436e-07    16.1501937984496        0.508407722648952
7       93      DNA-dependent DNA replication
GO:0006260      1.90186696360858e-06    7.92832266037524        1.46508892118193
10      268     DNA replication
GO:0031297      5.4176636865537e-06     141.789473684211        0.0382672479413189
3       7       replication fork processing
GO:0000724      1.00390326144296e-05    20.1632882882883        0.289737734412843
5       53      double-strand break repair via homologous recombination
GO:0000725      1.10163471052765e-05    19.7504136789851        0.295204484118746
5       54      recombinational repair
GO:0051320      1.28279379400116e-05    10.1768790849673        0.781745207944087
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7       143     S phase
Tissue: Heart_Left_Ventricle=>Lung      Type:   asymmetric
SourceGene:     RP11-705O3.1(ENSG00000246174.2)
TargetGeneSet:  RP11    TIGD2   GYPA    PCDHA5  TDP2    ABHD11  DEFA4   DEFA3
FAM108B1        MS4A3   TMEM121 MPO     CST2    RHOT1P2
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0050832      1.89422397636428e-07    424.264705882353        0.0124558854058543
3       20      defense response to fungus
GO:0009620      9.02902190532709e-07    240.2   0.0205522109196595      3       33
response to fungus
Tissue: Heart_Left_Ventricle=>Lung      Type:   asymmetric
SourceGene:     RP11-723D22.3(ENSG00000253829.1)
TargetGeneSet:  RPL11   7SK     RP4     RPL5    OCLM    ASXL2   UBC     RPL15   RP11
USP4    SLCO2A1 RPL35A  RPL34   RPS14   RPS10   RPL10A  MRPS12  KRIT1   IMMP2L  CTD
RPL30   RPS6    GKAP1   HSD17B3 SNORD90 LRRC8A  RPS24   RPL13AP5        C10orf12
PTPRE   RPS13   PRDX5   FAU     PFDN5   RBMS1P1 MDM2    CHST11  ESD     RPS3AP6
RPLP1   NFATC2IP        CDYL2   ALOX15B RPL26   FOXO3B  RFFL    RPL17   RPL27
ZNF813  RPS9    NCOA3   ARFGEF2 MID2
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      2.5603980931057e-31     151.313888888889        0.277074250916892
19      91      translational termination
GO:0006414      5.05762996742098e-30    126.557674418605        0.31970105875026
19      105     translational elongation
GO:0006614      5.05762996742098e-30    126.557674418605        0.31970105875026
19      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      6.1519748877624e-30     125.094252873563        0.322745830738357
19      106     cotranslational protein targeting to membrane
GO:0045047      6.1519748877624e-30     125.094252873563        0.322745830738357
19      106     protein targeting to ER
GO:0072599      6.1519748877624e-30     125.094252873563        0.322745830738357
19      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      5.56638703863715e-29    109.839191919192        0.35928309459553
19      118     protein localization to endoplasmic reticulum
GO:0000184      6.61303269373228e-29    108.7332        0.362327866583627       19
119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      8.09971816547013e-27    82.1893939393939        0.459760570202754
19      151     viral genome expression
GO:0019083      8.09971816547013e-27    82.1893939393939        0.459760570202754
19      151     viral transcription
GO:0006413      9.24146203052846e-27    81.5657142857143        0.462805342190852
19      152     translational initiation
GO:0006612      1.0534310133535e-26     80.9513432835821        0.46585011417895
19      153     protein targeting to membrane
GO:0043624      1.0534310133535e-26     80.9513432835821        0.46585011417895
19      153     cellular protein complex disassembly
GO:0043241      2.00007357656436e-26    78.0120863309352        0.481073974119438
19      158     protein complex disassembly
GO:0072594      5.01990939016781e-26    64.4157608695652        0.621133485571933
20      204     establishment of protein localization to organelle
GO:0000956      7.61359271306488e-26    72.2354666666667        0.514566465988513
19      169     nuclear-transcribed mRNA catabolic process
GO:0034623      1.35576286702987e-25    69.8807741935484        0.529790325929001
19      174     cellular macromolecular complex disassembly
GO:0006402      2.12402765554839e-25    68.1036477987421        0.541969413881392
19      178     mRNA catabolic process
GO:0032984      2.37230667119594e-25    67.67325        0.54501418586949        19
179     macromolecular complex disassembly
GO:0006401      3.40229111940558e-24    58.107311827957 0.62417825756003        19
205     RNA catabolic process
GO:0019058      3.47933016120422e-23    50.8877358490566        0.703342329250571
19      231     viral infectious cycle
GO:0022415      3.42058338548897e-22    44.6728630705394        0.791640716905404
19      260     viral reproductive process
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GO:0071845      1.86427534219837e-21    40.5581886792453        0.864715244619749
19      284     cellular component disassembly at cellular level
GO:0022411      2.43672401642247e-21    39.9437918215613        0.87689433257214
19      288     cellular component disassembly
GO:0033365      4.22101928156436e-20    28.1892073874567        1.44017715037022
21      473     protein localization to organelle
GO:0006605      1.18992594108223e-18    25.6112334801762        1.44322192235831
20      474     protein targeting
GO:0016032      1.1618245029038e-17     24.5856481481481        1.37319216663207
19      451     viral reproduction
GO:0006364      2.51065623580698e-08    27.9102814154361        0.316656286762162
7       104     rRNA processing
GO:0042273      3.63450224529092e-08    179.9875        0.0365372638571725      4
12      ribosomal large subunit biogenesis
GO:0016072      3.71045693642895e-08    26.2734190501181        0.334924918690748
7       110     rRNA metabolic process
GO:0042254      2.99457733795892e-07    19.0055196041112        0.453671026226559
7       149     ribosome biogenesis
GO:0022613      3.33587853221997e-07    14.531490015361 0.685073697321985       8
225     ribonucleoprotein complex biogenesis
GO:0071843      5.27937993328423e-07    13.6373256373256        0.727700505155353
8       239     cellular component biogenesis at cellular level
GO:0034470      2.17447811327912e-06    13.933342669094 0.608954397619542       7
200     ncRNA processing
Tissue: Heart_Left_Ventricle=>Lung      Type:   asymmetric
SourceGene:     RP3-322G13.7(ENSG00000234832.1)
TargetGeneSet:  RP11    SNORA55 CYP4Z2P ITGB5-AS1       MSMO1   SAP30   CTD
HMGCS1  PCDHB9  PPP1R16A        RP13    UPF3AP3 IKZF5   NTN4    MAP1LC3B2
ZDHHC20-IT1     C14orf1 MVD     CYCS    RBBP9   RPL36P4 MT
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0016126      1.138892003711e-07      127.928888888889        0.0474707632689779
4       49      sterol biosynthetic process
GO:0016125      4.10560577174981e-06    49.815652173913 0.115286139367518       4
119     sterol metabolic process
GO:0006694      7.8338182759668e-06     42.0617647058824        0.13563075219708
4       140     steroid biosynthetic process
GO:0006695      8.7311967723947e-06     98.1613636363636        0.0416580167462459
3       43      cholesterol biosynthetic process
Tissue: Lung=>Heart_Left_Ventricle      Type:   asymmetric
SourceGene:     RP4-604G5.1(ENSG00000237640.1)
TargetGeneSet:  KLHL17  NPPB    RP11    GDI2P2  DPYD-AS1        ATXN7L2 MYOC
PFN1P1  MIR4426 FTH1P2  ZNF692  DPY30   GALNT3  RPL37A  ILKAP   PDCD6IP RPL7AP11
EEF1A1P25       RAP2B   CXCL5   TMSB4XP8        TNIP3   CTD     RPS23   FAM193B
GTF2H4  LYPLA2P1        RPL24P4 RP1     RPL23P8 EGFR    PDGFRL  FAM160B2
KIAA1875        ADCK5   ROR2    SKA2L   C9orf114        C10orf62        C11orf10
MIR1304 NOP2    EEF1A1P33       AAAS    TESPA1  RPL41   SPPL3   PUS1    RPS11P5
RPS29   CASC5   C16orf79        IRX6    YWHAE   GLP2R   PRR11   INTS2   RPL38
SLC38A10        CCDC137 NCLN    SNRPEP4 C19orf79        QTRT1   TRMT1   AP1M1
GRIK5   RP4     RPL24P2 C20orf24        RPS21   UCKL1   NCAM2   CTA     SGSM3
MAPK8IP2        PSMA6P2 PRICKLE3        PGAM4   FAM199X RP3     FTH1P8
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0070972      9.71104964429525e-08    22.534009009009 0.383779669227043       7
118     protein localization to endoplasmic reticulum
GO:0006415      4.60459441584333e-07    24.6525107604017        0.295965677115771
6       91      translational termination
GO:0019080      5.24239948151167e-07    17.3298611111111        0.491107881807487
7       151     viral genome expression
GO:0019083      5.24239948151167e-07    17.3298611111111        0.491107881807487
7       151     viral transcription
GO:0006414      1.07442747741021e-06    21.1456023651146        0.341498858210504
6       105     translational elongation
GO:0006614      1.07442747741021e-06    21.1456023651146        0.341498858210504
6       105     SRP-dependent cotranslational protein targeting to membrane
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GO:0006613      1.13612011101643e-06    20.9326829268293        0.3447512282887 6
106     cotranslational protein targeting to membrane
GO:0045047      1.13612011101643e-06    20.9326829268293        0.3447512282887 6
106     protein targeting to ER
GO:0072599      1.13612011101643e-06    20.9326829268293        0.3447512282887 6
106     establishment of protein localization to endoplasmic reticulum
GO:0000184      2.23897097097223e-06    18.507662421757 0.387032039305238       6
119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019058      8.88767604249368e-06    11.078125       0.75129748806311        7
231     viral infectious cycle
GO:0006413      9.22796613593862e-06    14.2913464751086        0.494360251885683
6       152     translational initiation
GO:0006612      9.58122597442802e-06    14.1931309109009        0.497612621963878
6       153     protein targeting to membrane
GO:0043624      9.58122597442802e-06    14.1931309109009        0.497612621963878
6       153     cellular protein complex disassembly
GO:0043241      1.15159550618145e-05    13.7214377406932        0.513874472354854
6       158     protein complex disassembly
GO:0016032      1.2308528359795e-05     7.48142414860681        1.46681890526607
9       451     viral reproduction
GO:0000956      1.68955941365674e-05    12.785575340416 0.549650543215002       6
169     nuclear-transcribed mRNA catabolic process
GO:0022415      1.91468811180636e-05    9.78824110671937        0.845616220330773
7       260     viral reproductive process
GO:0034623      1.99335748672826e-05    12.4006968641115        0.565912393605979
6       174     cellular macromolecular complex disassembly
Tissue: Lung=>Heart_Left_Ventricle      Type:   cluster
SourceGene:     RP4-604G5.1(ENSG00000237640.1)
TargetGeneSet:  KLHL17  NPPB    RP11    GDI2P2  DPYD-AS1        ATXN7L2 MYOC
PFN1P1  MIR4426 FTH1P2  ZNF692  DPY30   GALNT3  RPL37A  ILKAP   PDCD6IP RPL7AP11
EEF1A1P25       RAP2B   CXCL5   TMSB4XP8        TNIP3   CTD     RPS23   FAM193B
GTF2H4  LYPLA2P1        RPL24P4 RP1     RPL23P8 EGFR    PDGFRL  FAM160B2
KIAA1875        ADCK5   ROR2    SKA2L   C9orf114        C10orf62        C11orf10
MIR1304 NOP2    EEF1A1P33       AAAS    TESPA1  RPL41   SPPL3   PUS1    RPS11P5
RPS29   CASC5   C16orf79        IRX6    YWHAE   GLP2R   PRR11   INTS2   RPL38
SLC38A10        CCDC137 NCLN    SNRPEP4 C19orf79        QTRT1   TRMT1   AP1M1
GRIK5   RP4     RPL24P2 C20orf24        RPS21   UCKL1   NCAM2   CTA     SGSM3
MAPK8IP2        PSMA6P2 PRICKLE3        PGAM4   FAM199X RP3     FTH1P8
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0070972      9.71104964429525e-08    22.534009009009 0.383779669227043       7
118     protein localization to endoplasmic reticulum
GO:0006415      4.60459441584333e-07    24.6525107604017        0.295965677115771
6       91      translational termination
GO:0019080      5.24239948151167e-07    17.3298611111111        0.491107881807487
7       151     viral genome expression
GO:0019083      5.24239948151167e-07    17.3298611111111        0.491107881807487
7       151     viral transcription
GO:0006414      1.07442747741021e-06    21.1456023651146        0.341498858210504
6       105     translational elongation
GO:0006614      1.07442747741021e-06    21.1456023651146        0.341498858210504
6       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.13612011101643e-06    20.9326829268293        0.3447512282887 6
106     cotranslational protein targeting to membrane
GO:0045047      1.13612011101643e-06    20.9326829268293        0.3447512282887 6
106     protein targeting to ER
GO:0072599      1.13612011101643e-06    20.9326829268293        0.3447512282887 6
106     establishment of protein localization to endoplasmic reticulum
GO:0000184      2.23897097097223e-06    18.507662421757 0.387032039305238       6
119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019058      8.88767604249368e-06    11.078125       0.75129748806311        7
231     viral infectious cycle
GO:0006413      9.22796613593862e-06    14.2913464751086        0.494360251885683
6       152     translational initiation
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GO:0006612      9.58122597442802e-06    14.1931309109009        0.497612621963878
6       153     protein targeting to membrane
GO:0043624      9.58122597442802e-06    14.1931309109009        0.497612621963878
6       153     cellular protein complex disassembly
GO:0043241      1.15159550618145e-05    13.7214377406932        0.513874472354854
6       158     protein complex disassembly
GO:0016032      1.2308528359795e-05     7.48142414860681        1.46681890526607
9       451     viral reproduction
GO:0000956      1.68955941365674e-05    12.785575340416 0.549650543215002       6
169     nuclear-transcribed mRNA catabolic process
GO:0022415      1.91468811180636e-05    9.78824110671937        0.845616220330773
7       260     viral reproductive process
GO:0034623      1.99335748672826e-05    12.4006968641115        0.565912393605979
6       174     cellular macromolecular complex disassembly
Tissue: Lung=>Heart_Left_Ventricle      Type:   asymmetric


SourceGene:     VENTXP6(ENSG00000254105.1)      VENT homeobox pseudogene 6



TargetGeneSet:  LIMS1   NDUFB3  CNPPD1  RP11    RP1     LSM5    SDHDP2  RPL8
RPS13   EEF1A1P33       RPS29   RPS17L  RPL38   ELMO2   ALG12   MED14-AS1

GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term


GO:0000956      3.75E-09        75.06573181     0.152031001     6       169
nuclear-transcribed mRNA catabolic process


GO:0006402      5.13E-09        71.09302326     0.160127327     6       178     mRNA
catabolic process


GO:0006415      1.10E-08        104.3023256     0.081862847     5       91
translational termination


GO:0006401      1.20E-08        61.33094042     0.184416303     6       205     RNA
catabolic process


GO:0006414      2.26E-08        89.6125 0.094457131     5       105
translational elongation


GO:0006614      2.26E-08        89.6125 0.094457131     5       105
SRP-dependent cotranslational protein targeting to membrane


GO:0006613      2.37E-08        88.71905941     0.095356723     5       106
cotranslational protein targeting to membrane


GO:0045047      2.37E-08        88.71905941     0.095356723     5       106
protein targeting to ER


GO:0072599      2.37E-08        88.71905941     0.095356723     5       106
establishment of protein localization to endoplasmic reticulum
```

GO:0070972	4.07E-08	79.23119469	0.106151823	5	118	protein localization to endoplasmic reticulum
GO:0000184	4.25E-08	78.53070175	0.107051415	5	119	"nuclear-transcribed mRNA catabolic process, nonsense-mediated decay"
GO:0019080	1.40E-07	61.18150685	0.13583835	5	151	viral genome expression
GO:0019083	1.40E-07	61.18150685	0.13583835	5	151	viral transcription
GO:0006413	1.45E-07	60.76105442	0.136737942	5	152	translational initiation
GO:0006612	1.50E-07	60.34628378	0.137637534	5	153	protein targeting to membrane
GO:0043624	1.50E-07	60.34628378	0.137637534	5	153	cellular protein complex disassembly
GO:0043241	1.76E-07	58.35375817	0.142135492	5	158	protein complex disassembly
GO:0034623	2.84E-07	52.76997041	0.15652896	5	174	cellular macromolecular complex disassembly
GO:0032984	3.27E-07	51.23563218	0.161026919	5	179	macromolecular complex disassembly
GO:0072594	6.27E-07	44.72047739	0.183516712	5	204	establishment of protein localization to organelle
GO:0019058	1.16E-06	39.30309735	0.207805688	5	231	viral infectious cycle
GO:0022415	2.08E-06	34.7622549	0.233893848	5	260	viral reproductive process
GO:0071845	3.20E-06	31.71818996	0.25548405	5	284	cellular component disassembly at cellular level
GO:0022411	3.43E-06	31.2610424	0.259082416	5	288	cellular component disassembly

Tissue: Lung=>Muscle_Skeletal Type: asymmetric
SourceGene: CALR(ENSG00000179218.6)
TargetGeneSet: C1orf192 C2orf44 OLA1 SNORD19B RP11 PCNP

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SLC41A3 TBCA    DEK     CSNK2B  NT5C3   ZKSCAN5 EIF3E   EIF3F   RPL27A  RPS13
KDM5A   CLEC4A  VPS29   RPLP0   TPT1    RNASEH2B        C14orf132       RPAP1   MGA
SPG11   RPS15A  DNAJC7  SDK2    CTD     IER3IP1 RPSAP58 ZNF526  ZNF765  ZSWIM1
PRR14L  C22orf32        RPL10   EIF1AY
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006413      9.23058599239458e-09    34.4665517241379        0.283994187253477
7       152     translational initiation
GO:0000184      7.05889254764862e-08    36.1845764854614        0.222337554494499
6       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006401      7.28458370460635e-08    25.1469696969697        0.383018476230019
7       205     RNA catabolic process
GO:0000956      5.65205978561604e-07    24.9973707274321        0.315756695038406
6       169     nuclear-transcribed mRNA catabolic process
GO:0006415      6.41277891250554e-07    37.8911205073996        0.170022835789911
5       91      translational termination
GO:0006402      7.66472280893686e-07    23.6744186046512        0.332572140336309
6       178     mRNA catabolic process
GO:0006414      1.3080209252186e-06     32.5545454545455        0.196180195142205
5       105     translational elongation
GO:0006614      1.3080209252186e-06     32.5545454545455        0.196180195142205
5       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.3710283642215e-06     32.2299729972997        0.198048577953083
5       106     cotranslational protein targeting to membrane
GO:0045047      1.3710283642215e-06     32.2299729972997        0.198048577953083
5       106     protein targeting to ER
GO:0072599      1.3710283642215e-06     32.2299729972997        0.198048577953083
5       106     establishment of protein localization to endoplasmic reticulum
GO:0070972      2.33117693976938e-06    28.783185840708 0.220469171683621       5
118     protein localization to endoplasmic reticulum
GO:0019058      3.49388704343774e-06    18.0304761904762        0.43159642931285
6       231     viral infectious cycle
GO:0022415      6.89985689854706e-06    15.9392575928009        0.485779530828316
6       260     viral reproductive process
GO:0019080      7.81678864797814e-06    22.2260273972603        0.282125804442599
5       151     viral genome expression
GO:0019083      7.81678864797814e-06    22.2260273972603        0.282125804442599
5       151     viral transcription
GO:0006612      8.33446558546097e-06    21.9226044226044        0.285862570064355
5       153     protein targeting to membrane
GO:0043624      8.33446558546097e-06    21.9226044226044        0.285862570064355
5       153     cellular protein complex disassembly
GO:0043241      9.74664991833363e-06    21.198752228164 0.295204484118746       5
158     protein complex disassembly
GO:0016032      1.42153456865043e-05    11.0202702702703        0.842640647706041
7       451     viral reproduction
GO:0034623      1.55609181597683e-05    19.170252824099 0.325098609092796       5
174     cellular macromolecular complex disassembly
GO:0032984      1.78441369704505e-05    18.6128526645768        0.334440523147187
5       179     macromolecular complex disassembly
Tissue: Muscle_Skeletal=>Lung   Type:   asymmetric
SourceGene:     CTD-3064C13.1(ENSG00000255372.1)
TargetGeneSet:  RPL22   RPL5    RP11    RPL15   DNAJC13 KLHL24  HMGCS1  BTF3    CTB
RPS14   RP3     RPL10A  EEF1A1  RAC1    TOMM7   UQCRB   EIF3H   EEF1D   IDI2-AS1
PFN1P11 RPS13   CTSF    DHCR7   IL18BP  B3GAT1  TPT1    GZMH    MAPKBP1 RPL4
ANKFY1  RPS11   PNPLA4
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      2.0142792696908e-15     88.7244582043344        0.196180195142205
10      105     translational elongation
GO:0006415      3.63613987228667e-12    72.7507926442613        0.170022835789911
8       91      translational termination
GO:0006413      4.95086588893475e-12    49.9335664335664        0.283994187253477
9       152     translational initiation
GO:0006614      1.17345503194058e-11    62.1899077590884        0.196180195142205
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8       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.26775622401036e-11    61.5510204081633        0.198048577953083
8       106     cotranslational protein targeting to membrane
GO:0045047      1.26775622401036e-11    61.5510204081633        0.198048577953083
8       106     protein targeting to ER
GO:0072599      1.26775622401036e-11    61.5510204081633        0.198048577953083
8       106     establishment of protein localization to endoplasmic reticulum
GO:0070972      3.03203010637571e-11    54.7904306220096        0.220469171683621
8       118     protein localization to endoplasmic reticulum
GO:0000184      3.24673383521069e-11    54.2930298719772        0.222337554494499
8       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0072594      7.01935279172028e-11    36.4846153846154        0.381150093419141
9       204     establishment of protein localization to organelle
GO:0019080      2.21326302210561e-10    42.0493191019507        0.282125804442599
8       151     viral genome expression
GO:0019083      2.21326302210561e-10    42.0493191019507        0.282125804442599
8       151     viral transcription
GO:0006612      2.45931590628955e-10    41.4635208711434        0.285862570064355
8       153     protein targeting to membrane
GO:0043624      2.45931590628955e-10    41.4635208711434        0.285862570064355
8       153     cellular protein complex disassembly
GO:0043241      3.1811205942258e-10     40.0673684210526        0.295204484118746
8       158     protein complex disassembly
GO:0000956      5.44445628484361e-10    37.3010787839163        0.315756695038406
8       169     nuclear-transcribed mRNA catabolic process
GO:0034623      6.86790688362788e-10    36.1648700063412        0.325098609092796
8       174     cellular macromolecular complex disassembly
GO:0006402      8.22921123361849e-10    35.3040247678019        0.332572140336309
8       178     mRNA catabolic process
GO:0032984      8.6040489338959e-10     35.0951061865189        0.334440523147187
8       179     macromolecular complex disassembly
GO:0006401      2.52017424606074e-09    30.4076943628106        0.383018476230019
8       205     RNA catabolic process
GO:0019058      6.4533641082341e-09     26.8133113051688        0.43159642931285
8       231     viral infectious cycle
GO:0022415      1.62842937280258e-08    23.6791979949875        0.485779530828316
8       260     viral reproductive process
GO:0071845      3.23747950135079e-08    21.58352402746  0.530620718289392       8
284     cellular component disassembly at cellular level
GO:0022411      3.60866072584282e-08    21.2691729323308        0.538094249532904
8       288     cellular component disassembly
GO:0016032      7.37343343458781e-08    15.816742081448 0.842640647706041       9
451     viral reproduction
GO:0033365      1.10786645196307e-07    15.0431034482759        0.88374506954536
9       473     protein localization to organelle
GO:0006605      1.12801165729686e-07    15.0096774193548        0.885613452356238
9       474     protein targeting
Tissue: Lung=>Muscle_Skeletal   Type:   asymmetric
SourceGene:     DCTN1(ENSG00000204843.7)
TargetGeneSet:  GNL2    C1orf109        DPH2    SORT1   LRIF1   PFDN2   PAPPA2
TIMM17A BROX    SRSF7   PSME4   RAB1A   CNNM3   MKI67IP NUP35   ANKAR   MARS2
C2orf47 PPIL3   WDR12   STK36   RAMP1   LSM3    ARF4    MITF    CCDC58  ABTB1   UBA5
USP13   GRPEL1  GPR125  ATP8A1  OCIAD1  PAICS   EGF     GAB1    ANAPC10 CLPTM1L
BRIX1   C5orf43 SRFBP1  PPP2CA  HSPA9   MRPL22  PAK1IP1 TPMT    HLA-DMA PPIL1
MAD2L1BP        PHF3    NDUFAF4 HECA    LTV1    MALSU1  FKBP14  GGCT    GATSL2
ASB15   MKRN1   SORBS3  FAM219A DNAJB5  SEC61B  MRPL50  DPM2    ZER1    ZNF25
TIMM23  PPIF    PGAM1   MXI1    RP11    HIPK3   FIBP    DNAJB13 TMEM126A
ARHGAP42        NOP2    DTX3    CDK4    CTDSP2  CCT2    COX6A1  TBC1D4  ZBTB25
BCRP2   COX16   CINP    CTD     UNKL    C16orf91        IFT140  NPIPP1  MPHOSPH6
TIMM22  ANKFY1  C1QBP   ATP1B2  ERAL1   MAP3K3  DDX5    MEP1B   MRPL4   ANKRD27
TIMM50  SRSF6   SDC4    ATP5E   FBXW11P1        C21orf33        RP3     PLA2G6
NHP2L1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
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GO:0006457      1.34450967259763e-07    9.26133254015467        1.39007681129334
11      216     protein folding
GO:0022613      1.79241599838792e-06    7.92546931913701        1.44799667843056
10      225     ribonucleoprotein complex biogenesis
GO:0071843      3.0822405348495e-06     7.43357710317252        1.5380942495329 10
239     cellular component biogenesis at cellular level
GO:0006839      4.65300458254365e-06    11.966794533685 0.669296242474569       7
104     mitochondrial transport
GO:0042254      5.14077077224417e-06    9.48986232790989        0.958895578160681
8       149     ribosome biogenesis
GO:0006626      1.84154687313195e-05    17.6778656126482        0.32821258044426
5       51      protein targeting to mitochondrion
Tissue: Lung=>Muscle_Skeletal   Type:   cluster
SourceGene:     DCTN1(ENSG00000204843.7)
TargetGeneSet:  GNL2    C1orf109        DPH2    SORT1   LRIF1   PFDN2   PAPPA2
TIMM17A BROX    SRSF7   PSME4   RAB1A   CNNM3   MKI67IP NUP35   ANKAR   MARS2
C2orf47 PPIL3   WDR12   STK36   RAMP1   LSM3    ARF4    MITF    CCDC58  ABTB1   UBA5
USP13   GRPEL1  GPR125  ATP8A1  OCIAD1  PAICS   EGF     GAB1    ANAPC10 CLPTM1L
BRIX1   C5orf43 SRFBP1  PPP2CA  HSPA9   MRPL22  PAK1IP1 TPMT    HLA-DMA PPIL1
MAD2L1BP        PHF3    NDUFAF4 HECA    LTV1    MALSU1  FKBP14  GGCT    GATSL2
ASB15   MKRN1   SORBS3  FAM219A DNAJB5  SEC61B  MRPL50  DPM2    ZER1    ZNF25
TIMM23  PPIF    PGAM1   MXI1    RP11    HIPK3   FIBP    DNAJB13 TMEM126A
ARHGAP42        NOP2    DTX3    CDK4    CTDSP2  CCT2    COX6A1  TBC1D4  ZBTB25
BCRP2   COX16   CINP    CTD     UNKL    C16orf91        IFT140  NPIPP1  MPHOSPH6
TIMM22  ANKFY1  C1QBP   ATP1B2  ERAL1   MAP3K3  DDX5    MEP1B   MRPL4   ANKRD27
TIMM50  SRSF6   SDC4    ATP5E   FBXW11P1        C21orf33        RP3     PLA2G6
NHP2L1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006457      1.34450967259763e-07    9.26133254015467        1.39007681129334
11      216     protein folding
GO:0022613      1.79241599838792e-06    7.92546931913701        1.44799667843056
10      225     ribonucleoprotein complex biogenesis
GO:0071843      3.0822405348495e-06     7.43357710317252        1.5380942495329 10
239     cellular component biogenesis at cellular level
GO:0006839      4.65300458254365e-06    11.966794533685 0.669296242474569       7
104     mitochondrial transport
GO:0042254      5.14077077224417e-06    9.48986232790989        0.958895578160681
8       149     ribosome biogenesis
GO:0006626      1.84154687313195e-05    17.6778656126482        0.32821258044426
5       51      protein targeting to mitochondrion
Tissue: Muscle_Skeletal=>Lung   Type:   asymmetric
SourceGene:     EIF1AY(ENSG00000198692.5)
TargetGeneSet:  EIF2B4  UBC     DYSF    IL18RAP LIPA    CXCR1   TBC1D5  ALAS1
RPL24   TMED10P2        UTS2D   RP11    BTF3    NSA2    TBCA    KRT8P32 ETF1
PCDHGB7 RPS14   SRPK1   SKAP2   IMPDH1  EEF1D   BAAT    EDF1    RPL27A  SBF2    CTSF
RPL36A  TARSL2  C16orf5 RPL17   CALR    FFAR2   SNRPD2  RPL18   RPL13A
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      1.67918420777686e-11    57.574297188755 0.201508546121376       8
91      translational termination
GO:0006414      5.39567704313388e-11    49.2164948453608        0.23250986090928
8       105     translational elongation
GO:0000184      1.48643933171072e-10    42.966966966967 0.263511175697184       8
119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006413      1.05747743506729e-09    33.0439814814815        0.336585703411529
8       152     translational initiation
GO:0043624      1.11416252329696e-09    32.8137931034483        0.338800083039236
8       153     cellular protein complex disassembly
GO:0043241      1.43893936799346e-09    31.7088888888889        0.349871981177773
8       158     protein complex disassembly
GO:0000956      2.45436106968739e-09    29.51966873706  0.374230157082555       8
169     nuclear-transcribed mRNA catabolic process
GO:0006614      2.53183530314578e-09    40.9171428571429        0.23250986090928
7       105     SRP-dependent cotranslational protein targeting to membrane
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GO:0006613      2.70673351802074e-09    40.5010101010101        0.234724240536987
7       106     cotranslational protein targeting to membrane
GO:0045047      2.70673351802074e-09    40.5010101010101        0.234724240536987
7       106     protein targeting to ER
GO:0072599      2.70673351802074e-09    40.5010101010101        0.234724240536987
7       106     establishment of protein localization to endoplasmic reticulum
GO:0034623      3.0912646162229e-09     28.6204819277108        0.385302055221092
8       174     cellular macromolecular complex disassembly
GO:0006402      3.69940779345068e-09    27.9392156862745        0.394159573731922
8       178     mRNA catabolic process
GO:0032984      3.86671722201437e-09    27.7738791423002        0.396373953359629
8       179     macromolecular complex disassembly
GO:0070972      5.74981541988534e-09    36.0922522522523        0.261296796069476
7       118     protein localization to endoplasmic reticulum
GO:0006401      1.1234998341734e-08     24.0642978003384        0.453947823680022
8       205     RNA catabolic process
GO:0019058      2.85383685772976e-08    21.219730941704 0.511521694000415       8
231     viral infectious cycle
GO:0019080      3.19859803578109e-08    27.7569444444444        0.334371323783821
7       151     viral genome expression
GO:0019083      3.19859803578109e-08    27.7569444444444        0.334371323783821
7       151     viral transcription
GO:0006612      3.50308231415754e-08    27.3728767123288        0.338800083039236
7       153     protein targeting to membrane
GO:0022415      7.13683891621245e-08    18.739417989418 0.575738703203931       8
260     viral reproductive process
GO:0071845      1.40834573230078e-07    17.0809178743961        0.628883814268909
8       284     cellular component disassembly at cellular level
GO:0022411      1.56786621481419e-07    16.8321428571429        0.637741332779738
8       288     cellular component disassembly
GO:0072594      2.51491040811721e-07    20.2140101522843        0.451733444052315
7       204     establishment of protein localization to organelle
GO:0016032      4.60034359857129e-06    10.5161775771257        0.998685212096049
8       451     viral reproduction
GO:0033365      6.53335266389927e-06    10.0028673835125        1.04740156390561
8       473     protein localization to organelle
GO:0006605      6.63550110170467e-06    9.98068669527897        1.04961594353332
8       474     protein targeting
Tissue: Lung=>Muscle_Skeletal   Type:   asymmetric
SourceGene:     ENSG00000217643.1
TargetGeneSet:  ACAP3   TNFRSF25        CROCCP3 C1orf63 CPT2    DOCK7   SGIP1   RP4
HFM1    MTMR11  FAM189B PEX19   B4GALT3 KCNF1   MSH6    STON1   GFPT1   POLR1A
ARL6IP6 RFTN2   SLC23A3 TAMM41  KIAA1143        CCDC12  RRP9    PPP4R2  UBA5    RP11
PARL    ZNF718  HGFAC   OCIAD1  EXOSC9  GAB1    TMA16   LPCAT1  YTHDC2  SRFBP1
SLC23A2 IK      NHLRC1  HCG20   RP1     TRMT11  HECA    VIP     NSUN5   CLIP2
AGAP3   GNRH1   PPP2R2A GDAP1   NOL6    FANCC   XPA     STXBP1  FPGS    URM1
C9orf106        USP20   EXOSC2  EDF1    SLC34A3 ARHGAP21        ECD     SEC23IP
KCNQ1-AS1       DNAJC24 PEX16   FNBP4   BEST1   ANKRD13D        TCIRG1  ATG16L2
SRSF8   TECTA   RARG    NPFF    AVIL    THAP2   SNRPF   U4      FAM207BP
MRP63   NUPL1   STK24-AS1       FAM70B  C14orf21        SCFD1   SOCS6   ZBTB1   ERH
ABCD4   ACYP1   C15orf44        COMMD4  FAM103A1        MRPL28  ALG1    PMM2    MAZ
ITGAX   CCDC102A        KATNB1  DYNC1LI2        KLHDC4  TRAPPC2L        SNORD68 PIGS
TBC1D3  KLHL11  VPS25   ALYREF  ENOSF1  RNMT    CABLES1 IMPACT  CXXC1   CIRBP   CAPS
PDE4A   SAMD1   MEF2BNB URI1    WDR88   MED29   TIMM50  RUVBL2  MBOAT7  TMEM238
ZNF667  MZF1    ANKRD5  CBFA2T2 PABPC1L STX16   USP16   C21orf67        RAB9A
FAM3C2  RBM3    HSD17B10        TSR2    HNRNPH2 FERP1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0071843      1.54298032144831e-06    7.09411549707602        1.76963531935506
11      239     cellular component biogenesis at cellular level
Tissue: Lung=>Muscle_Skeletal   Type:   cluster
SourceGene:     ENSG00000217643.1
TargetGeneSet:  ACAP3   TNFRSF25        CROCCP3 C1orf63 CPT2    DOCK7   SGIP1   RP4
HFM1    MTMR11  FAM189B PEX19   B4GALT3 KCNF1   MSH6    STON1   GFPT1   POLR1A
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ARL6IP6 RFTN2   SLC23A3 TAMM41  KIAA1143        CCDC12  RRP9    PPP4R2  UBA5    RP11
PARL    ZNF718  HGFAC   OCIAD1  EXOSC9  GAB1    TMA16   LPCAT1  YTHDC2  SRFBP1
SLC23A2 IK      NHLRC1  HCG20   RP1     TRMT11  HECA    VIP     NSUN5   CLIP2
AGAP3   GNRH1   PPP2R2A GDAP1   NOL6    FANCC   XPA     STXBP1  FPGS    URM1
C9orf106        USP20   EXOSC2  EDF1    SLC34A3 ARHGAP21        ECD     SEC23IP
KCNQ1-AS1       DNAJC24 PEX16   FNBP4   BEST1   ANKRD13D        TCIRG1  ATG16L2
SRSF8   TECTA   RARG    NPFF    AVIL    THAP2   SNRPF   U4      FAM207BP
MRP63   NUPL1   STK24-AS1       FAM70B  C14orf21        SCFD1   SOCS6   ZBTB1   ERH
ABCD4   ACYP1   C15orf44        COMMD4  FAM103A1        MRPL28  ALG1    PMM2    MAZ
ITGAX   CCDC102A        KATNB1  DYNC1LI2        KLHDC4  TRAPPC2L        SNORD68 PIGS
TBC1D3  KLHL11  VPS25   ALYREF  ENOSF1  RNMT    CABLES1 IMPACT  CXXC1   CIRBP   CAPS
PDE4A   SAMD1   MEF2BNB URI1    WDR88   MED29   TIMM50  RUVBL2  MBOAT7  TMEM238
ZNF667  MZF1    ANKRD5  CBFA2T2 PABPC1L STX16   USP16   C21orf67        RAB9A
FAM3C2  RBM3    HSD17B10        TSR2    HNRNPH2 FERP1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0071843      1.54298032144831e-06    7.09411549707602        1.76963531935506
11      239     cellular component biogenesis at cellular level
Tissue: Lung=>Muscle_Skeletal   Type:   asymmetric
SourceGene:     OCA2(ENSG00000104044.10)
TargetGeneSet:  CPT2    THEM5   CHTOP   KLHL29  RAB10   MGAT4A  MFF     RP11    LDB2
RASGRF2 EIF4EBP3        GEMIN5  TSPYL4  RSPO3   FAM220A TSPAN13 TRGC1   DBNL    CDK6
ACHE    PPP2R2A PDP1    KIAA2026        FRMD3   USP20   FAM78A  ARRDC1  BMI1    KLLN
BET1L   MAP4K2  SIPA1   ANKRD42 FLI1    EFNB2   RHOJ    CTD     FMN1    CD2BP2
DYNC1LI2        AKAP1   ZFP161  SOGA2   LONP1   SAMD1   MEF2BNB URI1    ERCC2
RUVBL2  PRPF6   H1F0    GSPT2
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0000244      3.61442722939206e-07    400.25  0.0161926510276105      3       6
assembly of spliceosomal tri-snRNP
GO:0000387      1.35215838565712e-06    60.8888888888889        0.0836620303093212
4       31      spliceosomal snRNP assembly
Tissue: Muscle_Skeletal=>Lung   Type:   asymmetric
SourceGene:     OR7C1(ENSG00000127530.2)
TargetGeneSet:  RP11    CD53    SETP9   ARHGAP30        TRAF3IP3        WIPF1
EEF1A1P25       TMED11P IRF2    DOCK2   BTN3A2  IKZF1   FDPSP2  NCKAP1L ARL11
SLC7A7  SNX20   EVI2B   PRR22   CD37    SASH3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0046631      9.23103529146026e-07    73.6358974358974        0.0794408691440039
4       82      alpha-beta T cell activation
GO:0046638      2.89385018698768e-06    145.555555555556        0.02906373261366
3       30      positive regulation of alpha-beta T cell differentiation
GO:0046637      7.00204710918774e-06    106.142506142506        0.0387516434848799
3       40      regulation of alpha-beta T cell differentiation
GO:0046635      8.7311967723947e-06     98.1613636363636        0.0416580167462459
3       43      positive regulation of alpha-beta T cell activation
GO:0030217      1.20235178036476e-05    37.5921052631579        0.151131409591032
4       156     T cell differentiation
GO:0045582      1.64793124999097e-05    78.4745454545454        0.0513459276174659
3       53      positive regulation of T cell differentiation
GO:0002639      1.82525001619232e-05    481.066666666667        0.00678153760985399
2       7       positive regulation of immunoglobulin production
GO:0046634      1.84342500519685e-05    75.4458041958042        0.0532835097917099
3       55      regulation of alpha-beta T cell activation
Tissue: Muscle_Skeletal=>Lung   Type:   asymmetric
SourceGene:     RASA3-IT1(ENSG00000232487.1)
TargetGeneSet:  RPL11   RP11    RPL32   LNP1    RPL35A  GNPDA2  FAM198B RPL37
ARHGAP26        RPS14   RPL30   RPL35   DNAJC9  PRKRIR  COX16   RPS21   CRLF2
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      5.2570415996395e-15     230.586345381526        0.0881599889281019
8       91      translational termination
GO:0006414      1.71575130044712e-14    197.113402061856        0.10172306414781
8       105     translational elongation
GO:0006614      1.71575130044712e-14    197.113402061856        0.10172306414781
8       105     SRP-dependent cotranslational protein targeting to membrane
```

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GO:0006613      1.85512348484428e-14    195.08843537415 0.102691855234932       8
106     cotranslational protein targeting to membrane
GO:0045047      1.85512348484428e-14    195.08843537415 0.102691855234932       8
106     protein targeting to ER
GO:0072599      1.85512348484428e-14    195.08843537415 0.102691855234932       8
106     establishment of protein localization to endoplasmic reticulum
GO:0070972      4.47983465610689e-14    173.660606060606        0.114317348280396
8       118     protein localization to endoplasmic reticulum
GO:0000184      4.80092081827107e-14    172.084084084084        0.115286139367518
8       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      3.35814083575264e-13    133.277389277389        0.146287454155422
8       151     viral genome expression
GO:0019083      3.35814083575264e-13    133.277389277389        0.146287454155422
8       151     viral transcription
GO:0006413      3.54338439066552e-13    132.342592592593        0.147256245242544
8       152     translational initiation
GO:0006612      3.73748925539744e-13    131.420689655172        0.148225036329666
8       153     protein targeting to membrane
GO:0043624      3.73748925539744e-13    131.420689655172        0.148225036329666
8       153     cellular protein complex disassembly
GO:0043241      4.85395133590566e-13    126.995555555556        0.153068991765276
8       158     protein complex disassembly
GO:0000956      8.38147272952354e-13    118.227743271222        0.163725693723618
8       169     nuclear-transcribed mRNA catabolic process
GO:0034623      1.06155147079757e-12    114.626506024096        0.168569649159228
8       174     cellular macromolecular complex disassembly
GO:0006402      1.2760738371205e-12     111.898039215686        0.172444813507716
8       178     mRNA catabolic process
GO:0032984      1.33527505900153e-12    111.235867446394        0.173413604594838
8       179     macromolecular complex disassembly
GO:0072594      3.83959375516869e-12    96.8775510204082        0.197633381772888
8       204     establishment of protein localization to organelle
GO:0006401      3.99402407328448e-12    96.3790186125212        0.19860217286001
8       205     RNA catabolic process
GO:0019058      1.04445206758584e-11    84.9865470852018        0.223790741125182
8       231     viral infectious cycle
GO:0022415      2.69809871595179e-11    75.0529100529101        0.25188568265172
8       260     viral reproductive process
GO:0071845      5.46934795574173e-11    68.4106280193237        0.275136668742648
8       284     cellular component disassembly at cellular level
GO:0022411      6.11620460408393e-11    67.4142857142857        0.279011833091136
8       288     cellular component disassembly
GO:0016032      2.15543429215612e-09    42.1188863807374        0.436924780292021
8       451     viral reproduction
GO:0033365      3.13802233915605e-09    40.063082437276 0.458238184208705       8
473     protein localization to organelle
GO:0006605      3.19068290243744e-09    39.9742489270386        0.459206975295827
8       474     protein targeting
GO:0022613      1.56277436514447e-06    35.9015151515151        0.21797799460245
5       225     ribonucleoprotein complex biogenesis
GO:0071843      2.10343614093234e-06    33.7203228869896        0.231541069822158
5       239     cellular component biogenesis at cellular level
GO:0006364      2.39727680017796e-06    57.348  0.100754273060688       4       104
rRNA processing
GO:0016072      2.99988324947846e-06    54.0792452830189        0.10656701958342
4       110     rRNA metabolic process
GO:0042254      1.00270629752182e-05    39.4262068965517        0.144349871981178
4       149     ribosome biogenesis
GO:0030490      1.82525001619232e-05    481.066666666667        0.00678153760985399
2       7       maturation of SSU-rRNA
Tissue: Lung=>Muscle_Skeletal   Type:   asymmetric
SourceGene:     RLBP1(ENSG00000140522.7)
TargetGeneSet:  LRRC8D  C1orf68 PTPRC   LINC00467       RP11    PLEK    NGLY1   RP1
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TTYH3   ST7-OT4 TRIM14  SUSD1   OR5B2   PTPN6   TWF1    ATF1    LCP1    TSHR
PSTPIP1 CORO1A  ITGAX   RAB11FIP4       VAV1    IFI30   HCST    LGALS7B SIGLEC9 HCK
NCF4    CTA     PDZD4
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0007229      5.26466458883855e-06    42.7440476190476        0.117638917721957
4       68      integrin-mediated signaling pathway
GO:0008064      1.28328803890419e-05    33.7330981775426        0.147048647152446
4       85      regulation of actin polymerization or depolymerization
GO:0030832      1.34432130162966e-05    33.3193960511034        0.148778631236593
4       86      regulation of actin filament length
GO:0007015      1.81297937854322e-05    18.7315789473684        0.337346896408553
5       195     actin filament organization
Tissue: Muscle_Skeletal=>Lung   Type:   asymmetric
SourceGene:     RP11-417L19.4(ENSG00000255992.1)
TargetGeneSet:  RP4     CDC20   DEPDC1  WDR26   SGOL1   RP1     HIPK2   RPL3P9  SF1
DNAJC12 FZD4    RP11    C15orf41        FAM149B2        PLK1    KIF18B  U6
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0060041      7.98517850623222e-07    79.7166666666667        0.0780568818766867
4       94      retina development in camera-type eye
GO:0051488      1.32441885892811e-05    577.36  0.00581274652273199     2       7
activation of anaphase-promoting complex activity
GO:0043010      1.85010637569267e-05    35.064039408867 0.171891218600789       4
207     camera-type eye development
Tissue: Muscle_Skeletal=>Lung   Type:   cluster
SourceGene:     RP11-462G12.2(ENSG00000262888.1)
TargetGeneSet:  IGKJ5   IGKC    IGKJ4   IGKJ3   IGKJ2   IGKJ1   IGKV1-12
IGKV1-27        IGKV1-33        IGKV1D-27       TM4SF1-AS1      CHRD    IGJ
CALML5  RP11    IGHG1   IGHG3   IGHJ6   IGHJ5   IGHJ3   IGHV4-34        IGHV5-51
KRT10   DSC2    IGLV2-14        IGLL5   IGLC1   IGLC3   IGLC4
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006958      1.83629841921271e-10    266.574074074074        0.0380596498512214
5       50      complement activation, classical pathway
GO:0006956      6.06437703370626e-10    206.637931034483        0.0479551588125389
5       63      complement activation
GO:0002455      7.12155292763391e-10    199.722222222222        0.0494775448065878
5       65      humoral immune response mediated by circulating immunoglobulin
GO:0072376      2.33865100137353e-09    155.443722943723        0.062417825756003
5       82      protein activation cascade
GO:0016064      1.08748917995986e-08    112.688679245283        0.0844924226697114
5       111     immunoglobulin mediated immune response
GO:0019724      1.24433927273075e-08    109.564220183486        0.0867760016607847
5       114     B cell mediated immunity
GO:0006959      1.75213588880413e-08    102.01566951567 0.0928655456369801      5
122     humoral immune response
GO:0002449      8.47891311072625e-08    73.4465020576132        0.127119230503079
5       167     lymphocyte mediated immunity
GO:0002460      1.26787130696983e-07    67.5378787878788        0.137775932461421
5       181     adaptive immune response based on somatic recombination of immune
receptors built from immunoglobulin superfamily domains
GO:0002250      1.98391196917433e-07    61.5155440414508        0.150716213410837
5       198     adaptive immune response
GO:0002443      2.72274185450078e-07    57.5809061488673        0.160611722372154
5       211     leukocyte mediated immunity
GO:0002253      1.52998646745843e-06    40.0963718820862        0.227596706110304
5       299     activation of immune response
GO:0050778      4.02276505197398e-06    32.6857010213556        0.277074250916892
5       364     positive regulation of immune response
GO:0002252      5.36131152318692e-06    30.7502187226597        0.293820496851429
5       386     immune effector process
Tissue: Muscle_Skeletal=>Lung   Type:   asymmetric
SourceGene:     RP11-706O15.5(ENSG00000205663.4)
TargetGeneSet:  RPL11   RPL5    RPL31   ALDH7A1P2       RPL37A  RPL32   RP11
RPL35A  RPL34   RPL37   CTB     PANK3   RPL10A  SLC4A2  CHPF2   FAM150A UQCRB
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RPL30   POLR2K  SCRIB   RPS6    C9orf103        SLC27A4 UNC5B   RPS24   RPS25
C12orf39        SNORA49 SAP18   TPT1    EGLN3   POMT2   MAPKBP1 RPL4    FBXO22
PDPK1   CTD     PKD1P6  SLC12A4 RPL23A  UBA52   RPS11   TMC2    MAFIPL  MIS18A-AS1
PNPLA4  GPC3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      1.13924126257327e-28    164.716216216216        0.232994256452841
17      91      translational termination
GO:0006414      1.59539864162419e-27    138.376136363636        0.268839526676355
17      105     translational elongation
GO:0006614      1.59539864162419e-27    138.376136363636        0.268839526676355
17      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.89763757700381e-27    136.811797752809        0.271399903120891
17      106     cotranslational protein targeting to membrane
GO:0045047      1.89763757700381e-27    136.811797752809        0.271399903120891
17      106     protein targeting to ER
GO:0072599      1.89763757700381e-27    136.811797752809        0.271399903120891
17      106     establishment of protein localization to endoplasmic reticulum
GO:0019080      1.16101996113734e-26    101.724574594381        0.386616843125043
18      151     viral genome expression
GO:0019083      1.16101996113734e-26    101.724574594381        0.386616843125043
18      151     viral transcription
GO:0070972      1.3368781209105e-26     120.455940594059        0.302124420455332
17      118     protein localization to endoplasmic reticulum
GO:0000184      1.55763730660219e-26    119.266666666667        0.304684796899869
17      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006413      1.25360192660306e-24    89.9048148148148        0.38917721956958
17      152     translational initiation
GO:0006612      1.40844113849234e-24    89.2375 0.391737596014117       17      153
protein targeting to membrane
GO:0043624      1.40844113849234e-24    89.2375 0.391737596014117       17      153
cellular protein complex disassembly
GO:0043241      2.49139715694258e-24    86.0429078014184        0.4045394782368 17
158     protein complex disassembly
GO:0000956      8.18727855160578e-24    79.7546052631579        0.432703619126704
17      169     nuclear-transcribed mRNA catabolic process
GO:0034623      1.3685780068508e-23     77.1875796178344        0.445505501349388
17      174     cellular macromolecular complex disassembly
GO:0006402      2.04134419859622e-23    75.2487577639751        0.455747007127534
17      178     mRNA catabolic process
GO:0032984      2.25257810251158e-23    74.779012345679 0.458307383572071       17
179     macromolecular complex disassembly
GO:0019058      3.21621458870359e-23    63.1623424759081        0.59144695868798
18      231     viral infectious cycle
GO:0072594      2.22050743212406e-22    64.6681818181818        0.522316794685489
17      204     establishment of protein localization to organelle
GO:0006401      2.41809254046337e-22    64.3196808510638        0.524877171130026
17      205     RNA catabolic process
GO:0022415      2.81584247458275e-22    55.479773814702 0.665697875579545       18
260     viral reproductive process
GO:0071845      6.73842211348502e-20    45.037265917603 0.727146910248426       17
284     cellular component disassembly at cellular level
GO:0022411      8.56072118352137e-20    44.359963099631 0.737388416026573       17
288     cellular component disassembly
GO:0016032      5.77770676639793e-18    30.5892792026255        1.15472977648606
18      451     viral reproduction
GO:0033365      3.72077288339009e-16    26.018201754386 1.21105805826586        17
473     protein localization to organelle
GO:0006605      3.8539867726553e-16     25.959409190372 1.2136184347104 17      474
protein targeting
GO:0022613      1.39806468068982e-06    15.194495412844 0.57608470002076        7
225     ribonucleoprotein complex biogenesis
GO:0042254      1.9398878296968e-06     19.3155876381683        0.38149609023597
6       149     ribosome biogenesis
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GO:0071843      2.09082168711077e-06    14.2635057471264        0.611929970244274
7       239     cellular component biogenesis at cellular level
GO:0042273      3.34571139845119e-06    141.225490196078        0.0307245173344405
3       12      ribosomal large subunit biogenesis
GO:0006364      6.3609947487871e-06     22.5931186868687        0.266279150231818
5       104     rRNA processing
GO:0016072      8.37237154329821e-06    21.2931547619048        0.281641408899038
5       110     rRNA metabolic process
GO:0042274      1.22788070669489e-05    84.7    0.0460867760016608      3       18
ribosomal small subunit biogenesis
Tissue: Muscle_Skeletal=>Lung   Type:   asymmetric
SourceGene:     SDS(ENSG00000135094.4)
TargetGeneSet:  VPS45   RPS7    RPL15   CTB     EEF1A1P6        CTA     TRBV7-8 MYPN
RPS3AP5 FBXL15  RPL27A  RP11    C11orf31        CTD     NME3    RPL13   RPL26
MRPL34  RPL13A  NOSIP
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      4.01611449165716e-10    101.294117647059        0.100754273060688
6       91      translational termination
GO:0006414      9.61586459350121e-10    86.8848484848485        0.11625493045464
6       105     translational elongation
GO:0006614      9.61586459350121e-10    86.8848484848485        0.11625493045464
6       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.01867392935224e-09    86.01   0.117362120268494       6       106
cotranslational protein targeting to membrane
GO:0045047      1.01867392935224e-09    86.01   0.117362120268494       6       106
protein targeting to ER
GO:0072599      1.01867392935224e-09    86.01   0.117362120268494       6       106
establishment of protein localization to endoplasmic reticulum
GO:0070972      1.95364559544598e-09    76.7303571428571        0.130648398034738
6       118     protein localization to endoplasmic reticulum
GO:0000184      2.05615156802194e-09    76.046017699115 0.131755587848592       6
119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      8.65497447098544e-09    59.1310344827586        0.167185661891911
6       151     viral genome expression
GO:0019083      8.65497447098544e-09    59.1310344827586        0.167185661891911
6       151     viral transcription
GO:0006413      9.00527408901662e-09    58.7219178082192        0.168292851705764
6       152     translational initiation
GO:0006612      9.36723534542493e-09    58.3183673469388        0.169400041519618
6       153     protein targeting to membrane
GO:0043624      9.36723534542493e-09    58.3183673469388        0.169400041519618
6       153     cellular protein complex disassembly
GO:0043241      1.13628486543256e-08    56.3802631578947        0.174935990588887
6       158     protein complex disassembly
GO:0000956      1.70119170987948e-08    52.5349693251534        0.187115078541277
6       169     nuclear-transcribed mRNA catabolic process
GO:0034623      2.0256353412196e-08     50.9535714285714        0.192651027610546
6       174     cellular macromolecular complex disassembly
GO:0006402      2.32062780153623e-08    49.7546511627907        0.197079786865961
6       178     mRNA catabolic process
GO:0032984      2.39967536614885e-08    49.4635838150289        0.198186976679815
6       179     macromolecular complex disassembly
GO:0072594      5.23432551511703e-08    43.1424242424242        0.225866722026157
6       204     establishment of protein localization to organelle
GO:0006401      5.38891409876322e-08    42.9226130653266        0.226973911840011
6       205     RNA catabolic process
GO:0019058      1.09526014563922e-07    37.8933333333333        0.255760847000208
6       231     viral infectious cycle
GO:0022415      2.20453366736355e-07    33.4984251968504        0.287869351601965
6       260     viral reproductive process
GO:0071845      3.70908453898079e-07    30.5546762589928        0.314441907134454
6       284     cellular component disassembly at cellular level
GO:0022411      4.02707066625748e-07    30.1127659574468        0.318870666389869
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6       288     cellular component disassembly
GO:0016032      5.48524295696051e-06    18.8629213483146        0.499342606048024
6       451     viral reproduction
GO:0033365      7.21412751227361e-06    17.9460385438972        0.523700781952806
6       473     protein localization to organelle
GO:0006605      7.30218217842615e-06    17.9064102564103        0.52480797176666
6       474     protein targeting
Tissue: Lung=>Muscle_Skeletal   Type:   cluster
SourceGene:     TTC12(ENSG00000149292.11)
TargetGeneSet:  RHD     MACF1   GPBP1L1 DIEXF   ATAD2B  LGALSL  SLC1A4  MAP4K4
SS18L2  FAM198A ARF4    RP11    TBL1XR1 TNIP2   RELL1   NFKB1   PPP1R14BP3
CLPTM1L NLN     PIK3R1  ANKRD32 HBEGF   E2F3    FKBP5   APOBEC2 CENPQ   FKBP1C
HDAC2   RP3     HIVEP2  PDGFA   HOXA5   IGFBP3  YWHAG   RBM48   AZIN1   OPLAH
TTLL11  PRRC2B  WDR5    UBAC1   ARHGAP21        ABI1    ARID5B  TSPAN15 FUT11
PANK1   C10orf2 PCGF6   TEAD1   TTC12   FAIM2   PCBP2   KCTD10  SACS    SHISA2
FOXO1   GRTP1   PARP2   STRN3   TJP1    HIC1    PER1    PMP22   AKAP10  UBE2O
NPTX1   TSHZ3   B4GALT5 PPM1F   TMEM184B        CSNK1E  PDGFB   RBBP7
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
Tissue: Lung=>Muscle_Skeletal   Type:   cluster
SourceGene:     ZNF673(ENSG00000147121.10)
TargetGeneSet:  ACAP3   ALPL    ZBTB40  HMGN2   SNRNP40 UROD    RP11    HAX1
C1orf112        GS1     LINC00467       INTS7   CCDC85A TIA1    MKI67IP WDR75
MRPS36P1        SLC22A14        TMEM42  MON1A   RUVBL1  PLS1    ACAP2   TM4SF19
TMA16   CTD     GEMIN5  NUDCD2  B4GALT7 C6orf62 BYSL    MMS22L  MICAL1  FAM126A
GNAI1   SLC4A2  PABPC1  ZNF706  NOL3    C8orf55 KIAA0020        NOL6    SWI5
USP20   EXOSC2  RBM17   AFAP1L2 KCNC1   NAT10   POLR2G  ESRRA   MAP4K2  MUS81
TCIRG1  NEU3    CLNS1A  SIDT2   PVRL1   CLEC2D  LOH12CR1        DTX3    MDM1
RIC8B   ISCU    MAP1LC3B2       TRMT5   DCAF4   SMEK1   HMGN2P5 CHRNA7  HEXA    NMB
AEN     SBK1    RABEP2  RRAD    SLC43A2 DPH1    CTDNEP1 GPS2    TP53I13 TUBG1
UBE2O   AFMID   HNRNPA1P7       CCDC68  ANKRD24 DCAF15  SAMD1   SNRPA   KCNJ14  CD37
ZNF628  ZNF324B C20orf72        NAA20   HM13-AS1        RBL1    C20orf132
FAM210B SYCP2   ZGPAT   SETD4   DGCR8   HMOX1   NCF4    ZC4H2   PIN4    UTP14A
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0008380      7.88259161784815e-06    6.7049735348815 1.72105736627223        10
323     RNA splicing
GO:0000377      1.25598439456655e-05    8.3868677905945 1.08698359975088        8
204     RNA splicing, via transesterification reactions with bulged adenosine as
nucleophile
GO:0000398      1.25598439456655e-05    8.3868677905945 1.08698359975088        8
204     nuclear mRNA splicing, via spliceosome
GO:0000375      1.4973605780224e-05     8.17535510851539        1.11362535464674
8       209     RNA splicing, via transesterification reactions
GO:0034660      1.9847296795506e-05     6.76054987212276        1.51858002906373
9       285     ncRNA metabolic process
Tissue: Lung=>Nerve_Tibial      Type:   cluster
SourceGene:     ACSL3(ENSG00000123983.9)
TargetGeneSet:  CEP104  UBR4    HMGCL   GBP7    HIPK1   CRTC2   ATP1A4  TARBP1
ITSN2   SMPD4   PKP4    RAX     RP11    THAP4   SETD5   CHCHD4  C3orf75 DHX30   NEK4
CGGBP1  RPL7AP11        UBQLN4P1        NDUFB5  WHSC2   CCNI    WWC2    CTD
SPATA9  CTB     TCOF1   ZNF300  ATOX1   UBLCP1  RP3     BRD2    C6orf106
FOXP4   FRS3    HMGN3   SMPDL3A TAB2    FBXO5   LSM5    GSTK1   KAT6A   FAM82B
ZNF572  EIF2C2  FAM83H  CCL19   ATP8B5P PHF2    ODF2    PRRC2B  UCK1    EHMT1   WAC
PARD3   PPRC1   NOLC1   MXI1    ZRANB1  CTBP2   PPP2R2D PHRF1   NUP98   ZNF143
SPTY2D1 INCENP  NXF1    SNX15   MRPL49  SLC25A45        FIBP    SART1   KLC2
KDM2A   CLNS1A  7SK     PCSK7   ZNF384  ATN1    CCDC91  DDX23   KCNH3   PHC1P1
PRDM4   GCN1L1  EP400   A2LD1   RBM23   GSTZ1   IFI27L1 DENND4A SIN3A   AP3B2
AXIN1   MAPK8IP3        RNPS1   CREBBP  NOMO1   NOMO3   SETD1A  ZC3H18  LINC00304
RP13    FOXO3B  SOCS7   NT5C3L  ANKRD40 MAP3K3  ABCA10  SYNGR2  FOXK2   ZNF625
CHERP   FAM187B SUPT5H  MAP3K10 ZNF574  ZNF526  CLPTM1  CLASRP  TRAPPC6A
SCAF1   ZNF473  ZNF71   NCOA5   ZBP1    ADRM1   SCAF4   C21orf67        EP300   SBF1
GAPDHP1 RPS2P55 DDX3X   RP6     TIMP1   FOXO4   IDS
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006397      4.88462197370097e-07    5.56202168367347        3.1199916960764 15
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399     mRNA processing
Tissue: Lung=>Nerve_Tibial      Type:   asymmetric
SourceGene:     ENSG00000211482.1
TargetGeneSet:  TMEM234 LAMTOR2 RP11    TMSB10  CAPG    CHRNA1  UBE2E3  SPCS1   PDHB
UQCRQ   ATOX1   PTTG1   GCNT2   DEFA6   FAM54A  RP1     NDUFA4  CUL1    TAF5
PHRF1   MIR611  KLC2    REP15   ATP5G2  RPL41   SLC16A7 GCN1L1  EP400   GOLGA3
LPAR6   LRFN5   NPC2    KCNK13  KLHL25  CTD     PKD1P6  MLLT6   FOXK2   RP13
COX6B1  POLR2I  MAP3K10 NDUFA3  SNRPB2  RP4     ROMO1   CTSZ    MIR647  TTLL1   SBF1
DDX3X   CXorf26 NDUFA1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0045333      2.53312645571106e-07    19.4730994152047        0.442183931907826
7       142     cellular respiration
GO:0015980      4.12017193659578e-06    10.2012112446895        0.955989204899315
8       307     energy derivation by oxidation of organic compounds
GO:0022904      1.15325666764779e-05    19.6634615384615        0.298941249740502
5       96      respiratory electron transport chain
Tissue: Nerve_Tibial=>Lung      Type:   asymmetric
SourceGene:     ENSG00000223461.1
TargetGeneSet:  HS6ST1P1        STMN1   KIF2C   ATRX    IQGAP3  TNFSF13B        RRM2
SLC5A6  HMGN2P21        NCAPH   BUB1    CKAP2L  C2orf27B        FABP5P10
ENO1P4  MYL3    CACNA1D CCDC66  RP11    SPSB4   SIAH2   MSANTD1 NCAPG   EDNRA
NEIL3   ZNF131  CDC25C  RP1     KIFC1   APOBEC2 LAMA4   BTF3L4P3        SAMD9L
DNAJB9  NCAPG2  PBK     PHF19   KIF11   HOGA1   E2F8    FAT3    RAD51AP1
CDCA3   WBP11   ESPL1   DLGAP5  RAD51   KIAA0101        ANP32BP1        HMGN2P3
CES1P1  HERPUD1 CENPN   FANCA   AURKB   C17orf67        RPS10L  GINS1   TPX2
CPT1B
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0000280      5.22653288661906e-14    21.7272259392692        1.0656701958342 15
350     nuclear division
GO:0007067      5.22653288661906e-14    21.7272259392692        1.0656701958342 15
350     mitosis
GO:0000087      7.89044901168891e-14    21.0824587706147        1.09611791571518
15      360     M phase of mitotic cell cycle
GO:0048285      1.17693520690794e-13    20.4740165128703        1.12656563559615
15      370     organelle fission
GO:0051301      6.44458844443446e-09    11.9036931818182        1.37623693862016
12      452     cell division
GO:0007059      8.38176051439041e-09    24.0319865319865        0.426268078333679
8       140     chromosome segregation
GO:0000070      3.57368219700349e-07    41.8502331002331        0.149193827416788
5       49      mitotic sister chromatid segregation
GO:0000819      4.83790765365382e-07    39.1707583196945        0.158328143381081
5       52      sister chromatid segregation
GO:0051983      7.59729081247084e-07    71.935  0.073074527714345       4       24
regulation of chromosome segregation
GO:0007017      2.26535970998001e-06    9.39040178571429        1.1965953913224 9
393     microtubule-based process
GO:0007052      2.86790487866996e-06    49.5793103448276        0.100477475607224
4       33      mitotic spindle organization
GO:0007051      4.20160213903285e-06    24.4991452991453        0.243581759047817
5       80      spindle organization
GO:0000226      1.52310376407441e-05    10.2140499277904        0.819043664798284
7       269     microtubule cytoskeleton organization
Tissue: Nerve_Tibial=>Lung      Type:   asymmetric
SourceGene:     FOLR4(ENSG00000183560.4)
TargetGeneSet:  DDX11L1 PAQR7   DMBX1   CMPK1   GNG5    S100A10 TCEB1P21        GNLY
CCDC72  RP11    LINC00578       HNRPDL  MRPS36  CTB     PPIA    ZNF92   FIS1
TRBV5-6 GTF2E2  COX6C   ATP6V1C1        CHMP5   PCDH15  TMEM9B  ATP5L   KLRB1
HEBP1   GYS2    MYL6    COX6A1  ACIN1   PPP2R5C SRP14   MGA     NDUFAB1 RPL27
SUMO2   MYL12A  MYL12B  C18orf32        NDUFA13 PPIAP22 ATP5J   SEC14L3 COX7B
ZBTB33
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      4.87906245786462e-09    36.3421529539688        0.252439277558646
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7       96      respiratory electron transport chain
GO:0022900      5.00125557113411e-08    25.4005588011176        0.352363158258944
7       134     electron transport chain
GO:0015980      7.43733814647176e-08    14.6997222865078        0.807279773026088
9       307     energy derivation by oxidation of organic compounds
GO:0045333      7.46046853932828e-08    23.8819593787336        0.373399764722165
7       142     cellular respiration
GO:0006091      1.22530510802485e-06    10.3650728335116        1.1254584457823 9
428     generation of precursor metabolites and energy
Tissue: Lung=>Nerve_Tibial      Type:   asymmetric
SourceGene:     GFAP(ENSG00000131095.5)
TargetGeneSet:  UTP11L  ANKRD13C        EVI5    PFDN2   MRPL33  C1D     SUGT1P2
SEMA3B  UBA3    ATG3    RP11    IL12A   SUB1    TAF9    FAM174A UQCRQ   CTB     TUBB
RANP1   COX7A2  PSMB1   RPA3    NDUFA4  MALSU1  HUS1    TRIM56  FIS1    PSMC2
DCTN6   COX6C   TTC35   EXOSC4  PRSS3   DCTN3   PSMB7   ATP5C1  FAM149B1
SNORA19 NDUFS8  CWF19L2 MRP63   POMP    MZT1    L2HGDH  SNORA70 PSMA3   ERH
GTF2A2  COX5A   DNAJA4  PSMA4   MRPL28  NFATC3  SMYD4   PSMB6   TXNDC17 DHRS7C
PSMB3   AATK    IER3IP1 SEC11C  UQCR11  NFIC    PIN1    UBE2S   TGM3    SNRPB2
ZMAT5   CCDC160
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0051443      2.37160466144218e-11    37.5686388807928        0.317763476576016
9       82      positive regulation of ubiquitin-protein ligase activity
GO:0051351      3.67800011272365e-11    35.6070737772865        0.333264133969967
9       86      positive regulation of ligase activity
GO:0051438      1.00693999163763e-10    31.492296404989 0.372015777454847       9
96      regulation of ubiquitin-protein ligase activity
GO:0051340      1.46005668686652e-10    30.0996025251344        0.387516434848799
9       100     regulation of ligase activity
GO:0000216      6.3792202051005e-10     33.6244131455399        0.306137983530551
8       79      M/G1 transition of mitotic cell cycle
GO:0031575      8.63789621157269e-10    32.2545045045045        0.317763476576016
8       82      mitotic cell cycle G1/S transition checkpoint
GO:0031145      9.5309813187546e-10     31.8222222222222        0.321638640924504
8       83      anaphase-promoting complex-dependent proteasomal ubiquitin-dependent
protein catabolic process
GO:0031398      1.25636639401995e-09    23.1685899747566        0.492145872257975
9       127     positive regulation of protein ubiquitination
GO:0071779      1.27078945669152e-09    30.5918803418803        0.333264133969967
8       86      G1/S transition checkpoint
GO:0006521      2.02662410128543e-09    40.9857142857143        0.220884367863816
7       57      regulation of cellular amino acid metabolic process
GO:2000045      3.94522660797564e-09    26.1978021978022        0.383641270500311
8       99      regulation of G1/S transition of mitotic cell cycle
GO:0006977      5.8120202579892e-09     34.7118644067797        0.255760847000208
7       66      DNA damage response, signal transduction by p53 class mediator
resulting in cell cycle arrest
GO:0072413      5.8120202579892e-09     34.7118644067797        0.255760847000208
7       66      signal transduction involved in mitotic cell cycle checkpoint
GO:0072431      5.8120202579892e-09     34.7118644067797        0.255760847000208
7       66      signal transduction involved in mitotic cell cycle G1/S transition
DNA damage checkpoint
GO:0072474      5.8120202579892e-09     34.7118644067797        0.255760847000208
7       66      signal transduction involved in mitotic cell cycle G1/S checkpoint
GO:0051436      6.47080923363157e-09    34.1309523809524        0.259636011348696
7       67      negative regulation of ubiquitin-protein ligase activity involved in
mitotic cell cycle
GO:0072401      6.47080923363157e-09    34.1309523809524        0.259636011348696
7       67      signal transduction involved in DNA integrity checkpoint
GO:0072404      6.47080923363157e-09    34.1309523809524        0.259636011348696
7       67      signal transduction involved in G1/S transition checkpoint
GO:0072422      6.47080923363157e-09    34.1309523809524        0.259636011348696
7       67      signal transduction involved in DNA damage checkpoint
GO:0072395      7.19193217728347e-09    33.5690866510539        0.263511175697184
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7       68      signal transduction involved in cell cycle checkpoint
GO:0000209      1.02305678494934e-08    17.9433090705487        0.623901460106567
9       161     protein polyubiquitination
GO:0033238      1.07991473500473e-08    31.4945054945055        0.279011833091136
7       72      regulation of cellular amine metabolic process
GO:0051352      1.07991473500473e-08    31.4945054945055        0.279011833091136
7       72      negative regulation of ligase activity
GO:0051437      1.07991473500473e-08    31.4945054945055        0.279011833091136
7       72      positive regulation of ubiquitin-protein ligase activity involved in
mitotic cell cycle
GO:0051444      1.07991473500473e-08    31.4945054945055        0.279011833091136
7       72      negative regulation of ubiquitin-protein ligase activity
GO:0031571      1.19090254014592e-08    31.0151515151515        0.282886997439624
7       73      mitotic cell cycle G1/S transition DNA damage checkpoint
GO:0002479      1.44211901233994e-08    30.0987394957983        0.2906373261366 7
75      antigen processing and presentation of exogenous peptide antigen via MHC
class I, TAP-dependent
GO:0031396      1.48415781669281e-08    17.1449217181855        0.651027610545983
9       168     regulation of protein ubiquitination
GO:0051439      1.9024701276404e-08     28.8209255533199        0.302262819182064
7       78      regulation of ubiquitin-protein ligase activity involved in mitotic
cell cycle
GO:0042590      2.08123048151715e-08    28.4186507936508        0.306137983530551
7       79      antigen processing and presentation of exogenous peptide antigen via
MHC class I
GO:0071158      2.2740239072208e-08     28.027397260274 0.310013147879039       7
80      positive regulation of cell cycle arrest
GO:0002478      2.94569981048109e-08    26.9154135338346        0.321638640924504
7       83      antigen processing and presentation of exogenous peptide antigen
GO:0000077      3.41402806989042e-08    19.4986338797814        0.503771365303439
8       130     DNA damage checkpoint
GO:0019884      3.48110141843876e-08    26.2216117216117        0.329388969621479
7       85      antigen processing and presentation of exogenous antigen
GO:0000082      3.59390157517707e-08    15.3818968626037        0.720780568818767
9       186     G1/S transition of mitotic cell cycle
GO:0000084      4.32819461581721e-08    18.8743386243386        0.519272022697391
8       134     S phase of mitotic cell cycle
GO:0031570      4.85946306035468e-08    18.5768229166667        0.527022351394367
8       136     DNA integrity checkpoint
GO:0007093      5.76145194306118e-08    18.147582697201 0.538647844439831       8
139     mitotic cell cycle checkpoint
GO:0031397      6.05117384076545e-08    24.0504201680672        0.356515120060895
7       92      negative regulation of protein ubiquitination
GO:0045333      6.80409505498185e-08    17.7375621890547        0.550273337485295
8       142     cellular respiration
GO:0051320      7.18594164906072e-08    17.6049382716049        0.554148501833783
8       143     S phase
GO:0022904      8.13551220948746e-08    22.9630818619583        0.372015777454847
7       96      respiratory electron transport chain
GO:2000602      8.90378995282056e-08    17.0935251798561        0.569649159227735
8       147     regulation of interphase of mitotic cell cycle
GO:0043161      9.80205424264059e-08    13.5909574468085        0.809909348833991
9       209     proteasomal ubiquitin-dependent protein catabolic process
GO:0002474      1.0070905787803e-07     22.2096273291925        0.383641270500311
7       99      antigen processing and presentation of peptide antigen via MHC class
I
GO:0010498      1.29897464201097e-07    13.1248843663275        0.837035499273407
9       216     proteasomal protein catabolic process
GO:0048002      1.83640985175241e-07    20.2178217821782        0.418517749636703
7       108     antigen processing and presentation of peptide antigen
GO:0030330      3.18000147089335e-07    18.5519480519481        0.453394228773095
7       117     DNA damage response, signal transduction by p53 class mediator
GO:0000075      3.40784712969514e-07    11.6389370833714        0.937789772334095
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9       242     cell cycle checkpoint
GO:0072331      4.4735319198022e-07     17.5849753694581        0.476645214864023
7       123     signal transduction by p53 class mediator
GO:0071156      7.076942782611e-07      10.6182728410513        1.02304338800083
9       264     regulation of cell cycle arrest
GO:0022900      8.00066537061481e-07    16.0494938132733        0.519272022697391
7       134     electron transport chain
GO:0042770      1.07533269909024e-06    15.3190118152524        0.542523008788319
7       140     signal transduction in response to DNA damage
GO:0007050      1.30476957963186e-06    8.49945500787211        1.42993564459207
10      369     cell cycle arrest
GO:0051329      1.66080666485495e-06    8.26322611052198        1.46868728807695
10      379     interphase of mitotic cell cycle
GO:0090068      1.78711354681157e-06    14.1378968253968        0.585149816621687
7       151     positive regulation of cell cycle process
GO:0019882      1.86781761245699e-06    14.0394088669951        0.589024980970175
7       152     antigen processing and presentation
GO:0051325      2.0040363970074e-06     8.08326605927805        1.49968860286485
10      387     interphase
GO:0010565      2.03840210248302e-06    13.846452866861 0.596775309667151       7
154     regulation of cellular ketone metabolic process
GO:0007346      2.21855020581098e-06    9.18432479374729        1.17417479759186
9       303     regulation of mitotic cell cycle
GO:0015980      2.47100756082141e-06    9.05847493931172        1.18967545498581
9       307     energy derivation by oxidation of organic compounds
GO:0010564      3.66142377567205e-06    7.52851915626345        1.60431804027403
10      414     regulation of cell cycle process
GO:0045786      5.90980336392712e-06    7.11129212911109        1.69344682028925
10      437     negative regulation of cell cycle
GO:0044106      6.39627865973228e-06    11.5413961038961        0.709155075773303
7       183     cellular amine metabolic process
GO:0006511      9.84736623766474e-06    7.57326940365598        1.41055982284963
9       364     ubiquitin-dependent protein catabolic process
GO:0019941      1.14704978264928e-05    7.42312213471259        1.43768597328905
9       371     modification-dependent protein catabolic process
GO:0009308      1.22023885936851e-05    10.4029304029304        0.782783198394575
7       202     amine metabolic process
GO:0043632      1.22332329984429e-05    7.36053628679685        1.44931146633451
9       374     modification-dependent macromolecule catabolic process
GO:0051603      1.67323685365422e-05    7.06243001119821        1.50743893156183
9       389     proteolysis involved in cellular protein catabolic process
Tissue: Nerve_Tibial=>Lung      Type:   asymmetric
SourceGene:     GPRC5A(ENSG00000013588.5)
TargetGeneSet:  YARS    SARS    RP11    HADH    GARS    C9orf9  SRGN    CFL1P1  CARS
KRTAP5-10       KRR1    ITGA11  MPRIP   RAD23A  CYP4F2  SLC1A5  SETD4   TSR2
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006418      7.49326144892686e-08    145.393939393939        0.0431804027402948
4       48      tRNA aminoacylation for protein translation
GO:0034660      8.52978289875066e-08    43.4992319508449        0.2563836412705 6
285     ncRNA metabolic process
GO:0043038      9.60922540719905e-08    136.085106382979        0.0458791779115632
4       51      amino acid activation
GO:0043039      9.60922540719905e-08    136.085106382979        0.0458791779115632
4       51      tRNA aminoacylation
GO:0006399      3.59118375176098e-06    52.5876951331497        0.112448965469518
4       125     tRNA metabolic process
Tissue: Lung=>Nerve_Tibial      Type:   asymmetric
SourceGene:     GSTA1(ENSG00000243955.1)
TargetGeneSet:  UQCRH   CSRP3   KCNC4   C1orf54 LHX4    LHX9    RP11    ERLEC1
GPAT2   LYAR    CRMP1   CC2D2A  ATP1B1P1        NDUFS6  TMEM14C RHAG    TMEM120A
PTPN12  PUS7    LINC00032       ATP5C1  NCOA4   IFIT2   MYOF    BBIP1   NDUFS3
MRPL16  NDUFA9  KRR1    FRMD6   CHURC1  TDP1    NDUFB1  WASH3P  HCFC1R1 USP31
ZNF629  COX4I1  SMARCE1 KRT223P PSMG2   COX6B1  RP3     ROMO1   DNTTIP1 MRPL39
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VDAC1P2 TCEAL8  NDUFA1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      3.96471358198034e-12    47.7997775305895        0.265725555324891
9       96      respiratory electron transport chain
GO:0022900      8.28557327429333e-11    33.1803870967742        0.370908587640994
9       134     electron transport chain
GO:0045333      1.39661050307714e-10    31.1671113267039        0.393052383918068
9       142     cellular respiration
GO:0006119      1.94109208173366e-10    59.726678550208 0.160542523008788       7
58      oxidative phosphorylation
GO:0042773      3.0024573107284e-09     61.8507890961263        0.130094803127811
6       47      ATP synthesis coupled electron transport
GO:0042775      3.0024573107284e-09     61.8507890961263        0.130094803127811
6       47      mitochondrial ATP synthesis coupled electron transport
GO:0006120      4.43961605146332e-08    66.2672811059908        0.0996470832468341
5       36      mitochondrial electron transport, NADH to ubiquinone
GO:0015980      1.20183139616916e-07    13.7494046330375        0.849768182132724
9       307     energy derivation by oxidation of organic compounds
GO:0006091      1.95011088415191e-06    9.69497266918161        1.18469310082347
9       428     generation of precursor metabolites and energy
Tissue: Nerve_Tibial=>Lung      Type:   asymmetric
SourceGene:     IGKV1OR2-118(ENSG00000219041.3)
TargetGeneSet:  DRAM2   KRT8P29 CNIH4   MAT2A   IL1R2   STEAP3  TNNC1   WDR52   CNBP
RP11    LINC00578       TMEM128 PCDHA5  GS1     SGCE    PENK    C8orf34 RPL8
OR1L8   RPL35   MRPL41  ZNF37BP VDAC2   RPL27A  FDX1    ATP5L   C12orf57
RIC8B   HMGB3P4 TCEB2   RPL19   MYO5B   RPL36   EIF3K   ZNF814  DPH3P1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0019080      3.67143006109308e-07    26.8551724137931        0.292574908310844
6       151     viral genome expression
GO:0019083      3.67143006109308e-07    26.8551724137931        0.292574908310844
6       151     viral transcription
GO:0006413      3.81729724848633e-07    26.6693648816936        0.294512490485088
6       152     translational initiation
GO:0006415      7.76820389467076e-07    36.2411526794742        0.176319977856204
5       91      translational termination
GO:0006414      1.58320955019598e-06    31.1369565217391        0.20344612829562
5       105     translational elongation
GO:0006614      1.58320955019598e-06    31.1369565217391        0.20344612829562
5       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.6593771554176e-06     30.8265174343521        0.205383710469864
5       106     cotranslational protein targeting to membrane
GO:0045047      1.6593771554176e-06     30.8265174343521        0.205383710469864
5       106     protein targeting to ER
GO:0072599      1.6593771554176e-06     30.8265174343521        0.205383710469864
5       106     establishment of protein localization to endoplasmic reticulum
GO:0070972      2.81950870580034e-06    27.5298191612159        0.228634696560792
5       118     protein localization to endoplasmic reticulum
GO:0000184      2.93925737315813e-06    27.2864225781846        0.230572278735036
5       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019058      4.38768208778296e-06    17.209696969697 0.447581482250363       6
231     viral infectious cycle
GO:0022415      8.65002609782669e-06    15.213672154617 0.503771365303439       6
260     viral reproductive process
GO:0006612      1.00600473682889e-05    20.9679788484136        0.296450072659332
5       153     protein targeting to membrane
GO:0043624      1.00600473682889e-05    20.9679788484136        0.296450072659332
5       153     cellular protein complex disassembly
GO:0043241      1.17612249258428e-05    20.2756464904802        0.306137983530551
5       158     protein complex disassembly
GO:0000956      1.62952306616806e-05    18.9011134676564        0.327451387447236
5       169     nuclear-transcribed mRNA catabolic process
GO:0034623      1.87599746165927e-05    18.3354772317983        0.337139298318455
5       174     cellular macromolecular complex disassembly
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Tissue: Lung=>Nerve_Tibial      Type:   asymmetric
SourceGene:     IGLV4-69(ENSG00000211637.2)
TargetGeneSet:  PRDM16  CLCN6   RPL11   BMP8B   DOCK7   RP11    SORT1   SLC27A3
C1orf9  RPS6KC1 FIGLA   PDCL3   FHL2    SCN7A   CRTAP   ABHD14B GFM1    KIAA0232
C1QTNF7 SPP1    FNIP2   CTD     RPL37   EEF1A1P19       HMGCR   PAQR8   EEF1A1
NDUFAF4 PERP    PLAGL1  RP4     INSIG1  PHYHIP  MRPS35  RPL30   PABPC1  EIF3H
SCRIB   GPSM1   MAMDC4  IDI1    SEC61A2 TOLLIP  UBXN1   FAU     BCRP1   NCAM1
RPL18AP3        AHSA1   MAP1A   POLG    GAS7    MAPK7   HDHD2   ACAA2   BCL2
LMNB2   PIAS4   EMR4P   ELAVL1  PRKCSH  RPL18A  RPS16   TTYH1   RPL28   RPL24P2
EIF3L   SAMM50  XG      PNMA5   RPL10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      1.75572187950827e-11    29.5046439628483        0.443221922358314
10      105     translational elongation
GO:0006413      3.2225444616925e-11     22.2324822695035        0.641616497128226
11      152     translational initiation
GO:0000184      1.55267453698717e-09    22.4685314685315        0.502318178672756
9       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006415      4.0524739989832e-09     26.0186406001364        0.384125666043872
8       91      translational termination
GO:0006614      1.26995874179205e-08    22.2415872398366        0.443221922358314
8       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.3691395478107e-08     22.0130920292645        0.447443083523632
8       106     cotranslational protein targeting to membrane
GO:0045047      1.3691395478107e-08     22.0130920292645        0.447443083523632
8       106     protein targeting to ER
GO:0072599      1.3691395478107e-08     22.0130920292645        0.447443083523632
8       106     establishment of protein localization to endoplasmic reticulum
GO:0006612      1.43143685183038e-08    17.1225961538462        0.645837658293544
9       153     protein targeting to membrane
GO:0070972      3.19308852501457e-08    19.5951972555746        0.498097017507439
8       118     protein localization to endoplasmic reticulum
GO:0000956      3.40335834635391e-08    15.3930288461538        0.71337623693862
9       169     nuclear-transcribed mRNA catabolic process
GO:0006402      5.3308649991659e-08     14.5640646335913        0.751366687426476
9       178     mRNA catabolic process
GO:0072594      1.71549864677873e-07    12.5991124260355        0.861116877724725
9       204     establishment of protein localization to organelle
GO:0006401      1.78842527534319e-07    12.5339481946625        0.865338038890042
9       205     RNA catabolic process
GO:0019080      2.17490132258189e-07    15.0383955666975        0.637395335962909
8       151     viral genome expression
GO:0019083      2.17490132258189e-07    15.0383955666975        0.637395335962909
8       151     viral transcription
GO:0043624      2.40656914726628e-07    14.8288874430709        0.645837658293544
8       153     cellular protein complex disassembly
GO:0043241      3.08040556832121e-07    14.3295597484277        0.66694346412013
8       158     protein complex disassembly
GO:0019058      4.91070992933821e-07    11.045738045738 0.975088229188292       9
231     viral infectious cycle
GO:0034623      6.43090629727571e-07    12.933848601955 0.734482042765207       8
174     cellular macromolecular complex disassembly
GO:0032984      7.9724984921292e-07     12.5512523446982        0.755587848591793
8       179     macromolecular complex disassembly
GO:0022415      1.31819270190311e-06    9.74954030033711        1.09750190298249
9       260     viral reproductive process
Tissue: Lung=>Nerve_Tibial      Type:   asymmetric
SourceGene:     MICF(ENSG00000233265.1)
TargetGeneSet:  HSPB11  RP4     NAP1L4P1        C1orf54 ZNF672  PTRHD1  RP11
HACE1   COX6C   CTBP2   NDUFS3  MRPL16  ATP5L   TBCEL   RPSAP51 HIGD1C  STAT6
ST6GALNAC4P1    PLEKHG3 IFI27L2 NDUFB10 COX4I1  PVR     MAVS    ERGIC3  DHRSX
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      6.76611078259766e-08    65.6730769230769        0.112933361013079
5       96      respiratory electron transport chain
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GO:0022900      3.59926044765517e-07    46.2047803617571        0.157636149747422
5       134     electron transport chain
GO:0045333      4.80373639711739e-07    43.4823600973236        0.167047263165179
5       142     cellular respiration
Tissue: Nerve_Tibial=>Lung      Type:   asymmetric
SourceGene:     PIGK(ENSG00000142892.10)
TargetGeneSet:  UBE4B   SPEN    ARHGEF10L       RNF11   TTC24   RP11    KRT8P29
RAB4A   FEZ2    MDH1    NFU1    COX5B   KLHL18  CHMP2B  ANKRD17 SLC25A4 CCT6P2
NDUFS4  PTCD2   FAM174A PHACTR1 CNR1    RN5S216 SEPT7   CHCHD2  EIF4H   FZD1
NDUFA5  METTL2A CTD     RAB2A   IMPDH1P6        NDUFA8  MRPL41  ATP5C1  ANKRD22
ABCC2   FBXL15  PTPMT1  C11orf31        CPSF7   RAB6A   TMEM123 PHC1    STAT6   AVIL
COX6A1  ZNF605  ACIN1   TSSK6   HMGB1P14        VRK1    SIVA1   SRP14   GANC
RAB11A  MRPL46  FAM173A NME3    LSMD1   KRT31   AANAT   MYL12B  NDUFV2  IER3IP1
C18orf32        ATP5D   DAPK3   TRAPPC5 ZNF414  ZNF558  RBM42   ZNF428  ZNF284
SIGLEC10        NOP56   SCAND1  ATP5J   DGCR6L  CHCHD10 RAB9A   ZFX     COX7B
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      1.37277815089332e-11    30.2325581395349        0.431804027402948
10      96      respiratory electron transport chain
GO:0045333      3.1726615113612e-11     22.1663839411931        0.63871012386686
11      142     cellular respiration
GO:0022900      3.88793784774641e-10    20.9120234604106        0.602726454916615
10      134     electron transport chain
GO:0006119      6.70860201440995e-09    33.9232589587559        0.260881599889281
7       58      oxidative phosphorylation
GO:0015980      1.00411779914637e-08    10.8149664214902        1.38087329596568
12      307     energy derivation by oxidation of organic compounds
GO:0006091      4.55303983869757e-08    8.41626506024096        1.92512628883814
13      428     generation of precursor metabolites and energy
GO:0009206      7.10485190235733e-06    21.7136363636364        0.269877517126842
5       60      purine ribonucleoside triphosphate biosynthetic process
GO:0009145      7.71248956275583e-06    21.3244047619048        0.274375475745623
5       61      purine nucleoside triphosphate biosynthetic process
GO:0009201      1.05610168824303e-05    19.8972222222222        0.292367310220746
5       65      ribonucleoside triphosphate biosynthetic process
GO:0009205      1.14367548275899e-05    5.8510101010101 2.22648951629645        11
495     purine ribonucleoside triphosphate metabolic process
GO:0009144      1.23331147428029e-05    5.80138129933212        2.24448135077157
11      499     purine nucleoside triphosphate metabolic process
GO:0009142      1.41720677300219e-05    18.6484375      0.310359144695869       5
69      nucleoside triphosphate biosynthetic process
GO:0006120      1.97063151171034e-05    29.4139344262295        0.161926510276105
4       36      mitochondrial electron transport, NADH to ubiquinone
Tissue: Nerve_Tibial=>Lung      Type:   asymmetric
SourceGene:     RAD52(ENSG00000002016.11)
TargetGeneSet:  MRPL20  DFFB    UBE4B   ARHGEF19        CDC42   IFI6    SNHG3   RP11
MSH4    RP4     APH1A   INTS3   UBQLN4  CCT3    FAM78B  BRP44   CSRP1   RAB4A
ADCY3   SLC5A6  MORN2   NFU1    AUP1    RNF181  CHMP3   COX5B   CKAP2L  CCDC115
TMEM194B        SATB2   SPAG16  BCS1L   STK36   CYP8B1  TNNC1   SPCS1   SLC25A26
SUCLG2  CCDC48  CNBP    COL6A5  RNF7    GRK7    NAALADL2-AS2    PARL    RTP4
TMEM128 ANKRD17 TMSB4XP8        PPA2    NDUFC1  C4orf27 CCT6P2  SLC1A3  ZNF131
NDUFS4  FAM174A CTB     RP1     TMEM14C TMEM14B ZDHHC20P1       C6orf130
C6orf226        CNR1    LINC00271       PEX7    AIG1    C6orf72 WDR27   LSM5
CHCHD2  EIF4H   FZD1    SGCE    PILRB   DUS4L   CAV2    NDUFA5  METTL2A UBN2
ASH2L   C8orf40 PKIA    DECR1   COX6C   POLR2K  NDUFB9  NSMCE2  CHRAC1  CHMP5
MED27   ATP5C1  C1DP1   ZNF37BP C10orf116       AGAP11  ABCC2   AP2A2   TNNI2
ZNF195  TMEM9B  PLEKHA7 PIGCP1  ALKBH3  CPSF7   PLA2G16 DRAP1   KDM2A   CLNS1A
TMEM123 CARD16  ATM     C11orf1 HYOU1   RAD52   DAZAP2  MYL6    PAN2    LUM
SLC41A2 RIC8B   UBE3B   COX6A1  MLEC    GOLGA3  ZNF605  POMP    SPG20   ACIN1
MAP3K9  POMT2   TRIP11  NDUFB1  IFI27   SRP14   PLA2G4E WDR61   SRRM2   TCEB2
CLDN9   PKD1P1  NDUFAB1 TNRC6A  SULT1A1 MIR4519 PSMB10  SERPINF2        CTD
NLGN2   CTC1    TEKT3   SLC46A1 HMGB1P24        CNTNAP1 SUPT4H1 MTMR4   SKA2
ICAM2   ATP5H   TBC1D16 MYL12A  MYL12B  C18orf32        MUM1    TRAPPC5 ZNF558
HOOK2   DCAF15  ZNF793  FAM98C  ZNF428  NAPA    SNRNP70 VSIG10L PPP1R12C
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ZSCAN22 DSTN    DTD1    CHMP4B  RALY    PKIG    PABPC1L RP3     ZMYND8  SLC17A9
ATP5J   SNRPD3  PRR14L  ZFX     TSR2    ACRC    CXorf41 AKAP14  APLN    EMD
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      2.38067494063953e-11    15.9031841652324        1.01640024911771
13      96      respiratory electron transport chain
GO:0045333      3.05580499993376e-10    11.1499550359712        1.50342536848661
14      142     cellular respiration
GO:0022900      1.65293176557921e-09    10.8796340023613        1.4187253477268 13
134     electron transport chain
GO:0015980      1.61968757953848e-07    5.62149145910151        3.25036329665767
16      307     energy derivation by oxidation of organic compounds
GO:0006120      1.91302751155676e-06    19.4122448979592        0.381150093419141
6       36      mitochondrial electron transport, NADH to ubiquinone
GO:0006119      2.48576023154465e-06    13.3936341659952        0.614075150508615
7       58      oxidative phosphorylation
GO:0042773      9.58122597442801e-06    14.1931309109009        0.497612621963878
6       47      ATP synthesis coupled electron transport
GO:0042775      9.58122597442801e-06    14.1931309109009        0.497612621963878
6       47      mitochondrial ATP synthesis coupled electron transport
GO:0006091      1.23508777015847e-05    3.93621997023599        4.53145111064978
16      428     generation of precursor metabolites and energy
Tissue: Lung=>Nerve_Tibial      Type:   asymmetric
SourceGene:     RP11-645C24.1(ENSG00000185864.12)
TargetGeneSet:  ISG15   NADK    CEP104  RP11    WDTC1   IFI6    EYA3    ATPIF1
KHDRBS1 PIGK    IFI44   LPPR5   NBPF8   NBPF10  NBPF24  INTS3   CRTC2   DCST2
PFN1P1  MDM4    PUM2    MORN2   GALNT5  BTF3L4P2        SPC25   UBE2E3  TRIP12  ING5
UBE2E1  SPCS1   FTH1P23 RPL7AP11        SNORA4  CCNI    BMP2K   TMSB4XP8
NDUFC1  C5orf55 RBBP4P1 SUB1    CTD     FAM174A UQCRQ   TCOF1   C6orf226        PEX6
C6orf108        RP3     NDUFA4  CCDC126 CDK13   GS1     GTF2IRD2B       SGCE
PILRB   PPP1R35 DUS4L   ARF5    RBM28   C7orf49 GSTK1   ZNF862  C8orf59 COX6C
KIAA2026        C9orf133        GKAP1   SEC61B  TSC1    TUBBP5  ATP5C1  PBLD    DNA2
CALM2P2 FGFBP3  CPSF7   NXF1    SNX15   RCE1    RAD52   GYS2    MED13L  GCN1L1  PXN
MLXIP   MPHOSPH8        IPO5    ACIN1   DHRS2   CTAGE5  PSMA3   ZNF410  PROX2   NEK9
NDUFB1  IFI27L1 IFI27   PPP1R13B        HMGN2P5 TUBGCP4 NPRL3   IFT140  PDXDC1
USP31   ITFG1   C17orf85        TXNDC17 NEURL4  CTC1    FLII    EPN2    NPEPPS
ATP5H   LLGL2   EPG5    IER3IP1 UQCR11  PIP5K1C INSR    ANKLE1  ANKRD27 PPP1R13L
SLC17A7 TBC1D17 SNRPB2  LPIN3   GDAP1L1 BCAS4   SS18L1  LINC00478       H1F0    RP6
TIMP1   MORC4   PGRMC1  NDUFA1  LINC00087       VAMP7
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      1.38635549180869e-08    16.9655172413793        0.637741332779738
9       96      respiratory electron transport chain
GO:0022900      2.53676180473649e-07    11.7765517241379        0.890180610338385
9       134     electron transport chain
GO:0045333      4.15805339285461e-07    11.0619652579725        0.943325721403363
9       142     cellular respiration
GO:0015980      8.65198381291436e-07    6.80871670702179        2.03944363711854
12      307     energy derivation by oxidation of organic compounds
GO:0006091      4.86402676188033e-06    5.26114094933953        2.84326344197633
13      428     generation of precursor metabolites and energy
Tissue: Nerve_Tibial=>Lung      Type:   asymmetric
SourceGene:     RP11-74D7.1(ENSG00000259505.1)
TargetGeneSet:  RP11    S100A8  MNDA    CCDC85A FHL2    IL1RN   ZEB2-AS1
MYD88   LMOD3   HTR1F   SSR3    LIMCH1  LST1    C7orf31 MYO1G   PILRA   LYN     SYK
PIK3AP1 CATSPER1        LRRC23  STAC3   GLT1D1  LCP1    RNASE2  TRAV20  AQP9
RPS17L  GDE1    TOX3    CTU2    CENPBD1 BECN1   MEOX1   CD300E  MIR1227 C19orf38
TYROBP  FPR2    NLRP12  VSTM1   OSCAR   LILRA1  HCK     IFNGR2  IGLV3-16        CYBB
FTH1P8
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006954      6.28500911262047e-07    11.5604304635762        1.05501349387586
9       462     inflammatory response
GO:0031663      1.2605373894478e-06     62.0086206896552        0.0822088436786382
4       36      lipopolysaccharide-mediated signaling pathway
GO:0071216      3.21972438124354e-06    26.3641384388807        0.232925057089475
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5       102     cellular response to biotic stimulus
GO:0002757      1.33033524414724e-05    13.7690441533236        0.536641062902221
6       235     immune response-activating signal transduction
GO:0002764      1.80564638741489e-05    13.0174471992654        0.566327589786174
6       248     immune response-regulating signaling pathway
Tissue: Nerve_Tibial=>Lung      Type:   asymmetric
SourceGene:     RPL23AP80(ENSG00000213035.3)
TargetGeneSet:  AGTRAP  EFHD2   SH3BGRL3        GBP1    GBP4    FCRL6   RAB7L1
OR14L1P ARHGAP25        SHISA5  ZBTB20-AS4      MYLK-AS2        LRRC33  CD38
CXCL9   CXCL10  HERC3   LRBA    ST8SIA4 STC2    GMNN    UBD     HLA-F   HCG4P11 HCP5
PSMB8   PSMB9   TAP1    RSPO3   HIVEP2  TRGC2   RP11    DENND4C SH2D3C  C9orf167
MAP4K2  PLXNC1  DGKZP1  LCP1    PSME1   GZMH    GZMB    RTN1    CCDC88C WARS    RYR3
B2M     POLR2M  CILP    IL32    CORO1A  NLRC5   CDH5    PSMB10  PFN1    TRPV2   CCL5
ICAM2   BBC3    MED25   KIR2DL3 ITGB2   TYMP    NUDT10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0002479      9.70439617785782e-09    32.0684143222506        0.275067469379282
7       75      antigen processing and presentation of exogenous peptide antigen via
MHC class I, TAP-dependent
GO:0042590      1.40153348417612e-08    30.2783816425121        0.289737734412843
7       79      antigen processing and presentation of exogenous peptide antigen via
MHC class I
GO:0002478      1.985123929517e-08      28.6767734553776        0.304407999446405
7       83      antigen processing and presentation of exogenous peptide antigen
GO:0019884      2.34678722332923e-08    27.9375696767001        0.311743131963186
7       85      antigen processing and presentation of exogenous antigen
GO:0002474      6.80660493184403e-08    23.6630434782609        0.363089059580652
7       99      antigen processing and presentation of peptide antigen via MHC class
I
GO:0048002      1.24320184663247e-07    21.5408953938872        0.396097155906166
7       108     antigen processing and presentation of peptide antigen
GO:0019882      1.27460005119315e-06    14.9581709145427        0.557470071275344
7       152     antigen processing and presentation
GO:0034341      3.068198791441e-06      17.3775075987842        0.407099854681337
6       111     response to interferon-gamma
GO:0000216      1.00390326144296e-05    20.1632882882883        0.289737734412843
5       79      M/G1 transition of mitotic cell cycle
Tissue: Nerve_Tibial=>Lung      Type:   asymmetric
SourceGene:     RPL7AP11(ENSG00000242445.1)
TargetGeneSet:  WASH7P  TAS1R3  AKR7A2  NBPF8   FCRL5   LPIN1   IGKJ5   IGKC
IGKJ4   IGKJ2   IGKJ1   IGKV4-1 IGKV3-7 IGKV3-15        IGKV2-24        IGKV2-28
IGKV2-30        IGKV1-33        IGKV3D-11       HAT1    ACSL3   CGGBP1  LRRC34  IGJ
VTI1BP2 RP11    PCDHAC1 MUM1    FILIP1  GABRR2  NT5DC1  CLDN15  TPD52   PVT1    GLDC
LCN10   BMI1    ZNF32-AS2       IGHG2   IGHGP   IGHJ1   KIAA0125        HERC2P3
MRPL28  RPS12P27        CD79B   JSRP1   CD79A   FER1L4  CLDN14  IGLV1-36
IGLV3-16        IGLV3-12        IGLC2   DERL3   SAMM50  PIM2
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006958      5.39127483595445e-08    63.8933333333333        0.103799045048786
5       50      complement activation, classical pathway
GO:0006959      1.60955212150291e-07    30.8297413793103        0.253269669919037
6       122     humoral immune response
GO:0006956      1.7552478587324e-07     49.5275862068966        0.13078679676147
5       63      complement activation
GO:0002455      2.05671299082553e-07    47.87   0.134938758563421       5       65
humoral immune response mediated by circulating immunoglobulin
GO:0072376      6.62919932256574e-07    37.2571428571429        0.170230433880008
5       82      protein activation cascade
GO:0002253      2.0475684111775e-06     14.7264740917213        0.620718289391738
7       299     activation of immune response
GO:0016064      2.98603796326027e-06    27.0094339622642        0.230433880008304
5       111     immunoglobulin mediated immune response
GO:0019724      3.40548408730857e-06    26.2605504587156        0.236661822711231
5       114     B cell mediated immunity
GO:0050778      7.49754686067186e-06    11.9897698209719        0.755657047955159
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7       364     positive regulation of immune response
Tissue: Lung=>Nerve_Tibial      Type:   asymmetric
SourceGene:     SLC1A2(ENSG00000110436.6)
TargetGeneSet:  PODN    PRKAA2  RP4     ANKRD13C        MLLT11  MEX3A   UBXN2A  C1D
DGUOK   SSFA2   HSPE1   TIMP4   SUGT1P2 RP11    PRICKLE2        ATG3    ANXA3
ENOPH1  MRPS18C SNCA    RAP1GDS1        CISD2   UGT8    CTD     RNF130  TUBB    MNF1
MOCS1   COX7A2  RP1     QKI     SFT2D1  RPA3    NDUFA4  FIS1    FAM3C   PUF60
EXOSC4  PSMC3   POLR2G  SPCS2   ANGPTL5 ZBTB16  SIDT2   FEZ1    MRPL51  ACVR1B
UBE2N   C12orf76        COX6A1  MRP63   POMP    GTF2F2  MZT1    DAD1    MRPL52
PSME2   PSMA3   RN5S392 GATM    GTF2A2  FAM96B  IL34    GLOD4   PSMB6   TXNDC17
TRAPPC1 DHRS7C  PSMB3   STAT5A  ICT1    SEC11C  NFIC    PIN1    FDX1L   STX10
UBE2S   ISOC2   SNRPB2  DYNLRB1 MRPS6   ZMAT5   APOO
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0051443      7.56359909178388e-09    23.7904365904366        0.41422738910802
8       82      positive regulation of ubiquitin-protein ligase activity
GO:0051351      1.10808786561741e-08    22.5641025641026        0.43443360321085
8       86      positive regulation of ligase activity
GO:0051438      2.66028170384164e-08    19.986013986014 0.484949138467926       8
96      regulation of ubiquitin-protein ligase activity
GO:0051340      3.67391571978226e-08    19.1117056856187        0.505155352570756
8       100     regulation of ligase activity
GO:0031396      1.60633534296587e-07    12.575766509434 0.848660992318871       9
168     regulation of protein ubiquitination
GO:0031398      2.37452569917641e-07    14.7475113122172        0.641547297764861
8       127     positive regulation of protein ubiquitination
GO:0000216      2.80051382406854e-06    17.5485585769781        0.399072728530898
6       79      M/G1 transition of mitotic cell cycle
GO:0031145      3.74283272588697e-06    16.6322930800543        0.419278942633728
6       83      anaphase-promoting complex-dependent proteasomal ubiquitin-dependent
protein catabolic process
GO:0006521      9.77125334533065e-06    20.2573529411765        0.287938550965331
5       57      regulation of cellular amino acid metabolic process
GO:0010565      1.23102059570465e-05    10.2676767676768        0.777939242958965
7       154     regulation of cellular ketone metabolic process
GO:0000209      1.64392722055561e-05    9.79614325068871        0.813300117638918
7       161     protein polyubiquitination
Tissue: Nerve_Tibial=>Lung      Type:   asymmetric
SourceGene:     THNSL1(ENSG00000185875.8)
TargetGeneSet:  ISG15   SSU72   ATP13A2 IFI6    SDC3    YBX1    IFI44L  IFI44   GBP4
GABPB1  ZNF687  RNF187  CMPK2   SRSF7   UBE2E3  FGD5    SHISA5  RP11    RNF7    KLF3
KCNN2   PCYOX1L NRM     PSMB8   TAP1    C6orf106        FGFR1OP PSMB1   WIPI2   FIS1
PARP12  PTK2    LY6E    C9orf167        SEPHS1  GHITM   IFIT3   ACTR1A  RAB1B
NDUFS8  FDX1    ARHGEF12        NTN4    TFCP2   PAN2    SLC25A3 OAS3    OAS2
COX6A1  FBRSL1  ZNF219  ANKRD9  PSMA4   CTD     MRPL28  TCEB2   SBK1    ZNF267
CX3CL1  PSMB10  CHMP1A  GIT1    GJD3    SUPT4H1 TBX2    ATP5A1  PTBP1   UQCR11  AES
UBXN6   ZNF358  TRAPPC5 MAP2K7  TTC9B   EPN1    RBM39   SCAND1  STAU1   OGFR
ATP5J   MX1     SUMO3   DGCR2   ZMAT1   RP13
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0060337      1.12793285414446e-07    21.7022751895991        0.388623624662653
7       72      type I interferon-mediated signaling pathway
GO:0071357      1.12793285414446e-07    21.7022751895991        0.388623624662653
7       72      cellular response to type I interferon
GO:0034340      1.24219943078799e-07    21.3719590268886        0.39402117500519
7       73      response to type I interferon
Tissue: Nerve_Tibial=>Lung      Type:   asymmetric
SourceGene:     UBE2S(ENSG00000108106.8)
TargetGeneSet:  MTND1P23        MTND2P28        DVL1    RP11    JTB     BCAN
ATP1A2  MIR4426 ST13P19 ANKS1B  CTNNA2  C2orf77 ATP2B2  ARPP21  MOBP    RPL7AP31
H3F3AP6 CHCHD2P2        CTD     LIX1    RAB24   PPIAP29 MOG     7SK     EEF1A1P6
CDK6    STMN2   TG      AQP7P3  GRIN3A  TRAF2   OPALIN  COX15   INA     GPR123
SLC1A2  C11orf31        PPP2R5B CXCR5   KIF5A   LPCAT4  IQGAP1  HBA1    NME3
CACNG3  TRADD   TUSC5   TMEM11  GFAP    TCF3    PRKCSH  ZNF491  TSHZ3   TTYH1   PTK6
RP6     PLP1    HTR2C   RP1     FTH1P8  MT
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GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0060134      3.98256092190817e-06    135     0.0327312988720504      3       11
prepulse inhibition
GO:0010976      1.53398505003001e-05    31.3387888707038        0.151754203861324
4       51      positive regulation of neuron projection development
GO:0001964      1.62097344171137e-05    77.1107142857143        0.0505847346204415
3       17      startle response
Tissue: Lung=>Thyroid   Type:   asymmetric
SourceGene:     ATP9B(ENSG00000166377.13)
TargetGeneSet:  C1orf159        SLC45A1 WDTC1   CCDC28B TMEM234 RP4     HMCN1
COL5A2  FAM134A STK25   NIT2    CP      FGFBP1  RP11    CTD     PDLIM7  ADAMTS2
CD109   ADAT2   AP4M1   GFRA2   CTHRC1  ANXA2P2 DNM1    COL5A1  ZEB1    SLC25A45
CAPN5   KRR1P1  COL4A2-AS1      SCFD1   XRCC3   SLC28A2 COL1A1  PGPEP1  ZNF738
DPY19L3 CHMP2A  TSPY26P ADIG    COL9A3  LINC00266-1     TSSK1A  RGAG1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0030199      7.36751988167153e-09    98.8461538461538        0.0707909487232717
5       33      collagen fibril organization
GO:0043588      4.03512162778021e-06    45.3049645390071        0.10940419348142
4       51      skin development
Tissue: Thyroid=>Lung   Type:   asymmetric
SourceGene:     C1orf177(ENSG00000162398.7)
TargetGeneSet:  FGR     BTBD8   C1orf61 SELL    IKBKE   LBR     CCT4    IL1R2
SPOPL   SH3BP5  CMTM6   RP11    FAM208A FAM55C  MIR567  CPA3    CTD     TLR1    TLR6
KIT     FYB     CTB     MAP3K5  NCF1C   ATXN7L1 MTPN    PCMTD1  NTNG2   ABCA2   FUT7
ABI1    ACBD5   RASGEF1A        IKZF5   CLEC4D  IRAK3   PLXNC1  APAF1   GIT2
GLT1D1  ZDHHC20 TNFSF13B        C14orf118       CCNK    DYX1C1-CCPG1    CORO1A  TNS4
NKIRAS2 BECN1   FMNL1   UTP18   MBP     C19orf38        RAB8A   CD177   VSTM1
SIRPD   PMEPA1  ITGB2   IL17RA  GTPBP1  RP3     NFAM1   PANX2   CFP     PRAF2
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0002764      2.63465017376357e-06    10.7265151515152        0.892394989966092
8       248     immune response-regulating signaling pathway
GO:0050778      5.22588770360399e-06    8.28011791680314        1.30980554978894
9       364     positive regulation of immune response
GO:0002253      1.04359138787685e-05    8.81474539206498        1.07591170161235
8       299     activation of immune response
Tissue: Lung=>Thyroid   Type:   cluster
SourceGene:     CCDC104(ENSG00000163001.7)
TargetGeneSet:  WASH7P  MTND1P23        MTND2P28        NOL9    DFFA    CLCN6
DNAJC16 NECAP2  RP4     KDM1A   TCEB3   PAQR7   RP1     EYA3    MED18   YTHDF2
TXLNA   ZMYM6NB ZMYM1   EIF2C1  KDM4A   CCDC24  TOE1    IPP     NSUN4   SELRC1
DDX20   BCL9    RP11    RPRD2   GOLPH3L SCNM1   PYGO2   FLAD1   ETV3    HMGN1P4
RBBP5   ZC3H11B C2orf18 MSH6    ERLEC1  GPR75   DCTN1   C2orf68 KDM3A   TMEM127 LYG2
POLR1B  RBP4    AMMECR1L        STAM2   KRT8P15 RQCD1   EIF4E2  HMGB1P5 ACAA1
MYD88   PPM1M   PDE12   FAM3D   QTRTD1  MSL2    P2RY1   RAP2B   ABCF3   CRYGS
LRCH3   TADA2B  ENOPH1  AGPAT9  PLRG1   MARVELD2        PHAX    MTND5P11
RBM22   ABCF1   C6orf47 AGPAT1  ZBTB9   TAF8    RPL7L1  BEND6   FAM120B FTSJ2
FBXL18  INMT    AQP1    URGCP   YKT6    PURB    SNORA5A ZNF713  BAZ1B   FAM200A
ZNF498  MEPCE   GCC1    METTL2A SMO     ZC3HC1  ZNF212  ZNF746  CTD     INTS9   TTI2
SGK196  YTHDF3  PDP1    KIAA1429        TSPYL5  UTP23   TSSK5P1 ZNF517  RRAGA
KLHL9   STOML2  FOXE1   LINC00256B      ZBTB6   TBC1D13 EXOSC2  BRD3    C9orf167
C10orf140       THNSL1  ADO     AP3M1   ADK     SMC3    SIRT3   CHRNA10 SLC35C1
ARHGAP1 HEXIM1  BTBD18  MTA2    HNRNPUL2        ZBTB3   DPF2    C11orf68
EIF1AD  IL18BP  FAM76B  MSANTD4 PAFAH1B2        DDX6    PKNOX2  CERS5   SMUG1
ZC3H10  CAND1   TDG     BRAP    RNF6    KBTBD7  KCNRG   ALG11   CHAMP1  SALL2
RBM23   PROX2   DLST    MLH3    GOLGA8IP        TJP1    RNF111  PLEKHO2 FEM1B   NRG4
WASH3P  POLR3K  MAPK8IP3        THUMPD1 MAZ     TBC1D10B        CIAPIN1 CTRL
NFATC3  CHTF8   CENPBD1 PRDM7   VPS53   SLC16A13        TP53    ERAL1   CRLF3
ZNF830  TADA2A  MED1    WIPF2   IGFBP4  CNP     FAM134C VPS25   RUNDC1  ZNF652
PPP1R9B ANKRD40 TACO1   CANT1   ZBTB7A  FEM1A   ZNF557  ZNF562  FBXL12  ZNF440
ZNF429  C19orf12        ZNF526  BLOC1S3 CPT1C   SIGLEC7 ZNF613  ZNF542  ZNF264
ZNF543  ZNF547  ZNF549  ZNF134  AVP     FASTKD5 NANP    PLAGL2  NFS1    C20orf4
ZSWIM3  ZSWIM1  NCOA5   TP53RK  ZNFX1   PARD6B  ADNP    CSTF1   C20orf11
DNAJC28 SIM2    NDUFV3  NF2     NUP50   GEMIN8  GSPT2   SMC1A   BHLHB9
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GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
Tissue: Lung=>Thyroid   Type:   asymmetric
SourceGene:     CES1(ENSG00000198848.7)
TargetGeneSet:  NOL9    DNAJC16 RP11    WASF2   EYA3    ZSCAN20 EIF2C1  MFI2
SF3A3   RBBP5   DIEXF   HEATR1  FKBP1B  POLR1B  C2orf76 CLN5    ZXDC    UBQLN4P1
MYNN    ABCF3   RNF168  NOP14   SRP72   NUP155  CTB     DAGLB   ZNF713  MEPCE
CBLL1   TNPO3   PRSS37  TRIM35  SGK196  ZNF623  LINC00476       TBC1D13 EXOSC2  ADK
HIF1AN  C10orf2 SMC3    CTR9    SPTY2D1 NAT10   NUP160  ZBTB3   EIF1AD  DDX6
LPCAT3  KIAA1467        DDX23   CAND1   BRAP    SUPT16H C14orf21        HMGN2P5 TSR1
C17orf85        NLGN2   TMEM199 FLOT2   FAM134C FTSJ3   NOL11   CANT1   SUGP1
KCNJ14  C19orf76        ZNF264  ZNF543  ZNF304  ZNF547  ZNF749  DSTN    CRNKL1
COL18A1 RP13    UTP14A
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0071843      3.11080879409177e-11    15.9719764011799        1.05847346204415
13      239     cellular component biogenesis at cellular level
GO:0022613      2.4363836226506e-10     15.3564463705309        0.996470832468341
12      225     ribonucleoprotein complex biogenesis
GO:0022618      3.79493421339188e-06    16.6191398682681        0.420732129264411
6       95      ribonucleoprotein complex assembly
GO:0042254      4.08689031830945e-06    12.3196194712132        0.659885129056813
7       149     ribosome biogenesis
GO:0071826      5.11622235357972e-06    15.7296404988995        0.442875925541485
6       100     ribonucleoprotein complex subunit organization
GO:0006364      6.42344639483031e-06    15.0833919774806        0.460590962563144
6       104     rRNA processing
GO:0016072      8.88162284088054e-06    14.2072281167109        0.487163518095634
6       110     rRNA metabolic process
Tissue: Lung=>Thyroid   Type:   cluster
SourceGene:     CHIC2(ENSG00000109220.6)
TargetGeneSet:  TP73-AS1        KLHL21  ERRFI1  FBXO44  RP3     DNAJC16 TCEB3
TXLNA   RP4     YIPF1   CTH     ST7L    BCL2L15 GABPB1  SLC27A3 PYGO2   FLAD1   BAP1
NAV1    PFKFB2  IRF6    VSNL1   BRE     NFU1    AMMECR1L        STAM2   CFLAR   RP11
RQCD1   PSMD1   VGLL4   SATB1   CNOT10  MLH1    USP4    TFG     QTRTD1  TMEM39A
CCDC37  COPG1   KLHL24  CRYGS   UBXN7   TEC     SCFD2   ANKRD17 SOWAHB  MRPL1
SEC31A  SEC24D  TMEM154 DHX29   CTD     GTF2H2C ANKRA2  TMEM167A        ARSK
SAR1B   CAMK2A  MYOZ3   SAP30L  RARS    BNIP1   SNCB    GRM6    TRIM27  ABCF1
PPP1R10 HSPA1L  AGPAT1  LINC00336       PPIL1   BYSL    COQ3    RTN4IP1 SESN1
LATS1   IGF2R   DLL1    C7orf26 POLR2J4 TBL2    ZNF3    SRRT    CEP41   PPP2R2A
CEBPD   RAD21   PLAA    FAM219A GBA2    ALDH1B1 NCBP1   TGFBR1  C9orf91 GOLGA2  EDF1
CCNY    TIMM23  STOX1   PPP3CB  SEC24C  AP3M1   TBC1D12 ALDH18A1        ENTPD7  GBF1
RNU4-5P ZNF195  CHRNA10 C11orf42        MUC15   HIPK3   CAPRIN1 PSMC3   MTCH2
CTNND1  SLC22A20        UCP3    ACER3   ZBTB16  PAFAH1B2        ARCN1   NOP2    ASUN
PRKAG1  AQP6    CERS5   TFCP2   COPZ1   METTL1  METTL21B        ALDH1L2 CKAP4
MYO1H   KCTD10  ANAPC7  ZNF140  N4BP2L1 CYCSP34 TDRD3   GNPNAT1 ARG2    PGF
EIF2B2  DIO2    GTF2A1  PSMC1   CALM1   FAM181A MARK3   TJP1    TRIP4   C15orf39
NRG4    AKAP13  IGF1R   PMM2    UBFD1   DCTN5   CIAPIN1 GOT2    CTCF    HAS3
AFG3L1P TP53    KCNAB3  VAMP2   ZSWIM7  DRG2    UTP6    PIGW    PSME3   BRCA1
TMEM106A-AS1    UBTF    RSAD1   MBTD1   FAM100B ZNF562  ZNF44   MPV17L2 LSM4
ZNF429  ZNF565  ZNF790  PSMC4   ZNF470  ZNF586  ZNF135  ZNF544  FKBP1A  CDK5RAP1
MANBAL  SLC13A3 DOK5    RP1     CTSZ    LINC00315       ARL2BPP10       KREMEN1
L3MBTL2 APOO    BCOR    NDP     WBP5    RP6     LHFPL1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0048199      3.18112059422577e-10    40.0673684210526        0.295204484118746
8       27      vesicle targeting, to, from or within Golgi
GO:0006901      3.13155329490008e-09    28.1797530864198        0.382672479413189
8       35      vesicle coating
GO:0006900      5.04272049283586e-09    26.2326436781609        0.4045394782368 8
37      membrane budding
GO:0006903      5.04272049283586e-09    26.2326436781609        0.4045394782368 8
37      vesicle targeting
GO:0051650      4.45154798487893e-08    19.004  0.52480797176666        8       48
establishment of vesicle localization
GO:0051648      5.08809713526669e-07    13.3202339181287        0.710677461767352
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8       65      vesicle localization
GO:0031400      1.03206276884596e-06    5.15568641884431        3.28004982354162
15      300     negative regulation of protein modification process
GO:0002474      1.32864507079132e-06    9.53221476510067        1.08241644176874
9       99      antigen processing and presentation of peptide antigen via MHC class
I
GO:0051656      1.57335645071639e-06    9.32367960315144        1.10428344059235
9       101     establishment of organelle localization
GO:0048002      2.76127071889211e-06    8.660158633313  1.18081793647498        9
108     antigen processing and presentation of peptide antigen
GO:0032269      3.91005541938262e-06    4.33616061006926        4.13286277766245
16      378     negative regulation of cellular protein metabolic process
GO:0016050      6.73855416381985e-06    9.13092369477912        0.994948446474292
8       91      vesicle organization
GO:0035964      9.10906238497008e-06    41.2236652236652        0.14213549235347
4       13      COPI-coated vesicle budding
GO:0048194      9.10906238497008e-06    41.2236652236652        0.14213549235347
4       13      Golgi vesicle budding
GO:0048200      9.10906238497008e-06    41.2236652236652        0.14213549235347
4       13      Golgi transport vesicle coating
GO:0048205      9.10906238497008e-06    41.2236652236652        0.14213549235347
4       13      COPI coating of Golgi vesicle
GO:0051248      1.46951828398415e-05    3.87365778831404        4.59206975295827
16      420     negative regulation of protein metabolic process
GO:0031396      1.57121162212506e-05    6.04473144030106        1.83682790118331
10      168     regulation of protein ubiquitination
GO:0048207      1.70955476155306e-05    33.7237308146399        0.164002491177081
4       15      vesicle targeting, rough ER to cis-Golgi
GO:0048208      1.70955476155306e-05    33.7237308146399        0.164002491177081
4       15      COPII vesicle coating
GO:0090114      1.70955476155306e-05    33.7237308146399        0.164002491177081
4       15      COPII-coated vesicle budding
Tissue: Thyroid=>Lung   Type:   asymmetric
SourceGene:     CLEC17A(ENSG00000187912.7)
TargetGeneSet:  MXRA8   RPL11   PRDX3P2 RNF11   EFNA4   APOA2   SMG7    DIEXF
COX5B   MZT2B   SETD5   RPL15   CRTAP   RPL29   RP11    C4orf48 OCIAD1  WDFY3-AS2
RPL34   NDUFS4  SYNGAP1 C6orf162        LINC00271       C6orf72 SEPT7   GBAS
CHCHD2  NDUFA5  C8orf40 RAB2A   POLR2K  MRPL41  FAM204A RPLP2   SVIP    FAU
ATP5L   ZCRB1   ATXN2   SIVA1   RPLP1   AKAP13  TTLL13  NDUFB10 BCL7C   RPL13
WDR81   ALOX15B RPS7P1  CHST9   IER3IP1 ATP5D   RPS15   C19orf70        ZNF414
C19orf60        ZNF428  SEL1L2  ELMO2   MORC2   COX7B   TAF9B   FERP1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0000184      1.15108487616834e-12    40.9977064220183        0.345858418102553
10      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006415      3.90611021708204e-12    47.6507760532151        0.264479966784306
9       91      translational termination
GO:0019080      1.2699145793037e-11     31.6223404255319        0.438862362466265
10      151     viral genome expression
GO:0019083      1.2699145793037e-11     31.6223404255319        0.438862362466265
10      151     viral transcription
GO:0006414      1.45494050106561e-11    40.6619318181818        0.305169192443429
9       105     translational elongation
GO:0006614      1.45494050106561e-11    40.6619318181818        0.305169192443429
9       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.5866521412126e-11     40.2399250234302        0.308075565704795
9       106     cotranslational protein targeting to membrane
GO:0045047      1.5866521412126e-11     40.2399250234302        0.308075565704795
9       106     protein targeting to ER
GO:0072599      1.5866521412126e-11     40.2399250234302        0.308075565704795
9       106     establishment of protein localization to endoplasmic reticulum
GO:0000956      3.90262604607315e-11    28.0070754716981        0.491177081170853
10      169     nuclear-transcribed mRNA catabolic process
GO:0070972      4.21404579777737e-11    35.7798165137615        0.342952044841187
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9       118     protein localization to endoplasmic reticulum
GO:0006402      6.52857140390416e-11    26.4899553571429        0.517334440523147
10      178     mRNA catabolic process
GO:0006401      2.62586613772342e-10    22.7788461538462        0.595806518580029
10      205     RNA catabolic process
GO:0006413      4.11871732601169e-10    27.2078830260648        0.441768735727631
9       152     translational initiation
GO:0006612      4.36708395855424e-10    27.0170454545455        0.444675108988997
9       153     protein targeting to membrane
GO:0043624      4.36708395855424e-10    27.0170454545455        0.444675108988997
9       153     cellular protein complex disassembly
GO:0043241      5.81757041012065e-10    26.1012812690665        0.459206975295827
9       158     protein complex disassembly
GO:0019058      8.43176571987788e-10    20.0622171945701        0.671372223375545
10      231     viral infectious cycle
GO:0034623      1.37023776962067e-09    23.5438016528926        0.505708947477683
9       174     cellular macromolecular complex disassembly
GO:0032984      1.7604437071694e-09     22.8433155080214        0.520240813784513
9       179     macromolecular complex disassembly
GO:0022415      2.65183685286986e-09    17.69875        0.755657047955159       10
260     viral reproductive process
GO:0072594      5.56069320907923e-09    19.8797202797203        0.592900145318663
9       204     establishment of protein localization to organelle
GO:0022904      1.0207041821532e-08     32.1797752808989        0.279011833091136
7       96      respiratory electron transport chain
GO:0071845      9.73244793540003e-08    14.0171900826446        0.825410006227943
9       284     cellular component disassembly at cellular level
GO:0022900      1.03666298067087e-07    22.4913385826772        0.389454017023043
7       134     electron transport chain
GO:0022411      1.09661073000473e-07    13.8123167155425        0.837035499273407
9       288     cellular component disassembly
GO:0045333      1.54341118457122e-07    21.1466666666667        0.412705003113971
7       142     cellular respiration
GO:0016032      4.76546954001427e-07    9.89795918367347        1.31077434087606
10      451     viral reproduction
GO:0006119      6.63194113585121e-07    36.6037735849057        0.168569649159228
5       58      oxidative phosphorylation
GO:0033365      6.80668467421228e-06    8.19651253918495        1.37471455262612
9       473     protein localization to organelle
GO:0006605      6.92388962939753e-06    8.1782991202346 1.37762092588748        9
474     protein targeting
Tissue: Lung=>Thyroid   Type:   cluster
SourceGene:     DHX40(ENSG00000108406.4)
TargetGeneSet:  NOC2L   DNAJC16 ARHGEF19        ARHGEF19-AS1    PAQR7   RP11    NCDN
CCDC24  C1orf123        INSL5   WDR77   ST7L    MOV10   RP4     PIAS3   TARS2
FLAD1   CCT3    METTL13 DHX9    BAP1    NAV1    C1orf131        ODC1    EIF2B4
SRBD1   POLR1A  PSMD14  RQCD1   PSMD1   C3orf62 PBRM1   WNT5A   WNT5A-AS1
GRAMD1C QTRTD1  RNF13   MRPL47  KLHL24  EIF2B5  AP2M1   ABCF3   ALG3    PSMD2
SCFD2   PPAT    SEC31A  ETFDH   MFAP3L  TRAPPC11        DHX29   ARSB    PAIP2
GALNT10 SAP30L  TRIM27  PRR3    PTMAP1  TUBB    VARS    WDR46   PPIL1   AARS2
GPR63   RP1     LATS1   IQCE    YKT6    TBRG4   COPS6   ORC5    PUS7    METTL2A SMO
CEP41   SLC35B4 TTC26   ABCB8   SMARCD3 YBX1P4  BNIP3L  TRIM35  CHMP4C  VCP
STOML2  FXN     NCBP1   ANKS6   DNM1    NGB     C10orf114       C10orf140
RRP12   ENTPD7  RRP8    RCOR2   CD248   RIN1    C2CD2L  NOP2    COPS7A  TUBA1C
TFCP2   TARBP2  CYP27B1 METTL1  NT5DC3  ALDH1L2 CKAP4   POLR3B  MYO1H   KCTD10
ANAPC7  ATXN2   GTF2H3  PUS1    GOLGA3  N4BP2L1 PRMT5-AS1       PRMT5   ARG2
TUBGCP4 CTD     GLYR1   TBC1D10B        E2F4    CTCF    C16orf46        COX4NB
FAM57A  TSR1    ANKFY1  ERAL1   UTP6    LIG3    TADA2A  LEPREL4 PSME3   TMEM106A
ATXN7L3 UBTF    PNPO    RSAD1   INTS2   GPS1    NACC1   PRKACA  PIK3R2  RAB3A
C19orf12        ZNF790  PSMC4   GRWD1   ZNF135  NSFL1C  NOP56   ZNF341  ELMO2   ADNP
ZFP64   GTPBP5  PATZ1   L3MBTL2 KIAA0930        FAM123B
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0034660      6.22355165320264e-09    7.26736705996444        2.58355823126427
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16      285     ncRNA metabolic process
GO:0022613      1.60833835969351e-08    8.00121521448536        2.03965123520864
14      225     ribonucleoprotein complex biogenesis
GO:0071843      3.44876780339617e-08    7.49591642924976        2.16656286762162
14      239     cellular component biogenesis at cellular level
GO:0032269      1.68553856327261e-06    4.97185807922485        3.42661407515051
15      378     negative regulation of cellular protein metabolic process
GO:0022618      2.30828000140848e-06    10.6405008877675        0.861186077088091
8       95      ribonucleoprotein complex assembly
GO:0071826      3.4025624660899e-06     10.0586779780841        0.906511660092727
8       100     ribonucleoprotein complex subunit organization
GO:0051248      6.10921304185342e-06    4.44284802043423        3.80734897238945
15      420     negative regulation of protein metabolic process
GO:0071158      7.85092709955775e-06    11.0173442333186        0.725209328074182
7       80      positive regulation of cell cycle arrest
GO:0006521      1.22894247264736e-05    13.4296470588235        0.516711646252854
6       57      regulation of cellular amino acid metabolic process
GO:0034470      1.38935912753098e-05    6.14615050021749        1.81302332018545
10      200     ncRNA processing
GO:0031400      1.80428717651274e-05    4.91316526610644        2.71953498027818
12      300     negative regulation of protein modification process
GO:0031397      1.9787170992772e-05     9.45398481973434        0.833990727285309
7       92      negative regulation of protein ubiquitination
Tissue: Lung=>Thyroid   Type:   asymmetric
SourceGene:     ENSG00000203606.3
TargetGeneSet:  ZNF683  KIF21B  LRRN4   RPSA    XCR1    RSRC1   HELQ    RPL34   RP11
IL12B   ANKRD61 AHCYL2  RPS20   RPS6    RPL35   NRG3    RPL13AP5        MED17
RPL18AP3        RPS3AP6 FTLP14  CTD     RPS15   IL12RB1 UBA52   RPL13A  RPL28   RPS5
BACH1   SOX10   GRAP2   MAGEE2
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      1.07543866020772e-16    126.507936507937        0.151131409591032
10      91      translational termination
GO:0006414      4.76781576616223e-16    107.759398496241        0.17438239568196
10      105     translational elongation
GO:0006614      4.76781576616223e-16    107.759398496241        0.17438239568196
10      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      5.25979868331653e-16    106.629464285714        0.17604318040274
10      106     cotranslational protein targeting to membrane
GO:0045047      5.25979868331653e-16    106.629464285714        0.17604318040274
10      106     protein targeting to ER
GO:0072599      5.25979868331653e-16    106.629464285714        0.17604318040274
10      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      1.5921890154812e-15     94.7023809523809        0.195972597052107
10      118     protein localization to endoplasmic reticulum
GO:0000184      1.73672009496678e-15    93.826998689384 0.197633381772888       10
119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      1.98720990239267e-14    72.370820668693 0.250778492837866       10
151     viral genome expression
GO:0019083      1.98720990239267e-14    72.370820668693 0.250778492837866       10
151     viral transcription
GO:0006413      2.12526461752503e-14    71.8561368209256        0.252439277558646
10      152     translational initiation
GO:0006612      2.27186441596622e-14    71.3486513486513        0.254100062279427
10      153     protein targeting to membrane
GO:0043624      2.27186441596622e-14    71.3486513486513        0.254100062279427
10      153     cellular protein complex disassembly
GO:0043241      3.15009360763803e-14    68.9140926640927        0.26240398588333
10      158     protein complex disassembly
GO:0000956      6.23373642231738e-14    64.0970350404313        0.280672617811916
10      169     nuclear-transcribed mRNA catabolic process
GO:0034623      8.37322751028232e-14    62.1210801393728        0.288976541415819
10      174     cellular macromolecular complex disassembly
GO:0006402      1.05359344762146e-13    60.625  0.295619680298941       10      178
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mRNA catabolic process
GO:0032984      1.11494341089671e-13    60.262045646661 0.297280465019722       10
179     macromolecular complex disassembly
GO:0072594      4.16097052637557e-13    52.4042709867452        0.338800083039236
10      204     establishment of protein localization to organelle
GO:0006401      4.37045607501466e-13    52.1318681318681        0.340460867760017
10      205     RNA catabolic process
GO:0019058      1.44573429335072e-12    45.9146735617324        0.383641270500311
10      231     viral infectious cycle
GO:0022415      4.70042883773067e-12    40.5057142857143        0.431804027402948
10      260     viral reproductive process
GO:0071845      1.12918495204337e-11    36.8952033368092        0.471662860701682
10      284     cellular component disassembly at cellular level
GO:0022411      1.29696529821864e-11    36.3540596094553        0.478305999584804
10      288     cellular component disassembly
GO:0033365      6.99418000080748e-11    25.5769230769231        0.785551172929209
11      473     protein localization to organelle
GO:0006605      7.15427705087035e-11    25.5198537963117        0.78721195764999
11      474     protein targeting
GO:0016032      1.05208683112948e-09    22.6530612244898        0.749013909072037
10      451     viral reproduction
GO:0042274      3.23105168313163e-06    137.257142857143        0.0298941249740502
3       18      ribosomal small subunit biogenesis
GO:0072540      1.58285995353423e-05    655.681818181818        0.00664313888312228
2       4       T-helper 17 cell lineage commitment
GO:2000328      1.58285995353423e-05    655.681818181818        0.00664313888312228
2       4       regulation of T-helper 17 cell lineage commitment
GO:2000330      1.58285995353423e-05    655.681818181818        0.00664313888312228
2       4       positive regulation of T-helper 17 cell lineage commitment
Tissue: Thyroid=>Lung   Type:   asymmetric
SourceGene:     EXOC6B(ENSG00000144036.9)
TargetGeneSet:  RPL22   PIK3CD  CLCNKB  RP1     RPL11   NIPAL3  RPS8    S100A3
ARHGAP30        DUSP12  RGS18   RPS7    COMMD1  COA5    RPL31   RPL37A  GPBAR1
DDX11   RPL32   LSM3    RPL14   CCR2    C3orf27 RPL35A  MYL5    HTT     OCIAD1
RPL34   TLR2    RPL37   CTD     PLK2    ERCC8   CDC23   DOCK2   RUFY1   CSNK2B
HNRNPC  MEA1    IGF2R   LINC00473       AOAH    SBDS    MAGI2-AS3       PON2
IMPDH1  RP11    SPIN1   C9orf3  BAAT    EDF1    PIK3AP1 FAM204A RPLP2   RP13    CTR9
RPS13   SAA1    DEPDC7  PTPRJ   FAU     SIPA1   ARAP1-AS2       ATP5L   RPS25
C3AR1   B4GALNT1        APAF1   GLT8D2  PSPC1   RPL3P4  AQP9    CSK     C16orf70
GNA15   EMR2    POU2F2  RPL18   SIGLEC5 FPR2    ZNF813  LILRB4  SIRPG   CDS2    HCK
RP4     SLCO4A1 SH3BP1  PPARA   AFF2
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      1.22551557183846e-20    50.8444444444444        0.478582797038267
16      91      translational termination
GO:0006414      1.39415830001593e-19    42.8044943820225        0.552210919659539
16      105     translational elongation
GO:0006614      1.39415830001593e-19    42.8044943820225        0.552210919659539
16      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.63555547543825e-19    42.3259259259259        0.557470071275344
16      106     cotranslational protein targeting to membrane
GO:0045047      1.63555547543825e-19    42.3259259259259        0.557470071275344
16      106     protein targeting to ER
GO:0072599      1.63555547543825e-19    42.3259259259259        0.557470071275344
16      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      9.85193947891127e-19    37.3150326797386        0.620579890665006
16      118     protein localization to endoplasmic reticulum
GO:0000184      1.13375747411844e-18    36.9501618122977        0.625839042280811
16      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0043624      2.38731745532775e-18    30.1673728813559        0.804650197218186
17      153     cellular protein complex disassembly
GO:0043241      4.16889475989191e-18    29.0873903113355        0.830945955297211
17      158     protein complex disassembly
GO:0000956      1.33170191905417e-17    26.9615298840321        0.888796623071068
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17      169     nuclear-transcribed mRNA catabolic process
GO:0034623      2.19755195044071e-17    26.0937061427183        0.915092381150093
17      174     cellular macromolecular complex disassembly
GO:0006402      3.24419208790125e-17    25.4382566585956        0.936128987613314
17      178     mRNA catabolic process
GO:0032984      3.57067420166205e-17    25.2794517681523        0.941388139229119
17      179     macromolecular complex disassembly
GO:0019080      5.69250548323201e-17    28.1283950617284        0.794131893986575
16      151     viral genome expression
GO:0019083      5.69250548323201e-17    28.1283950617284        0.794131893986575
16      151     viral transcription
GO:0006413      6.33714914455192e-17    27.9196078431373        0.799391045602381
16      152     translational initiation
GO:0006612      7.04937307436429e-17    27.7138686131387        0.804650197218186
16      153     protein targeting to membrane
GO:0006401      3.58430859198859e-16    21.7435088351965        1.07812608124005
17      205     RNA catabolic process
GO:0072594      7.08232069808961e-15    20.1234042553191        1.07286692962425
16      204     establishment of protein localization to organelle
GO:0019058      4.99815591437332e-14    17.5627906976744        1.21486402325099
16      231     viral infectious cycle
GO:0071845      8.14201157117466e-14    15.2247825810957        1.49359905888866
17      284     cellular component disassembly at cellular level
GO:0022411      1.02371903515935e-13    14.9958096191131        1.51463566535188
17      288     cellular component disassembly
GO:0022415      3.13993713003726e-13    15.4437158469945        1.36737942010933
16      260     viral reproductive process
GO:0016032      1.33164525692891e-11    9.9926734092538 2.37187737872812        18
451     viral reproduction
GO:0033365      2.92686818870582e-11    9.49450549450549        2.48757871427583
18      473     protein localization to organelle
GO:0006605      3.03052855217993e-11    9.47300362976407        2.49283786589163
18      474     protein targeting
GO:0042273      3.38648218066051e-07    99.7708333333333        0.0631098193896616
4       12      ribosomal large subunit biogenesis
GO:0050900      4.6320715091572e-06     8.18881883685023        1.26745553940904
9       241     leukocyte migration
GO:0042254      1.29733160687055e-05    10.1685037762809        0.783613590754965
7       149     ribosome biogenesis
GO:0006364      1.74693870538412e-05    12.4871720116618        0.546951768043734
6       104     rRNA processing
Tissue: Lung=>Thyroid   Type:   asymmetric
SourceGene:     MEIS3(ENSG00000105419.10)
TargetGeneSet:  C1QA    C1QC    C1QB    RP4     RP11    CD84    SLAMF1  FCGR2A
TRIM54  C2orf68 IGKV4-1 IGKV1-5 IGKV3-20        IGKV2-28        CLASP1  WIPF1   BTD
TEX264  CD86    CTD     CD180   SMN2    DOCK2   MIR590  NCF1    PIK3CG  TMEM209 DOK2
TNFSF8  ZDHHC12 FAM78A  MS4A7   NCKAP1L RP13    LINC00543       RPL21P110
TRAV12-3        IGHA2   IGHA1   IGHV3-23        IGHV1-69        IGHV3-74
PLCB2   CD68    VAV1    MYO1F   TYROBP  MAP4K1  CEACAMP3        CD37    SIGLEC9 FPR3
LAIR1   C21orf128       ITGB2   IGLV3-1 IGLL5   IGLC1   NCF4    SH3BP1  APOBEC3F
VSIG4   CXCR3   ZDHHC15 SASH3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0002252      2.87071538339873e-17    25.4311594202899        1.20199294166494
18      386     immune effector process
GO:0006956      2.45869768457851e-13    66.4444444444444        0.196180195142205
9       63      complement activation
GO:0002443      1.2928520344683e-12     25.96071265418  0.657047955158813       12
211     leukocyte mediated immunity
GO:0006958      2.23355898765962e-12    73.945945945946 0.155698567573178       8
50      complement activation, classical pathway
GO:0072376      2.91685239485629e-12    49.0856164383562        0.255345650820012
9       82      protein activation cascade
GO:0006959      3.14566521722145e-12    36.4642857142857        0.379904504878555
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10      122     humoral immune response
GO:0002455      2.02913909719507e-11    54.4295874822191        0.202408137845132
8       65      humoral immune response mediated by circulating immunoglobulin
GO:0002250      3.90545676405975e-10    21.6079027355623        0.616566327589786
10      198     adaptive immune response
GO:0050778      7.41040877791082e-10    14.5185950413223        1.13348557193274
12      364     positive regulation of immune response
GO:0002253      1.34484561432163e-09    15.859681372549 0.931077434087606       11
299     activation of immune response
GO:0016064      1.59786108920534e-09    30.0246654421412        0.345650820012456
8       111     immunoglobulin mediated immune response
GO:0002449      1.83702363129305e-09    22.5443037974684        0.520033215694416
9       167     lymphocyte mediated immunity
GO:0019724      1.9780230461189e-09     29.1687914329424        0.354992734066847
8       114     B cell mediated immunity
GO:0002460      3.73693396883311e-09    20.6889534883721        0.563628814614906
9       181     adaptive immune response based on somatic recombination of immune
receptors built from immunoglobulin superfamily domains
GO:0046631      5.3171472034183e-06     23.2613636363636        0.255345650820012
5       82      alpha-beta T cell activation
GO:0042110      5.46578104487067e-06    9.79925262883462        0.993356861116878
8       319     T cell activation
GO:0046649      6.08926902884319e-06    8.24410377358491        1.34834959518372
9       433     lymphocyte activation
GO:0043372      1.86112825578915e-05    73.4285714285714        0.0529375129748806
3       17      positive regulation of CD4-positive, alpha-beta T cell
differentiation
Tissue: Lung=>Thyroid   Type:   asymmetric
SourceGene:     MORC2(ENSG00000133422.7)
TargetGeneSet:  RP4     C1orf159        UBE2J2  CEP104  DNAJC16 HSPB7   RP11    EYA3
KPNA7   TAL1    RP1     NFIA    SLC35A3 GOLPH3L UBQLN4  CCT3    POGK    CDC73
TMEM81  RBBP5   LINC00467       SMC6    TTC32   UBXN2A  PREB    SLC5A6  EIF2B4
ERLEC1  PNPT1   CCT4    SPR     CCT7    AUP1    RMND5A  MRPS5   ASTL    AMMECR1L
TFPI    HSPD1   HDLBP   NKIRAS1 ABHD5   GLYCTK  NEK4    PPP4R2  PTPLB   A4GNT
SLC25A36        ABCF3   CEP19   LRCH3   ZNF141  CLOCK   EIF4E   FAM105B ZFR
DNAJC21 CTD     IPO11   ZFYVE16 SHROOM1 CSNK1A1 TSPAN17 TRIM27  HCG20   HLA-DOB
RING1   TAF8    MTO1    PGM3    PEX7    NHSL1   AQP1    PURB    YWHAG   ZKSCAN1
AGFG2   CTA     C7orf53 CADPS2  SMO     NFE2L1  TRBV7-3 ABCF2   DNAJB6  KBTBD11
NEIL2   POLR3D  NKX3-1  PPP2R2A LSM12P1 KAT6A   C8orf40 ZHX1    IFNK    DNAJA1
TESK1   DCAF10  C9orf40 SUSD3   NIPSNAP3B       NOXA1   FBXO18  TAF3    BMS1
ZFAND4  P4HA1   AP2A2   RIC3    ETFA    MTA2    C11orf84        MARK2   STIP1   KLC2
RBM14   C11orf30        DDX10   C11orf92        PAFAH1B2        HSPA8   FKBP4
TULP3   C12orf33        KIAA1467        REP15   SLC35E3 CCT2    TDG     C12orf34
ATXN2   C12orf65        RPL22P19        RAN     PUS1    GOLGA3  RPL23AP67
MPHOSPH8        HSPH1   NHLRC3  DHRS12  SUGT1   A2LD1   PRMT5-AS1       PRMT5
ACIN1   SOCS6   DHRS7   AHSA1   HSP90AA1        GOLGA8IP        PPP1R14D
TP53BP1 AP4E1   TNFAIP8L3       PIGB    CSNK1G1 PEAK1   DNAJA4  CARHSP1 MAZ
SULT1A3 CD2BP2  TBC1D10B        DNAJA2  CCL22   GFOD2   MAF     GAN     ZDHHC7
KLHDC4  VPS53   DLG4    GIT1    CCL16   WIPF2   LEPREL4 SRP68   JMJD6   CANT1   RP13
ADAT3   SAFB    ELAVL1  ZNF562  CLEC17A LIN37   ZNF781  MAP3K10 MIA     IRGQ
MYPOP   KCNJ14  ZNF347  ZNF761  ZNF814  ZNF329  RP3     KRT18P4 KRT18P5 CRKL
TOP3B   SGSM1   MORC2   MID2
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006457      1.23318444524738e-09    8.17217391304348        2.30184762300187
16      216     protein folding
GO:0006986      9.67775375886308e-06    7.33293103448276        1.37471455262612
9       129     response to unfolded protein
GO:0035966      1.48379429324467e-05    6.92533260928591        1.44931146633451
9       136     response to topologically incorrect protein
GO:0006458      1.61056528419891e-05    12.8396396396396        0.543491799875441
6       51      'de novo' protein folding
Tissue: Lung=>Thyroid   Type:   asymmetric
SourceGene:     MRS2P2(ENSG00000257802.1)
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TargetGeneSet:  MTND1P23        MTND2P28        NOL9    SPEN    RP11    RP1
WASF2   EYA3    MED18   PHACTR4 PFN1P8  RPRD2   POGK    RBBP5   CICP5   RN5S78
GPR75   AAK1    POLR1A  RQCD1   QTRTD1  ANKRD17 CTD     APC     PHAX    CTB
MTND5P11        PCDH1   GFOD1   ZBTB9   TAF8    MTRNR2L9        URGCP   ZNF713
ZKSCAN5 MEPCE   CBLL1   ZNF800  TRIM35  KIAA1429        KLHL9   ZFP37   EXOSC2
PRINS   LRRC37A6P       AK3P5   DUPD1   PFN1P11 CHRNA10 MTRNR2L8        FNBP4
ZBTB3   MSANTD4 ZNF202  CD9     ACVRL1  PRKAB1  RBM22P2 ARGLU1  GOLGA8IP        TJP1
MGA     RPL35AP32       C15orf58        MAZ     FTO-IT1 NFATC3  SDR42E1 RNASEK
WIPF2   IGFBP4  FEM1A   ZNF557  ZNF317  ZNF562  ZNF440  ZNF44   ZNF429  LIN37
ZNF565  ZFP82   ZNF480  ZNF765  ZNF264  ZNF543  ZNF17   ZNF544  NCOA5   ADNP
NDUFV3  NF2     PRR14L  ZNF41   UTP14A
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
Tissue: Lung=>Thyroid   Type:   asymmetric
SourceGene:     OLA1(ENSG00000138430.11)
TargetGeneSet:  RP11    NCDN    CCDC24  VANGL1  METTL13 C1D     USP39   RPL31
CCDC74B BDP1    CAB39   TOP2B   ZNF860  XYLB    ZNF167  RPL29   POC1A   EIF4E3
IFT57   CNBP    LRCH3   LAMTOR3 ELOVL6  GTF2F2P1        HINT1   SKP1    PEX7
ATP6V1B2        RPS20   IMPDH1P6        ZNF618  ATP6V1G1        THNSL1  SUFU
C10orf32        C11orf58        FAM76B  ZC3H12C COPS7A  HOXC5   HMGB1   ITM2B
AKAP5   RPL4    C16orf59        RPL23A  RPL19   GPR142  CBX8    RPS15   SIN3B
ZNF536  SIGLEC7 LINC00493       ZFP64   PPM1F   CTPS2   RPS4X   BEX4    MIR224
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      3.21955477760918e-10    37.3116248778899        0.283371392983185
8       91      translational termination
GO:0006414      1.02297167185496e-09    31.8952354416272        0.326966991903675
8       105     translational elongation
GO:0006614      1.02297167185496e-09    31.8952354416272        0.326966991903675
8       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.10395183700959e-09    31.5675675675676        0.330080963255138
8       106     cotranslational protein targeting to membrane
GO:0045047      1.10395183700959e-09    31.5675675675676        0.330080963255138
8       106     protein targeting to ER
GO:0072599      1.10395183700959e-09    31.5675675675676        0.330080963255138
8       106     establishment of protein localization to endoplasmic reticulum
GO:0070972      2.60527694582146e-09    28.1002457002457        0.367448619472701
8       118     protein localization to endoplasmic reticulum
GO:0000184      2.78666132651158e-09    27.845142439737 0.370562590824164       8
119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0072594      1.06541617984882e-08    18.2192307692308        0.635250155698568
9       204     establishment of protein localization to organelle
GO:0019080      1.83321836171405e-08    21.5656775656776        0.470209674070999
8       151     viral genome expression
GO:0019083      1.83321836171405e-08    21.5656775656776        0.470209674070999
8       151     viral transcription
GO:0006413      1.93063668823183e-08    21.4144144144144        0.473323645422462
8       152     translational initiation
GO:0006612      2.03249372007879e-08    21.2652376514445        0.476437616773926
8       153     protein targeting to membrane
GO:0043624      2.03249372007879e-08    21.2652376514445        0.476437616773926
8       153     cellular protein complex disassembly
GO:0043241      2.61444317343914e-08    20.5491891891892        0.492007473531244
8       158     protein complex disassembly
GO:0000956      4.42016157169263e-08    19.1304347826087        0.526261158397343
8       169     nuclear-transcribed mRNA catabolic process
GO:0034623      5.54487334207817e-08    18.5477043308369        0.541831015154661
8       174     cellular macromolecular complex disassembly
GO:0006402      6.6144265321733e-08     18.106200317965 0.554286900560515       8
178     mRNA catabolic process
GO:0032984      6.90801909820277e-08    17.9990516832622        0.557400871911978
8       179     macromolecular complex disassembly
GO:0006605      1.55855312098603e-07    9.74291703722526        1.47602242059373
11      474     protein targeting
GO:0071845      1.83687142817769e-07    12.8463636363636        0.884367863815653
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9       284     cellular component disassembly at cellular level
GO:0006401      1.9656774814511e-07     15.5950061736864        0.638364127050031
8       205     RNA catabolic process
GO:0022411      2.06815135429612e-07    12.6586021505376        0.896823749221507
9       288     cellular component disassembly
GO:0019058      4.88983744313021e-07    13.7515452672403        0.719327382188084
8       231     viral infectious cycle
GO:0016032      9.5001796262223e-07     9.04761904761905        1.40440107951007
10      451     viral reproduction
GO:0022415      1.19467009618048e-06    12.1441441441441        0.809632551380527
8       260     viral reproductive process
GO:0033365      1.46260855257869e-06    8.60413452638075        1.47290844924227
10      473     protein localization to organelle
Tissue: Lung=>Thyroid   Type:   asymmetric
SourceGene:     PRKCDBP(ENSG00000170955.9)
TargetGeneSet:  CEP104  RP4     RP1     EYA3    PEF1    TAL1    RP11    INTS3
UBQLN4  CCT3    RBBP5   URB2    MFSD2B  SLC5A6  PCBP1-AS1       HTRA2   LMAN2L
ANKRD39 AMMECR1L        RBM43   CYP8B1  PHF7    NEK4    SLC25A36        KIAA0226
IDUA    FAM105B GABBR1  C6orf25 DAXX    USP42   METTL2A DNAJB6  NEIL2   CHMP7
KAT6A   DNAJA1  TBC1D13 FBXO18  CEP57L1P1       P4HA1   AP2A2   SLC35C1 C11orf84
STIP1   KLC2    RCE1    C11orf30        C2CD2L  HSPA8   SCN3B   FKBP4   REP15
GCN1L1  DYNLL1  C12orf65        MPHOSPH8        HSPH1   RFC3    PRMT5   SOCS6
ACOT2   DNAL1   AHSA1   HSP90AA1        BUB1B   PPP1R14D        PIGB    CTD
SH2D7   DNAJA4  PRC1    TELO2   USP31   MAZ     C17orf39        C17orf51        GIT1
PIP4K2B WIPF2   KAT2A   PSME3   UBE2Z   CDR2L   QRICH2  JMJD6   CSNK1D  ELOF1
DNAJB1  C19orf60        HIPK4   MIA     IRGQ    SMG9    NOVA2   ZNF329  ZSCAN22 RP3
LINC00478       SGSM1   NF2     PRR14L  LARGE   FAM123B ACRC
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006457      1.01918576706817e-08    12.2661683713611        1.09113556155283
11      216     protein folding
Tissue: Lung=>Thyroid   Type:   asymmetric
SourceGene:     RP11-114F3.5(ENSG00000255566.1)
TargetGeneSet:  DNAJC16 KIAA0090        TXLNA   SF3A3   EBNA1BP2        RP11    CTH
TMEM56  RLIMP2  PIAS3   BCL9    PSMD4   ADAR    FLAD1   FAM5B   NAV1    AKT3
POU3F3  PSMD14  TYW5    RQCD1   PSMD1   QTRTD1  RUVBL1  ALG3    PSMD2   PPAT    TET2
XBP1P1  GALNT10 PRR3    TUBB    VARS    ESR1    LINC00574       FAM71F1 SLC35B4
TAS2R5  TRIM35  OSGIN2  NCBP1   ANKS6   NGB     C10orf140       C11orf42
MRPL17  CAPRIN1 SLC1A2  GANAB   IL18BP  ASUN    METTL1  CAND1   POLR3B  PSME2
TUBGCP4 SRL     HSD3B7  CIAPIN1 TSR1    PIGW    PSMD3   PSME3   FAM100B PIK3R2
RAB3A   SOX12   NOP56   TRMT6   NCOA5   SEPT3   TTC3P1  UTP14A
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006521      4.22002709693428e-09    36.4992727272727        0.244550550134939
7       57      regulation of cellular amino acid metabolic process
GO:0031397      5.0530653684476e-09     25.2292768959436        0.394713168638849
8       92      negative regulation of protein ubiquitination
GO:0006977      1.20627742697857e-08    30.9121725731895        0.283163794893087
7       66      DNA damage response, signal transduction by p53 class mediator
resulting in cell cycle arrest
GO:0072413      1.20627742697857e-08    30.9121725731895        0.283163794893087
7       66      signal transduction involved in mitotic cell cycle checkpoint
GO:0072431      1.20627742697857e-08    30.9121725731895        0.283163794893087
7       66      signal transduction involved in mitotic cell cycle G1/S transition
DNA damage checkpoint
GO:0072474      1.20627742697857e-08    30.9121725731895        0.283163794893087
7       66      signal transduction involved in mitotic cell cycle G1/S checkpoint
GO:0051436      1.342519859634e-08      30.3948484848485        0.28745415542177
7       67      negative regulation of ubiquitin-protein ligase activity involved in
mitotic cell cycle
GO:0072401      1.342519859634e-08      30.3948484848485        0.28745415542177
7       67      signal transduction involved in DNA integrity checkpoint
GO:0072404      1.342519859634e-08      30.3948484848485        0.28745415542177
7       67      signal transduction involved in G1/S transition checkpoint
GO:0072422      1.342519859634e-08      30.3948484848485        0.28745415542177
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7       67      signal transduction involved in DNA damage checkpoint
GO:0072395      1.49159099716136e-08    29.8944858420268        0.291744515950453
7       68      signal transduction involved in cell cycle checkpoint
GO:0033238      2.23646394635328e-08    28.046993006993 0.308905958065186       7
72      regulation of cellular amine metabolic process
GO:0051352      2.23646394635328e-08    28.046993006993 0.308905958065186       7
72      negative regulation of ligase activity
GO:0051437      2.23646394635328e-08    28.046993006993 0.308905958065186       7
72      positive regulation of ubiquitin-protein ligase activity involved in mitotic
cell cycle
GO:0051444      2.23646394635328e-08    28.046993006993 0.308905958065186       7
72      negative regulation of ubiquitin-protein ligase activity
GO:0031571      2.46541900927055e-08    27.6201101928375        0.313196318593869
7       73      mitotic cell cycle G1/S transition DNA damage checkpoint
GO:0002479      2.98331980719466e-08    26.8040106951872        0.321777039651235
7       75      antigen processing and presentation of exogenous peptide antigen via
MHC class I, TAP-dependent
GO:0051439      3.93136073909734e-08    25.6660691421255        0.334648121237285
7       78      regulation of ubiquitin-protein ligase activity involved in mitotic
cell cycle
GO:0000216      4.29919710162785e-08    25.3078282828283        0.338938481765968
7       79      M/G1 transition of mitotic cell cycle
GO:0042590      4.29919710162785e-08    25.3078282828283        0.338938481765968
7       79      antigen processing and presentation of exogenous peptide antigen via
MHC class I
GO:0071158      4.69574322344922e-08    24.959402241594 0.343228842294651       7
80      positive regulation of cell cycle arrest
GO:0031575      5.58225818904681e-08    24.2904242424242        0.351809563352017
7       82      mitotic cell cycle G1/S transition checkpoint
GO:0051443      5.58225818904681e-08    24.2904242424242        0.351809563352017
7       82      positive regulation of ubiquitin-protein ligase activity
GO:0002478      6.07609077336516e-08    23.9691387559809        0.3560999238807 7
83      antigen processing and presentation of exogenous peptide antigen
GO:0031145      6.07609077336516e-08    23.9691387559809        0.3560999238807 7
83      anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein
catabolic process
GO:0019884      7.17524577732959e-08    23.3512820512821        0.364680644938067
7       85      antigen processing and presentation of exogenous antigen
GO:0051351      7.78498809155745e-08    23.054085155351 0.36897100546675        7
86      positive regulation of ligase activity
GO:0071779      7.78498809155745e-08    23.054085155351 0.36897100546675        7
86      G1/S transition checkpoint
GO:0051438      1.67020359586843e-07    20.4494382022472        0.411874610753581
7       96      regulation of ubiquitin-protein ligase activity
GO:0002474      2.06528439981576e-07    19.7784584980237        0.42474569233963
7       99      antigen processing and presentation of peptide antigen via MHC class
I
GO:2000045      2.06528439981576e-07    19.7784584980237        0.42474569233963
7       99      regulation of G1/S transition of mitotic cell cycle
GO:0051340      2.21333232867953e-07    19.5644183773216        0.429036052868314
7       100     regulation of ligase activity
GO:0048002      3.75371955881779e-07    18.0046804680468        0.463358937097779
7       108     antigen processing and presentation of peptide antigen
GO:0031396      5.59805003514572e-07    13.175  0.720780568818767       8       168
regulation of protein ubiquitination
GO:0030330      6.47889667386071e-07    16.5211570247934        0.501972181855927
7       117     DNA damage response, signal transduction by p53 class mediator
GO:0072331      9.0945033689989e-07     15.6600313479624        0.527714345028026
7       123     signal transduction by p53 class mediator
GO:0031398      1.12898228644264e-06    15.1337878787879        0.544875787142758
7       127     positive regulation of protein ubiquitination
GO:0000077      1.32138230143508e-06    14.7615668883962        0.557746868728808
7       130     DNA damage checkpoint
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GO:0000084      1.6200271999712e-06     14.2926270579814        0.57490831084354
7       134     S phase of mitotic cell cycle
GO:0031570      1.78934603801533e-06    14.0690627202255        0.583489031900907
7       136     DNA integrity checkpoint
GO:0007093      2.07094577702927e-06    13.7464187327824        0.596360113486956
7       139     mitotic cell cycle checkpoint
GO:0042770      2.17267426545028e-06    13.6421052631579        0.600650474015639
7       140     signal transduction in response to DNA damage
GO:0051320      2.5032781502014e-06     13.3383689839572        0.613521555601688
7       143     S phase
GO:2000602      3.0086052567158e-06     12.9536363636364        0.630682997716421
7       147     regulation of interphase of mitotic cell cycle
GO:0090068      3.59644367545003e-06    12.5902777777778        0.647844439831154
7       151     positive regulation of cell cycle process
GO:0019882      3.75749406192381e-06    12.5025705329154        0.652134800359837
7       152     antigen processing and presentation
GO:0010565      4.09769059308859e-06    12.3307359307359        0.660715521417203
7       154     regulation of cellular ketone metabolic process
GO:0022613      5.00227944008482e-06    9.67537122375832        0.965331118953706
8       225     ribonucleoprotein complex biogenesis
GO:0007346      5.32100917347733e-06    8.14112437427801        1.29997924019099
9       303     regulation of mitotic cell cycle
GO:0000209      5.49755148002312e-06    11.7644628099174        0.690748045117985
7       161     protein polyubiquitination
GO:0071843      7.79486493964174e-06    9.08000641333975        1.02539616635527
8       239     cellular component biogenesis at cellular level
GO:0044106      1.27238935544509e-05    10.2779958677686        0.785135976749014
7       183     cellular amine metabolic process
GO:0000082      1.41424410995654e-05    10.1036058913154        0.798007058335063
7       186     G1/S transition of mitotic cell cycle
GO:0006520      1.51770278059607e-05    6.28805620608899        1.87488755103453
10      437     cellular amino acid metabolic process
Tissue: Lung=>Thyroid   Type:   asymmetric
SourceGene:     RP11-252A24.3(ENSG00000261079.1)
TargetGeneSet:  RPL22   RPL11   RPS8    RP4     GNG5    RPL5    ABCA4   RP11
VANGL1  RPS27   OLFML2B SLC45A3 PROX1   RPS7    MYCN    DCTN1   COA5    RPL31
STEAP3-AS1      WDR75   TBC1D5  RPL15   RPL14   ZNF445  RPL29   CACNA1D CCDC66
RPL24   IGSF10  SUCNR1  NCBP2   WFS1    RPL34   GARS    RPS3A   WWC2-AS2        ING2
CDH10   NDUFAF2 TAF9    SKP1    ANXA6   LINC00340       CLIP2   C7orf58 SLC37A3
MRPS33  FNTA    RPL30   EIF3E   EBAG9   EIF3H   RPS6    TLN1    PGM5    ATP6V1G1
RPL12   ZNF488  RPS24   RPS3AP5 BLOC1S2 RPL27A  C11orf58        SVIP    BDNF
CYBASC3 INTS5   ARHGAP42        RPS25   RNF26   PPFIBP1 NAP1L1  RASSF9  GPN3    RPL6
TPT1    CYFIP1  RPS3AP6 RPL4    NEO1    SCAMP2  PEAK1   SEC11A  RPS15A  LYRM1
RPS7P1  RPL19   TANC2   CTD     RPL36   AP5S1   CDH22   HMGN1   SLC25A15P5
SNRPD3  RBFOX2  DMD     RPS4X   BEX5    HPRT1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0000184      3.65391600310303e-37    77.5978260869565        0.667012663483496
27      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006614      7.28082251612448e-37    85.5157652474108        0.588540585426614
26      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      9.61149598680075e-37    84.4409090909091        0.594145733859249
26      106     cotranslational protein targeting to membrane
GO:0045047      9.61149598680075e-37    84.4409090909091        0.594145733859249
26      106     protein targeting to ER
GO:0072599      9.61149598680075e-37    84.4409090909091        0.594145733859249
26      106     establishment of protein localization to endoplasmic reticulum
GO:0006415      1.04706135830411e-36    96.7532467532468        0.510068507369732
25      91      translational termination
GO:0006413      8.51277798678427e-36    60.6950699939136        0.851982561760432
28      152     translational initiation
GO:0070972      2.16200471202676e-35    73.3652173913043        0.661407515050861
26      118     protein localization to endoplasmic reticulum
GO:0006414      6.04349422700425e-35    79.7433035714286        0.588540585426614
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25      105     translational elongation
GO:0000956      1.07626458665364e-32    50.0985915492958        0.947270085115217
27      169     nuclear-transcribed mRNA catabolic process
GO:0019080      2.32797887638224e-32    53.872  0.846377413327797       26      151
viral genome expression
GO:0019083      2.32797887638224e-32    53.872  0.846377413327797       26      151
viral transcription
GO:0006612      3.3583026947795e-32     53.0161775232641        0.857587710193066
26      153     protein targeting to membrane
GO:0006402      4.75240277667812e-32    47.0827814569536        0.997716421008927
27      178     mRNA catabolic process
GO:0043624      1.73709570067169e-30    49.6721540178571        0.857587710193066
25      153     cellular protein complex disassembly
GO:0006401      2.597541189495e-30      39.8651685393258        1.14905542869006
27      205     RNA catabolic process
GO:0043241      4.08264984439921e-30    47.7879967776584        0.885613452356238
25      158     protein complex disassembly
GO:0034623      5.20334291210057e-29    42.6084611697028        0.975295827278389
25      174     cellular macromolecular complex disassembly
GO:0019058      7.32145164881366e-29    34.7205882352941        1.29478928793855
27      231     viral infectious cycle
GO:0072594      8.87435596441952e-29    37.6907048008172        1.14345028025742
26      204     establishment of protein localization to organelle
GO:0032984      1.09335072581424e-28    41.2105751391466        1.00332156944156
25      179     macromolecular complex disassembly
GO:0022415      1.92562465238357e-27    30.3369098712446        1.45733859248495
27      260     viral reproductive process
GO:0071845      5.81550425045238e-25    25.8570824524313        1.59186215486818
26      284     cellular component disassembly at cellular level
GO:0022411      8.38231358726506e-25    25.4551006245663        1.61428274859871
26      288     cellular component disassembly
GO:0016032      8.44656826549977e-25    19.4900097806343        2.52792194311812
30      451     viral reproduction
GO:0006605      1.83009408600185e-20    15.5738255033557        2.65684035706871
27      474     protein targeting
GO:0033365      2.65914396454758e-19    14.7243441122636        2.65123520863608
26      473     protein localization to organelle
GO:0042274      3.95076686206528e-08    72.6568825910931        0.10089267178742
5       18      ribosomal small subunit biogenesis
GO:0022613      4.75662848291033e-08    10.3949265687583        1.26115839734274
11      225     ribonucleoprotein complex biogenesis
GO:0071843      8.8068938230315e-08     9.74699248120301        1.33963047539963
11      239     cellular component biogenesis at cellular level
GO:0034660      5.16038454072388e-07    8.08425443169969        1.59746730330081
11      285     ncRNA metabolic process
GO:0042254      1.80178798662566e-06    11.0591664237832        0.835167116462529
8       149     ribosome biogenesis
GO:0006364      1.83261892452835e-06    13.9190582334912        0.58293543699398
7       104     rRNA processing
GO:0016072      2.6722829451218e-06     13.1027289425348        0.616566327589786
7       110     rRNA metabolic process
GO:0034470      1.5854029672272e-05     8.09246575342466        1.12102968652688
8       200     ncRNA processing
Tissue: Lung=>Thyroid   Type:   asymmetric
SourceGene:     RP11-321G12.1(ENSG00000259459.1)
TargetGeneSet:  FCRL5   FCRL2   FCRLA   SLAMF7  IGKJ4   IGKV4-1 IGKV1-9 IGKV3-15
IGKV1-17        IGKV3-20        IGKV2-28        IGKV2-30        IGKV1-39
IGKV3D-11       TMEM156 RP11    POU2AF1 TRAV10  IGHG2   IGHG3   IGHM    IGHJ6
IGHJ5   KIAA0125        IGHV6-1 IGHV4-4 IGHV3-7 IGHV3-11        IGHV3-23
IGHV3-30        IGHV4-39        IGHV1-46        IGHV1-69        CTD     UBE2I
TNFRSF17        TNFRSF13B       JSRP1   CD79A   IGLV1-51        IGLV1-44
IGLV3-25        IGLV2-23        IGLV3-19        IL2RG
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
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GO:0006958      1.512271440273e-11      178.388429752066        0.0588194588609785
6       50      complement activation, classical pathway
GO:0006959      4.65871068408555e-11    87.1591304347826        0.143519479620787
7       122     humoral immune response
GO:0006956      6.41139492144295e-11    137.578947368421        0.0741125181648329
6       63      complement activation
GO:0002455      7.78389893721975e-11    132.896764252696        0.076465296519272
6       65      humoral immune response mediated by circulating immunoglobulin
GO:0072376      3.26329245860814e-10    103.047846889952        0.0964639125320047
6       82      protein activation cascade
GO:0002449      4.28173735817395e-10    62.44875        0.196456992595668       7
167     lymphocyte mediated immunity
GO:0016064      2.07038944420833e-09    74.4363636363636        0.130579198671372
6       111     immunoglobulin mediated immune response
GO:0002443      2.2006586756438e-09     48.828431372549 0.248218116393329       7
211     leukocyte mediated immunity
GO:0019724      2.4338007599768e-09     72.3535353535353        0.134108366203031
6       114     B cell mediated immunity
GO:0002253      2.46469607360309e-08    33.9020547945205        0.351740363988651
7       299     activation of immune response
GO:0002460      3.92217118292969e-08    44.4436363636364        0.212926441076742
6       181     adaptive immune response based on somatic recombination of immune
receptors built from immunoglobulin superfamily domains
GO:0002250      6.69476686163987e-08    40.4602272727273        0.232925057089475
6       198     adaptive immune response
GO:0050778      9.50380640091185e-08    27.6019607843137        0.428205660507923
7       364     positive regulation of immune response
GO:0002252      1.41854204788672e-07    25.9591029023747        0.454086222406754
7       386     immune effector process
Tissue: Lung=>Thyroid   Type:   cluster
SourceGene:     RP11-61I13.2(ENSG00000240126.1)
TargetGeneSet:  TAS1R3  RPL22   ICMT    RPL11   RPS8    RP4     RPL5    RP11
PDIA3P  DUSP10  FAM177B RPS7    FNDC4   RPLP0P6 UBC     SLC1A4  RPL31   RPL23AP7
PSMD14  WIPF1   ZNF804A RPL32   RPL15   RPL14   STAB1   PBRM1   RPL24   LRRC33
RPL35A  CLNK    PCDH7   RPL34   RAPGEF2 ST8SIA4 CAMLG   CTB     GNB2L1  EXOC2
RPL10A  RPL39P3 SNHG5   UBE2J1  MRPS12  MBLAC1  RPS20   RPL30   LRRC14  FAM125B
RPL7A   ADAMTSL2        CARD9   RPL13AP5        GSTO1   CTBP2   CTD     RPS13
SLC37A2 PHB2    PPM1H   RPL6    RB1     TM9SF2  GNG2    C14orf166       IRF2BPL
RPL3P4  PLCB2   GALK2   RPS3AP6 RSL1D1  RPS15A  ADCY7   SNX20   RPL23A  RPL19   HAP1
RPL27   MRPL10  C18orf21        RPL17   WDR7    HMHA1   ANO8    RPL18A  UBA52
KCNN4   ALDH16A1        RPS11   RPL28   SIGLEC1 ZNFX1-AS1       EIF3D   RPL3
ALG12   EIF2S3  CYBB    WAS
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      6.90789313649414e-46    142.44234728895 0.478582797038267       29
91      translational termination
GO:0006414      7.3412890508891e-46     124.347826086957        0.552210919659539
30      105     translational elongation
GO:0006614      8.82178008367986e-44    116.089305711086        0.552210919659539
29      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.21058252063162e-43    114.573639126831        0.557470071275344
29      106     cotranslational protein targeting to membrane
GO:0045047      1.21058252063162e-43    114.573639126831        0.557470071275344
29      106     protein targeting to ER
GO:0072599      1.21058252063162e-43    114.573639126831        0.557470071275344
29      106     establishment of protein localization to endoplasmic reticulum
GO:0006413      2.45218234314814e-42    81.1522497704316        0.799391045602381
31      152     translational initiation
GO:0070972      4.18852763160563e-42    99.0423141286158        0.620579890665006
29      118     protein localization to endoplasmic reticulum
GO:0000184      5.52061833857549e-42    97.934988179669 0.625839042280811       29
119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006612      2.39608350147145e-40    75.5673382820785        0.804650197218186
30      153     protein targeting to membrane
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GO:0019080      1.16117058049162e-38    72.0852807813045        0.794131893986575
29      151     viral genome expression
GO:0019083      1.16117058049162e-38    72.0852807813045        0.794131893986575
29      151     viral transcription
GO:0043624      1.75930892269342e-38    70.9126630061771        0.804650197218186
29      153     cellular protein complex disassembly
GO:0043241      4.8426714214098e-38     68.1401946231239        0.830945955297211
29      158     protein complex disassembly
GO:0000956      3.98029982689823e-37    62.7378419452888        0.888796623071068
29      169     nuclear-transcribed mRNA catabolic process
GO:0034623      9.86271865464611e-37    60.5531914893617        0.915092381150093
29      174     cellular macromolecular complex disassembly
GO:0006402      1.99659358825539e-36    58.9110381265172        0.936128987613314
29      178     mRNA catabolic process
GO:0032984      2.37502413074469e-36    58.5141843971631        0.941388139229119
29      179     macromolecular complex disassembly
GO:0019058      1.2853668530197e-34     45.9896171317326        1.21486402325099
30      231     viral infectious cycle
GO:0072594      1.32394683462339e-34    50.0668693009119        1.07286692962425
29      204     establishment of protein localization to organelle
GO:0006401      1.53718455382506e-34    49.7788926499033        1.07812608124005
29      205     RNA catabolic process
GO:0022415      5.12477291362589e-33    40.1086956521739        1.36737942010933
30      260     viral reproductive process
GO:0071845      2.77080103453608e-30    34.1660408844389        1.49359905888866
29      284     cellular component disassembly at cellular level
GO:0022411      4.19204585584231e-30    33.6288507352337        1.51463566535188
29      288     cellular component disassembly
GO:0016032      3.99163768454759e-27    22.8891534391534        2.37187737872812
31      451     viral reproduction
GO:0006605      1.82993938591163e-26    21.6650112866817        2.49283786589163
31      474     protein targeting
GO:0033365      3.64606300734513e-25    20.5103543036608        2.48757871427583
30      473     protein localization to organelle
GO:0022613      2.40552140418525e-08    11.198490294752 1.18330911355616        11
225     ribonucleoprotein complex biogenesis
GO:0071843      4.47372398009831e-08    10.5004723346829        1.25693723617743
11      239     cellular component biogenesis at cellular level
GO:0042254      8.1785039138301e-08     13.658315565032 0.783613590754965       9
149     ribosome biogenesis
GO:0042273      3.38648218066051e-07    99.7708333333333        0.0631098193896616
4       12      ribosomal large subunit biogenesis
GO:0006364      1.74693870538412e-05    12.4871720116618        0.546951768043734
6       104     rRNA processing
Tissue: Lung=>Whole_Blood       Type:   asymmetric
SourceGene:     ALB(ENSG00000163631.11)
TargetGeneSet:  C8A     HHLA3   RP11    APCS    CFHR2   CFHR5   APOB    NAT8
RPL23AP7        SLC2A2  ALB     AFM     C9      DMGDH   BHMT    PLG     FGL1
CYP2C18 CYP2C9  CTD     APOA1   CMA1    SERPINA4        FOXA3   RP4     F9
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006957      1.10269643018981e-06    206.956937799043        0.021313403916684
3       14      complement activation, alternative pathway
GO:0072376      6.51653803394752e-06    40.8860398860399        0.124835651512006
4       82      protein activation cascade
GO:0001907      6.63126733129481e-06    1442.8  0.00456715798214656     2       3
killing by symbiont of host cells
GO:0044004      6.63126733129481e-06    1442.8  0.00456715798214656     2       3
disruption by symbiont of host cell
GO:0006579      1.32502969607106e-05    721.35  0.00608954397619542     2       4
amino-acid betaine catabolic process
Tissue: Whole_Blood=>Lung       Type:   cluster
SourceGene:     C9orf114(ENSG00000198917.6)
TargetGeneSet:  VPS13D  NFYC    DENND2D SLC50A1 ASH1L   PMF1    FCRL3   SLAMF6
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CDC73   RP11    TMEM18  PDIA6   ADCY3   DYNC2LI1        C2orf27B        METTL5
ABCB6   HDLBP   TMEM43  CCR2    SLC26A6 TSC22D2 TRAM1L1 BRIX1   PHF15   TXNDC15 PDF
LARP1   CANX    TRIM52  TXNDC5  E2F3    TOMM6   RP3     KDELR2  LSM5    IKZF1
ZKSCAN1 ORC5    CALU    PDIA4   ECD     RPP30   SFR1    SMNDC1  NUCB2   SPTBN2
CWF19L2 HYOU1   STT3A   KIAA0528        FKBP11  NUP37   HSP90B1 SLC41A2 MLEC
ZNF26   GTF3A   ESD     POLE2   RDH11   LINC00341       COMMD4  SNHG9   CLEC16A
SERPINF2        ACAP1   SPAG5-AS1       KIAA0100        CTB     AOC2    INO80C
LMAN1   CALR    JUND    PGPEP1  PCNA    MIS18A  RP4     PPARA   CRELD2  NCAPH2
PTCHD1  AR      MAGT1   TAF9B
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006457      8.21351440005903e-07    10.2717391304348        1.03134731160473
9       216     protein folding
GO:0006487      4.90339324014159e-06    15.8316722037652        0.43927755864646
6       92      protein N-linked glycosylation
GO:0032075      1.52772707948791e-05    18.3414446721311        0.315133900768113
5       66      positive regulation of nuclease activity
Tissue: Lung=>Whole_Blood       Type:   asymmetric
SourceGene:     CTB-85P21.2(ENSG00000259787.1)
TargetGeneSet:  VAV3-AS1        CD48    CAPN2   ARPC2   ANKMY1  UBA3    COL8A1
PDGFRA  TMSB4XP8        GTF2H5  TAS2R4  CTA     C9orf103        TMSB4XP4
WDR34   TNKS2   RP11    FEN1    CRABP1  CLSTN3  BIN2    DOCK9   WDHD1   TIPIN
GINS3   SIRT6   PPIAP22 RRM2P3  BEX4
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006260      1.98599441849477e-05    19.2409016838675        0.352363158258944
5       268     DNA replication
Tissue: Whole_Blood=>Lung       Type:   asymmetric
SourceGene:     ENSG00000261008.2
TargetGeneSet:  SMPDL3B CNTN2   NEK2    OR2L2   POU3F3  SYNPR   MIR922  MAD2L1
BRCC3   SAPCD1  GRM4    MCM3    RPS17P13        PRRT4   DEFA4   DEFA1   DEFA1B
DEFA3   RP11    IFIT1B  CALHM1  SIGIRR  C11orf41        TCN1    MS4A3   MMP8
TMTC1   SVOP    SKA3    TMX1    HERPUD1 MPO     AZU1    ELANE   CEACAM8 SHISA7  7SK
RP3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0050832      1.23515231214828e-10    252.842105263158        0.0332156944156114
5       20      defense response to fungus
GO:0009620      1.86399749503958e-09    135.328947368421        0.0548058957857588
5       33      response to fungus
GO:0031640      8.53536891126382e-08    130.954545454545        0.0431804027402948
4       26      killing of cells of other organism
GO:0044364      8.53536891126382e-08    130.954545454545        0.0431804027402948
4       26      disruption of cells of other organism
GO:0009617      9.56888627265752e-07    17.3211589113257        0.567988374506954
7       342     response to bacterium
GO:0045073      1.13864338687663e-06    205.957142857143        0.0215902013701474
3       13      regulation of chemokine biosynthetic process
GO:0042033      1.44760299206345e-06    187.220779220779        0.023250986090928
3       14      chemokine biosynthetic process
GO:0050755      1.80753155153579e-06    171.607142857143        0.0249117708117085
3       15      chemokine metabolic process
GO:0035821      3.93630713736036e-06    46.3387096774194        0.109611791571518
4       66      modification of morphology or physiology of other organism
GO:0001906      4.70590517975697e-06    44.1907692307692        0.114594145733859
4       69      cell killing
GO:0045079      7.92234085030777e-06    1311.45454545455        0.00498235416234171
2       3       negative regulation of chemokine biosynthetic process
Tissue: Whole_Blood=>Lung       Type:   asymmetric
SourceGene:     FHIT(ENSG00000189283.5)
TargetGeneSet:  TAGLN2  FAM150B ADCY3   CTD     FGF1    EBF1    CDCA7L  CA3
CCNT1   RP11    KL      MYL12A  ACER1   ZNF121  GATSL3  SEC14L2 GUCY2F  GPC3
MIR1184-2
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0045542      8.70129881364286e-06    801.888888888889        0.00484395543560999
2       5       positive regulation of cholesterol biosynthetic process
```

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GO:0090205      1.30447221048509e-05    601.375 0.00581274652273199     2       6
positive regulation of cholesterol metabolic process
Tissue: Lung=>Whole_Blood       Type:   cluster
SourceGene:     GABRA1(ENSG00000022355.10)
TargetGeneSet:  MTND2P28        GABRD   C1orf173        KCNJ9   RP3     ASTN1   RP11
VSNL1   POU3F3  SCN2A   KIF1A   SLC6A1  ARPP21  MOBP    CAMKV   CADPS   SYNPR
CADM2   TAGLN3  GAP43   ZIC1    SOX2-OT CXXC4   GRIA2   CTNND2  SPINK5  CAMK2A
TIMD4   GABRB2  CPLX2   NRSN1   BEND6   RIMS1   SNAP91  MYL7    VSTM2A  CALN1
FAM86B2 PSD3    PENK    STMN2   LY6H    SH3GL2  SLC25A16        GPR158  LGI1    INA
ANO3    SYT13   TMEM151A        SYT12   ELMOD1  OPCML   KCNA1   CNTN1   FAIM2
KCNC2   SYT1    SVOP    CTD     GABRB3  DDX11L9 CBLN1   MT3     VAT1L   EFNB3
PPP1R1B GFAP    DSG1    ST8SIA3 CELF5   CASP14  UNC13A  VSTM2B  PNMAL1  SLC8A2
TTYH1   SYT5    PEG3    SNAP25  NCAM2   SULT4A1 FRMPD4  TCEAL5  PLP1    GRIA3
H2AFB2
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0048489      1.89882609211438e-09    41.5080611823067        0.219223583143035
7       48      synaptic vesicle transport
GO:0016079      3.91936183998243e-09    59.8375 0.137014739464397       6       30
synaptic vesicle exocytosis
GO:0006836      6.43090363346774e-08    17.7371854613234        0.543491799875441
8       119     neurotransmitter transport
GO:0001505      8.32494509922324e-08    17.1154422788606        0.561760431804027
8       123     regulation of neurotransmitter levels
GO:0007269      1.20939271320294e-07    21.4850890366874        0.392775586464605
7       86      neurotransmitter secretion
GO:0003001      1.26303098339968e-05    7.24052803017315        1.44322192235831
9       316     generation of a signal involved in cell-cell signaling
GO:0023061      1.26303098339968e-05    7.24052803017315        1.44322192235831
9       316     signal release
Tissue: Lung=>Whole_Blood       Type:   asymmetric
SourceGene:     GAD2(ENSG00000136750.7)
TargetGeneSet:  MTND2P28        GABRD   NPPA    NCDN    PRCC    RP3     CNTN2
TMEM178 POU3F3  KIF1A   ARPP21  MOBP    CAMKV   GAP43   CTNND2  MTND5P11
CAMK2A  GABRA6  GABRA1  CPLX2   GRM4    RIMS1   SNAP91  DGKB    CALN1   GPR22
KCND2   NEFM    RP11    ZER1    GRIN1   PTPN5   ANO3    SYT13   SYT12   ELMOD1
C11orf87        OPCML   PRMT8   FAIM2   KCNC2   SYT1    GABRB3  PPP1R1B GFAP
ST8SIA3 CASP14  TTYH1   SNAP25  RIMS4   NCAM2   FRMPD4  TMEM35  PLP1    H2AFB2  MT
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006836      1.19686617063823e-07    21.7850609756098        0.395266763545775
7       119     neurotransmitter transport
GO:0016079      2.75548337057949e-06    50.2692307692308        0.0996470832468341
4       30      synaptic vesicle exocytosis
GO:0001505      3.08159567979656e-06    17.4432234432234        0.40855304131202
6       123     regulation of neurotransmitter levels
GO:0007612      5.74622045437605e-06    22.8257406817458        0.259082416441769
5       78      learning
GO:0007611      6.79349737194285e-06    15.0984126984127        0.46834129126012
6       141     learning or memory
GO:0048167      6.92221761903358e-06    21.9201346389229        0.269047124766452
5       81      regulation of synaptic plasticity
GO:0007269      9.29306926751621e-06    20.5598621877692        0.285654971974258
5       86      neurotransmitter secretion
GO:0050890      1.12668599004808e-05    13.7596525096525        0.511521694000415
6       154     cognition
GO:0048489      1.87251837297196e-05    29.6673553719008        0.159435333194935
4       48      synaptic vesicle transport
Tissue: Lung=>Whole_Blood       Type:   cluster
SourceGene:     HIST1H3G(ENSG00000256018.1)
TargetGeneSet:  DPH5    KIF14   IGKJ5   IGKC    IGKJ4   IGKJ1   IGKV1-5 BUB1
C2orf76 ITM2C   RP11    MUM1    TUBB    KIFC1   TMEM217 BHLHA15 PNOC    GINS4   MCM4
ADRA2A  ZWINT   BLNK    FEN1    CDCA5   POU2AF1 IGHG4   IGHGP   IGHG3   IGHJ3
IGHV3-15        IGHV3-23        IGHV3-48        CCNB2   PLK1    SHCBP1  GINS2
AURKB   CDC6    TYMS    RP4     MYBL2   TOX2    UBE2C   CDC45   IGLV6-57
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IGLV1-47 IGLV5-45 IGLV2-14 IGLV2-11 IGLV2-5 DERL3 EMID1

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0000280	3.56820526717671e-10	19.03232546706	0.847692201231749	11	350	nuclear division
GO:0007067	3.56820526717671e-10	19.03232546706	0.847692201231749	11	350	mitosis
GO:0000087	4.8108195251696e-10	18.4738538681948	0.871911978409799	11	360	M phase of mitotic cell cycle
GO:0048285	6.42971331608528e-10	17.9464948932219	0.896131755587849	11	370	organelle fission
GO:0051329	1.39906751290807e-08	15.2271002710027	0.917929555048094	10	379	interphase of mitotic cell cycle
GO:0006959	1.42054170376897e-08	31.0891304347826	0.29548128157221	7	122	humoral immune response
GO:0006271	1.63685597606566e-08	82.683908045977	0.0823472424053699	5	34	DNA strand elongation involved in DNA replication
GO:0051325	1.70633811698216e-08	14.8954907161804	0.937305376790533	10	387	interphase
GO:0022616	2.55089434850277e-08	74.9166666666667	0.0896131755587849	5	37	DNA strand elongation
GO:0010564	3.23201463478949e-08	13.8732673267327	1.00269877517127	10	414	regulation of cell cycle process
GO:0000075	8.77633934063887e-08	17.9575815131371	0.586118607708809	8	242	cell cycle checkpoint
GO:0006958	1.21229372537794e-07	53.2259259259259	0.12109888589025	5	50	complement activation, classical pathway
GO:0071156	1.71334688508739e-07	16.3888888888889	0.639402117500519	8	264	regulation of cell cycle arrest
GO:0051983	2.95970386617748e-07	92.8774193548387	0.0581274652273199	4	24	regulation of chromosome segregation
GO:0006956	3.93211835776371e-07	41.2586206896552	0.152584596221715	5	63	complement activation
GO:0002455	4.60480650898323e-07	39.8777777777778	0.157428551657325	5	65	humoral immune response mediated by circulating immunoglobulin
GO:0000084	7.39386892761105e-07	23.0948275862069	0.32454501418587	6	134	S phase of mitotic cell cycle
GO:0051301	9.05976370007049e-07	10.9183017885049	1.09473392844786	9	452	cell division
GO:0007059	9.56423966186795e-07	22.0514668039115	0.339076880492699	6	140	chromosome segregation
GO:0051320	1.08305274167737e-06	21.5640573873647	0.346342813646114	6	143	S phase
GO:0072376	1.47696702907015e-06	31.0367965367965	0.19860217286001	5	82	protein activation cascade
GO:0007050	2.15655126127038e-06	11.5358571868267	0.893709777870044	8	369	cell cycle arrest
GO:0006261	2.76009753716617e-06	27.1363636363636	0.225243927755865	5	93	DNA-dependent DNA replication
GO:0006260	3.00862339806096e-06	13.5584291187739	0.649090028371739	7	268	DNA replication
GO:0007017	3.44455065565553e-06	10.7982683982684	0.951837243097364	8	393	microtubule-based process
GO:0016064	6.59747971644911e-06	22.5	0.268839526676355	5	111	immunoglobulin mediated immune response
GO:0019724	7.51772815983643e-06	21.8761467889908	0.27610545982977	5	114	B cell mediated immunity
GO:0045786	7.52827705504051e-06	9.66036432703099	1.05840426268078	8	437	negative regulation of cell cycle
GO:0000083	1.94207783226368e-05	71.0378289473684	0.0532835097917099	3	22	regulation of transcription involved in G1/S phase of mitotic cell cycle

Tissue: Whole_Blood=>Lung Type: asymmetric

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SourceGene:     MMP3(ENSG00000149968.7)
TargetGeneSet:  SDHDP6  RP11    PPA2    TMCO6   C6orf72 C8orf82 FBXL15  DDX23   TEP1
MPG     SLC9A3R2        EIF3C   ATP5D   FAM108A1        ZNF358  FAM98C  RABAC1  A1BG
GATA5
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0014067      1.11832549800475e-05    656.090909090909        0.00539755034253685
2       6       negative regulation of phosphatidylinositol 3-kinase cascade
Tissue: Lung=>Whole_Blood       Type:   asymmetric
SourceGene:     MOG(ENSG00000204655.7)
TargetGeneSet:  MTND1P23        MTND2P28        RP11    RGS4    ARID4B-IT1
VSNL1   POU3F3  KIF1A   ARPP21  CAMKV   GABRB2  SNAP91  KCND2   DIRAS2  OPCML
PRMT8   KCNC2   HIGD1B  DYNLL2  UNC13A  SNAP25  FEM1AP1 CTA     FRMPD4  PLP1
GRIA3   H2AFB2
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
Tissue: Whole_Blood=>Lung       Type:   asymmetric
SourceGene:     PAMR1(ENSG00000149090.7)
TargetGeneSet:  RPS8    RP4     RPS7    UBC     DUSP19  RPL32   RP11    EPHB1
SLC30A9 SEPP1   DIMT1   TMEM14B HIST1H2BJ       HIST1H2AG       DPCR1   SEPT10P1
ZMYND11 RPL27A  RPL4    FTLP14  GCSH    RPS7P1  RPL19   TIMP2   RPS15   RPS5
DUSP18  CTA     RPL10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      6.30555352061827e-17    136.24881291548 0.144834267524739       10
91      translational termination
GO:0006414      2.79796175290637e-16    116.056680161943        0.167116462528545
10      105     translational elongation
GO:0006614      2.79796175290637e-16    116.056680161943        0.167116462528545
10      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      3.08687413255169e-16    114.839743589744        0.168708047885959
10      106     cotranslational protein targeting to membrane
GO:0045047      3.08687413255169e-16    114.839743589744        0.168708047885959
10      106     protein targeting to ER
GO:0072599      3.08687413255169e-16    114.839743589744        0.168708047885959
10      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      9.35135241104897e-16    101.994301994302        0.187807072174936
10      118     protein localization to endoplasmic reticulum
GO:0000184      1.02008682585083e-15    101.051517290049        0.189398657532351
10      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      1.16958569994575e-14    77.9432624113475        0.240329388969621
10      151     viral genome expression
GO:0019083      1.16958569994575e-14    77.9432624113475        0.240329388969621
10      151     viral transcription
GO:0006413      1.25091808835343e-14    77.3889490790899        0.241920974327036
10      152     translational initiation
GO:0006612      1.33729070090369e-14    76.8423883808499        0.243512559684451
10      153     protein targeting to membrane
GO:0043624      1.33729070090369e-14    76.8423883808499        0.243512559684451
10      153     cellular protein complex disassembly
GO:0043241      1.85483238175808e-14    74.2203742203742        0.251470486471524
10      158     protein complex disassembly
GO:0000956      3.6731013503907e-14     69.0324141267537        0.268977925403086
10      169     nuclear-transcribed mRNA catabolic process
GO:0034623      4.93531947415089e-14    66.9043151969981        0.27693585219016
10      174     cellular macromolecular complex disassembly
GO:0006402      6.21163297175937e-14    65.2930402930403        0.283302193619819
10      178     mRNA catabolic process
GO:0032984      6.57374934802155e-14    64.9021392808375        0.284893778977233
10      179     macromolecular complex disassembly
GO:0071845      1.52770223589797e-13    47.5289987789988        0.452010241505778
11      284     cellular component disassembly at cellular level
GO:0022411      1.78117443726344e-13    46.8294223826715        0.458376582935437
11      288     cellular component disassembly
GO:0072594      2.45722623718009e-13    56.4393338620143        0.324683412912601
10      204     establishment of protein localization to organelle
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GO:0006401      2.58110034705589e-13    56.1459566074951        0.326274998270016
10      205     RNA catabolic process
GO:0019058      8.55234752637089e-13    49.4500522102332        0.367656217562798
10      231     viral infectious cycle
GO:0022415      2.78571752229051e-12    43.6246153846154        0.413812192927825
10      260     viral reproductive process
GO:0016032      6.31199390872842e-10    24.397348683063 0.717804996194035       10
451     viral reproduction
GO:0033365      1.00237370241577e-09    23.2015284931052        0.752819874057159
10      473     protein localization to organelle
GO:0006605      1.02311616145228e-09    23.1498673740053        0.754411459414573
10      474     protein targeting
GO:0042274      2.82937347018751e-06    144.13  0.0286485364334648      3       18
ribosomal small subunit biogenesis
Tissue: Whole_Blood=>Lung       Type:   asymmetric
SourceGene:     RAB1C(ENSG00000233111.1)
TargetGeneSet:  TMEM222 RPS8    RP11    TMEM42  LTF     HCLS1   SPARCL1 CCNA2
HMGB2   CTD     HMMR    BOD1    BTNL9   KIFC1   CTSB    CDCA2   ESCO2   IL2RA
RBM17   ITGA8   SRGN    CCDC147 NCAPD2  C12orf57        CMAS    AGAP2   TMCC3
SELPLG  RP1     NUSAP1  BLM     SLC5A2  NKD1    TRAPPC2L        RPL19   BRCA1
RPS7P11 RFNG    SLC16A3 RPL18   RPL28   RPS5    TRIB3   MYLK2   CBLN4   MIOX    BEX2
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      3.77538272921322e-06    25.2413671599718        0.239291398519134
5       91      translational termination
GO:0006414      7.63268820961873e-06    21.6863636363636        0.27610545982977
5       105     translational elongation
GO:0006614      7.63268820961873e-06    21.6863636363636        0.27610545982977
5       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      7.99528987057395e-06    21.4701470147015        0.278735035637672
5       106     cotranslational protein targeting to membrane
GO:0045047      7.99528987057395e-06    21.4701470147015        0.278735035637672
5       106     protein targeting to ER
GO:0072599      7.99528987057395e-06    21.4701470147015        0.278735035637672
5       106     establishment of protein localization to endoplasmic reticulum
GO:0070972      1.34915910055372e-05    19.1740412979351        0.310289945332503
5       118     protein localization to endoplasmic reticulum
GO:0000184      1.40565085719009e-05    19.0045188729399        0.312919521140405
5       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
Tissue: Whole_Blood=>Lung       Type:   asymmetric
SourceGene:     RP11-369K16.1(ENSG00000251468.2)
TargetGeneSet:  ANAPC10P1       PMF1    NUF2    TNFSF13B        CCDC150 RP11
CEP19   CDC25C  RPL29P14        FTH1P15 PBK     ESPL1   TIMELESS        RFC3    PRC1
CTD     AURKB   UNK     AP5S1   GSTT1   NFAM1   SCML2   VDAC1P6 RBMY1KP
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0000280      2.50766476846914e-08    35.9515306122449        0.363296657670749
7       350     nuclear division
GO:0007067      2.50766476846914e-08    35.9515306122449        0.363296657670749
7       350     mitosis
GO:0000087      3.04437575889836e-08    34.9082861189802        0.373676562175628
7       360     M phase of mitotic cell cycle
GO:0048285      3.67569432426881e-08    33.922520661157 0.384056466680507       7
370     organelle fission
GO:0051301      1.44801125328211e-07    27.510393258427 0.469171683620511       7
452     cell division
GO:0007059      1.06022401963643e-05    38.2352941176471        0.1453186630683 4
140     chromosome segregation
Tissue: Whole_Blood=>Lung       Type:   cluster
SourceGene:     SORT1(ENSG00000134243.7)
TargetGeneSet:  TMEM51  SPEN    RP11    METTL13 GPR137B ERO1LB  SCN7A   CERS6
GOLGB1  KLF15   C4orf50 SPARCL1 LRRC16A RP3     KHDRBS2 HINT3   ADCY1   UPP1    POP1
AQP7P3  RHOBTB1 MICU1   SLC16A12        TMEM133 ITFG2   METTL7A IRAK3   NT5DC3
RAB35   FLT3    FOXO1   DNAJC3  PCNX    MGA     CHD9    MT1L    MT1M    MT1A    MT1X
GLOD4   TNFSF12 PNMT    MTMR4   NOTCH3  HIF3A   SAMHD1  TTPAL   NCOA3   KCNB1   H1F0
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MAGED2  RP6     MAGEC3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0071294      3.07587567160006e-06    145.515151515152        0.0298941249740502
3       12      cellular response to zinc ion
Tissue: Lung=>Whole_Blood       Type:   asymmetric
SourceGene:     WDR45L(ENSG00000141580.10)
TargetGeneSet:  MTND1P23        MTND2P28        SPSB1   ANGPTL7 RP11    BCAN
KCNJ10  HNRNPU  HADH    CIDEC   FOXP1   TAGLN3  AP2M1   ADIPOQ  BRD9    GABRA1
GABRP   HIST1H4H        COL12A1 HRCT1   DPP7    TPP1    MTRNR2L8        C11orf31
PACS1   TSKU    CRABP1  RP1     IGFBP6  PCBP2   NME3    CTA     NFATC3  SERPINF1
AP2B1   UBTF    GFAP    ARL16   SMARCA4 NUCB1-AS1       ADAM33  WISP2   MYH9
EIF2S3  NONO    USP26
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0050688      1.45278098400454e-05    31.8756936736959        0.149885821050446
4       57      regulation of defense response to virus
Tissue: Whole_Blood=>Lung       Type:   cluster
SourceGene:     all_source
TargetGeneSet:  ARL6IP5 SEC31B  DYNLL2  CDC42SE1        PSTPIP2 CATSPER1        RP11
OXT     SORT1   WDR69   UCN     C9orf114
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0042756      1.2041283328032e-05     601.458333333333        0.00553594906926856
2       8       drinking behavior
Tissue: Heart_Left_Ventricle=>Muscle_Skeletal   Type:   cluster
SourceGene:     CTD-2292M16.7(ENSG00000258459.1)
TargetGeneSet:  C1orf130        ZCCHC17 FABP3   MRPS15  DPH2    BTBD8   ANKRD20A14P
ATP1A2  TIMM17A SOX13   EML4    FBXO11  MDH1    SLC4A4  RPIA    COX5B   TXNDC9
C2orf29 RANBP2  NDUFB3  FAM117B THUMPD3 CRTAP   RP11    ACVR2B  MYL3    NDUFB4
SRPRB   MRPL47  MRPS18C CNGB1   NDUFC1  CMBL    JMY     TMEM167A        TTC37
UQCRQ   CNOT6   MRPS18B RRP36   CUL7    PHF3    SNAP91  BACH2   RTN4IP1 WISP3
NDUFA4  GGCT    CALU    MRPS33  MLL3    TNKS    VPS37A  MRPL15  UQCRB   COX6C
C9orf80 C9orf91 MRPL41  SVIL    PTPN20C MYPN    PPIF    MMS19   BCCIP   TMX2
LTBP2   NUMA1   SPCS2   TMEM126A        C11orf73        ATP5L   DNM1L   DUSP6
SLC25A3 SRRM4   SLC25A15        RALGAPA1        GLRX5   DYNC1H1 FAM96A  UACA
COX5A   ETFA    TSC2    PKD1    7SK     ZNF771  CIAPIN1 COQ9    COX4NB  C1QBP
SRP68P3 SUPT6H  ETV4    MRPL27  TACO1   ABCA5   ATP5H   SLC25A19        WDR45L
NDUFV2  NAPG    C18orf32        ACAA2   NEDD4L  ABCA7   UQCR11  ITGB1BP3
TIMM44  GADD45GIP1      ILVBL   COX6B1  RYR1    EIF3K   MRPS12  TBC1D17 SNORA51
TTC28   UQCR10  SLC16A8 RPS19BP1        NDUFA6  CLCN4   DMD     SLC9A7  RP1
RAP2C   MCF2    FUNDC2
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      5.09756556714145e-19    33.0004083299306        0.73074527714345
17      96      respiratory electron transport chain
GO:0045333      2.24818676451834e-17    22.4321528751753        1.08089405577469
18      142     cellular respiration
GO:0022900      1.82875161660439e-16    22.2229574487639        1.01999861601273
17      134     electron transport chain
GO:0015980      1.59850933047265e-12    10.187996031746 2.33686250086499        19
307     energy derivation by oxidation of organic compounds
GO:0006091      6.56007166244477e-11    7.58877995642702        3.25790602726455
20      428     generation of precursor metabolites and energy
GO:0042773      2.14085965668616e-09    28.7621920563097        0.357760708601481
8       47      ATP synthesis coupled electron transport
GO:0042775      2.14085965668616e-09    28.7621920563097        0.357760708601481
8       47      mitochondrial ATP synthesis coupled electron transport
GO:0006119      1.2177092509027e-08     22.4172549019608        0.441491938274168
8       58      oxidative phosphorylation
GO:0006120      2.74257268012291e-07    27.5211538461538        0.274029478928794
6       36      mitochondrial electron transport, NADH to ubiquinone
Tissue: Heart_Left_Ventricle=>Muscle_Skeletal   Type:   cluster
SourceGene:     DEFB1(ENSG00000164825.3)
TargetGeneSet:  RPL22   C1QA    C1QB    RPS8    RP11    FNBP1L  TKT     RGL1    SWT1
SRGAP3  SPTBN1  UBR3    FBLN2   RPL29   ABI3BP  RPL24   PSMD2   RPL35A  RPL34
RPS3A   CTD     PCDHB10 CSF1R   CTB     SLIT1   ADAMTS2 GFPT2   F13A1   RPL15P3
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RPS10   RPL10A  CLPS    NT5E    MRPS12  FNDC1   GPNMB   TRIP6   IRF5    RPL7
MATN2   NTRK2   RPL12   RPL7A   MRC1    ALOX5   TACR2   MYOF    ZNF195  RPL27A
RPS25   CD4     PFDN5   LRP1    GLIPR1  RPL6    GPC6    U6      RSL24D1 RPS3AP6 CILP
CORO2B  ISLR    ANPEP   LRRK1   USP7    PIEZO1  RPL13   RPL26   PSMD3   CHAD
TIMP2   RPL17   PRTN3   HRC     WISP2   ARSD-AS1        GPR64   RPS4X   DOCK11  ELF4
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      1.87298754884005e-26    71.2350628930818        0.453394228773095
19      91      translational termination
GO:0006414      3.60489204692822e-25    59.5802983764809        0.523147187045879
19      105     translational elongation
GO:0006614      3.60489204692822e-25    59.5802983764809        0.523147187045879
19      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      4.3767684978085e-25     58.8913467794405        0.528129541208221
19      106     cotranslational protein targeting to membrane
GO:0045047      4.3767684978085e-25     58.8913467794405        0.528129541208221
19      106     protein targeting to ER
GO:0072599      4.3767684978085e-25     58.8913467794405        0.528129541208221
19      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      3.87288690757928e-24    51.7095483133219        0.587917791156321
19      118     protein localization to endoplasmic reticulum
GO:0000184      4.59256530536703e-24    51.1888679245283        0.592900145318663
19      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006612      1.70868344544392e-23    41.1972238288028        0.762300186838281
20      153     protein targeting to membrane
GO:0043624      1.70868344544392e-23    41.1972238288028        0.762300186838281
20      153     cellular protein complex disassembly
GO:0043241      3.33498848053864e-23    39.690635451505 0.78721195764999        20
158     protein complex disassembly
GO:0034623      2.44910218365854e-22    35.526973026973 0.866929624247457       20
174     cellular macromolecular complex disassembly
GO:0032984      4.38389985809079e-22    34.3976777939042        0.891841395059165
20      179     macromolecular complex disassembly
GO:0019080      5.30012675642439e-22    38.692538593482 0.752335478513598       19
151     viral genome expression
GO:0019083      5.30012675642439e-22    38.692538593482 0.752335478513598       19
151     viral transcription
GO:0006413      6.03599514109242e-22    38.3989218328841        0.757317832675939
19      152     translational initiation
GO:0000956      4.81784431727102e-21    34.0064150943396        0.842017853435748
19      169     nuclear-transcribed mRNA catabolic process
GO:0071845      9.37713762928254e-21    23.7079389312977        1.41498858210504
22      284     cellular component disassembly at cellular level
GO:0022411      1.27352754784725e-20    23.3448120300752        1.43491799875441
22      288     cellular component disassembly
GO:0006402      1.32172620845689e-20    32.061231755073 0.886859040896824       19
178     mRNA catabolic process
GO:0019058      7.75447417905815e-20    25.8257382427999        1.15092381150093
20      231     viral infectious cycle
GO:0072594      1.83307320726844e-19    27.5049464558899        1.01640024911771
19      204     establishment of protein localization to organelle
GO:0006401      2.01319926029769e-19    27.3551430310408        1.02138260328005
19      205     RNA catabolic process
GO:0022415      8.22254859659035e-19    22.6586538461538        1.29541208220884
20      260     viral reproductive process
GO:0016032      1.91219579250783e-16    14.3076923076923        2.24704172721611
22      451     viral reproduction
GO:0033365      6.926931938195e-15      12.6872722540344        2.35665351878763
21      473     protein localization to organelle
GO:0006605      7.22293049273841e-15    12.6583560576548        2.36163587294997
21      474     protein targeting
GO:0071843      2.73842229720722e-06    8.78819875776398        1.19078264479967
9       239     cellular component biogenesis at cellular level
GO:0042254      9.04735715293693e-06    10.7972914409534        0.742370770188914
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7       149     ribosome biogenesis
GO:0022613      1.54948743400183e-05    8.15783410138249        1.12102968652688
8       225     ribonucleoprotein complex biogenesis
Tissue: Heart_Left_Ventricle=>Muscle_Skeletal   Type:   asymmetric
SourceGene:     ELMO1-AS1(ENSG00000224101.1)
TargetGeneSet:  SLC2A5  MIR186  MFSD2B  SFTPB   RAX     VILL    PILRA   SFTPC
FAM163B LRRC18  SFTPA2  SFTPA1  SFTPD   HBB     CTD     HBA1    RP3     ALAS2
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0007585      5.63941214389412e-10    195.54347826087 0.0458791779115632      5
51      respiratory gaseous exchange
GO:0071732      1.56486111333871e-05    524.836363636364        0.00629714206629299
2       7       cellular response to nitric oxide
Tissue: Heart_Left_Ventricle=>Muscle_Skeletal   Type:   asymmetric
SourceGene:     ENSG00000232970.1
TargetGeneSet:  RP11    TTLL7   GBP5    CSDE1   LCE1A   NR1I3   EBF3    DYSF
COX5B   FASTKD1 C2orf88 CCDC150 CCDC58  PLS1    MB21D2  HAUS3   SDHA    SDHAP3
COX7C   C6orf136        UQCRB   PTPDC1  OLFML2A MRPL41  VDAC2   COMTD1  GOT1
FBXL15  NRAP    ARNTL   ATP5L   USP5    B4GALNT1        SLC25A3 C15orf57
COX5A   IDH3A   PAQR4   C16orf62        UQCRC2  MLYCD   RILP    ASPA    PSMD11
C18orf25        EIF3K   RP4     SLMO2   DDT     KIAA0930        USP11   RPL23AP83
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0045333      3.75947048454087e-11    37.1737998843262        0.343920835928309
9       142     cellular respiration
GO:0022904      2.64221223061685e-09    40.2443820224719        0.23250986090928
7       96      respiratory electron transport chain
GO:0022900      2.7271926015933e-08     28.1279527559055        0.32454501418587
7       134     electron transport chain
GO:0015980      3.40707675026016e-08    16.3993288590604        0.743547159366134
9       307     energy derivation by oxidation of organic compounds
GO:0006091      4.42283451323363e-08    13.3952153110048        1.03660646322054
10      428     generation of precursor metabolites and energy
GO:0009060      3.02273220774707e-06    48.8217317487267        0.10172306414781
4       42      aerobic respiration
Tissue: Muscle_Skeletal=>Heart_Left_Ventricle   Type:   asymmetric
SourceGene:     ENSG00000243454.1
TargetGeneSet:  ZBTB48  COL24A1 BNIPL   TRAPPC12-AS1    COL3A1  COL5A2  FILIP1L RP11
CCDC80  KIT     PDE5A   FAM198B LPCAT1  PCDHGC5 MAPK14  EPB41L2 NFE2L3  CTHRC1
COL14A1 OGN     ASPN    ECM2    ANKS6   COL5A1  CDH23   POLL    LRRC55  LUM
DACT1   C17orf62        ZNF600  ZNF525  C20orf202       CDH26   CAPN6
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0030199      4.28224736216947e-09    111.762422360248        0.0639402117500519
5       33      collagen fibril organization
GO:0030198      1.81828795030155e-08    30.8852813852814        0.311950730053283
7       161     extracellular matrix organization
GO:0043062      1.89797129607994e-08    30.6838709677419        0.313888312227527
7       162     extracellular structure organization
Tissue: Muscle_Skeletal=>Heart_Left_Ventricle   Type:   asymmetric
SourceGene:     ENSG00000256240.1
TargetGeneSet:  PRPF38A MIR4426 NFU1    RPL37A  RP11    RPS23   CTD     TRIM27
ANKRD20A4       NDUFA8  RPS13   RPS29   RPL38   RPS21   GPM6B
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      4.7286271313409e-11     168.870588235294        0.0755657047955159
6       91      translational termination
GO:0006414      1.13596912439202e-10    144.848484848485        0.0871911978409799
6       105     translational elongation
GO:0006614      1.13596912439202e-10    144.848484848485        0.0871911978409799
6       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.20369630057904e-10    143.39  0.0880215902013702      6       106
cotranslational protein targeting to membrane
GO:0045047      1.20369630057904e-10    143.39  0.0880215902013702      6       106
protein targeting to ER
GO:0072599      1.20369630057904e-10    143.39  0.0880215902013702      6       106
establishment of protein localization to endoplasmic reticulum
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GO:0070972      2.31510341395467e-10    127.919642857143        0.0979862985260536
6       118     protein localization to endoplasmic reticulum
GO:0000184      2.43715605442804e-10    126.778761061947        0.0988166908864438
6       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      1.03374025467577e-09    98.5793103448276        0.125389246418933
6       151     viral genome expression
GO:0019083      1.03374025467577e-09    98.5793103448276        0.125389246418933
6       151     viral transcription
GO:0006413      1.07583659143465e-09    97.8972602739726        0.126219638779323
6       152     translational initiation
GO:0006612      1.11934651153124e-09    97.2244897959184        0.127050031139714
6       153     protein targeting to membrane
GO:0043624      1.11934651153124e-09    97.2244897959184        0.127050031139714
6       153     cellular protein complex disassembly
GO:0043241      1.35943709635315e-09    93.9934210526316        0.131201992941665
6       158     protein complex disassembly
GO:0000956      2.04064203149548e-09    87.5828220858896        0.140336308905958
6       169     nuclear-transcribed mRNA catabolic process
GO:0034623      2.43273019696167e-09    84.9464285714286        0.144488270707909
6       174     cellular macromolecular complex disassembly
GO:0006402      2.78967451431039e-09    82.9476744186046        0.147809840149471
6       178     mRNA catabolic process
GO:0032984      2.885389111653e-09      82.4624277456647        0.148640232509861
6       179     macromolecular complex disassembly
GO:0072594      6.33155322571186e-09    71.9242424242424        0.169400041519618
6       204     establishment of protein localization to organelle
GO:0006401      6.52010748867559e-09    71.5577889447236        0.170230433880008
6       205     RNA catabolic process
GO:0019058      1.33344527646106e-08    63.1733333333333        0.191820635250156
6       231     viral infectious cycle
GO:0022415      2.70267879691018e-08    55.8464566929134        0.215902013701474
6       260     viral reproductive process
GO:0071845      4.57347393629197e-08    50.9388489208633        0.235831430350841
6       284     cellular component disassembly at cellular level
GO:0022411      4.97033799076331e-08    50.2021276595745        0.239152999792402
6       288     cellular component disassembly
GO:0016032      7.04124660609916e-07    31.447191011236 0.374506954536018       6
451     viral reproduction
GO:0033365      9.30996519068124e-07    29.9186295503212        0.392775586464605
6       473     protein localization to organelle
GO:0006605      9.42588157413463e-07    29.8525641025641        0.393605978824995
6       474     protein targeting
Tissue: Muscle_Skeletal=>Heart_Left_Ventricle   Type:   asymmetric
SourceGene:     HTR7(ENSG00000148680.10)
TargetGeneSet:  RPL11   RP11    PSMD4   UBC     GNLY    EEF1B2  RPS3A   BTF3    CTB
RPS10   COPS6   RPL30   HAS2    PSMB7   URM1    GSTO1   TALDO1  RPLP2   RPS13
RPL14P1 CYP51P2 RPS3AP6 PSMB6   NLGN2   RPL23A  RPL17   PSMC5   TTC39C  ZNF121
KANK2   ZNF69   UBA52   RPL13A  HSD17B10        CSAG1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      8.79632144056685e-19    102.709677419355        0.21797799460245
12      105     translational elongation
GO:0006415      1.63837225706366e-17    103.783552631579        0.18891426198879
11      91      translational termination
GO:0006614      8.48006399289468e-17    88.2402015677492        0.21797799460245
11      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      9.45049397256069e-17    87.3052631578947        0.220053975503425
11      106     cotranslational protein targeting to membrane
GO:0045047      9.45049397256069e-17    87.3052631578947        0.220053975503425
11      106     protein targeting to ER
GO:0072599      9.45049397256069e-17    87.3052631578947        0.220053975503425
11      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      3.20574582608876e-16    77.4490900147565        0.244965746315134
11      118     protein localization to endoplasmic reticulum
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GO:0000184      3.5279711938347e-16     76.7266081871345        0.24704172721611
11      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0016032      2.08323179173028e-15    32.0756880733945        0.936267386340046
15      451     viral reproduction
GO:0019080      5.16753494456863e-15    59.0567669172932        0.313473116047332
11      151     viral genome expression
GO:0019083      5.16753494456863e-15    59.0567669172932        0.313473116047332
11      151     viral transcription
GO:0006413      5.56390451368096e-15    58.6338185890258        0.315549096948308
11      152     translational initiation
GO:0006612      5.98762366075637e-15    58.2168272794663        0.317625077849284
11      153     protein targeting to membrane
GO:0043624      5.98762366075637e-15    58.2168272794663        0.317625077849284
11      153     cellular protein complex disassembly
GO:0043241      8.57846919587909e-15    56.2169709989259        0.328004982354162
11      158     protein complex disassembly
GO:0000956      1.81720686333755e-14    52.2628247834777        0.350840772264895
11      169     nuclear-transcribed mRNA catabolic process
GO:0034623      2.51352674312269e-14    50.6419115272845        0.361220676769774
11      174     cellular macromolecular complex disassembly
GO:0006402      3.23563366621432e-14    49.4150646076269        0.369524600373677
11      178     mRNA catabolic process
GO:0032984      3.44329372861052e-14    49.1174812030075        0.371600581274652
11      179     macromolecular complex disassembly
GO:0072594      1.46307605867581e-13    42.6801199890919        0.423500103799045
11      204     establishment of protein localization to organelle
GO:0006401      1.54414914668809e-13    42.4571351058058        0.425576084700021
11      205     RNA catabolic process
GO:0019058      5.73980054119701e-13    37.3710526315789        0.479551588125389
11      231     viral infectious cycle
GO:0022415      2.09096768632073e-12    32.9511731135067        0.539755034253685
11      260     viral reproductive process
GO:0071845      5.46196938724066e-12    30.0034702139965        0.589578575877102
11      284     cellular component disassembly at cellular level
GO:0022411      6.35672814117802e-12    29.5618468554057        0.597882499481005
11      288     cellular component disassembly
GO:2000045      1.02214241136263e-09    47.4021739130435        0.205522109196595
7       99      regulation of G1/S transition of mitotic cell cycle
GO:0033365      1.28085356945784e-09    17.4924812030075        0.981938966161511
11      473     protein localization to organelle
GO:0006605      1.30966144978202e-09    17.4534500397863        0.984014947062487
11      474     protein targeting
GO:0006977      3.91936183998244e-09    59.8375 0.137014739464397       6       66
DNA damage response, signal transduction by p53 class mediator resulting in cell
cycle arrest
GO:0072413      3.91936183998244e-09    59.8375 0.137014739464397       6       66
signal transduction involved in mitotic cell cycle checkpoint
GO:0072431      3.91936183998244e-09    59.8375 0.137014739464397       6       66
signal transduction involved in mitotic cell cycle G1/S transition DNA damage
checkpoint
GO:0072474      3.91936183998244e-09    59.8375 0.137014739464397       6       66
signal transduction involved in mitotic cell cycle G1/S checkpoint
GO:0051436      4.29873094196168e-09    58.8524590163934        0.139090720365373
6       67      negative regulation of ubiquitin-protein ligase activity involved in
mitotic cell cycle
GO:0072401      4.29873094196168e-09    58.8524590163934        0.139090720365373
6       67      signal transduction involved in DNA integrity checkpoint
GO:0072404      4.29873094196168e-09    58.8524590163934        0.139090720365373
6       67      signal transduction involved in G1/S transition checkpoint
GO:0072422      4.29873094196168e-09    58.8524590163934        0.139090720365373
6       67      signal transduction involved in DNA damage checkpoint
GO:0072395      4.70801029401529e-09    57.8991935483871        0.141166701266348
6       68      signal transduction involved in cell cycle checkpoint
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GO:0051352	6.68216269281093e-09	54.375	0.149470624870251	6	72	negative regulation of ligase activity
GO:0051437	6.68216269281093e-09	54.375	0.149470624870251	6	72	positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
GO:0051444	6.68216269281093e-09	54.375	0.149470624870251	6	72	negative regulation of ubiquitin-protein ligase activity
GO:0031571	7.27017602897557e-09	53.5597014925373	0.151546605771227	6	73	mitotic cell cycle G1/S transition DNA damage checkpoint
GO:0002479	8.57510599745578e-09	52	0.155698567573178	6	75	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent
GO:0051439	1.08915271556663e-08	49.8229166666667	0.161926510276105	6	78	regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
GO:0000216	1.17698986002428e-08	49.1369863013699	0.164002491177081	6	79	M/G1 transition of mitotic cell cycle
GO:0042590	1.17698986002428e-08	49.1369863013699	0.164002491177081	6	79	antigen processing and presentation of exogenous peptide antigen via MHC class I
GO:0071158	1.27060535538087e-08	48.4695945945946	0.166078472078057	6	80	positive regulation of cell cycle arrest
GO:0031575	1.47636597233999e-08	47.1875	0.170230433880008	6	82	mitotic cell cycle G1/S transition checkpoint
GO:0051443	1.47636597233999e-08	47.1875	0.170230433880008	6	82	positive regulation of ubiquitin-protein ligase activity
GO:0002478	1.58913587152108e-08	46.5714285714286	0.172306414780984	6	83	antigen processing and presentation of exogenous peptide antigen
GO:0031145	1.58913587152108e-08	46.5714285714286	0.172306414780984	6	83	anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process
GO:2000602	1.63425650901189e-08	31.045652173913	0.305169192443429	7	147	regulation of interphase of mitotic cell cycle
GO:0019884	1.83610184479699e-08	45.3860759493671	0.176458376582935	6	85	antigen processing and presentation of exogenous antigen
GO:0051351	1.97099177666051e-08	44.815625	0.178534357483911	6	86	positive regulation of ligase activity
GO:0071779	1.97099177666051e-08	44.815625	0.178534357483911	6	86	G1/S transition checkpoint
GO:0031397	2.96382080598767e-08	41.671511627907	0.190990242889765	6	92	negative regulation of protein ubiquitination
GO:0051438	3.83125302602106e-08	39.8083333333333	0.199294166493668	6	96	regulation of ubiquitin-protein ligase activity
GO:0002474	4.61104909350121e-08	38.5161290322581	0.205522109196595	6	99	antigen processing and presentation of peptide antigen via MHC class I
GO:0051340	4.89836579529392e-08	38.1037234042553	0.207598090097571	6	100	regulation of ligase activity
GO:0048002	7.77374940761755e-08	35.0955882352941	0.224205937305377	6	108	antigen processing and presentation of peptide antigen
GO:0000082	8.28495259004838e-08	24.2152052465387	0.386132447581482	7	186	G1/S transition of mitotic cell cycle
GO:0030330	1.25433059224399e-07	32.2297297297297	0.242889765414158	6	117	DNA damage response, signal transduction by p53 class mediator
GO:0072331	1.68967505186815e-07	30.5641025641026	0.255345650820012	6	123	signal transduction by p53 class mediator
GO:0031398	2.04375567662649e-07	29.5454545454545	0.263649574423915	6	127	positive regulation of protein ubiquitination
GO:0000077	2.34758725350849e-07	28.8245967741935	0.269877517126842	6	130	DNA damage checkpoint
GO:0000084	2.80959714360291e-07	27.916015625	0.278181440730745	6	134	S phase of mitotic cell cycle
GO:0031570	3.06719228726957e-07	27.4826923076923	0.282333402532697			

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6       136     DNA integrity checkpoint
GO:0007093      3.48975113536308e-07    26.8571428571429        0.288561345235624
6       139     mitotic cell cycle checkpoint
GO:0042770      3.64079545731552e-07    26.6548507462687        0.2906373261366 6
140     signal transduction in response to DNA damage
GO:0051320      4.12650314043875e-07    26.0656934306569        0.296865268839527
6       143     S phase
GO:0090068      5.68762218632599e-07    24.6137931034483        0.313473116047332
6       151     positive regulation of cell cycle process
GO:0019882      5.91289054146557e-07    24.4434931506849        0.315549096948308
6       152     antigen processing and presentation
GO:0000209      8.28994291915284e-07    23.0096774193548        0.334232925057089
6       161     protein polyubiquitination
GO:0031396      1.06371034376703e-06    22.0046296296296        0.348764791363919
6       168     regulation of protein ubiquitination
GO:0007346      2.23664730534032e-06    14.5233548766157        0.62902221299564
7       303     regulation of mitotic cell cycle
GO:0043161      3.78521980910599e-06    17.5098522167488        0.433880008303924
6       209     proteasomal ubiquitin-dependent protein catabolic process
GO:0010498      4.57725075111673e-06    16.9178571428571        0.448411874610754
6       216     proteasomal protein catabolic process
GO:0006521      5.52175345972073e-06    41.7068214804064        0.118330911355616
4       57      regulation of cellular amino acid metabolic process
GO:0000075      8.78757779016714e-06    15.0264830508475        0.502387378036122
6       242     cell cycle checkpoint
GO:0051329      9.76062238866366e-06    11.4940392706872        0.786796761469794
7       379     interphase of mitotic cell cycle
GO:0051325      1.1183273928385e-05     11.245652173913 0.8034046086776 7       387
interphase
GO:0033238      1.40738090422235e-05    32.472850678733 0.149470624870251       4
72      regulation of cellular amine metabolic process
GO:0071156      1.44265095004602e-05    13.7238372093023        0.548058957857588
6       264     regulation of cell cycle arrest
GO:0010564      1.73202083240063e-05    10.4794359576968        0.859456093003944
7       414     regulation of cell cycle process
Tissue: Heart_Left_Ventricle=>Muscle_Skeletal   Type:   asymmetric
SourceGene:     ITPKA(ENSG00000137825.6)
TargetGeneSet:  TMEM52  UBAP2L  HADH    HADHB   RPLP0P6 UGP2    RUVBL1  DCUN1D1
ZDHHC19 ETFDH   NUDT3   EPHA7   RP11    SND1    ZNF703  TOR1B   FAM213A NXF1
HOXC9   ACADVL  DHX40   ECH1    PIGT    RAB9A
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006635      1.41289059246051e-08    88.1066176470588        0.0813784513182479
5       56      fatty acid beta-oxidation
GO:0009062      3.81315591051784e-08    71.2648809523809        0.0988166908864438
5       68      fatty acid catabolic process
GO:0072329      8.16074322110899e-08    60.625  0.114801743823957       5       79
monocarboxylic acid catabolic process
GO:0019395      1.32806728447555e-07    54.6798780487805        0.126427236869421
5       87      fatty acid oxidation
GO:0034440      1.57526132238458e-07    52.7389705882353        0.13078679676147
5       90      lipid oxidation
GO:0044242      1.28190144385319e-06    33.8494318181818        0.199086568403571
5       137     cellular lipid catabolic process
GO:0030258      1.81557241724748e-06    31.443661971831 0.213618434710401       5
147     lipid modification
GO:0016054      5.76208919702338e-06    24.6011740331492        0.270292713307038
5       186     organic acid catabolic process
GO:0046395      5.76208919702338e-06    24.6011740331492        0.270292713307038
5       186     carboxylic acid catabolic process
GO:0044282      1.24698933640249e-05    20.8582746478873        0.316794685488894
5       218     small molecule catabolic process
GO:0032787      1.67535472839315e-05    14.2126582278481        0.582727838903882
6       401     monocarboxylic acid metabolic process
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Tissue: Muscle_Skeletal=>Heart_Left_Ventricle   Type:   cluster
SourceGene:     MYH13(ENSG00000006788.6)
TargetGeneSet:  SSU72   PARK7   DDI2    RPL11   RP4     BTBD8   RPL5    CSDE1   HAX1
NOS1AP  SNRPE   RP11    UBC     AAK1    POLR1B  EEF1B2  WDR48   RPL14   UBE2K   ANK2
RPS3A   SERF1B  RAD50   GNB2L1  HIVEP1  PPIAP29 SRSF3   COQ3    PNISR   ARID1B  PPIA
RPS3AP26        PNPLA8  ZNF467  RPL30   ZNF706  DEPTOR  GBA2    RNF20   ZNF483  MRRF
ARPC5L  APBB1IP RPS24   RPS3AP5 ZDHHC16 PPIAP19 UROS    GLRX3   RPL27A  DDX6
COX14   ACVR1B  PFDN5   C12orf73        RPL6    GTF3A   POMP    COX17P1 METTL17
VTI1B   TMED8   CDC42BPB        GANC    RPS3AP6 RNU6    CD276   MRPL28  RPS15A
RPL26   RPS7P1  SYNRG   RPL19   RPL27   RPS7P11 RPS2P48 SRSF1   SRSF2   MYL12B
NDUFV2  TXNL4A  C19orf35        RIN2    ARFGEF2 PPIAP22 ATP5O   HMGB1P10
APOL6   APOL2   APOBEC3C        XRCC6   C22orf32        PIGA    RPL9P7  EEF1B2P3
RPS2P55 RP6     SPIN4   RPS23P8 MED12   COX7B
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      2.6903825884287e-16     34.8791208791209        0.559476852812954
14      105     translational elongation
GO:0006415      1.3332248432203e-15     37.2291666666667        0.48487993910456
13      91      translational termination
GO:0070972      1.45054291603114e-15    30.491452991453 0.628745415542177       14
118     protein localization to endoplasmic reticulum
GO:0006614      9.16193873515715e-15    31.5329483695652        0.559476852812954
13      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.03994866934022e-14    31.1917002688172        0.564805203792125
13      106     cotranslational protein targeting to membrane
GO:0045047      1.03994866934022e-14    31.1917002688172        0.564805203792125
13      106     protein targeting to ER
GO:0072599      1.03994866934022e-14    31.1917002688172        0.564805203792125
13      106     establishment of protein localization to endoplasmic reticulum
GO:0000184      4.8362029249584e-14     27.341391509434 0.634073766521348       13
119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0000956      2.30569410904471e-13    20.3856630824373        0.900491315479898
14      169     nuclear-transcribed mRNA catabolic process
GO:0034623      3.45338973426966e-13    19.7416666666667        0.927133070375753
14      174     cellular macromolecular complex disassembly
GO:0006402      4.72796873249243e-13    19.2547425474255        0.948446474292437
14      178     mRNA catabolic process
GO:0032984      5.1080815321368e-13     19.1367003367003        0.953774825271608
14      179     macromolecular complex disassembly
GO:0019058      1.05742489747585e-12    15.8579749103943        1.2308490761885 15
231     viral infectious cycle
GO:0019080      1.08608954059873e-12    20.9542572463768        0.80458099785482
13      151     viral genome expression
GO:0019083      1.08608954059873e-12    20.9542572463768        0.80458099785482
13      151     viral transcription
GO:0006413      1.1827488475147e-12     20.8020458633094        0.809909348833991
13      152     translational initiation
GO:0006612      1.28722352384582e-12    20.6520089285714        0.815237699813162
13      153     protein targeting to membrane
GO:0043624      1.28722352384582e-12    20.6520089285714        0.815237699813162
13      153     cellular protein complex disassembly
GO:0043241      1.9480621205499e-12     19.9328663793103        0.841879454709017
13      158     protein complex disassembly
GO:0006401      3.27946995097057e-12    16.5014543339151        1.09231195073005
14      205     RNA catabolic process
GO:0022415      5.83733746363248e-12    13.9522712310731        1.38537125458446
15      260     viral reproductive process
GO:0072594      5.01185158014528e-11    15.0833606020942        1.08698359975088
13      204     establishment of protein localization to organelle
GO:0071845      2.5819617408704e-10     11.6082304526749        1.51325167808456
14      284     cellular component disassembly at cellular level
GO:0022411      3.10317216976828e-10    11.4355231143552        1.53456508200125
14      288     cellular component disassembly
GO:0016032      1.47811966170085e-09    8.40489918974939        2.40308629160612
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16      451     viral reproduction
GO:0071843      5.14402960702649e-08    10.3406432748538        1.27347588402187
11      239     cellular component biogenesis at cellular level
GO:0033365      1.6986105728012e-07     6.73686758654079        2.52031001314788
14      473     protein localization to organelle
GO:0022613      3.02358418324044e-07    9.82922596320722        1.19887897031347
10      225     ribonucleoprotein complex biogenesis
GO:0042273      3.57045597231164e-07    98.3972602739726        0.0639402117500519
4       12      ribosomal large subunit biogenesis
GO:0006605      1.16729083679998e-06    6.13032131236443        2.52563836412705
13      474     protein targeting
GO:0071826      1.50487845944361e-05    12.8378783338328        0.532835097917099
6       100     ribonucleoprotein complex subunit organization
Tissue: Heart_Left_Ventricle=>Muscle_Skeletal   Type:   asymmetric
SourceGene:     NELF(ENSG00000165802.14)
TargetGeneSet:  UBR4    FABP3   MACF1   HECTD3  C1orf52 CCDC18  RPS27   MTX1
HAPLN2  RP11    DUSP12  SLC19A2 LRRN2   PARP1   C2orf28 ETAA1   TPRKB   RETSAT
COX5B   COA5    MAP4K4  NDUFB3  EFHD1   MYEOV2  HDLBP   FAM208A GXYLT2  GAP43
NDUFB4  C3orf37 HAUS3   DOK7    WDFY3   MRPS36  COX7C   ID4     VARS    TAF11   CUL7
DST     BACH2   COQ3    EIF3B   NDUFA4  PHF14   GGCT    TRIM56  NDUFA5  KIAA1549
DEFB1   UBE2V2  ARMC1   UQCRB   COX6C   MRPL13  TLN1    CLTA    FYTTD1P1
MRPL41  CWF19L1 PCGF6   C10orf88        TRIM44  NDUFS8  C11orf73        FZD4
TMEM135 ATP5L   ERC1    USP5    SLC25A3 GPN3    EXOSC8  FREM2   SAMD4A  SYNE2
SMEK1   NDUFB1  DYNC1H1 SIVA1   C15orf29        SLC12A6 CCPG1   VPS13C  COX5A   ETFA
PEX11A  MPG     TRAF7   PAQR4   NOMO2   ARL6IP1 UQCRC2  MLYCD   TRIM16  SUPT6H
TMEM106A        MRPL27  ACSF2   TACO1   ATP5H   C18orf21        ACAA2   CNDP2
PQLC1   UQCR11  COX6B1  ECH1    CYP2G1P GEMIN7  RP1     MAP1LC3A        PI4KA   MPST
C22orf46        NDUFB11 UBE2A
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      7.13933868438904e-22    43.3572874493927        0.624455055013494
18      96      respiratory electron transport chain
GO:0022900      3.95593074504116e-19    29.0764519056261        0.871635180956335
18      134     electron transport chain
GO:0045333      1.15776440546362e-18    27.1852716468591        0.92367310220746
18      142     cellular respiration
GO:0015980      9.91986481979411e-13    11.5290475323256        1.9969552280119 18
307     energy derivation by oxidation of organic compounds
GO:0006091      2.86043603514395e-11    8.63934800325998        2.78402878693516
19      428     generation of precursor metabolites and energy
GO:0006119      3.47605471064466e-09    26.6176744186047        0.377274929070653
8       58      oxidative phosphorylation
GO:0042773      1.99865711717415e-08    28.7985632183908        0.305722787350356
7       47      ATP synthesis coupled electron transport
GO:0042775      1.99865711717415e-08    28.7985632183908        0.305722787350356
7       47      mitochondrial ATP synthesis coupled electron transport
GO:0006120      1.07279395697902e-07    32.5613636363636        0.23417064563006
6       36      mitochondrial electron transport, NADH to ubiquinone
Tissue: Heart_Left_Ventricle=>Muscle_Skeletal   Type:   asymmetric
SourceGene:     OR7A5(ENSG00000188269.3)
TargetGeneSet:  C1orf52 RP11    PCNXL2  UBC     RPL24   RPL35A  RPL34   LSM6
COX7C   CTD     MRPS12  NAA38   RPL27A  USP5    SIPA1L1 SEC11A  RPS7P1  RPL27   CHAD
RPL17   WDR7    SNORA68
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006614      7.26569440883648e-14    147.814432989691        0.11625493045464
8       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      7.85492180676036e-14    146.295918367347        0.117362120268494
8       106     cotranslational protein targeting to membrane
GO:0045047      7.85492180676036e-14    146.295918367347        0.117362120268494
8       106     protein targeting to ER
GO:0072599      7.85492180676036e-14    146.295918367347        0.117362120268494
8       106     establishment of protein localization to endoplasmic reticulum
GO:0070972      1.89402554759958e-13    130.227272727273        0.130648398034738
8       118     protein localization to endoplasmic reticulum
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GO:0006612      1.5733295426454e-12     98.551724137931 0.169400041519618       8
153     protein targeting to membrane
GO:0006415      3.39176939742113e-12    132.87962962963 0.100754273060688       7
91      translational termination
GO:0000956      3.52125634699605e-12    88.6583850931677        0.187115078541277
8       169     nuclear-transcribed mRNA catabolic process
GO:0006402      5.355101126179e-12      83.9117647058823        0.19707978686596l
8       178     mRNA catabolic process
GO:0006414      9.46494166699606e-12    113.785714285714        0.11625493045464
7       105     translational elongation
GO:0072594      1.60610344859003e-11    72.6479591836735        0.225866722026157
8       204     establishment of protein localization to organelle
GO:0006401      1.67049389414366e-11    72.2741116751269        0.226973911840011
8       205     RNA catabolic process
GO:0000184      2.31164452652353e-11    99.4652777777778        0.131755587848592
7       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      1.2505211822669e-10     77.1890432098765        0.167185661891911
7       151     viral genome expression
GO:0019083      1.2505211822669e-10     77.1890432098765        0.167185661891911
7       151     viral transcription
GO:0006413      1.31017098892955e-10    76.6513409961686        0.168292851705764
7       152     translational initiation
GO:0043624      1.3722330701249e-10     76.12100456621  0.169400041519618       7
153     cellular protein complex disassembly
GO:0043241      1.7216091487359e-10     73.5746872700515        0.174935990588887
7       158     protein complex disassembly
GO:0034623      3.3947602590686e-10     66.4510978043912        0.192651027610546
7       174     cellular macromolecular complex disassembly
GO:0032984      4.14230218725797e-10    64.4967700258398        0.198186976679815
7       179     macromolecular complex disassembly
GO:0019058      2.46507857012528e-09    49.34375        0.255760847000208       7
231     viral infectious cycle
GO:0022415      5.60903100281073e-09    43.5985946420729        0.287869351601965
7       260     viral reproductive process
GO:0071845      1.03407170427426e-08    39.7537103890894        0.314441907134454
7       284     cellular component disassembly at cellular level
GO:0022411      1.1390980188622e-08     39.1767497034401        0.318870666389869
7       288     cellular component disassembly
GO:0033365      1.26914402183488e-08    30.0430107526882        0.523700781952806
8       473     protein localization to organelle
GO:0006605      1.29027933970099e-08    29.9763948497854        0.52480797176666
8       474     protein targeting
GO:0016032      2.46764369267241e-07    24.5087587587588        0.499342606048024
7       451     viral reproduction
Tissue: Muscle_Skeletal=>Heart_Left_Ventricle   Type:   asymmetric
SourceGene:     PTBP2(ENSG00000117569.12)
TargetGeneSet:  AURKAIP1        BTBD8   KIAA1107        GNAI3   OTUD7B  ZBTB37  SWT1
SUSD4   UBC     NFU1    COX5B   TSPO    NBEAL1  ASB1    WDR48   ZNF501  BCL6
NAP1L5  RP11    NDUFS6  TRIM23  COX7C   LARP1   CREBRF  HIGD2A  RNF44   COX7A2
SLC18B1 MRPS24  PSPH    GATSL2  SRI     ATP5J2  GATS    RPS26P31        GSTK1   CTD
RPL30   COX6C   FBXO32  FAM49B  ZFP41   CYC1    NDUFB6  C9orf131        NDUFA8
OLFML2A PRRC2B  CAMSAP1 ENTPD2  CREM    NDUFB8  NDUFS3  COX8A   EFEMP2  NDUFS8
PFDN5   ITGA5   WIBG    FITM1   PROX2   LINC00521       COX5A   WDR24   UNKL
RPL3L   NDUFB10 TCEB2   YPEL3   RBL2    PSMB6   NT5M    HELZ    RECQL5  ALYREF
SNRPD1  ATP5D   C19orf70        NDUFB7  COX6B1  POLR2I  NDUFA3  MAPRE1  CEP250
ATP9A   PPIAP22 ATP5O   MRPL40  RP4     HUWE1   COX7B
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      5.88938071504012e-28    73.8080495356037        0.471662860701682
20      96      respiratory electron transport chain
GO:0022900      7.71309560013103e-25    49.0746474028208        0.658362743062764
20      134     electron transport chain
GO:0045333      2.61492795940944e-24    45.8309225329476        0.697667981454571
20      142     cellular respiration
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GO:0015980      1.60320971903948e-17    19.2566782810685        1.50833852328559
20      307     energy derivation by oxidation of organic compounds
GO:0006091      9.75352417986163e-15    13.4294502114571        2.10283025396166
20      428     generation of precursor metabolites and energy
GO:0006120      8.3589123933997e-14     77.1666666666667        0.176873572763131
9       36      mitochondrial electron transport, NADH to ubiquinone
GO:0006119      1.83556053078907e-13    48.948087431694 0.284962978340599       10
58      oxidative phosphorylation
GO:0042773      1.15940979052487e-12    54.7869269949066        0.230918275551865
9       47      ATP synthesis coupled electron transport
GO:0042775      1.15940979052487e-12    54.7869269949066        0.230918275551865
9       47      mitochondrial ATP synthesis coupled electron transport
Tissue: Muscle_Skeletal=>Heart_Left_Ventricle   Type:   asymmetric
SourceGene:     QDPR(ENSG00000151552.7)
TargetGeneSet:  THRAP3  GNG5    ADCK3   FH      NFU1    TSPO    UGGT1   TNS1
SLC9C1  ARHGAP31        POU5F1P6        RP11    ANTXR2  BNIP1   PPP2R5D MDN1
FBXL18  C7orf41 IGFBP3  DPY19L2P4       GSTK1   TCEB1   COX6C   NDUFB9  FAM49B  CYC1
TSSK5P1 SMARCA2 NDUFB6  FAM122A C9orf174        RNF20   MUSK    NDUFA8  ARPC5L
PCGF5   SUFU    PDCD4   CSRP3   PHF21A  NDUFS3  PDE2A   TMTC1   TMED8   CDC42BPB
HERC2   LRRC49  NDUFB10 ECI1    SNX29   CSDAP1  RBL2    MT1X    KLHL36  KIAA0513
ZNF624  MLX     NFE2L1  ERN1    NDUFV2  FAM210A C19orf70        DDX39A  ZNF570  RP1
KCNB1   GGA1    SLC16A8 UQCRFS1P1       C22orf46        RP4     PACSIN2 ACOT9
RPL9P7  GAPDHP1 TIMM17B COX7B   MBNL3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      1.92258326527859e-10    29.0141987829615        0.398588332987337
9       96      respiratory electron transport chain
GO:0015980      2.94117361601686e-10    13.262483716891 1.27465227319909        13
307     energy derivation by oxidation of organic compounds
GO:0045333      3.02432975593257e-10    21.6045454545455        0.589578575877102
10      142     cellular respiration
GO:0022900      3.83137500848125e-09    20.1402352941176        0.556362881461491
9       134     electron transport chain
GO:0006120      7.00893603321913e-09    53.1888888888889        0.149470624870251
6       36      mitochondrial electron transport, NADH to ubiquinone
GO:0006091      1.6391297759747e-08     9.31494488592669        1.77703965123521
13      428     generation of precursor metabolites and energy
GO:0042773      3.72981637460749e-08    38.8888888888889        0.195142204691717
6       47      ATP synthesis coupled electron transport
GO:0042775      3.72981637460749e-08    38.8888888888889        0.195142204691717
6       47      mitochondrial ATP synthesis coupled electron transport
GO:0006119      1.35720446957882e-07    30.6388888888889        0.240813784513182
6       58      oxidative phosphorylation
Tissue: Muscle_Skeletal=>Heart_Left_Ventricle   Type:   cluster
SourceGene:     RNY4P14(ENSG00000200526.1)
TargetGeneSet:  DFFB    ZBTB48  LRRC38  COL16A1 CCDC28B COL24A1 GSTM5   BNIPL   RGS5
RP11    PLA2G4A ANTXR1  LINC00152       XIRP2   FRZB    COL3A1  COL5A2  FN1
DOCK10  FBLN2   ROBO1   FILIP1L CCDC80  WDR52   TNIK    DCUN1D1 FAM184B KIT
SEPT11  HPGDS   CXXC4   PDE5A   FAM198B CPE     LPCAT1  PTGER4  PHF15   TGFBI
PCDHGC5 ARSI    TRIM41  MAPK14  RP1     PM20D2  MARCKS  SLC35F1 EPB41L2 FNDC1   LFNG
NFE2L3  VWC2    COL1A2  SLC12A9 EBF2    PLAT    MSC     CTHRC1  COL14A1 FREM1
GLIPR2  RG9MTD3 OGN     ASPN    ECM2    ANKS6   COL15A1 NCS1    COL5A1  CCDC3
ARHGAP22        CDH23   POLL    OLFML1  LRRC55  NRXN2   ZC3H12C SCN4B   KCNA5
LRRC10  LUM     ANO4    GPR133  LPAR6   DACT1   SERPINA3        ALDH1A2 FTSJD1
CENPN   CAMTA2  MFAP4   STAT3   EZH1    MRC2    CDC42EP4        TIMP2   C17orf62
ARHGAP28        MOB3A   ZNF558  ANKRD27 WDR62   PSMC4   ZNF600  ZNF525  ZNF671
PTPRT   PARD6B  CDH26   COL6A1  COL6A2  TOB2    CAPN6   LHFPL1  PLS3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0030198      3.56054065301709e-09    13.5361904761905        0.980416580167462
11      161     extracellular matrix organization
GO:0043062      3.80116888912781e-09    13.445600756859 0.986506124143658       11
162     extracellular structure organization
GO:0030199      4.16435072997243e-08    38.8509485094851        0.200954951214449
6       33      collagen fibril organization
```

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GO:0071230      2.09866096359796e-06    28.781124497992 0.21313403916684        5
35      cellular response to amino acid stimulus
GO:0071229      4.70749855958424e-06    23.9742302543507        0.249671303024012
5       41      cellular response to acid
GO:0071418      1.27485675500892e-05    19.1673360107095        0.304477198809771
5       50      cellular response to amine stimulus
GO:0071417      1.54890956021022e-05    18.3491412458344        0.316656286762162
5       52      cellular response to organic nitrogen
Tissue: Heart_Left_Ventricle=>Muscle_Skeletal   Type:   asymmetric
SourceGene:     RP1-163G9.1(ENSG00000177133.5)
TargetGeneSet:  GDI2P2  RP11    TMEM183A        KRT18P12        FAM179A MDH1    UGP2
VAMP8   COX5B   SPPL2B  GIGYF2  PLCL2   PLCL2-AS1       ZNF621  ZDHHC3  TEX264  PDHB
ZBTB20  NDUFB4  C3orf55 LIMCH1  EGF     MRPS36  UQCRQ   GUSBP2  XPO5    WDR11
IFNGR1  PHACTR2 NDUFA4  POR     TMEM120A        CTB     ERVW-1  NDUFA5  GSTK1
HMBOX1  CTD     VDAC3   IMPA1   C8orf38 TAF1L   MRPL41  TIMM23  MYPN    MMS19
FADS3   TMEM135 LDHB    DDX23   ASIC1   HOXC9   SLC25A3 CHPT1   FREM2   EDNRB
CMTM5   SAMD4A  LGALS3  DYNC1H1 CHKB    GANC    COX5A   RPUSD1  GRIN2A  UQCRC2
TMCO7   ADAT1   VPS53   RPS4XP17        NF1     KRT32   ATP5H   METRNL  NDUFV2
ACAA2   FBN3    RYR1    LIPE    SBK2    URB1    CECR2   ASB11   TCEAL2  UBE2A
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0045333      6.25226838176364e-11    20.6318768096868        0.678015362258667
11      142     cellular respiration
GO:0022904      7.01828460502807e-10    24.6465517241379        0.458376582935437
9       96      respiratory electron transport chain
GO:0022900      7.1571976333513e-10     19.4887916894478        0.639817313680714
10      134     electron transport chain
GO:0006091      1.21707375563813e-09    9.39534570890503        2.04359559892049
15      428     generation of precursor metabolites and energy
GO:0015980      2.03692193812284e-08    10.0531668153434        1.46585011417895
12      307     energy derivation by oxidation of organic compounds
GO:0006119      8.0674877637956e-06     21.1217570754717        0.27693585219016
5       58      oxidative phosphorylation
Tissue: Heart_Left_Ventricle=>Muscle_Skeletal   Type:   asymmetric
SourceGene:     RP1-228H13.1(ENSG00000227311.1)
TargetGeneSet:  RP11    NUDT4P1 IL6R    TMEM17  HDAC4   ATP13A4-AS1     RPS10
RPL10A  VPS26A  VDAC2   EIF3F   NUDT4   TIMM9   RP3     IGHD    TGM7    MRPS34  CTD
RPL13   EIF3K   RPL18   FUNDC2
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006413      1.37968195674388e-08    53.3798256537983        0.178811154937375
6       152     translational initiation
GO:0006612      6.95845230174473e-07    40.2195945945946        0.179987544114594
5       153     protein targeting to membrane
GO:0072594      2.87729689222389e-06    29.8052763819095        0.239983392152792
5       204     establishment of protein localization to organelle
GO:0006415      3.28912916443026e-06    50.7409372236958        0.107051415126981
4       91      translational termination
GO:0006414      5.82364233891752e-06    43.6648895658797        0.123520863608055
4       105     translational elongation
GO:0006614      5.82364233891752e-06    43.6648895658797        0.123520863608055
4       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      6.04765176555914e-06    43.2337858220211        0.124697252785274
4       106     cotranslational protein targeting to membrane
GO:0045047      6.04765176555914e-06    43.2337858220211        0.124697252785274
4       106     protein targeting to ER
GO:0072599      6.04765176555914e-06    43.2337858220211        0.124697252785274
4       106     establishment of protein localization to endoplasmic reticulum
GO:0070972      9.26148736805911e-06    38.6504723346829        0.138813922911909
4       118     protein localization to endoplasmic reticulum
GO:0000184      9.57670561999659e-06    38.3117056856187        0.139990312089129
4       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
Tissue: Heart_Left_Ventricle=>Muscle_Skeletal   Type:   asymmetric
SourceGene:     SRSF1(ENSG00000136450.6)
TargetGeneSet:  NKAIN1  USP33   KCNC4   BRP44   FAM129A MDH1    TIA1    SUCLG1
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CNNM3   COX5B   FASTKD1 NDUFB3  ICA1L   CRTAP   NDUFB5  MB21D2  RAB28   FAT4
PHF17   NDUFC1  UFSP2   MRPS36  COX7C   CTXN3   CTB     GNL1    UHRF1BP1
MTRNR2L9        ELFN1   GATS    NDUFA5  SP6     SDCBP   HEY1    UQCRB   MTERFD1 AUH
C9orf106        C9orf142        MRPL41  MLLT10  VDAC2   RP11    NDUFS8  CHKA
ATP5L   POU6F1  SLC25A3 BRI3BP  ZNF839  GOLGA8IP        COX5A   UBE2Q2  UQCRC2
MYH13   MYH1    MTRNR2L1        SRSF1   DHX40   ATP5H   ECSIT   EIF3K   MYBPC2
PSMD4P1 MYO18B  TTC28   UQCR10  C22orf46        CPT1B   APOO    SLC9A7  NDUFB11
GAGE2D  AR
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0045333      9.61868886345563e-22    52.4592432432432        0.530620718289392
17      142     cellular respiration
GO:0022904      3.17953538779795e-19    61.1006097560976        0.358729499688603
14      96      respiratory electron transport chain
GO:0022900      4.11300559421583e-17    41.64125        0.500726593315342       14
134     electron transport chain
GO:0015980      5.4562090248746e-16     22.3503261882572        1.14718704587918
17      307     energy derivation by oxidation of organic compounds
GO:0006091      7.85300294206473e-15    17.0573170731707        1.59933568611169
18      428     generation of precursor metabolites and energy
GO:0006119      3.67604008661309e-11    49.9026086956522        0.216732406061864
8       58      oxidative phosphorylation
GO:0042773      3.81102226867521e-10    53.456914893617 0.175627984222545       7
47      ATP synthesis coupled electron transport
GO:0042775      3.81102226867521e-10    53.456914893617 0.175627984222545       7
47      mitochondrial ATP synthesis coupled electron transport
GO:0006120      2.08094257316656e-07    47.2876892692561        0.134523562383226
5       36      mitochondrial electron transport, NADH to ubiquinone
GO:0009060      1.75417182913406e-05    30.2294736842105        0.156944156113764
4       42      aerobic respiration
Tissue: Heart_Left_Ventricle=>Muscle_Skeletal   Type:   asymmetric
SourceGene:     SUSD2(ENSG00000099994.10)
TargetGeneSet:  NDUFS2  FAM129A TRMT61B SUCLG1  ANKRD36 NIF3L1  NDUFB3  LRRC3B  PDHB
MLF1    COX18   RAB33B  RICTOR  MRPS30  IL6ST   COQ3    RTN4IP1 C6orf203        SGK1
STAG3   RP11    MRPL15  PGM5P1  PDSS1   RHOBTB1 PPIF    GHITM   FZD4    CD9
AP5M1   DIO2    SLC25A29        ETFA    UQCRC2  CIAPIN1 GLG1    TEX2    METRNL
ATP5A1  PSMD4P1 C21orf33        ARVCF   HPS4    NDUFA6  APOO    TIMM8A  SLC25A5
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0045333      2.16383598522514e-09    29.3978383942357        0.363573455124213
8       142     cellular respiration
GO:0015980      3.39155268413446e-09    17.6044394562913        0.78603556847277
10      307     energy derivation by oxidation of organic compounds
GO:0006091      7.95810263568277e-08    12.401205032784 1.09584111826171        10
428     generation of precursor metabolites and energy
GO:0022904      1.44492783454821e-07    30.8043010752688        0.245796138675524
6       96      respiratory electron transport chain
GO:0022900      1.04301560891696e-06    21.601814516129 0.343090443567919       6
134     electron transport chain
GO:0006119      1.39768675208686e-05    32.2334455667789        0.148501833783129
4       58      oxidative phosphorylation
Tissue: Muscle_Skeletal=>Heart_Left_Ventricle   Type:   asymmetric
SourceGene:     TRDN(ENSG00000186439.7)
TargetGeneSet:  MTND2P28        AURKAIP1        MRPL20  RPL5    HBXIP   ZNF687
EEF1B2  UBE2F   MAP4    RPL29   THOC7   HTT-AS1 MRAP    RP11    RPS3A   MTND5P11
CTB     NQO2    SRSF3   HDDC2   FBXL18  CYCS    MRPS24  TCEB1   AK1     METTL11A
GLRX3   RPL27A  NDUFS3  PFDN5   RAP1B   RPL6    HERC2P10        PHGR1   ZFAND6
STUB1   ECI1    RPS15A  METTL16 TMEM93  TXNDC17 STX8    RPS7P1  RPL27   ICT1
NDUFV2  RPL17   C19orf70        RPL36   ZNF121  MRPL4   ECSIT   MRPS12  ERCC1
AP2S1   RP13    COX7B   GLA
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      1.57116185129279e-13    50.5291005291005        0.283371392983185
10      91      translational termination
GO:0006414      6.83719788344114e-13    43.0406015037594        0.326966991903675
10      105     translational elongation
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GO:0022415	1.51654404867934e-11	20.7595307917889	0.809632551380527
12	260	viral reproductive process
GO:0019080	2.68062413950479e-11	28.9057750759878	0.470209674070999
10	151	viral genome expression
GO:0019083	2.68062413950479e-11	28.9057750759878	0.470209674070999
10	151	viral transcription
GO:0006614	2.839953166158e-11	37.265625	0.326966991903675	9
105	SRP-dependent cotranslational protein targeting to membrane
GO:0043624	3.05645861104189e-11	28.4975024975025	0.476437616773926
10	153	cellular protein complex disassembly
GO:0006613	3.09646487107332e-11	36.8788659793814	0.330080963255138
9	106	cotranslational protein targeting to membrane
GO:0045047	3.09646487107332e-11	36.8788659793814	0.330080963255138
9	106	protein targeting to ER
GO:0072599	3.09646487107332e-11	36.8788659793814	0.330080963255138
9	106	establishment of protein localization to endoplasmic reticulum
GO:0043241	4.2098732973947e-11	27.5250965250965	0.492007473531244
10	158	protein complex disassembly
GO:0070972	8.20550790764881e-11	32.7912844036697	0.367448619472701
9	118	protein localization to endoplasmic reticulum
GO:0019058	8.63871384160125e-11	20.8617647058824	0.719327382188084
11	231	viral infectious cycle
GO:0000184	8.85686637461013e-11	32.4909090909091	0.370562590824164
9	119	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0034623	1.09543149198663e-10	24.8118466898955	0.541831015154661
10	174	cellular macromolecular complex disassembly
GO:0032984	1.44894676833757e-10	24.0693153000845	0.557400871911978
10	179	macromolecular complex disassembly
GO:0072594	5.23025518826207e-10	20.9307805596465	0.635250155698568
10	204	establishment of protein localization to organelle
GO:0016032	6.5912322409242e-10	12.9554794520548	1.40440107951007
13	451	viral reproduction
GO:0071845	7.81150313155869e-10	16.7488687782805	0.884367863815653
11	284	cellular component disassembly at cellular level
GO:0006413	7.96884843940991e-10	24.9353146853147	0.473323645422462
9	152	translational initiation
GO:0006612	8.44779860055398e-10	24.7604166666667	0.476437616773926
9	153	protein targeting to membrane
GO:0022411	9.0561627267405e-10	16.5023359524315	0.896823749221507
11	288	cellular component disassembly
GO:0000956	2.04094139108864e-09	22.259375	0.526261158397343	9
169	nuclear-transcribed mRNA catabolic process
GO:0006402	3.22575021615126e-09	21.060650887574	0.554286900560515	9
178	mRNA catabolic process
GO:0006401	1.11181915330089e-08	18.125	0.638364127050031	9	205
RNA catabolic process
GO:0033365	1.46260855257869e-06	8.60413452638075	1.47290844924227
10	473	protein localization to organelle
GO:0006605	1.49077133793387e-06	8.58497536945813	1.47602242059373
10	474	protein targeting
Tissue: Nerve_Tibial=>Muscle_Skeletal	Type:	asymmetric



SourceGene:	AAK1(ENSG00000115977.13)	AP2 associated kinase 1



TargetGeneSet:	MTND2P28	PLEKHM2	RPL11	RPS27	KLHL12	MRPL55	EIF5B
EEF1B2	ENTPD3-AS1	RPL29	RP11	RPL34	MTND5P11	SYNPO	MTRNR2L9
```

RPS3AP26 MTUS1 PCM1 RPS20 RPL30 7SK RPS24 RPS3AP5 MTRNR2L8
RBMS1P1 COX17P1 DNAJC3 GOLGA8IP ADCY7 MTRNR2L1 RPL23A RPS7P11
PRR15L RPS2P48 LYPD3 CTA ITIH6 RPL39 MT

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0006414	1.59E-16	125.7368421	0.159850529	10	105	translational elongation
GO:0006415	4.83E-15	121.1285178	0.138537125	9	91	translational termination
GO:0006413	7.13E-15	83.84389671	0.231402671	10	152	translational initiation
GO:0006614	1.83E-14	103.3629808	0.159850529	9	105	SRP-dependent cotranslational protein targeting to membrane
GO:0006613	2.00E-14	102.2902458	0.161372915	9	106	cotranslational protein targeting to membrane
GO:0045047	2.00E-14	102.2902458	0.161372915	9	106	protein targeting to ER
GO:0072599	2.00E-14	102.2902458	0.161372915	9	106	establishment of protein localization to endoplasmic reticulum
GO:0070972	5.39E-14	90.95271701	0.179641547	9	118	protein localization to endoplasmic reticulum
GO:0000184	5.82E-14	90.11958042	0.181163933	9	119	"nuclear-transcribed mRNA catabolic process, nonsense-mediated decay"

GO:0019080	5.17E-13	69.65492958	0.229880285	9	151	viral genome expression
GO:0019083	5.17E-13	69.65492958	0.229880285	9	151	viral transcription
GO:0006612	5.83E-13	68.67788462	0.232925057	9	153	protein targeting to membrane
GO:0043624	5.83E-13	68.67788462	0.232925057	9	153	cellular protein complex disassembly
GO:0043241	7.82E-13	66.35002581	0.240536987	9	158	protein complex disassembly
GO:0000956	1.44E-12	61.74086538	0.257283233	9	169	nuclear-transcribed mRNA catabolic process
GO:0034623	1.88E-12	59.84895105	0.264895163	9	174	cellular macromolecular complex disassembly
GO:0006402	2.31E-12	58.41602185	0.270984707	9	178	mRNA catabolic process
GO:0032984	2.43E-12	58.06832579	0.272507093	9	179	macromolecular complex disassembly
GO:0072594	7.92E-12	50.53491124	0.310566743	9	204	establishment of protein localization to organelle
GO:0006401	8.28E-12	50.27354788	0.312089129	9	205	RNA catabolic process

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GO:0019058      2.42E-11        44.3045738      0.351671165     9       231
viral infectious cycle

GO:0022415      6.98E-11        39.10573092     0.395820358     9       260
viral reproductive process

GO:0071845      1.53E-10        35.63244755     0.432357622     9       284
cellular component disassembly at cellular level

GO:0022411      1.74E-10        35.11166253     0.438447166     9       288
cellular component disassembly

GO:0016032      8.99E-09        21.90793596     0.686596083     9       451
viral reproduction

GO:0033365      1.36E-08        20.83637268     0.720088575     9       473
protein localization to organelle

GO:0006605      1.39E-08        20.79007444     0.721610961     9       474
protein targeting

Tissue: Muscle_Skeletal=>Nerve_Tibial   Type:   asymmetric

SourceGene:     C10orf107(ENSG00000183346.6)

TargetGeneSet:  CELA3A  ZBTB40  EFNA1   CACNA1S ACTA1   TEX261  REG1A   HTR5BP  NEB
EXOSC7  RP11    PGM2    TPH2    RPL37   SPINK1  DDX39B  RP3     C6orf203
PRSS1   PRSS3P2 LOXL2   RPL10AP2        ST13P6  C9orf72 IL15RA  IPMK    MYPN
CYP2C9  NRAP    PNLIPRP1        TSPAN9  TMTC3   MYBPC1  MYL2    MEG8    IQGAP1
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RPL3L CTD GP2 ATP2A1 CTRB2 RPS4XP17 MYH2 MYH1 UNC45B
KRT10 TMEM99 CCDC40 ZNF254 CKM MYBPC2 TNNC2 PVALB C22orf32
MTHFD1P1

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0030049	1.03E-11	95.31534091	0.107951007	7	39	muscle filament sliding
GO:0033275	1.03E-11	95.31534091	0.107951007	7	39	actin-myosin filament sliding
GO:0070252	1.80E-11	87.12727273	0.11625493	7	42	actin-mediated cell contraction
GO:0030048	2.20E-10	58.57400932	0.163310498	7	59	actin filament-based movement
GO:0006936	6.96E-10	20.643377	0.661545914	10	239	muscle contraction
GO:0003012	1.97E-09	18.43098958	0.736281226	10	266	muscle system process
GO:0006941	1.88E-06	29.26734694	0.20759809	5	75	striated muscle contraction
GO:0003009	1.85E-05	72.94763514	0.052591516	3	19	skeletal muscle contraction

GO:0030029	1.98E-05	8.247051887	1.195764999	8	432
actin filament-based process

Tissue: Nerve_Tibial=>Muscle_Skeletal	Type:	asymmetric

SourceGene:	CD93(ENSG00000125810.8)

TargetGeneSet:	RPL22	RPS27	PEX19	C1orf192		RHOQP2	TFPI	PHACTR2
EEF1A1P6		RP11	HMCN2	RPL7A	RPS3AP5	ATP5G2	NCKAP1L	UPF3A	RPL13
TLCD2	CLDN7	TIMM13	ATP5SL	ZNF630	VDAC1P1	APOOL

GOBPID	Pvalue	OddsRatio		ExpCount		Count	Size	Term

GO:0006612	3.57E-09	72.90816327	0.148225036	6	153
protein targeting to membrane

GO:0072594	2.01E-08	53.93560606	0.197633382	6	204
establishment of protein localization to organelle

GO:0000184	6.57E-08	69.80019493	0.115286139	5	119
"nuclear-transcribed mRNA catabolic process, nonsense-mediated decay"

GO:0000956	3.79E-07	48.350271	0.163725694	5	169
nuclear-transcribed mRNA catabolic process

GO:0006402	4.90E-07	45.80603725	0.172444814	5	178	mRNA
catabolic process

GO:0006401	9.87E-07	39.54722222	0.198602173	5	205	RNA
catabolic process

GO:0006415	1.40E-06	65.97701149	0.088159989	4	91
translational termination

GO:0006414	2.49E-06	56.77623762	0.101723064	4	105
translational elongation

GO:0006614	2.49E-06	56.77623762	0.101723064	4	105

SRP-dependent cotranslational protein targeting to membrane

GO:0006613 2.59E-06 56.21568627 0.102691855 4 106
cotranslational protein targeting to membrane

GO:0045047 2.59E-06 56.21568627 0.102691855 4 106
protein targeting to ER

GO:0072599 2.59E-06 56.21568627 0.102691855 4 106
establishment of protein localization to endoplasmic reticulum

GO:0033365 2.86E-06 22.43576017 0.458238184 6 473
protein localization to organelle

GO:0006605 2.90E-06 22.38621795 0.459206975 6 474
protein targeting

GO:0070972 3.97E-06 50.25614035 0.114317348 4 118
protein localization to endoplasmic reticulum

GO:0019080 1.06E-05 38.88435374 0.146287454 4 151
viral genome expression

GO:0019083 1.06E-05 38.88435374 0.146287454 4 151
viral transcription

GO:0006413 1.08E-05 38.61891892 0.147256245 4 152
translational initiation

GO:0043624 1.11E-05 38.35704698 0.148225036 4 153
cellular protein complex disassembly

GO:0043241 1.26E-05 37.0987013 0.153068992 4 158
protein complex disassembly

GO:0072321 1.83E-05 481.0666667 0.006781538 2 7
chaperone-mediated protein transport

GO:0034623 1.85E-05 33.56941176 0.168569649 4 174
cellular macromolecular complex disassembly

Tissue: Nerve_Tibial=>Muscle_Skeletal Type: asymmetric
SourceGene: ENSG00000239291.1
TargetGeneSet: RPL22 CAMTA1-IT1 CLSTN1 RPS27 PPP1R12B CICP5

```
SH3YL1  RPS7    BIRC6   SMYD5   RANBP2  NEB     TTC21B  EEF1B2  UBE2F   ATG4B
DTYMK   RP11    AP2M1   ZAR1    HNRPDL  SUB1    C5orf28 CENPH   FAM174A TCERG1  TUBB
PPIL1   PPP2R5D RP1     MTRNR2L9        PHF3    ARID1B  MALSU1  DDX56   PPIA
BAIAP2L1        RPS3AP26        CUX1    SLC13A4 MLL3    TNKS    PCMTD1  TCEB1
OTUD6B  ANXA2P2 SPTLC1  DENND1A RPL35   RPL7A   SVIL    EIF6    BCCIP   TSG101
RPL18AP3        MED4-AS1        RNF31   C14orf166       DYNC1H1 HERC2   HERC1
SNRPA1  SOX8    CTD     GLOD4   RPL17P43        SUPT6H  TNRC6C  WDR45L  IER3IP1
C18orf32        TXNL4A  GADD45GIP1      ZNF486  RPSAP58 TSHZ3   RYR1    RPS19   RPS5
EIF2S2  PPIAP22 C21orf119       ERVH48-1        SF3A1   RBX1    DMD-AS2 ITIH6
CXorf26 RPL39   RPL10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      7.31754245214919e-11    25.0631578947368        0.508615320739049
10      105     translational elongation
GO:0006415      4.93542301124678e-10    25.7279088364654        0.440799944640509
9       91      translational termination
GO:0019058      9.82518356581008e-10    13.3793103448276        1.11895370562591
12      231     viral infectious cycle
GO:0006614      1.79383947513436e-09    21.9544057377049        0.508615320739049
9       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.95280987937582e-09    21.7265506168667        0.513459276174659
9       106     cotranslational protein targeting to membrane
GO:0045047      1.95280987937582e-09    21.7265506168667        0.513459276174659
9       106     protein targeting to ER
GO:0072599      1.95280987937582e-09    21.7265506168667        0.513459276174659
9       106     establishment of protein localization to endoplasmic reticulum
GO:0019080      2.66776487282486e-09    16.8321513002364        0.731437270777109
10      151     viral genome expression
GO:0019083      2.66776487282486e-09    16.8321513002364        0.731437270777109
10      151     viral transcription
GO:0006413      2.84480329887681e-09    16.712441314554 0.736281226212719       10
152     translational initiation
GO:0016032      3.07835109852793e-09    8.72289407839867        2.18462390146011
15      451     viral reproduction
GO:0022415      3.76473354170724e-09    11.7906006674082        1.2594284132586 12
260     viral reproductive process
GO:0070972      5.0787447552387e-09     19.3183937434201        0.571586741401979
9       118     protein localization to endoplasmic reticulum
GO:0000184      5.47334037527631e-09    19.1414307004471        0.576430696837589
9       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006612      4.95047982223002e-08    14.5870901639344        0.741125181648329
9       153     protein targeting to membrane
GO:0043624      4.95047982223002e-08    14.5870901639344        0.741125181648329
9       153     cellular protein complex disassembly
GO:0043241      6.53728633758801e-08    14.0926394542854        0.765344958826379
9       158     protein complex disassembly
GO:0000956      1.16648791459562e-07    13.1136270491803        0.818628468618089
9       169     nuclear-transcribed mRNA catabolic process
GO:0022613      1.20242275180982e-07    10.9813953488372        1.08988997301225
10      225     ribonucleoprotein complex biogenesis
GO:0034623      1.49724472349781e-07    12.7117734724292        0.842848245796139
9       174     cellular macromolecular complex disassembly
GO:0006402      1.81792370708096e-07    12.407411000097 0.862224067538579       9
178     mRNA catabolic process
GO:0032984      1.90686320250573e-07    12.3335583413693        0.867068022974189
9       179     macromolecular complex disassembly
GO:0071843      2.11000230823148e-07    10.2998544395924        1.15770534911079
10      239     cellular component biogenesis at cellular level
GO:0072594      5.76541966419243e-07    10.7334174022699        0.988166908864438
9       204     establishment of protein localization to organelle
GO:0006401      6.00713892035634e-07    10.6779023084644        0.993010864300048
9       205     RNA catabolic process
GO:0071845      8.77339691245854e-06    7.5680476900149 1.37568334371324        9
284     cellular component disassembly at cellular level
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GO:0022411      9.81661683224337e-06    7.4574299312533 1.39505916545568        9
288     cellular component disassembly
GO:0033365      1.55450055012712e-05    5.61702986279257        2.29119092104353
11      473     protein localization to organelle
Tissue: Nerve_Tibial=>Muscle_Skeletal   Type:   asymmetric
SourceGene:     ENSG00000239791.1
TargetGeneSet:  SEPN1   RP11    RPLP0P6 ZAP70   RPL37A  PPIAP16 RPL35A  RPL34
RPS23   CTD     RPL39P3 RPL7    GS1     AQP9    RPL35   RPL13AP5        RPLP2
ORAOV1  ST13P11 SLC11A2 RPS29   PLEKHD1 C15orf52        RPS3AP6 ZNF774  PDZD9
RPL27   S1PR4   WIZ     REPS2   RP13    RP3     RPL10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      2.1887296438331e-18     139.781914893617        0.167116462528545
11      105     translational elongation
GO:0006415      6.30555352061827e-17    136.24881291548 0.144834267524739       10
91      translational termination
GO:0006614      2.79796175290637e-16    116.056680161943        0.167116462528545
10      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      3.08687413255169e-16    114.839743589744        0.168708047885959
10      106     cotranslational protein targeting to membrane
GO:0045047      3.08687413255169e-16    114.839743589744        0.168708047885959
10      106     protein targeting to ER
GO:0072599      3.08687413255169e-16    114.839743589744        0.168708047885959
10      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      9.35135241104897e-16    101.994301994302        0.187807072174936
10      118     protein localization to endoplasmic reticulum
GO:0000184      1.02008682585083e-15    101.051517290049        0.189398657532351
10      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      1.16958569994575e-14    77.9432624113475        0.240329388969621
10      151     viral genome expression
GO:0019083      1.16958569994575e-14    77.9432624113475        0.240329388969621
10      151     viral transcription
GO:0006413      1.25091808835343e-14    77.3889490790899        0.241920974327036
10      152     translational initiation
GO:0006612      1.33729070090369e-14    76.8423883808499        0.243512559684451
10      153     protein targeting to membrane
GO:0043624      1.33729070090369e-14    76.8423883808499        0.243512559684451
10      153     cellular protein complex disassembly
GO:0043241      1.85483238175808e-14    74.2203742203742        0.251470486471524
10      158     protein complex disassembly
GO:0000956      3.6731013503907e-14     69.0324141267537        0.268977925403086
10      169     nuclear-transcribed mRNA catabolic process
GO:0034623      4.93531947415089e-14    66.9043151969981        0.27693585219016
10      174     cellular macromolecular complex disassembly
GO:0006402      6.21163297175937e-14    65.2930402930403        0.283302193619819
10      178     mRNA catabolic process
GO:0032984      6.57374934802155e-14    64.9021392808375        0.284893778977233
10      179     macromolecular complex disassembly
GO:0072594      2.45722623718009e-13    56.4393338620143        0.324683412912601
10      204     establishment of protein localization to organelle
GO:0006401      2.58110034705589e-13    56.1459566074951        0.326274998270016
10      205     RNA catabolic process
GO:0019058      8.55234752637089e-13    49.4500522102332        0.367656217562798
10      231     viral infectious cycle
GO:0022415      2.78571752229051e-12    43.6246153846154        0.413812192927825
10      260     viral reproductive process
GO:0071845      6.70239269057421e-12    39.7361033127456        0.452010241505778
10      284     cellular component disassembly at cellular level
GO:0022411      7.70023687149939e-12    39.1532927504151        0.458376582935437
10      288     cellular component disassembly
GO:0016032      6.31199390872842e-10    24.397348683063 0.717804996194035       10
451     viral reproduction
GO:0033365      1.00237370241577e-09    23.2015284931052        0.752819874057159
10      473     protein localization to organelle
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GO:0006605      1.02311616145228e-09    23.1498673740053        0.754411459414573
10      474     protein targeting
Tissue: Nerve_Tibial=>Muscle_Skeletal   Type:   asymmetric



SourceGene:     FBXO18(ENSG00000134452.12)      "F-box protein, helicase, 18"



TargetGeneSet:  ACAP3   OTUD3   HP1BP3  C1orf63 TRAPPC3 ERMAP   PPAP2B  ACTG1P4 RP11
RC3H1   UCHL5   WNT9A   RPLP0P6 LINC00152       MCM6    RFTN2   RPL37A  SLC23A3
IL17RC  ACAA1   KIAA1143        PTPLB   CCNL1   MYL5    AADAT   RANBP3L RPS23   CTD
GCNT2   CDKAL1  STK19   AGER    NOTCH4  RPL10A  SNHG5   ELMO1   GNRH1   NR6A1   BMI1
USP54   FGFBP3  RPL13AP5        PIDD    RPLP2   TNNT3   MEN1    NADSYN1 MSANTD2 ANO2
FGFR1OP2        PUS7L   SLC11A2 RPS29   PIAS1   PRC1    RPS15A  GDPD3   C16orf57
NFAT5   CCL16   RPL27   RPS15   PDE4A   RPS16   CARD8   RPS5P2  ACRC    FERP1
LINC00087

GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term



GO:0006414      3.25E-12        35.84962406     0.377828524     10      105
translational elongation



GO:0006415      3.06E-11        36.54367555     0.327451387     9       91
translational termination



GO:0006614      1.13E-10        31.18386628     0.377828524     9       105
SRP-dependent cotranslational protein targeting to membrane



GO:0006613      1.23E-10        30.86022537     0.381426891     9       106
```

						cotranslational protein targeting to membrane
GO:0045047	1.23E-10	30.86022537	0.381426891	9	106	protein targeting to ER
GO:0072599	1.23E-10	30.86022537	0.381426891	9	106	establishment of protein localization to endoplasmic reticulum
GO:0070972	3.25E-10	27.4397269	0.424607294	9	118	protein localization to endoplasmic reticulum
GO:0000184	3.50E-10	27.18837209	0.428205661	9	119	"nuclear-transcribed mRNA catabolic process, nonsense-mediated decay"
GO:0000956	3.79E-10	21.32374963	0.608124005	10	169	nuclear-transcribed mRNA catabolic process
GO:0006402	6.31E-10	20.16865079	0.640509307	10	178	mRNA catabolic process
GO:0006401	2.50E-09	17.34310134	0.737665213	10	205	RNA catabolic process

GO:0019080	2.93E-09	21.01424828	0.543353401	9	151	viral genome expression
GO:0019083	2.93E-09	21.01424828	0.543353401	9	151	viral transcription
GO:0006413	3.11E-09	20.86583184	0.546951768	9	152	translational initiation
GO:0006612	3.29E-09	20.71947674	0.550550135	9	153	protein targeting to membrane
GO:0043624	3.29E-09	20.71947674	0.550550135	9	153	cellular protein complex disassembly
GO:0043241	4.37E-09	20.01716872	0.568541969	9	158	protein complex disassembly
GO:0034623	1.02E-08	18.05581395	0.62611584	9	174	cellular macromolecular complex disassembly

GO:0032984	1.31E-08	17.51860465	0.644107674	9	179	macromolecular complex disassembly
GO:0072594	4.06E-08	15.24579606	0.734066847	9	204	establishment of protein localization to organelle
GO:0019058	1.18E-07	13.36612194	0.831222753	9	231	viral infectious cycle
GO:0022415	3.22E-07	11.79764662	0.935575393	9	260	viral reproductive process
GO:0071845	6.76E-07	10.74976744	1.021936198	9	284	cellular component disassembly at cellular level
GO:0022411	7.60E-07	10.59264816	1.036329666	9	288	cellular component disassembly
GO:0016032	3.87E-06	7.53590325	1.62286347	10	451	viral reproduction

Tissue: Nerve_Tibial=>Muscle_Skeletal Type: asymmetric

SourceGene: GORASP1(ENSG00000114745.9) "golgi reassembly stacking protein 1, 65kDa"

TargetGeneSet: RPL22 SFN RP4 MFI2 RPL5 RP11 AP4B1 TMEM79
SUPT7L OLA1 RPL15 PROK2 RPL34 SPOCK3 CENPH CTD CTB HCG27 RPL7
EIF3E EIF3H RPS24 PCNXL3 CCND1 RPS25 DNAJC3 TRAPPC6B RPL4
LINGO1 TMEM104 RDH13 PRDX4

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0006413	8.90E-14	59.16321458	0.283994187	10	152	translational initiation
GO:0000184	5.30E-13	65.06363636	0.222337554	9	119	"nuclear-transcribed mRNA catabolic process, nonsense-mediated decay"
GO:0006415	3.64E-12	72.75079264	0.170022836	8	91	translational termination
GO:0006414	1.17E-11	62.18990776	0.196180195	8	105	translational elongation
GO:0006614	1.17E-11	62.18990776	0.196180195	8	105	SRP-dependent cotranslational protein targeting to membrane
GO:0006613	1.27E-11	61.55102041	0.198048578	8	106	cotranslational protein targeting to membrane
GO:0045047	1.27E-11	61.55102041	0.198048578	8	106	protein targeting to ER
GO:0072599	1.27E-11	61.55102041	0.198048578	8	106	establishment of protein localization to endoplasmic reticulum

GO:0000956	1.29E-11	44.575	0.315756695	9	169	nuclear-transcribed mRNA catabolic process
GO:0006402	2.06E-11	42.17455621	0.33257214	9	178	mRNA catabolic process
GO:0070972	3.03E-11	54.79043062	0.220469172	8	118	protein localization to endoplasmic reticulum
GO:0006401	7.33E-11	36.29591837	0.383018476	9	205	RNA catabolic process
GO:0019080	2.21E-10	42.0493191	0.282125804	8	151	viral genome expression
GO:0019083	2.21E-10	42.0493191	0.282125804	8	151	viral transcription
GO:0006612	2.46E-10	41.46352087	0.28586257	8	153	protein targeting to membrane
GO:0043624	2.46E-10	41.46352087	0.28586257	8	153	cellular protein complex disassembly
GO:0043241	3.18E-10	40.06736842	0.295204484	8	158	protein complex disassembly
GO:0034623	6.87E-10	36.16487001	0.325098609	8	174	cellular macromolecular complex disassembly
GO:0032984	8.60E-10	35.09510619	0.334440523	8	179	macromolecular complex disassembly
GO:0072594	2.42E-09	30.56498389	0.381150093	8	204	establishment of protein localization to organelle
GO:0019058	6.45E-09	26.81331131	0.431596429	8	231	viral infectious cycle

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GO:0022415      1.63E-08        23.67919799     0.485779531     8       260
viral reproductive process



GO:0071845      3.24E-08        21.58352403     0.530620718     8       284
cellular component disassembly at cellular level



GO:0022411      3.61E-08        21.26917293     0.53809425      8       288
cellular component disassembly



GO:0033365      1.11E-07        15.04310345     0.88374507      9       473
protein localization to organelle



GO:0006605      1.13E-07        15.00967742     0.885613452     9       474
protein targeting



GO:0016032      1.11E-06        13.28834502     0.842640648     8       451
viral reproduction



Tissue: Nerve_Tibial=>Muscle_Skeletal   Type:   asymmetric
SourceGene:     HMGN5(ENSG00000198157.6)
TargetGeneSet:  RPL22   AGTRAP  C1orf144        HMGN2   MRPS15  RSPO1   KIAA0494
ZFYVE9  FOXD3   RABGGTB RP11    AGL     HBXIP   HIPK1   RPS27   ATP8B2  FAM189B HCN3
CCT3    XPR1    LINC00467       SRP9    C1orf95 SRSF7   COX7A2L RHOQ    CCT4
MKI67IP HSPD1   HSPE1   CLN5    ITPR1   RPL15   LAMB2   RPL24   MYLK    MAP6D1  ADD1
SLIT2   PDE5A   RPS3A   SORBS2  RBBP4P1 NDUFS4  PTCD2   BTF3    TBCA    CTB
SLIT1   KCNMB1  NPM1    RPL26L1 LRRC16A RPL10A  TBX18   AKD1    RPF2    RP3     TRDN
LTV1    TAB2    FNDC1   PSMB1   SDK1    EEF1A1P6        MRPL32  SEC61G  RPS3AP26
ZSCAN21 FIS1    MRPS33  KRBA1   SFTPC   SCARA5  HOOK3   MRPS35  WWP1    EIF3E
TTC35   KIAA0020        NTRK2   RPL35   RPL7A   DNLZ    EDF1    CAMK1D  COMMD3
TIMM23  HK1     RPS24   RPS3AP5 SFXN4   IGF2    STIM1   TMEM109 MRPL21  LAMTOR1
TMEM126A        SNORA8  PHLDB1  SOX5    POLR2KP1        IKZF4   RNF41   SDSL
CCDC92  PUS1    IFT88   MRP63   PRMT5-AS1       C14orf166       ACTN1   BCRP2
SRP14   JMJD8   LYRM1   HMGN2P3 TGFB1I1 PARD6A  GABARAPL2       WWOX    GCSH
C1QBP   STX8    KCNJ12  STAC2   VAT1    ANKRD40 MSI2    SRSF1   SLC16A5 TRAPPC8
C18orf21        CNN1    FAM71E1 TSEN34  PPP6R1  SNRPB2  AHCY    MYL9    CHD6
TCP10L  MRPL40  FOXRED2 NHP2L1  ATXN10  ZC3H12B HMGN5   TRMT2B  BEX2    DOCK11
SLC9A6
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006614      5.73767343535094e-12    17.9582686335404        0.908241644176874
13      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      6.49249560224171e-12    17.763920890937 0.916891564597606       13
106     cotranslational protein targeting to membrane
GO:0045047      6.49249560224171e-12    17.763920890937 0.916891564597606       13
106     protein targeting to ER
GO:0072599      6.49249560224171e-12    17.763920890937 0.916891564597606       13
106     establishment of protein localization to endoplasmic reticulum
GO:0070972      2.60182755677225e-11    15.7204931972789        1.02069060964639
13      118     protein localization to endoplasmic reticulum
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GO:0006414	1.01566689419554e-10	16.2523551241793	0.908241644176874
12	105	translational elongation
GO:0006612	6.94494928981492e-10	11.7613520408163	1.32343782437202
13	153	protein targeting to membrane
GO:0006415	5.79974161324413e-09	15.2925389157273	0.787142758286624
10	91	translational termination
GO:0000184	6.22590156196839e-09	12.7028914879792	1.02934053006712
11	119	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0043624	8.10272368894881e-09	10.6834871022406	1.32343782437202
12	153	cellular protein complex disassembly
GO:0043241	1.16593388123638e-08	10.3139774518123	1.36668742647568
12	158	protein complex disassembly
GO:0072594	2.3080843883101e-08	8.58989341810022	1.76458376582935
13	204	establishment of protein localization to organelle
GO:0034623	3.43845483812788e-08	9.28482464765651	1.50508615320739
12	174	cellular macromolecular complex disassembly
GO:0032984	4.71013040491334e-08	9.00365640400615	1.54833575531105
12	179	macromolecular complex disassembly
GO:0006413	8.04011240743188e-08	9.70729127783999	1.31478790395128
11	152	translational initiation
GO:0000956	2.36908829095149e-07	8.65245391960915	1.46183655110373
11	169	nuclear-transcribed mRNA catabolic process
GO:0006402	3.9945788384366e-07	8.18095388171026	1.53968583489032
11	178	mRNA catabolic process
GO:0019080	7.30958509555701e-07	8.74807277212458	1.30613798353055
10	151	viral genome expression
GO:0019083	7.30958509555701e-07	8.74807277212458	1.30613798353055
10	151	viral transcription
GO:0019058	7.5054439855748e-07	6.8405867377864 1.99813161718912	12
231	viral infectious cycle
GO:0006401	1.61889016522879e-06	7.02893832519443	1.77323368625009
11	205	RNA catabolic process
GO:0022415	2.59639333784596e-06	6.0282614901513 2.24897930939035	12
260	viral reproductive process
GO:0071845	6.43058633558557e-06	5.48698594482041	2.45657739948792
12	284	cellular component disassembly at cellular level
GO:0022411	7.41205255207756e-06	5.40592535590612	2.49117708117085
12	288	cellular component disassembly
GO:0016032	8.03903518619091e-06	4.34424520433695	3.90111410975019
15	451	viral reproduction
GO:0033365	1.41529228327999e-05	4.12901945216356	4.0914123590063 15
473	protein localization to organelle
Tissue: Nerve_Tibial=>Muscle_Skeletal	Type:	cluster




SourceGene:	HMGN5(ENSG00000198157.6)	high mobility group nucleosome
binding domain 5
```

TargetGeneSet: RPL22 AGTRAP C1orf144 HMGN2 MRPS15 RSPO1 KIAA0494
ZFYVE9 FOXD3 RABGGTB RP11 AGL HBXIP HIPK1 RPS27 ATP8B2 FAM189B HCN3
CCT3 XPR1 LINC00467 SRP9 C1orf95 SRSF7 COX7A2L RHOQ CCT4
MKI67IP HSPD1 HSPE1 CLN5 ITPR1 RPL15 LAMB2 RPL24 MYLK MAP6D1 ADD1
SLIT2 PDE5A RPS3A SORBS2 RBBP4P1 NDUFS4 PTCD2 BTF3 TBCA CTB
SLIT1 KCNMB1 NPM1 RPL26L1 LRRC16A RPL10A TBX18 AKD1 RPF2 RP3 TRDN
LTV1 TAB2 FNDC1 PSMB1 SDK1 EEF1A1P6 MRPL32 SEC61G RPS3AP26
ZSCAN21 FIS1 MRPS33 KRBA1 SFTPC SCARA5 HOOK3 MRPS35 WWP1 EIF3E
TTC35 KIAA0020 NTRK2 RPL35 RPL7A DNLZ EDF1 CAMK1D COMMD3
TIMM23 HK1 RPS24 RPS3AP5 SFXN4 IGF2 STIM1 TMEM109 MRPL21 LAMTOR1
TMEM126A SNORA8 PHLDB1 SOX5 POLR2KP1 IKZF4 RNF41 SDSL
CCDC92 PUS1 IFT88 MRP63 PRMT5-AS1 C14orf166 ACTN1 BCRP2
SRP14 JMJD8 LYRM1 HMGN2P3 TGFB1I1 PARD6A GABARAPL2 WWOX GCSH
C1QBP STX8 KCNJ12 STAC2 VAT1 ANKRD40 MSI2 SRSF1 SLC16A5 TRAPPC8
C18orf21 CNN1 FAM71E1 TSEN34 PPP6R1 SNRPB2 AHCY MYL9 CHD6
TCP10L MRPL40 FOXRED2 NHP2L1 ATXN10 ZC3H12B HMGN5 TRMT2B BEX2 DOCK11
SLC9A6

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0006614	5.74E-12	17.95826863	0.908241644	13	105	SRP-dependent cotranslational protein targeting to membrane
GO:0006613	6.49E-12	17.76392089	0.916891565	13	106	cotranslational protein targeting to membrane

GO:0045047	6.49E-12	17.76392089	0.916891565	13	106
protein targeting to ER					
GO:0072599	6.49E-12	17.76392089	0.916891565	13	106
establishment of protein localization to endoplasmic reticulum					
GO:0070972	2.60E-11	15.7204932	1.02069061	13	118
protein localization to endoplasmic reticulum					
GO:0006414	1.02E-10	16.25235512	0.908241644	12	105

translational elongation

GO:0006612 6.94E-10 11.76135204 1.323437824 13 153
protein targeting to membrane

GO:0006415 5.80E-09 15.29253892 0.787142758 10 91
translational termination

GO:0000184 6.23E-09 12.70289149 1.02934053 11 119
"nuclear-transcribed mRNA catabolic process, nonsense-mediated decay"

GO:0043624	8.10E-09	10.6834871	1.323437824	12	153
cellular protein complex disassembly

GO:0043241	1.17E-08	10.31397745	1.366687426	12	158
protein complex disassembly

GO:0072594	2.31E-08	8.589893418	1.764583766	13	204
establishment of protein localization to organelle

GO:0034623	3.44E-08	9.284824648	1.505086153	12	174
cellular macromolecular complex disassembly

GO:0032984	4.71E-08	9.003656404	1.548335755	12	179	macromolecular complex disassembly
GO:0006413	8.04E-08	9.707291278	1.314787904	11	152	translational initiation
GO:0000956	2.37E-07	8.65245392	1.461836551	11	169	nuclear-transcribed mRNA catabolic process
GO:0006402	3.99E-07	8.180953882	1.539685835	11	178	mRNA catabolic process

GO:0019080	7.31E-07	8.748072772	1.306137984	10	151	viral genome expression
GO:0019083	7.31E-07	8.748072772	1.306137984	10	151	viral transcription
GO:0019058	7.51E-07	6.840586738	1.998131617	12	231	viral infectious cycle
GO:0006401	1.62E-06	7.028938325	1.773233686	11	205	RNA catabolic process

GO:0022415	2.60E-06	6.02826149	2.248979309	12	260
viral reproductive process					
GO:0071845	6.43E-06	5.486985945	2.456577399	12	284
cellular component disassembly at cellular level					
GO:0022411	7.41E-06	5.405925356	2.491177081	12	288
cellular component disassembly					
GO:0016032	8.04E-06	4.344245204	3.90111411	15	451
viral reproduction					

```
GO:0033365      1.42E-05        4.129019452     4.091412359     15      473
protein localization to organelle









Tissue: Nerve_Tibial=>Muscle_Skeletal   Type:   asymmetric



SourceGene:     KIAA1456(ENSG00000250305.3)     putative methyltransferase




TargetGeneSet:  ZBTB48  ADPRHL2 RP11    RPS7    ROCK2   RPL37A  RPL35A  LMLN
ZNF827  MYLIP   DEK     ZBTB12  RPS18   RPL39P3 HIP1    DBF4    RPS20   RPL30
EEF1D   RPL8    FRMD3   RPL35   RPL13AP5        FAU     RPS3    RPS25   ATP5G2
RPL41   TPT1    RPL36A  SIX1    RPS3AP6 RPLP1   C16orf13        CASP16  RPS15A
RPL13   RPS7P1  RPL23A  RPL27   ZFP161  RPS15   DAPK3   C19orf43        GLTSCR2 TMC2
C21orf33        TCN2    GS1     PQBP1

GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term



GO:0006414      4.82E-31        150.7059801     0.290637326     19      105
translational elongation



GO:0006415      4.13E-30        160.6998755     0.251885683     18      91
translational termination



GO:0006614      6.86E-29        134.7084639     0.290637326     18      105
SRP-dependent cotranslational protein targeting to membrane
```

GO:0006613	8.25E-29	133.1683884	0.293405301	18	106	cotranslational protein targeting to membrane
GO:0045047	8.25E-29	133.1683884	0.293405301	18	106	protein targeting to ER
GO:0072599	8.25E-29	133.1683884	0.293405301	18	106	establishment of protein localization to endoplasmic reticulum
GO:0070972	6.59E-28	117.09	0.326620995	18	118	protein localization to endoplasmic reticulum
GO:0000184	7.75E-28	115.9225923	0.32938897	18	119	"nuclear-transcribed mRNA catabolic process, nonsense-mediated decay"
GO:0019080	7.26E-26	87.83458647	0.417964155	18	151	viral genome expression
GO:0019083	7.26E-26	87.83458647	0.417964155	18	151	viral transcription
GO:0006413	8.22E-26	87.17299864	0.420732129	18	152	translational initiation
GO:0006612	9.30E-26	86.52121212	0.423500104	18	153	protein targeting to membrane

GO:0043624	9.30E-26	86.52121212	0.423500104	18	153	cellular protein complex disassembly
GO:0043241	1.70E-25	83.40194805	0.437339976	18	158	protein complex disassembly
GO:0000956	6.03E-25	77.2667068	0.467787696	18	169	nuclear-transcribed mRNA catabolic process
GO:0034623	1.04E-24	74.76398601	0.481627569	18	174	cellular macromolecular complex disassembly
GO:0006402	1.59E-24	72.87443182	0.492699467	18	178	mRNA catabolic process
GO:0032984	1.77E-24	72.41671372	0.495467442	18	179	macromolecular complex disassembly
GO:0019058	3.43E-24	60.59770889	0.639402118	19	231	viral infectious cycle
GO:0072594	2.00E-23	62.57331378	0.564666805	18	204	establishment of protein localization to organelle
GO:0006401	2.19E-23	62.23432183	0.56743478	18	205	RNA catabolic process

GO:0022415	3.40E-23	53.19699664	0.719673379	19	260	viral reproductive process
GO:0071845	8.58E-21	43.50820232	0.786104768	18	284	cellular component disassembly at cellular level
GO:0022411	1.11E-20	42.85151515	0.797176666	18	288	cellular component disassembly
GO:0016032	1.22E-18	29.27700617	1.248356515	19	451	viral reproduction
GO:0033365	2.96E-18	27.81445353	1.309251955	19	473	protein localization to organelle
GO:0006605	8.18E-17	25.0388756	1.312019929	18	474	protein targeting
GO:0042274	1.56E-05	77.81621622	0.049823542	3	18	ribosomal small subunit biogenesis

Tissue: Nerve_Tibial=>Muscle_Skeletal Type: asymmetric

SourceGene: LPP(ENSG00000145012.8)

TargetGeneSet: RPL22 RPL11 BRD8 LRIF1 RPS27 RPS7 NEB RPL37A
GAL3ST2 SCAP RP11 RPL24 ZBTB38 RPL35A LMLN HNRPDL RPL34 LARP1B LSM6
RPS3A TNFAIP8 NUDCD2 CSNK2B RPS18 RPL10A ENPP5 RPL39P3 LTV1 OGDH
ZMIZ2 C7orf63 TECPR1 C8orf40 RPS20 RPL30 RPL35 ADRA2A ZNF32-AS2
VPS26A RPS24 FAU CWC15 RPS25 ATP5G2 RPL41 UFM1 TPT1 COMMD6
TIMM9 KLF13 RPS3AP6 RPLP1 TCEB2 NUBP1 RPS15A MIR4519 VMO1 RPL23A
RPL27 SEH1L UBA52 SNRPD2 SNRPB2 LINC00493 RANBP1 TNRC6B UXT
RPL10

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0006415	6.05E-39	150.9323968	0.36523424	24	91	translational termination
GO:0006414	2.95E-37	124.7233115	0.421424123	24	105	translational elongation
GO:0006614	2.95E-37	124.7233115	0.421424123	24	105	SRP-dependent cotranslational protein targeting to membrane
GO:0006613	3.81E-37	123.1936872	0.425437686	24	106	cotranslational protein targeting to membrane
GO:0045047	3.81E-37	123.1936872	0.425437686	24	106	protein targeting to ER

GO:0072599	3.81E-37	123.1936872	0.425437686	24	106	establishment of protein localization to endoplasmic reticulum
GO:0070972	6.62E-36	107.3767209	0.473600443	24	118	protein localization to endoplasmic reticulum
GO:0000184	8.27E-36	106.2390093	0.477614006	24	119	"nuclear-transcribed mRNA catabolic process, nonsense-mediated decay"
GO:0019080	4.93E-35	85.78042328	0.606048024	25	151	viral genome expression
GO:0019083	4.93E-35	85.78042328	0.606048024	25	151	viral transcription
GO:0006612	7.03E-35	84.42826705	0.614075151	25	153	protein targeting to membrane
GO:0000956	1.00E-33	74.9631734	0.67829216	25	169	nuclear-transcribed mRNA catabolic process

GO:0006402	3.97E-33	70.50901169	0.714414227	25	178	mRNA catabolic process
GO:0006413	4.83E-33	78.66727941	0.610061587	24	152	translational initiation
GO:0043624	5.72E-33	78.05198358	0.614075151	24	153	cellular protein complex disassembly
GO:0043241	1.30E-32	75.11325724	0.634142966	24	158	protein complex disassembly
GO:0072594	1.43E-31	60.15744033	0.818766867	25	204	establishment of protein localization to organelle
GO:0034623	1.52E-31	67.02588235	0.698359975	24	174	cellular macromolecular complex disassembly
GO:0006401	1.63E-31	59.81902357	0.82278043	25	205	RNA catabolic process
GO:0032984	3.11E-31	64.84098672	0.71842779	24	179	macromolecular complex disassembly

GO:0019058	3.63E-30	52.17343336	0.92713307	25	231	viral infectious cycle
GO:0022415	7.65E-29	45.6415216	1.0435264	25	260	viral reproductive process
GO:0071845	2.93E-26	38.37013575	1.139851913	24	284	cellular component disassembly at cellular level
GO:0022411	4.12E-26	37.77807487	1.155906166	24	288	cellular component disassembly
GO:0016032	1.10E-25	28.69468959	1.810116947	27	451	viral reproduction
GO:0033365	2.57E-22	23.58123647	1.898415335	25	473	protein localization to organelle
GO:0006605	2.71E-22	23.52702976	1.902428898	25	474	protein targeting

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GO:0022613      2.52E-07        12.05527211     0.903051692     9       225
ribonucleoprotein complex biogenesis




GO:0071843      4.19E-07        11.31029281     0.959241575     9       239
cellular component biogenesis at cellular level




GO:0042254      2.08E-06        13.77478597     0.598020898     7       149
ribosome biogenesis




Tissue: Nerve_Tibial=>Muscle_Skeletal   Type:   asymmetric
SourceGene:     MORN2(ENSG00000188010.8)
TargetGeneSet:  RP1     CLSTN1  MTOR    ATP13A2 MAGOH   RP4     LRIF1   PMF1
DUSP12  TIMM17A SNRPE   SRP9    OBSCN   C1D     TPRKB   DGUOK   TMEM131 COA5
UNC50   MMADHC  NEB     C2orf47 SLC23A3 HDLBP   LSM3    SS18L2  VPRBP   RAD54L2 RP11
CHMP2B  RG9MTD1 CCDC58  PEX5L   MYL5    SLBP    7SK     LARP1B  LSM6    SUB1    TAF9
CTD     MRPL22  UBLCP1  SYCP2L  BAG6    CSNK2B  HNRNPC  MDGA1   C6orf226        CUL7
HMGN3   SNHG5   C6orf162        LSM5    DDX56   GS1     ACN9    TRRAP   BUD31   CUX1
SPDYE2  NAA38   SSBP1   PCM1    LSM1    UBE2V2  RPS20   ARMC1   TCEB1   C8orf59
OTUD6B  POLR2K  PLEC    DENND1A PRRC2B  C10orf31        HSPA14  SAR1A   CHCHD1
KAT6B   PCGF6   BCCIP   IMMP1L  API5    CWC15   DCUN1D5 PPHLN1  WIBG    UBE3B   POMP
ITM2B   C14orf166       PSMA3   ERH     SLIRP   SNW1    C15orf23        MAP2K5
ZNF592  SNRPA1  MRPL28  TSC2    SRRM2   NOMO1   CAMTA2  MYH10   FLII    GPR179
PSMG2   FHOD3   IER3IP1 C18orf32        SDHAF1  SNRPB   SNRPB2  LINC00493
CEP250  DPM1    ATP5E   WRB     SF3A1   GGA1    SLC16A8 TNRC6B  PSMD10  VBP1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0000375      2.71123063330777e-11    12.1580756013746        1.51858002906373
15      209     RNA splicing, via transesterification reactions
GO:0008380      1.57731304071045e-10    8.86363636363636        2.34689640855304
17      323     RNA splicing
GO:0000377      2.37050046335867e-10    11.4623481781377        1.48225036329666
14      204     RNA splicing, via transesterification reactions with bulged
adenosine as nucleophile
GO:0000398      2.37050046335867e-10    11.4623481781377        1.48225036329666
14      204     nuclear mRNA splicing, via spliceosome
GO:0006397      5.27576295806882e-10    7.58349171870758        2.89910732821258
18      399     mRNA processing
GO:0043248      1.27733847387696e-05    105.455882352941        0.0508615320739049
3       7       proteasome assembly
Tissue: Nerve_Tibial=>Muscle_Skeletal   Type:   asymmetric
```

SourceGene: NCOA6(ENSG00000198646.7) nuclear receptor coactivator 6

TargetGeneSet: TMEM51 PPIH ZYG11B COL24A1 RP11 GJA5 NMNAT2 SRGAP3
ASAP2 PTPN4 RPL15 SERP1 BTF3 CTD PRELID2 HNRNPC RPL10A UFL1 RPA3
CLIP2 IMMP2L EXTL3 DCTN6 IKBKB RPL35 FUT11 MARVELD1 CALHM2 GRK5
RPLP2 ELP4 EIF3M COMMD9 C11orf10 PCNXL3 ARHGEF17 NRIP2
KLHDC5 STAT6 DNAJC3-AS1 PLEKHG3 RPLP1 LINGO1 IL16 ZNF768 CDH11 CHD3
STX8 RPS15 USF2 SPINT2 RPS19 SNRPD2 RPS9 RPS5 CSRP2BP ZNFX1-AS1
SUSD2 ARSD ARSD-AS1 RP3 HPRT1

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0006415	9.46E-12	42.48747528	0.289668535	9	91	translational termination
GO:0019080	3.39E-11	28.10086682	0.480658778	10	151	viral genome expression
GO:0019083	3.39E-11	28.10086682	0.480658778	10	151	viral transcription
GO:0006414	3.51E-11	36.25591216	0.334232925	9	105	translational elongation
GO:0006614	3.51E-11	36.25591216	0.334232925	9	105	SRP-dependent cotranslational protein targeting to membrane

GO:0006413	3.63E-11	27.90101721	0.483841949	10	152	translational initiation
GO:0006613	3.83E-11	35.87963221	0.337416096	9	106	cotranslational protein targeting to membrane
GO:0045047	3.83E-11	35.87963221	0.337416096	9	106	protein targeting to ER
GO:0072599	3.83E-11	35.87963221	0.337416096	9	106	establishment of protein localization to endoplasmic reticulum
GO:0070972	1.01E-10	31.90280188	0.375614144	9	118	protein localization to endoplasmic reticulum
GO:0000184	1.09E-10	31.61056511	0.378797315	9	119	"nuclear-transcribed mRNA catabolic process, nonsense-mediated decay"
GO:0072594	6.60E-10	20.34793814	0.649366826	10	204	establishment of protein localization to organelle
GO:0006612	1.04E-09	24.08952703	0.487025119	9	153	protein targeting to membrane

GO:0043624	1.04E-09	24.08952703	0.487025119	9	153	cellular protein complex disassembly
GO:0043241	1.38E-09	23.27299111	0.502940973	9	158	protein complex disassembly
GO:0019058	2.21E-09	17.8280543	0.735312435	10	231	viral infectious cycle
GO:0000956	2.51E-09	21.65625	0.537955851	9	169	nuclear-transcribed mRNA catabolic process
GO:0034623	3.25E-09	20.99262899	0.553871704	9	174	cellular macromolecular complex disassembly
GO:0006402	3.97E-09	20.4900048	0.566604387	9	178	mRNA catabolic process
GO:0032984	4.17E-09	20.36804452	0.569787558	9	179	macromolecular complex disassembly
GO:0022415	6.90E-09	15.72777778	0.827624386	10	260	viral reproductive process

GO:0006401	1.37E-08	17.6338941	0.652549997	9	205	RNA catabolic process
GO:0071845	2.24E-07	12.4982801	0.904020483	9	284	cellular component disassembly at cellular level
GO:0022411	2.53E-07	12.31560593	0.916753166	9	288	cellular component disassembly
GO:0016032	1.18E-06	8.795666415	1.435609992	10	451	viral reproduction
GO:0033365	1.81E-06	8.364530838	1.505639748	10	473	protein localization to organelle
GO:0006605	1.85E-06	8.345905172	1.508822919	10	474	protein targeting

Tissue: Nerve_Tibial=>Muscle_Skeletal   Type: asymmetric

SourceGene: PHF8(ENSG00000172943.13)   PHD finger protein 8 (histone lysine

```
demethylase)







TargetGeneSet:  WDTC1   RP11    DLGAP3  C1orf168        ILF2    IL6R    DUSP12
TBX19   TIMM17A RPLP0P6 TMEM131 WIPF1   RFTN2   CLK1    RPL37A  LSM3    EBP
P4HTM   NISCH   ABTB1   IFT122  NPHP3-AS1       MRPL47  PEX5L   PARL    EVC2
MRFAP1L1        WDR1    UBE2K   NUP54   GAB1    NSUN2   RPS23   HIST1H2AG
SYNGAP1 RPL39P3 SERAC1  CLDN15  CAPZA2  OPN1SW  ARMC1   FAM92A1 INTS8   ENY2
PUF60   C8orf33 MIRLET7DHG      RPL35   C9orf173        HSPA14  FGFBP3  TM9SF3
BCCIP   RPLP2   CHRNA10 FADS3   FAU     MRPL21  SNORA25 WBP11   CPM     METAP2
SNRPF   RPL18AP3        RFC3    RPS29   METTL21D        ERH     POMT2   SLIRP   SNW1
MAGEL2  RPS3AP6 MAP2K5  RPLP1   UNC45A  C16orf91        PKD1    ALG1    RPS15A
PYDC1   HSD11B2 MBTPS1  MIR22HG ANKFY1  SREBF1  RPS7P1  RPL27   HOXB4   ABCA6
H3F3B   RHBDF2  WDR45L  RPS15   ANKRD27 ZFP14   TMEM91  RPS19   ZNF17   SNRPB
SNRPB2  SRC     ZNF334  HSPA13  LGALS1  RP1     SYTL4   RPL36A

GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term









GO:0006414      1.28E-12        24.55225806     0.632136184     12      105
translational elongation








GO:0006415      6.28E-12        25.84276316     0.54785136      11      91
translational termination








GO:0006614      3.09E-11        21.97228443     0.632136184     11      105
SRP-dependent cotranslational protein targeting to membrane
```

GO:0006613	3.43E-11	21.73947368	0.638156529	11	106
cotranslational protein targeting to membrane					
GO:0045047	3.43E-11	21.73947368	0.638156529	11	106
protein targeting to ER					
GO:0072599	3.43E-11	21.73947368	0.638156529	11	106
establishment of protein localization to endoplasmic reticulum					
GO:0070972	1.11E-10	19.2851697	0.710400664	11	118
protein localization to endoplasmic reticulum					
GO:0043624	1.15E-10	16.13957447	0.921112726	12	153
cellular protein complex disassembly					

GO:0000184	1.22E-10	19.10526316	0.716421009	11	119	"nuclear-transcribed mRNA catabolic process, nonsense-mediated decay"
GO:0043241	1.68E-10	15.58136986	0.951214449	12	158	protein complex disassembly
GO:0072594	2.47E-10	13.03587095	1.228150301	13	204	establishment of protein localization to organelle
GO:0000956	3.67E-10	14.47847134	1.01743824	12	169	nuclear-transcribed mRNA catabolic process
GO:0034623	5.14E-10	14.02666667	1.047539963	12	174	cellular macromolecular complex disassembly

GO:0006402	6.68E-10	13.68481928	1.071621341	12	178	mRNA catabolic process
GO:0032984	7.13E-10	13.60191617	1.077641686	12	179	macromolecular complex disassembly
GO:0019080	1.59E-09	14.70526316	0.909072037	11	151	viral genome expression
GO:0019083	1.59E-09	14.70526316	0.909072037	11	151	viral transcription
GO:0006413	1.71E-09	14.59994401	0.915092381	11	152	translational initiation

GO:0006612	1.83E-09	14.49610823	0.921112726	11	153	protein targeting to membrane
GO:0006605	2.63E-09	7.390403251	2.853643346	17	474	protein targeting
GO:0006401	3.36E-09	11.74797927	1.234170646	12	205	RNA catabolic process
GO:0071845	1.26E-07	8.289411765	1.70977787	12	284	cellular component disassembly at cellular level
GO:0033365	1.28E-07	6.325509461	2.847623002	15	473	protein localization to organelle
GO:0019058	1.32E-07	9.305263158	1.390699606	11	231	viral infectious cycle

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GO:0022411      1.46E-07        8.166956522     1.733859248     12      288
cellular component disassembly




GO:0022415      4.33E-07        8.204660748     1.565289599     11      260
viral reproductive process




GO:0016032      1.57E-05        5.075170843     2.71517542      12      451
viral reproduction




Tissue: Muscle_Skeletal=>Nerve_Tibial   Type:   asymmetric



SourceGene:     PLXNA1(ENSG00000114554.7)       plexin A1



TargetGeneSet:  GNB1    RPL22   SLC6A9  RPS8    RP11    RPS27   SYT12   ATP1B1
TP53BP2 TGIF2P1 ASAP2   HPCAL1  TMEM178 UBC     CLASP1  BSN-AS2 RPL29   RPS3A
ADAMTS16        CTB     RPL10A  GLI3    ARPC1B  FAM200A XKR4    EIF3E   RPS6
```

S1PR3 RPL12 RPS3AP5 NAV2 AMBRA1 GANAB RDX COMMD6 DICER1-AS1
DTWD1 RPS3AP6 NPTN RPL13 RPL26 KANSL1-AS1 CTD RPL18 ZNF419
SNORD86 FOXRED2 MICALL1 RP2 SMC1A NLGN3 RPL39 RPS4Y1

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0043624	1.19E-22	79.39937435	0.391737596	16	153	cellular protein complex disassembly
GO:0000184	1.76E-22	93.81555944	0.304684797	15	119	"nuclear-transcribed mRNA catabolic process, nonsense-mediated decay"
GO:0043241	2.03E-22	76.5767941	0.404539478	16	158	protein complex disassembly
GO:0006415	2.95E-22	113.3359684	0.232994256	14	91	translational termination
GO:0034623	1.00E-21	68.74502712	0.445505501	16	174	cellular macromolecular complex disassembly
GO:0032984	1.60E-21	66.61291265	0.458307384	16	179	macromolecular complex disassembly
GO:0006414	2.48E-21	95.80602007	0.268839527	14	105	translational elongation
GO:0006614	2.48E-21	95.80602007	0.268839527	14	105	SRP-dependent cotranslational protein targeting to membrane

GO:0006613	2.85E-21	94.75803403	0.271399903	14	106	cotranslational protein targeting to membrane
GO:0045047	2.85E-21	94.75803403	0.271399903	14	106	protein targeting to ER
GO:0072599	2.85E-21	94.75803403	0.271399903	14	106	establishment of protein localization to endoplasmic reticulum
GO:0006413	8.10E-21	71.05341739	0.38917722	15	152	translational initiation
GO:0070972	1.38E-20	83.7541806	0.30212442	14	118	protein localization to endoplasmic reticulum
GO:0000956	4.17E-20	63.13459268	0.432703619	15	169	nuclear-transcribed mRNA catabolic process
GO:0006402	9.28E-20	59.61098717	0.455747007	15	178	mRNA catabolic process
GO:0019080	4.98E-19	63.43319581	0.386616843	14	151	viral genome expression
GO:0019083	4.98E-19	63.43319581	0.386616843	14	151	viral transcription

GO:0006612	6.01E-19	62.51172975	0.391737596	14	153	protein targeting to membrane
GO:0006401	8.05E-19	51.0430622	0.524877171	15	205	RNA catabolic process
GO:0071845	2.89E-18	40.21606254	0.72714691	16	284	cellular component disassembly at cellular level
GO:0022411	3.61E-18	39.61344538	0.737388416	16	288	cellular component disassembly
GO:0072594	3.66E-17	45.56887872	0.522316795	14	204	establishment of protein localization to organelle
GO:0019058	2.11E-16	39.82328191	0.591446959	14	231	viral infectious cycle
GO:0022415	1.11E-15	35.05691057	0.665697876	14	260	viral reproductive process
GO:0033365	2.06E-13	20.77610163	1.211058058	15	473	protein localization to organelle
GO:0006605	2.12E-13	20.72935235	1.213618435	15	474	protein targeting

```
GO:0016032      2.16E-12        19.4685106      1.154729776     14      451
viral reproduction



Tissue: Muscle_Skeletal=>Nerve_Tibial   Type:   asymmetric
SourceGene:     RP11-241I20.3(ENSG00000234335.1)
TargetGeneSet:  RPL22   PQLC2   RPL11   RP4     PDC     RP11    GALNT2  PREB    PIGF
UBC     RPL31   FOXD4L1 BIN1    RPL32   RPP14   RPL35A  MSANTD1 HERC5   RPL34   CTD
RPL37   MIP     HOMER1  ZFYVE16 RPS23   TCF7    GABRP   RPL10A  RPL39P3 HDAC2
MRPS12  PERP    SNX9    STEAP1B HNRNPA2B1       SLC12A9 SHH     RPS20   GRIP1
RPL30   PUF60   RPS6    RPL12   SLC27A4 COBRA1  FBXO18  RPS24   RPL13AP5
RPS13   MTA2    LRRN4CL RNU2-2  FAU     CCL13   CDK2AP2 RPS3    RPS25   HYOU1
HEBP1   GXYLT1  PFDN5   RPL41   NACA    RPL14P1 DAO     RPS29   KIAA0317        SLTM
RPS3AP6 RPS15A  TMC7    FBXL19  RPL26   ARHGAP44        RPL23A  RPL17   PNMT
ERBB2   RPL27   PHB     ARHGDIA LMNB2   UBA52   RPS16   ZNF780A ZNF235  SNRPD2
RPL18   ZNF534  RPL28   ZNFX1-AS1       TAF4    RPS21   ZNF74   BCR     GAL3ST1
EIF3L   RANGAP1 PPP1R3F RP13    RAB40A  GPC4    MTM1    HAUS7   PLXNB3  MT
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      1.2517819831294e-47     127.402873563218        0.560445643900076
31      91      translational termination
GO:0006414      2.38409111527322e-45    103.198508853681        0.646668050653934
31      105     translational elongation
GO:0006614      2.38409111527322e-45    103.198508853681        0.646668050653934
31      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      3.35632427922435e-45    101.815402298851        0.652826793993495
31      106     cotranslational protein targeting to membrane
GO:0045047      3.35632427922435e-45    101.815402298851        0.652826793993495
31      106     protein targeting to ER
GO:0072599      3.35632427922435e-45    101.815402298851        0.652826793993495
31      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      1.54020609043224e-43    87.6981767736821        0.726731714068231
31      118     protein localization to endoplasmic reticulum
GO:0000184      2.0746181668463e-43     86.6955329153605        0.732890457407792
31      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      1.19778126380658e-41    67.1938670204924        0.929970244273753
32      151     viral genome expression
GO:0019083      1.19778126380658e-41    67.1938670204924        0.929970244273753
32      151     viral transcription
GO:0006413      1.51132929845921e-41    66.6292397660819        0.936128987613314
32      152     translational initiation
GO:0006612      1.22704965767786e-39    62.3855285472018        0.942287730952875
31      153     protein targeting to membrane
GO:0043624      1.22704965767786e-39    62.3855285472018        0.942287730952875
31      153     cellular protein complex disassembly
GO:0043241      3.64283852177859e-39    59.90836274776  0.973081447650682       31
158     protein complex disassembly
GO:0000956      3.49951970397202e-38    55.0904547726137        1.04082762438586
31      169     nuclear-transcribed mRNA catabolic process
GO:0034623      9.26909437636963e-38    53.1455268869062        1.07162134108366
31      174     cellular macromolecular complex disassembly
GO:0006402      1.97576698886417e-37    51.684846352334 1.09625631444191        31
178     mRNA catabolic process
GO:0032984      2.38021148919808e-37    51.3320130475303        1.10241505778147
31      179     macromolecular complex disassembly
GO:0072594      3.91513174939744e-37    46.3157894736842        1.2563836412705 32
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204     establishment of protein localization to organelle
GO:0006401      2.08165844613826e-35    43.5818470075307        1.26254238461006
31      205     RNA catabolic process
GO:0019058      2.57901084196969e-35    39.9555673102354        1.42266971143865
32      231     viral infectious cycle
GO:0022415      1.31789591896921e-33    34.8020929516774        1.60127326828593
32      260     viral reproductive process
GO:0071845      7.43165661525524e-31    29.8063922584162        1.7490831084354 31
284     cellular component disassembly at cellular level
GO:0022411      1.15646006109395e-30    29.3341607406414        1.77371808179365
31      288     cellular component disassembly
GO:0006605      4.45999507696312e-29    20.5561883067578        2.91924434295204
35      474     protein targeting
GO:0033365      8.38935600606502e-28    19.6057983019259        2.91308559961248
34      473     protein localization to organelle
GO:0016032      3.45248063126365e-27    19.6578947368421        2.77759324614214
33      451     viral reproduction
GO:0042274      6.36193153430945e-08    65.7005494505494        0.110857380112103
5       18      ribosomal small subunit biogenesis
GO:0022613      1.19098339368093e-06    8.32911392405063        1.38571725140129
10      225     ribonucleoprotein complex biogenesis
GO:0071843      2.0552278343414e-06     7.81217179813167        1.47193965815514
10      239     cellular component biogenesis at cellular level
GO:0006364      3.46465097984344e-06    12.5540608498868        0.640509307314373
7       104     rRNA processing
GO:0042254      3.69092665497524e-06    9.96129936082655        0.91765275759463
8       149     ribosome biogenesis
GO:0016072      5.03748474613913e-06    11.8177835661852        0.67746176735174
7       110     rRNA metabolic process
Tissue: Muscle_Skeletal=>Nerve_Tibial   Type:   asymmetric
SourceGene:     RP11-302M6.4(ENSG00000232236.1)
TargetGeneSet:  RPS8    RP11    RP4     CAMSAP2 SLC35F3 EIF3FP3 FGF5    CTB
HLA-DOA RPL10A  ESRP1   BAALC   RPS6    RPL12   RPL7A   LINC00173       RPS15A
RPL26   CCDC144C        CDR2L   NFATC1  CTD     FTL     RPL28   FIZ1    ZNF787
RPL10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      1.64695369752928e-15    143.171840354767        0.12594284132586
9       91      translational termination
GO:0006414      6.25396002161484e-15    122.173295454545        0.1453186630683 9
105     translational elongation
GO:0006614      6.25396002161484e-15    122.173295454545        0.1453186630683 9
105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      6.8295141899155e-15     120.9053420806  0.146702650335617       9
106     cotranslational protein targeting to membrane
GO:0045047      6.8295141899155e-15     120.9053420806  0.146702650335617       9
106     protein targeting to ER
GO:0072599      6.8295141899155e-15     120.9053420806  0.146702650335617       9
106     establishment of protein localization to endoplasmic reticulum
GO:0070972      1.84411327786449e-14    107.504587155963        0.163310497543423
9       118     protein localization to endoplasmic reticulum
GO:0000184      1.99361931307001e-14    106.519834710744        0.16469448481074
9       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      1.77829104397303e-13    82.330985915493 0.208982077364888       9
151     viral genome expression
GO:0019083      1.77829104397303e-13    82.330985915493 0.208982077364888       9
151     viral transcription
GO:0006413      1.8889053476204e-13     81.7495232040687        0.210366064632205
9       152     translational initiation
GO:0006612      2.00557506904523e-13    81.1761363636364        0.211750051899523
9       153     protein targeting to membrane
GO:0043624      2.00557506904523e-13    81.1761363636364        0.211750051899523
9       153     cellular protein complex disassembly
GO:0043241      2.69020382903067e-13    78.424649176327 0.218669988236108       9
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158     protein complex disassembly
GO:0000956      4.96844691928321e-13    72.9767045454546        0.233893848176597
9       169     nuclear-transcribed mRNA catabolic process
GO:0034623      6.47784464322384e-13    70.7404958677686        0.240813784513182
9       174     cellular macromolecular complex disassembly
GO:0006402      7.96437183648954e-13    69.0467993544917        0.246349733582451
9       178     mRNA catabolic process
GO:0032984      8.38021161068123e-13    68.6358288770054        0.247733720849768
9       179     macromolecular complex disassembly
GO:0072594      2.74006229750891e-12    59.7314685314685        0.282333402532697
9       204     establishment of protein localization to organelle
GO:0006401      2.86389527912518e-12    59.4225417439703        0.283717389800014
9       205     RNA catabolic process
GO:0019058      8.40737870340574e-12    52.3673218673219        0.31970105875026
9       231     viral infectious cycle
GO:0022415      2.43158646465357e-11    46.2223831944947        0.359836689502457
9       260     viral reproductive process
GO:0071845      5.35711693096786e-11    42.1170247933884        0.393052383918068
9       284     cellular component disassembly at cellular level
GO:0022411      6.06971959474303e-11    41.5014662756598        0.398588332987337
9       288     cellular component disassembly
GO:0016032      3.21091968451894e-09    25.8948992184286        0.62417825756003
9       451     viral reproduction
GO:0033365      4.87194104762567e-09    24.6283307210031        0.654625977441008
9       473     protein localization to organelle
GO:0006605      4.96274204060114e-09    24.5736070381232        0.656009964708325
9       474     protein targeting
GO:0022613      1.12128380665978e-05    21.5318181818182        0.311397135146357
5       225     ribonucleoprotein complex biogenesis
GO:0071843      1.50187593401244e-05    20.2236467236467        0.330772956888797
5       239     cellular component biogenesis at cellular level
Tissue: Muscle_Skeletal=>Nerve_Tibial   Type:   asymmetric
SourceGene:     RP11-307I14.2(ENSG00000220105.2)
TargetGeneSet:  RP4     RP11    RPL11   RPS3A   RPL10A  EPHB6   RPS20   RPL7
POLR1E  USP2    GEMIN2  RPS3AP6 RPL17
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      4.7286271313409e-11     168.870588235294        0.0755657047955159
6       91      translational termination
GO:0006414      1.13596912439202e-10    144.848484848485        0.0871911978409799
6       105     translational elongation
GO:0006614      1.13596912439202e-10    144.848484848485        0.0871911978409799
6       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.20369630057904e-10    143.39  0.0880215902013702      6       106
cotranslational protein targeting to membrane
GO:0045047      1.20369630057904e-10    143.39  0.0880215902013702      6       106
protein targeting to ER
GO:0072599      1.20369630057904e-10    143.39  0.0880215902013702      6       106
establishment of protein localization to endoplasmic reticulum
GO:0070972      2.31510341395467e-10    127.919642857143        0.0979862985260536
6       118     protein localization to endoplasmic reticulum
GO:0000184      2.43715605442804e-10    126.778761061947        0.0988166908864438
6       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      1.03374025467577e-09    98.5793103448276        0.125389246418933
6       151     viral genome expression
GO:0019083      1.03374025467577e-09    98.5793103448276        0.125389246418933
6       151     viral transcription
GO:0006413      1.07583659143465e-09    97.8972602739726        0.126219638779323
6       152     translational initiation
GO:0006612      1.11934651153124e-09    97.2244897959184        0.127050031139714
6       153     protein targeting to membrane
GO:0043624      1.11934651153124e-09    97.2244897959184        0.127050031139714
6       153     cellular protein complex disassembly
GO:0043241      1.35943709635315e-09    93.9934210526316        0.131201992941665
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6       158     protein complex disassembly
GO:0000956      2.04064203149548e-09    87.5828220858896        0.140336308905958
6       169     nuclear-transcribed mRNA catabolic process
GO:0034623      2.43273019696167e-09    84.9464285714286        0.144488270707909
6       174     cellular macromolecular complex disassembly
GO:0006402      2.78967451431039e-09    82.9476744186046        0.147809840149471
6       178     mRNA catabolic process
GO:0032984      2.885389111653e-09      82.4624277456647        0.148640232509861
6       179     macromolecular complex disassembly
GO:0072594      6.33155322571186e-09    71.9242424242424        0.169400041519618
6       204     establishment of protein localization to organelle
GO:0006401      6.52010748867559e-09    71.5577889447236        0.170230433880008
6       205     RNA catabolic process
GO:0019058      1.33344527646106e-08    63.1733333333333        0.191820635250156
6       231     viral infectious cycle
GO:0022415      2.70267879691018e-08    55.8464566929134        0.215902013701474
6       260     viral reproductive process
GO:0071845      4.57347393629197e-08    50.9388489208633        0.235831430350841
6       284     cellular component disassembly at cellular level
GO:0022411      4.97033799076331e-08    50.2021276595745        0.239152999792402
6       288     cellular component disassembly
GO:0016032      7.04124660609916e-07    31.447191011236 0.374506954536018       6
451     viral reproduction
GO:0033365      9.30996519068124e-07    29.9186295503212        0.392775586464605
6       473     protein localization to organelle
GO:0006605      9.42588157413463e-07    29.8525641025641        0.393605978824995
6       474     protein targeting
Tissue: Muscle_Skeletal=>Skin_Sun_Exposed_Lower_leg     Type:   asymmetric
SourceGene:     CDKN2D(ENSG00000129355.5)
TargetGeneSet:  CLCN6   SNHG3   ZNF691  PALMD   FCGR1B  PPIAL4B CHD1L   PRUNE   SHC1
RHBG    SUPT7L  PLB1    MTHFD2  EN1     TANC1   SLC6A6  RP11    NBEAL2  MRPS18AP1
QRICH1  HNRPDL  CCDC127 NSUN2   LIFR-AS1        LARP1   BEND3   MTHFD1L MEOX2
TRIM4   YBX1P2  CHPF2   TNFRSF10B       HEATR7A MIRLET7D        FPGS    OTUD1
LZTS2   PTPRE   CTD     METTL15 TBRG1   DHX37   SPRY2   CBLN3   CDKL1   CRIP2
CYP19A1 SCAPER  CLCN7   EME2    CA4     LINC00338       NPLOC4  ZNF844  LGI4
CAPN12  RTN2    ETFB    FAM113A ASXL1   TRAPPC10        FTCD    PI4KA   CES5AP1
SREBF2  NOX1    MTMR1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006730      4.40453268055253e-08    66.5694444444444        0.0996470832468341
5       32      one-carbon metabolic process
GO:0006760      6.95682568325645e-07    73.8741976893453        0.071621341083662
4       23      folic acid-containing compound metabolic process
GO:0009396      3.33486209636152e-06    146.928571428571        0.0311397135146357
3       10      folic acid-containing compound biosynthetic process
GO:0042558      4.00301924421348e-06    45.2399685287175        0.108988997301225
4       35      pteridine-containing compound metabolic process
GO:0046653      1.5360388194886e-05     79.0824175824176        0.0498235416234171
3       16      tetrahydrofolate metabolic process
Tissue: Muscle_Skeletal=>Skin_Sun_Exposed_Lower_leg     Type:   asymmetric
SourceGene:     CELA2B(ENSG00000215704.4)
TargetGeneSet:  MTND1P23        CELA2A  CELA3B  CELA3A  ODF2L   REG1A   LARS2   RP11
CLPS    RP1     CPA2    CPA1    PRSS1   PNLIP   PNLIPRP1        PNLIPRP2
PLA2G1B GP2     CTRB1   THAP8   DHDH    KLK3    NXT1    ETS2    CECR9
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0007586      1.21835570087734e-10    70.2352941176471        0.158397342744447
7       109     digestion
GO:0044241      4.45140475278301e-09    308.427807486631        0.021797799460245
4       15      lipid digestion
Tissue: Muscle_Skeletal=>Skin_Sun_Exposed_Lower_leg     Type:   asymmetric
SourceGene:     CHPT1(ENSG00000111666.5)
TargetGeneSet:  RPL11   TAF12   ALG6    PRUNE   PSMB4   BRP44   C1orf35 HIST3H2A
RAB4A   RPS7    UCN     DPY30   UBC     TPRKB   COX5B   OXSM    DALRD3  RASSF1  LIAS
NUDT10  OSTC    PRMT10  UBE2B   CAMLG   MRPL22  CTB     C6orf130        MRPL2
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COX7A2  ASF1A   C6orf72 GTF2H5  BRP44L  LINC00174       TMEM60  FNTA    C8orf76
MAPK15  C9orf123        CCL19   RP11    CLTA    FAM206A ENTPD2  ATP5C1  FAM188A
COMMD3  CUL2    RPL13AP5        CPXM2   RARRES3 KBTBD3  PLEKHG6 GPN3    MRP63   GPX2
COX16   C15orf24        C16orf48        RPS7P1  CCL13   RPL27   ARHGAP27
C18orf32        SEC11C  XAB2    SLC25A42        FAM98C  CLDND2  TNNI3   TRAPPC2
SPEF1   CDK5RAP1        PSMA7   ATP5J   PMM1    IL3RA   COX7B   PSMD10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0031398      1.68165736274848e-05    12.6340023612751        0.544875787142758
6       127     positive regulation of protein ubiquitination
Tissue: Muscle_Skeletal=>Skin_Sun_Exposed_Lower_leg     Type:   asymmetric
SourceGene:     CTD-2576F9.2(ENSG00000260521.1)
TargetGeneSet:  RP1     AKIRIN1 RP11    USP21   HNRNPU  COQ10B  ZNF654  ERAP1
ZCCHC10 DIAPH1  PGBD1   DDX56   RPS3AP34        PTDSS1  PABPC1  FAM91A1 ATP6V1G1
FAM73B  ACBD5   FAM35A  EIF6    BBOX1   AHNAK   STT3A   GOLT1B  CCDC65  PCBP2   TBK1
ACTR6   ABHD13  SLC22A17        MBIP    MED6    YLPM1   WDR76   CTD     CDH1
TERF2IP RP13    RPA1    DYNLL2  EEF2    PRKCSH  WDR83   ZNF506  SS18L1  OSBPL2
MAFIPL  SMC1A   MSN
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0000377      7.24601949011397e-07    16.8390862944162        0.522316794685489
7       204     RNA splicing, via transesterification reactions with bulged
adenosine as nucleophile
GO:0000398      7.24601949011397e-07    16.8390862944162        0.522316794685489
7       204     nuclear mRNA splicing, via spliceosome
GO:0000375      8.52766533219009e-07    16.416501650165 0.535118676908172       7
209     RNA splicing, via transesterification reactions
GO:0008380      1.5104647807121e-05     10.4099156118143        0.827001591585357
7       323     RNA splicing
Tissue: Muscle_Skeletal=>Skin_Sun_Exposed_Lower_leg     Type:   asymmetric
SourceGene:     ENSG00000232926.1
TargetGeneSet:  PGD     CTPS    SZT2    RP4     NAP1L4P1        RP11    MLLT11  CCT3
ARHGEF11        GDF7    SLC5A6  FNDC4   RPL36AP15       MREG    TRIP12  SLC4A7
NT5DC2  HTR1F   LRRC58  KPNA1   SEC61A1 SRPRB   UBQLN4P1        LETM1   MT1P2
ACSL1   NSUN2   SV2C    HOMER1  VDAC1   LARP1   PRELID1 E2F3    XPO5    RP1
BEND3   LINC00473       FBXL18  SEPT7P3 TRRAP   TRIM4   TFR2    ADCK2   ABCF2
UBE3C   PRKDC   MAPRE1P1        HEATR7A FAM120A DDX21   UNC5B   TMEM123 NOLC1
TP53I11 RPS6KA4 PITPNM1 PCSK7   MARS    CYP27B1 XPOT    MVK     EP400   MYCBP2
IFI27L2 TYRO3   COX5A   ZNF592  FURIN   TRAF7   CTD     FAM86A  USP7    ABCC1
SLC7A5  ACACA   ACLY    PSME3   PYCR1   FASN    LMNB2   PNPLA6  DNMT1   CILP2
TMEM145 GART    TRAPPC10        SEPT5   PPPDE2  SREBF2  PNPLA3  HUWE1   ZMAT1
ZDHHC9  NSDHL
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0035338      1.64408893497176e-06    60.3571428571429        0.0896823749221507
4       18      long-chain fatty-acyl-CoA biosynthetic process
GO:0035336      2.58360213421859e-06    52.8051470588235        0.0996470832468341
4       20      long-chain fatty-acyl-CoA metabolic process
GO:0046949      2.58360213421859e-06    52.8051470588235        0.0996470832468341
4       20      fatty-acyl-CoA biosynthetic process
GO:0035384      3.17951037573131e-06    49.6955017301038        0.104629437409176
4       21      thioester biosynthetic process
GO:0071616      3.17951037573131e-06    49.6955017301038        0.104629437409176
4       21      acyl-CoA biosynthetic process
GO:0035337      5.5816118277697e-06     42.2323529411765        0.119576499896201
4       24      fatty-acyl-CoA metabolic process
GO:0019432      6.35430074420932e-06    22.2807835820896        0.26406477060411
5       53      triglyceride biosynthetic process
GO:0046460      7.64369646350815e-06    21.3865671641791        0.274029478928794
5       55      neutral lipid biosynthetic process
GO:0046463      7.64369646350815e-06    21.3865671641791        0.274029478928794
5       55      acylglycerol biosynthetic process
Tissue: Muscle_Skeletal=>Skin_Sun_Exposed_Lower_leg     Type:   asymmetric
SourceGene:     ENSG00000235978.2
TargetGeneSet:  RP11    WDR3    TMOD4   UCK2    ADCY3   SLC5A6  CAD     RGPD2
PIKFYVE NT5DC2  C3orf26 PLXNA1  HES1    LETM1   TBC1D14 LARP1   NOP16   PAK1IP1
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POU5F1  MDN1    TRRAP   TFR2    IMPDH1  MAK16   RDH10   CTA     C9orf114
OR52N4  NEU3    DDN     DNAJC14 UTP20   DDX55   DHX37   EP400   DDX51   TMTC4
ATP11A  SPINT1  CTD     PDPR    KCNAB3  C17orf67        LINC00338       DOT1L
TRMT1   SNORA68 CYP2G1P ZNF587  ACTG1P3 NOP56   PTPN1   GART    RRP1B   MCM3AP
NBEAP3  ADSL    CLCN5   RHOXF2
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0009156      2.8836915130135e-08     72.9361054766734        0.0917583558231264
5       34      ribonucleoside monophosphate biosynthetic process
GO:0009124      4.49086546209502e-08    66.0845588235294        0.0998546813369317
5       37      nucleoside monophosphate biosynthetic process
GO:0009161      5.90853733529536e-08    62.1885813148789        0.105252231679469
5       39      ribonucleoside monophosphate metabolic process
GO:0009123      1.38749459309604e-07    51.5459110473458        0.124143657878348
5       46      nucleoside monophosphate metabolic process
GO:0009112      6.88112536845422e-07    36.394523326572 0.170022835789911       5
63      nucleobase metabolic process
GO:0009260      4.08040004898645e-06    24.7871972318339        0.242889765414158
5       90      ribonucleotide biosynthetic process
Tissue: Skin_Sun_Exposed_Lower_leg=>Muscle_Skeletal     Type:   asymmetric
SourceGene:     ENSG00000236935.1
TargetGeneSet:  SFPQ    ACBD6   RP11    RPL10A  RPL35   RPS25   RPL41   RPLP1
RPL13   SNORD12 ARSFP1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      1.46219002870474e-12    506.752941176471        0.0503771365303439
6       91      translational termination
GO:0006414      3.52440227959429e-12    434.666666666667        0.0581274652273199
6       105     translational elongation
GO:0006614      3.52440227959429e-12    434.666666666667        0.0581274652273199
6       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      3.73542049121313e-12    430.29  0.0586810601342468      6       106
cotranslational protein targeting to membrane
GO:0045047      3.73542049121313e-12    430.29  0.0586810601342468      6       106
protein targeting to ER
GO:0072599      3.73542049121313e-12    430.29  0.0586810601342468      6       106
establishment of protein localization to endoplasmic reticulum
GO:0070972      7.20504798139751e-12    383.866071428571        0.065324199017369
6       118     protein localization to endoplasmic reticulum
GO:0000184      7.58671052977975e-12    380.442477876106        0.0658777939242959
6       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      3.24266868858932e-11    295.820689655172        0.0835928309459553
6       151     viral genome expression
GO:0019083      3.24266868858932e-11    295.820689655172        0.0835928309459553
6       151     viral transcription
GO:0006413      3.37552499800433e-11    293.77397260274 0.0841464258528822      6
152     translational initiation
GO:0006612      3.51288101484549e-11    291.755102040816        0.084700020759809
6       153     protein targeting to membrane
GO:0043624      3.51288101484549e-11    291.755102040816        0.084700020759809
6       153     cellular protein complex disassembly
GO:0043241      4.27147087778567e-11    282.059210526316        0.0874679952944433
6       158     protein complex disassembly
GO:0000956      6.42877757668172e-11    262.822085889571        0.0935575392706387
6       169     nuclear-transcribed mRNA catabolic process
GO:0034623      7.67317996887295e-11    254.910714285714        0.096325513805273
6       174     cellular macromolecular complex disassembly
GO:0006402      8.80746571102475e-11    248.912790697674        0.0985398934329804
6       178     mRNA catabolic process
GO:0032984      9.11183454247686e-11    247.456647398844        0.0990934883399073
6       179     macromolecular complex disassembly
GO:0072594      2.01147052447413e-10    215.833333333333        0.112933361013079
6       204     establishment of protein localization to organelle
GO:0006401      2.07186910357011e-10    214.733668341709        0.11348695592006
6       205     RNA catabolic process
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GO:0019058      4.26375714687163e-10    189.573333333333        0.127880423500104
6       231     viral infectious cycle
GO:0022415      8.70238502331617e-10    167.586614173228        0.143934675800983
6       260     viral reproductive process
GO:0071845      1.48114719337377e-09    152.859712230216        0.157220953567227
6       284     cellular component disassembly at cellular level
GO:0022411      1.61122524367783e-09    150.648936170213        0.159435333194935
6       288     cellular component disassembly
GO:0016032      2.37432063915819e-08    94.3685393258427        0.249671303024012
6       451     viral reproduction
GO:0033365      3.15616285494933e-08    89.7815845824411        0.261850390976403
6       473     protein localization to organelle
GO:0006605      3.19623654221233e-08    89.5833333333333        0.26240398588333
6       474     protein targeting
Tissue: Muscle_Skeletal=>Skin_Sun_Exposed_Lower_leg     Type:   cluster
SourceGene:     FABP4(ENSG00000170323.4)
TargetGeneSet:  MTND2P28        CCNL2   TMEM240 FBXO44  ZBTB40  SYF2    C1orf63
RBBP4   THRAP3  JAK1    RPS27   NTRK1   TKT     VAMP4   FAM129A CNTN2   PARP1
C1orf35 MRPL55  KCNK1   C2orf18 YPEL5   DPY30   UBC     FAM136A DCTN1   ZFAND2B
TRIP12  MAP4    CLDND1  C3orf15 COPG1   CCNL1   ARAP2   H2AFZ   RP11    MYO10
ATG12   HINT1   PCDHB6  LARP1   FAM193B DEK     LEMD2   DEFA6   PNISR   C7orf23
HIPK2   PAF1    TTC35   LY6D    CD72    FAM206A UBAC1   COMMD3  ZEB1-AS1
ARHGAP12        CHST3   C10orf118       NSMCE4A CCDC88B ANKRD13D        PICALM
CEP57   KBTBD3  TBRG1   GOLGA2B NFYB    ARL6IP4 MTRF1   TPT1-AS1        RCN1P2
ARGLU1  DCUN1D2 KLHDC2  U6      NEK9    WARS    ANKRD9  LPCAT4  AKAP13  CHD2    CTD
RHBDF1  FOPNL   LONP2   C16orf48        HSDL1   SPG7    TP53    RPL26   GSDMB   CLTC
IER3IP1 MALT1   FAM69C  FGF22   ALKBH7  CCDC114 CYTH2   ZNF772  KIF3B   BCL2L13 RP1
MPST    TRABD   AKAP17A MAGED1  MSN
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
Tissue: Skin_Sun_Exposed_Lower_leg=>Muscle_Skeletal     Type:   asymmetric
SourceGene:     FAM207BP(ENSG00000228797.2)
TargetGeneSet:  AHDC1   TMEM56  ATP5F1  B3GALNT2        C2orf28 COX5B   GULP1   ICOS
THUMPD3 GRPEL1  PPARGC1A        ATP8A1  TIFA    RP11    C5orf63 SH3RF2  MRPS18B
KCNK17  FAXC    STXBP5  NDUFA4  DNAH11  TBRG4   GTF2I   AGBL3   MRPS33  MRPL13
ISCA1   AS3MT   IMMP1L  CYBASC3 IFT46   C14orf142       RPL9P25 TSPAN3  MRPL46
UQCRC2  ZNF821  CHAD    ATP5H   ICAM3   ZNF627  MAST3   COX6B1  MRPS12  GPCPD1  CHD6
C21orf33        DNMT3L  C22orf25        NDUFA6  BTK
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022900      4.94758116199299e-12    34.9071358748778        0.398726731714068
10      134     electron transport chain
GO:0045333      2.80930273241364e-10    28.4111012826183        0.422531312711923
9       142     cellular respiration
GO:0022904      3.37738933946109e-10    37.1948051948052        0.285654971974258
8       96      respiratory electron transport chain
GO:0006091      3.31242845336531e-08    11.5333483213429        1.27354508338523
11      428     generation of precursor metabolites and energy
GO:0015980      2.34362402309278e-07    12.5335570469799        0.913500795792679
9       307     energy derivation by oxidation of organic compounds
Tissue: Muscle_Skeletal=>Skin_Sun_Exposed_Lower_leg     Type:   cluster
SourceGene:     PLEKHA4(ENSG00000105559.5)
TargetGeneSet:  NADK    DNAJC11 PGD     MTHFR   DDI2    SYF2    CSMD2   SZT2
BCAR3   TSPAN2  FOXE1   SHC1    IER5    CD55    PPP2R5A CICP13  ADCY3   OTOF
SLC5A6  CAD     CRIM1   MTHFD2  HOXD9   MREG    SGPP2   TRIP12  MYRIP   ZNF621
NICN1   PARP9   ATR     RPL22L1 LETM1   TMEM165 RP11    CYP2U1  SLC25A4 MCCC2
CETN3   SMAD5-AS1       ZNF225  PPP2R2B HMGXB3  LARP1   ID4     E2F3    SKIV2L  XPO5
SLC29A1 MRAP2   MDN1    AIM1    CCDC28A MTHFD1L FBXL18  MEOX2   CLIP2   GNG11
TRRAP   AKR1B10 GIMAP7  CHD7    POP1    RAD21   DPAGT1  IARS    KIAA0368
NUP188  FAM208B OTUD1   CICP9   SIRT1   SLC25A16        PCBD1   RP13    C10orf116
AGAP11  EML3    C11orf68        AIP     NEU3    DIXDC1  KCNJ1   CD9     CLEC7A
HOXC10  DNAJC14 XPOT    ATP6V0A2        EP400   CRYL1   RNF31   AKAP5   EVL
TRAF3   CTD     PLA2G4E WDR73   TSC2    USP7    IRX5    SLC7A6  CIRH1A  ADAT1
VPS53   TSR1    RP1     CAMTA2  CDK5R1  GAS2L2  ACACA   PSME3   EFTUD2  PPM1D   TLK2
C17orf28        SGSH    FN3K    BCL2    ILF3    GCDH    TRMT1   DPY19L3 MLL4
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C19orf55        MEGF8   SIGLEC10        NLRP12  ZNF587  MAVS    PAX1    APCDD1L GART
PEX26   FAM156B TCEAL7
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006732      6.17803174840816e-07    7.82166918049271        1.61082278043042
11      206     coenzyme metabolic process
GO:0051186      3.37181934434477e-06    6.50008379420144        1.91578437478375
11      245     cofactor metabolic process
Tissue: Muscle_Skeletal=>Skin_Sun_Exposed_Lower_leg     Type:   asymmetric
SourceGene:     PROCR(ENSG00000101000.3)
TargetGeneSet:  SKI     ICMT    ZBTB48  PGD     PEX14   FBLIM1  RP11    SEPN1   RP1
EIF2C1  INSL3   CTPS    MUTYH   RP4     ALX3    CTTNBP2NL       MAN1A2  CDC42SE1
CHTOP   SNORA58 SHC1    ASH1L   ARHGEF11        UCK2    MPZL1   ABL2    ATP2B4
TP53BP2 GALNT2  ATAD2B  ADCY3   ASXL2   GPR113  SLC5A6  CAD     YPEL5   ASB3
AFTPH   TEX261  UGGT1   TMEM163 ACVR2A  FMNL2   MTX2    CWC22   PIKFYVE RNF25
SGPP2   COL4A4  HDAC4   ARL8B   TBC1D5  HIGD1A  CCDC12  PRKAR2A ZNF654  CLDND1
KIAA2018        NCK1    PIK3CB  UBQLN4P1        GPR87   BCL6    HES1    LETM1
ZBTB49  MRFAP1L1        TBC1D14 PCDH7   TEC     CHIC2   GSX2    CLOCK   RASGEF1B
HELQ    SGMS2   ANAPC10 LSM6    UBE2B   ANKHD1  FBXO38  NDST1   LARP1   MAT2B
SLC2A3P1        NEURL1B CTB     DUSP1   ARL10   NSD1    CANX    ZKSCAN4 UHRF1BP1
DEFA6   FBXO9   PTP4A1  PHF3    MDN1    MCM9    CCDC28A PPIL4   FOXK1   ARL4A
CCT6P3  ZNF394  FAM200A C7orf59 EPHB4   PRKRIP1 DNAJB9  IMPDH1  KLHDC10 HIPK2   RHEB
GS1     KIAA1456        KCNU1   PRKDC   ATP6V1H TMEM68  PTDSS1  POP1    PABPC1
TTC35   ST3GAL1 CTA     EPPK1   RGP1    FAM120A GRIN3A  SNX33   MIR181A2HG
NUP188  TOR1B   WDR5    NACC2   KLF6    OTUD1   RAB18   C10orf25        ZFAND4
P4HA1   C10orf28        TAF5    DUSP5   PPP2R2D HRAS    ZBED5   TUT1    CTSC
AMOTL1  C11orf63        SIAE    SRPR    ERC1    TULP3   CDKN1B  ITPR2   FKBP11
TUBA1C  TMBIM6  ACVR1B  SARNP   DDIT3   SLC25A3 EID3    C12orf76        UNC119B
RSRC2   RPL21   AKAP11  MYCBP2  IPO5    CHAMP1  RNF31   TSSK6   BNIP3P1 ARF6
CHMP4BP1        MED6    ANGEL1  ALKBH1  SPATA7  BTBD7   WARS    TRAF3   CDC42BPB
HERC2   C15orf24        RNF111  CLK3    CTD     UBN1    FAM86A  NOMO2   SMG1    COG7
NFATC2IP        KCTD13  PRSS8   ARMC5   CNOT1   CMTM4   CBFB    PSKH1   CDH1
GABARAPL2       TERF2IP MAP1LC3B        ZNF778  GLOD4   C17orf48        TOM1L2
MYO15A  USP22   NF1     LRRC37B RHOT1   NLE1    ACACA   SOCS7   NR1D1   STAT3
PSME3   DUSP3   SPOP    LRRC59  TOB1    MPO     PPM1D   TLK2    H3F3B   EXOC7
JMJD6   SLC26A11        NPLOC4  TGIF1   TUBB6   DSG3    PMAIP1  TMX3    LMNB2   EEF2
XAB2    ZNF426  PIN1    ZNF627  ZNF563  DCAF15  AKAP8L  ZFP36   DEDD2   MEGF8
PHLDB3  ZNF225  PPP1R37 PRKD2   ZNF616  ZNF766  CNOT3   ZNF587  CENPB   PROCR
DNTTIP1 VAPB    C20orf151       C20orf20        TMEM50B GART    ATP6V1E1        NF2
SREBF2  CDKL5   SMC1A   HUWE1   MSN     PHKA1   TTC3P1  EIF4A1P10       PSMD10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
Tissue: Muscle_Skeletal=>Skin_Sun_Exposed_Lower_leg     Type:   cluster
SourceGene:     PROCR(ENSG00000101000.3)
TargetGeneSet:  SKI     ICMT    ZBTB48  PGD     PEX14   FBLIM1  RP11    SEPN1   RP1
EIF2C1  INSL3   CTPS    MUTYH   RP4     ALX3    CTTNBP2NL       MAN1A2  CDC42SE1
CHTOP   SNORA58 SHC1    ASH1L   ARHGEF11        UCK2    MPZL1   ABL2    ATP2B4
TP53BP2 GALNT2  ATAD2B  ADCY3   ASXL2   GPR113  SLC5A6  CAD     YPEL5   ASB3
AFTPH   TEX261  UGGT1   TMEM163 ACVR2A  FMNL2   MTX2    CWC22   PIKFYVE RNF25
SGPP2   COL4A4  HDAC4   ARL8B   TBC1D5  HIGD1A  CCDC12  PRKAR2A ZNF654  CLDND1
KIAA2018        NCK1    PIK3CB  UBQLN4P1        GPR87   BCL6    HES1    LETM1
ZBTB49  MRFAP1L1        TBC1D14 PCDH7   TEC     CHIC2   GSX2    CLOCK   RASGEF1B
HELQ    SGMS2   ANAPC10 LSM6    UBE2B   ANKHD1  FBXO38  NDST1   LARP1   MAT2B
SLC2A3P1        NEURL1B CTB     DUSP1   ARL10   NSD1    CANX    ZKSCAN4 UHRF1BP1
DEFA6   FBXO9   PTP4A1  PHF3    MDN1    MCM9    CCDC28A PPIL4   FOXK1   ARL4A
CCT6P3  ZNF394  FAM200A C7orf59 EPHB4   PRKRIP1 DNAJB9  IMPDH1  KLHDC10 HIPK2   RHEB
GS1     KIAA1456        KCNU1   PRKDC   ATP6V1H TMEM68  PTDSS1  POP1    PABPC1
TTC35   ST3GAL1 CTA     EPPK1   RGP1    FAM120A GRIN3A  SNX33   MIR181A2HG
NUP188  TOR1B   WDR5    NACC2   KLF6    OTUD1   RAB18   C10orf25        ZFAND4
P4HA1   C10orf28        TAF5    DUSP5   PPP2R2D HRAS    ZBED5   TUT1    CTSC
AMOTL1  C11orf63        SIAE    SRPR    ERC1    TULP3   CDKN1B  ITPR2   FKBP11
TUBA1C  TMBIM6  ACVR1B  SARNP   DDIT3   SLC25A3 EID3    C12orf76        UNC119B
RSRC2   RPL21   AKAP11  MYCBP2  IPO5    CHAMP1  RNF31   TSSK6   BNIP3P1 ARF6
CHMP4BP1        MED6    ANGEL1  ALKBH1  SPATA7  BTBD7   WARS    TRAF3   CDC42BPB
HERC2   C15orf24        RNF111  CLK3    CTD     UBN1    FAM86A  NOMO2   SMG1    COG7
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NFATC2IP        KCTD13  PRSS8   ARMC5   CNOT1   CMTM4   CBFB    PSKH1   CDH1
GABARAPL2       TERF2IP MAP1LC3B        ZNF778  GLOD4   C17orf48        TOM1L2
MYO15A  USP22   NF1     LRRC37B RHOT1   NLE1    ACACA   SOCS7   NR1D1   STAT3
PSME3   DUSP3   SPOP    LRRC59  TOB1    MPO     PPM1D   TLK2    H3F3B   EXOC7
JMJD6   SLC26A11        NPLOC4  TGIF1   TUBB6   DSG3    PMAIP1  TMX3    LMNB2   EEF2
XAB2    ZNF426  PIN1    ZNF627  ZNF563  DCAF15  AKAP8L  ZFP36   DEDD2   MEGF8
PHLDB3  ZNF225  PPP1R37 PRKD2   ZNF616  ZNF766  CNOT3   ZNF587  CENPB   PROCR
DNTTIP1 VAPB    C20orf151       C20orf20        TMEM50B GART    ATP6V1E1        NF2
SREBF2  CDKL5   SMC1A   HUWE1   MSN     PHKA1   TTC3P1  EIF4A1P10       PSMD10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
Tissue: Muscle_Skeletal=>Skin_Sun_Exposed_Lower_leg     Type:   asymmetric
SourceGene:     RBPJL(ENSG00000124232.6)
TargetGeneSet:  CELA2A  CELA3B  CELA3A  REG1B   REG1A   HIST1H2BL       CLPS    CGA
CPA2    CPA1    PRSS1   PRSS3P1 PNLIP   PNLIPRP1        PNLIPRP2        RPL29P25
PLA2G1B GP2     MT1H    CTRB2   CTRB1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0007586      5.69496585169008e-13    103.193519351935        0.14331188153069
8       109     digestion
GO:0044241      2.88633145415972e-09    349.6   0.0197218185592693      4       15
lipid digestion
GO:0022617      1.33863255514118e-05    81.8125 0.0473323645422462      3       36
extracellular matrix disassembly
Tissue: Muscle_Skeletal=>Skin_Sun_Exposed_Lower_leg     Type:   cluster
SourceGene:     RP11-439E19.1(ENSG00000225300.1)
TargetGeneSet:  RP11    FOXE1   C4BPAP2 REL     FAM126B CFLAR   GPBAR1  POC1A
ITGB5-AS1       STAG1   ECT2    CRYGS   RAC1P2  LNX1-AS1        CCNA2   FAM160A1
KIFC1   PRKAR1B ANLN    MIR671  XKR6    EXOSC3  TCEB2P4 AGAP7   AFAP1L2 GVINP1
INCENP  THSD1P1 MYCBP2-AS2      BUB1B   UBE2Q2  C15orf42        PRC1    NPIP
HEXIM2  FAM108A5P       GSTT2   FGD1    KIF4A   MED12
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0051301      4.07559802103047e-07    15.7466216216216        0.750674693792817
8       452     cell division
GO:0000910      1.61460133934954e-05    31.86   0.156113763753373       4       94
cytokinesis
GO:0000280      1.79929748081699e-05    13.6463178294574        0.581274652273199
6       350     nuclear division
GO:0007067      1.79929748081699e-05    13.6463178294574        0.581274652273199
6       350     mitosis
Tissue: Skin_Sun_Exposed_Lower_leg=>Muscle_Skeletal     Type:   asymmetric
SourceGene:     RPL32P29(ENSG00000244270.1)
TargetGeneSet:  SRM     PKP1    QARS    RP11    WDR43   POLR1A  SS18L2  LETM1   GUF1
SCFD2   SNRNP48 RP1     AIMP2   TRGV4   GLIS3   TRUB2   PDCD11  DUSP5   CCDC59
ANAPC5  WARS    SAT2    ELAC2   FARSA   PSMF1   ATRN    RAB22A  RRP1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0034660      1.67741032307719e-08    24.0373752389042        0.493045463981731
8       285     ncRNA metabolic process
GO:0006399      5.74670433869465e-08    37.9663865546218        0.216248010518303
6       125     tRNA metabolic process
GO:0006418      1.2875089575768e-06     62.2597402597403        0.0830392360390284
4       48      tRNA aminoacylation for protein translation
GO:0043038      1.64778958528933e-06    58.273556231003 0.0882291882914677      4
51      amino acid activation
GO:0043039      1.64778958528933e-06    58.273556231003 0.0882291882914677      4
51      tRNA aminoacylation
Tissue: Muscle_Skeletal=>Skin_Sun_Exposed_Lower_leg     Type:   cluster
SourceGene:     SEPT10P1(ENSG00000253541.1)
TargetGeneSet:  RPS8    IPP     HBXIP   BRP44   ACP1    ERLEC1  REL     SENP2
CXCR2   THOC7   PCNP    RP11    PARL    RPS3A   ZDHHC11 VTA1    BRP44L  RPS3AP26
ZNF277  CTD     DCTN6   PAF1    RPS6    RP13    ATP6V1G1        CUL2    ANAPC16
FAM204A MUC5AC  TMPRSS5 HELB    ARL1    GPN3    GTF3A   MEG8    RPS3AP6 RPL26
RPL17   ARX     VBP1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022415      8.04580785927588e-07    17.0434782608696        0.539755034253685
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7       260     viral reproductive process
GO:0006415      1.11526350705577e-06    33.3372093023256        0.18891426198879
5       91      translational termination
GO:0006414      2.26931234975104e-06    28.642  0.21797799460245        5       105
translational elongation
GO:0006614      2.26931234975104e-06    28.642  0.21797799460245        5       105
SRP-dependent cotranslational protein targeting to membrane
GO:0006613      2.37821394029656e-06    28.3564356435644        0.220053975503425
5       106     cotranslational protein targeting to membrane
GO:0045047      2.37821394029656e-06    28.3564356435644        0.220053975503425
5       106     protein targeting to ER
GO:0072599      2.37821394029656e-06    28.3564356435644        0.220053975503425
5       106     establishment of protein localization to endoplasmic reticulum
GO:0072594      3.29101373818799e-06    17.9583333333333        0.423500103799045
6       204     establishment of protein localization to organelle
GO:0070972      4.03532583692599e-06    25.3238938053097        0.244965746315134
5       118     protein localization to endoplasmic reticulum
GO:0000184      4.20622731218036e-06    25.1    0.24704172721611        5       119
nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019058      6.73288848653153e-06    15.7733333333333        0.479551588125389
6       231     viral infectious cycle
GO:0019080      1.34541121326142e-05    19.5547945205479        0.313473116047332
5       151     viral genome expression
GO:0019083      1.34541121326142e-05    19.5547945205479        0.313473116047332
5       151     viral transcription
GO:0006413      1.38916231216778e-05    19.4204081632653        0.315549096948308
5       152     translational initiation
GO:0006612      1.43401731253634e-05    19.2878378378378        0.317625077849284
5       153     protein targeting to membrane
GO:0043624      1.43401731253634e-05    19.2878378378378        0.317625077849284
5       153     cellular protein complex disassembly
GO:0043241      1.67554828197996e-05    18.6509803921569        0.328004982354162
5       158     protein complex disassembly
Tissue: Skin_Sun_Exposed_Lower_leg=>Muscle_Skeletal     Type:   asymmetric
SourceGene:     SHROOM1(ENSG00000164403.9)
TargetGeneSet:  C1orf144        CATSPER4        SFN     MACF1   C1orf50 KIAA0494
S100A4  TNFSF13B        RP11    CENPO   DYSF    GPR155  ILKAP   HSPBAP1 TMEM108
SCARNA7 WDR1    MAP1B   TXNDC15 CTNNA1  PCDHB14 NDST1   HIST1H2AG       CYP51A1 BPGM
NUP205  EXTL3   SFRP1   TTC35   MYOF    BNIP3   7SK     SLC43A3 TTC9C   MYEOV
SLC6A13 CDKN1B  BNIP3P1 HSPA2   AHNAK2  YPEL3   CDH11   NRN1L   PFAS    KRT16
TUBB6   SMARCA4 ZNF211  JPH2    COL18A1 NF2     RP3     RNF128  BGN
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
Tissue: Whole_Blood=>Muscle_Skeletal    Type:   asymmetric
SourceGene:     BCAN(ENSG00000132692.12)
TargetGeneSet:  GABRD   RP3     ERMN    SCN2A   MOBP    CAMKV   CTB     CPLX2
RPL7L1P3        TMEM130 RP11    VAT1    NEFL    DIRAS2  GRIN1   VPS26A  INA     BUB3
CEND1   SLC1A2  VAT1L   RUNDC3A GFAP    SYT4    LILRB3  SNAP25  SLC12A5 MYO18B
SEPT3   MLC1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006836      1.30506678399032e-06    33.0401662049861        0.197633381772888
5       119     neurotransmitter transport
GO:0001505      1.5371969226498e-06     31.9112399643176        0.20427652065601
5       123     regulation of neurotransmitter levels
GO:0001504      6.97436335720473e-06    102.907142857143        0.0381980485779531
3       23      neurotransmitter uptake
GO:0045104      1.02056064378552e-05    89.4658385093168        0.0431804027402948
3       26      intermediate filament cytoskeleton organization
GO:0045103      1.14687963909998e-05    85.7321428571429        0.0448411874610754
3       27      intermediate filament-based process
Tissue: Whole_Blood=>Muscle_Skeletal    Type:   asymmetric
SourceGene:     C6orf48(ENSG00000204387.7)
TargetGeneSet:  C1orf159        HECTD3  CYP4A22 RP11    INADL   DPYD    ATP5F1
HIST2H2BE       MTX1    FAM189B ACBD6   TSNAX   CEP170  TRMT61B C1D     TXNDC9
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NIF3L1  NDUFB3  ERBB4   ABCB6   PRRT3-AS1       SATB1   NR1D2   OXSM    GRM2
FAM208A UBXN7-AS1       MAN2A1  ARHGEF37        MRPL22  ARL10   HIST1H1E
MRPS18B TAF11   TEAD3   C6orf226        RRP36   DST     C6orf162        RTN4IP1
KPNA5   HECA    AIMP2   NDUFA4  PMPCB   AGAP3   DEFB1   PCM1    GDAP1   ZNF704
SMARCA2 MPDZ    FANCG   TESK1   STXBP1  FNBP1   ARHGAP21        SGMS1   SUPV3L1
RNF141  TEAD1   MPPED2  PEX16   PHF21A  PACS1   RBM4B   TEX12   APOA4   CBL     RARG
AVIL    TMEM19  MRPS31  MED4-AS1        TPP2    PLEK2   WDR25   LPCAT4  C15orf44
ETFA    MRPL46  MRPL28  PKD1    NOMO2   MAZ     NOD2    CIAPIN1 RP1     ZBTB4
COX10   GIT1    HSD17B1P1       PYCR1   NDUFV2  PQLC1   ABCA7   UQCR11  GIPC3
PGPEP1  RELB    PPP2R1A LINC00493       CDK5RAP1        RP3     NFATC2  ATP9A
FAM209B ITSN1   CTA     TMEM184B        CBX6    SMARCA1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      1.73404809983961e-06    14.0344101123596        0.577953082831638
7       96      respiratory electron transport chain
GO:0022900      1.58829521297848e-05    9.80895669291339        0.806726178119161
7       134     electron transport chain
Tissue: Whole_Blood=>Muscle_Skeletal    Type:   cluster
SourceGene:     C6orf48(ENSG00000204387.7)
TargetGeneSet:  C1orf159        HECTD3  CYP4A22 RP11    INADL   DPYD    ATP5F1
HIST2H2BE       MTX1    FAM189B ACBD6   TSNAX   CEP170  TRMT61B C1D     TXNDC9
NIF3L1  NDUFB3  ERBB4   ABCB6   PRRT3-AS1       SATB1   NR1D2   OXSM    GRM2
FAM208A UBXN7-AS1       MAN2A1  ARHGEF37        MRPL22  ARL10   HIST1H1E
MRPS18B TAF11   TEAD3   C6orf226        RRP36   DST     C6orf162        RTN4IP1
KPNA5   HECA    AIMP2   NDUFA4  PMPCB   AGAP3   DEFB1   PCM1    GDAP1   ZNF704
SMARCA2 MPDZ    FANCG   TESK1   STXBP1  FNBP1   ARHGAP21        SGMS1   SUPV3L1
RNF141  TEAD1   MPPED2  PEX16   PHF21A  PACS1   RBM4B   TEX12   APOA4   CBL     RARG
AVIL    TMEM19  MRPS31  MED4-AS1        TPP2    PLEK2   WDR25   LPCAT4  C15orf44
ETFA    MRPL46  MRPL28  PKD1    NOMO2   MAZ     NOD2    CIAPIN1 RP1     ZBTB4
COX10   GIT1    HSD17B1P1       PYCR1   NDUFV2  PQLC1   ABCA7   UQCR11  GIPC3
PGPEP1  RELB    PPP2R1A LINC00493       CDK5RAP1        RP3     NFATC2  ATP9A
FAM209B ITSN1   CTA     TMEM184B        CBX6    SMARCA1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      1.73404809983961e-06    14.0344101123596        0.577953082831638
7       96      respiratory electron transport chain
GO:0022900      1.58829521297848e-05    9.80895669291339        0.806726178119161
7       134     electron transport chain
Tissue: Whole_Blood=>Muscle_Skeletal    Type:   asymmetric
SourceGene:     LINC00422(ENSG00000224429.1)
TargetGeneSet:  KLHL21  CAMTA1  RP11    UBE2T   TMEM183A        JMJD4   RAB4A
ROCK2   EML6    MRPL30  CALCRL  TMEM42  SACM1L  PABPC1P10       TMED11P C4orf26
SKIV2L2 PTCD2   RAD50   GEMIN5  FARS2   C6orf62 BYSL    C6orf108        SNX14
SPDYE2  BPGM    RPL23AP53       TNFRSF10B       USP20   EXOSC2  DDB1    OVOL1
LOH12CR1        METTL7A B4GALNT1        CCL14   MAP1LC3B2       RCBTB2  NUBPL
SOCS6   ZBTB1   NEK9    DYNC1H1 VPS13C  MPI     DNAJA3  SBK1    LONP2   DYNC1LI2
HPR     ITGAE   TP53    TOM1L2  NLE1    MAPT    PNPO    PHOSPHO1        BCAS3
METTL4  SF3A2   HMG20B  BCL2L12 LINC00085       PSMF1   BID     EFCAB6  PNPLA4
UTP14A  LINC00087       BRCC3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022613      1.71308029564519e-06    11.3644560208375        0.840772264895163
8       225     ribonucleoprotein complex biogenesis
GO:0071843      2.68784995566008e-06    10.6651609260305        0.893086983599751
8       239     cellular component biogenesis at cellular level
Tissue: Muscle_Skeletal=>Whole_Blood    Type:   asymmetric
SourceGene:     MTFR1(ENSG00000066855.10)
TargetGeneSet:  RP11    PCSK9   CD101   POLR3GL CD1A    FAM110C PCYOX1  WDR54
IL18R1  ATRIP   MAPKAPK3        DUSP7   B4GALT4 PRLR    ARG1    LFNG    GATS    IRF5
LGI3    DRP2    GPR26   C9orf106        ARID5B  MYOF    ACP2    ARRB1   C11orf75
SLC37A2 SMARCD1 HVCN1   IRG1    FLVCR2  ZG16B   CBFA2T3 RPL7AP64        ASGR1
KCTD15  IL4I1   LILRB1  LILRB4  ADRBK2  PIK3IP1 CYBB
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0031623      9.38615227242075e-06    35.9125 0.134523562383226       4       54
receptor internalization
GO:0006898      1.41258191587134e-05    19.0535857104772        0.313888312227527
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5       126     receptor-mediated endocytosis
Tissue: Whole_Blood=>Muscle_Skeletal    Type:   asymmetric
SourceGene:     NCR1(ENSG00000189430.7)
TargetGeneSet:  FAM41C  PLOD1   RP3     FOXO6   RP11    UBE2T   SOCS5   EPHA4
GAL3ST2 LAMB2   DCAF16  MAP1B   ZNF277  GPR85   C8orf12 SPAG6   CSDA    SOCS6
RABEP2  HPR     ARHGAP23        GNA13   HMG20B  RGS19   ABCG1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0031103      9.78813257602548e-06    90.9726315789474        0.0426268078333679
3       28      axon regeneration
GO:0031102      1.62213937516522e-05    75.7842105263158        0.0502387378036122
3       33      neuron projection regeneration
Tissue: Whole_Blood=>Muscle_Skeletal    Type:   asymmetric
SourceGene:     NEFM(ENSG00000104722.8)
TargetGeneSet:  VPS13D  CACNA1A KCNJ9   VSNL1   CTNNA2  MOBP    CAMKV   SYNPR
TAGLN3  SPP1    LSM6    GRIA2   CPLX2   CTA     SFT2D1  TMEM130 RP11    NEFL
STMN4   DIRAS2  GRIN1   VPS26A  OPALIN  PSD     INA     GPR123  SLC1A2  PRMT8   SCG5
CKMT1B  FBXL16  GFAP    SYT4    SLC8A2  BCAT2   SNAP25  POLR3F  SLC12A5 MLC1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006836      5.86618827844923e-06    23.2374918778428        0.263511175697184
5       119     neurotransmitter transport
GO:0001505      6.89686640537397e-06    22.4435028248588        0.272368694208013
5       123     regulation of neurotransmitter levels
GO:0048791      1.42319897105304e-05    961.2   0.00664313888312228     2       3
calcium ion-dependent exocytosis of neurotransmitter
Tissue: Whole_Blood=>Muscle_Skeletal    Type:   asymmetric
SourceGene:     OLAH(ENSG00000152463.10)
TargetGeneSet:  CORT    PADI2   WNT4    AKR1A1  GADD45A TMEM206 JMJD4   EBF3    XDH
SOCS5   UGP2    ELMOD3  OSBPL6  ICA1L   ERBB4   EPHA4   EFHD1   ARL8B   ZDHHC3
TEX264  ANKDD1B CTB     SNX14   AGPAT5  VPS13B  ST3GAL1 SH3GLB2 VPS26A  MICU1
PANK1   SORBS1  SLC18A2 DDB1    IL18    RPUSD4  COPS7A  METTL7A ABCC4   RP11    SBK1
COX6A2  ABR     TP53    TP53I13 NLE1    MAPT    PNPO    EXOC7   METTL4  SMAD7
CRLF1   RELB    NNAT    RP1     MORC4   MTMR1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:2000379      1.77754256999733e-06    56.8379446640316        0.0896823749221507
4       27      positive regulation of reactive oxygen species metabolic process
Tissue: Muscle_Skeletal=>Whole_Blood    Type:   asymmetric
SourceGene:     PGM5(ENSG00000154330.6)
TargetGeneSet:  RP11    IGKJ5   IGKC    IGKJ1   IGKV4-1 IGKV1-9 IGKV3-20
IGKV2-24        IGKV3D-20       ENOPH1  TRRAP   GML     GLDC    RIN2    IGHG2
IGHV2-5 MRPL38  IGLV5-45        IGLV2-23        IGLV3-16        IGLL5   IGLC3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006958      1.14392769649748e-12    327.159090909091        0.0415196180195142
6       50      complement activation, classical pathway
GO:0006956      4.8685606027542e-12     252.315789473684        0.0523147187045879
6       63      complement activation
GO:0002455      5.91430420577553e-12    243.728813559322        0.0539755034253685
6       65      humoral immune response mediated by circulating immunoglobulin
GO:0072376      2.49206776864283e-11    188.986842105263        0.0680921735520033
6       82      protein activation cascade
GO:0016064      1.59480560469431e-10    136.514285714286        0.0921735520033216
6       111     immunoglobulin mediated immune response
GO:0019724      1.87641587000686e-10    132.694444444444        0.0946647290844924
6       114     B cell mediated immunity
GO:0006959      2.8358439605752e-10     123.474137931034        0.101307867967615
6       122     humoral immune response
GO:0002449      1.89926442395287e-09    88.6832298136646        0.138675524185178
6       167     lymphocyte mediated immunity
GO:0002460      3.08500589580792e-09    81.5085714285714        0.150301017230641
6       181     adaptive immune response based on somatic recombination of immune
receptors built from immunoglobulin superfamily domains
GO:0002250      5.29263894340719e-09    74.203125       0.164417687357276       6
198     adaptive immune response
GO:0002443      7.75190211419840e-09    69.4341463414634        0.17521278804235
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6       211     leukocyte mediated immunity
GO:0002253      6.21116986012747e-08    48.2798634812287        0.248287315756695
6       299     activation of immune response
GO:0050778      1.99278675894729e-07    39.3324022346369        0.302262819182064
6       364     positive regulation of immune response
GO:0002252      2.81797064242895e-07    36.9973684210526        0.32053145111065
6       386     immune effector process
Tissue: Whole_Blood=>Muscle_Skeletal    Type:   asymmetric
SourceGene:     PI3(ENSG00000124102.4)
TargetGeneSet:  RP11    RCC2    UBR4    WNT4    LYPLA2  MYOM3   RP3     CSMD2
MACF1   IPO13   TMEM53  AKR1A1  CYP4A22 PDZK1IP1-AS1    MIR761  WDR63   MTX1
HAPLN2  HDGF    SLC26A9 TSNAX   SIPA1L2 C2orf43 XDH     UGP2    CEP68   MYO7B   GPD2
OSBPL6  COL4A4  COL4A3  PDE6D   ARL8B   PRRT3   PRRT3-AS1       NR1D2   OXSM    RP13
FAM212A BZW1P2  WHSC1   EGF     ANAPC10 PDGFC   CKMT2   ANKRD32 SLC12A2 ARHGEF37
MRPL22  TUBB    JARID2  HIST1H1E        FKBP5   TMEM217 CUL7    MUT     BACH2   GJA1
RNF217  PLAGL1  ELN     LIMK1   MCM7    AGPAT5  FDFT1   IDO1    ZNF704  IMPA1
ST3GAL1 ZFAT-AS1        OPLAH   TESK1   AQP7P2  SEMA4D  HSDL2   ASTN2   TRIM32
USP6NL  SGMS1   RHOBTB1 TSPAN15 PANK1   TCTN3   GALNTL4 TEAD1   PEX16   PACS1
RPUSD4  CD9     GRASP   SUOX    TMCC3   GPR133  MRPS31  ABCC4   TEP1    C14orf135
FLVCR2  FOXN3   TTC7B   C14orf80        LPCAT4  FAM174B NOMO1   NOMO3   NOMO2   MAZ
PRRT2   COX6A2  LDHD    RNF166  CTD     RP1     UBE2G1  USP6    SLC2A4  SHBG    TP53
ALDH3A1 KSR1    TCAP    KRT13   ABCA8   KCTD2   SYNGR2  ARHGAP28        PMAIP1  BCL2
ZNF516  ABCA7   KLF16   FAM108A1        TIMM44  CYP4F22 CRLF1   RELB    BBC3
SPHK2   TGM3    VSX1    NNAT    B4GALT5 MIR133A2        TIMP3   KAL1    EGFL6
MTMR1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0046902      1.61334629839148e-06    66.3472222222222        0.0930039443637119
4       12      regulation of mitochondrial membrane permeability
Tissue: Whole_Blood=>Muscle_Skeletal    Type:   cluster
SourceGene:     PI3(ENSG00000124102.4)
TargetGeneSet:  RP11    RCC2    UBR4    WNT4    LYPLA2  MYOM3   RP3     CSMD2
MACF1   IPO13   TMEM53  AKR1A1  CYP4A22 PDZK1IP1-AS1    MIR761  WDR63   MTX1
HAPLN2  HDGF    SLC26A9 TSNAX   SIPA1L2 C2orf43 XDH     UGP2    CEP68   MYO7B   GPD2
OSBPL6  COL4A4  COL4A3  PDE6D   ARL8B   PRRT3   PRRT3-AS1       NR1D2   OXSM    RP13
FAM212A BZW1P2  WHSC1   EGF     ANAPC10 PDGFC   CKMT2   ANKRD32 SLC12A2 ARHGEF37
MRPL22  TUBB    JARID2  HIST1H1E        FKBP5   TMEM217 CUL7    MUT     BACH2   GJA1
RNF217  PLAGL1  ELN     LIMK1   MCM7    AGPAT5  FDFT1   IDO1    ZNF704  IMPA1
ST3GAL1 ZFAT-AS1        OPLAH   TESK1   AQP7P2  SEMA4D  HSDL2   ASTN2   TRIM32
USP6NL  SGMS1   RHOBTB1 TSPAN15 PANK1   TCTN3   GALNTL4 TEAD1   PEX16   PACS1
RPUSD4  CD9     GRASP   SUOX    TMCC3   GPR133  MRPS31  ABCC4   TEP1    C14orf135
FLVCR2  FOXN3   TTC7B   C14orf80        LPCAT4  FAM174B NOMO1   NOMO3   NOMO2   MAZ
PRRT2   COX6A2  LDHD    RNF166  CTD     RP1     UBE2G1  USP6    SLC2A4  SHBG    TP53
ALDH3A1 KSR1    TCAP    KRT13   ABCA8   KCTD2   SYNGR2  ARHGAP28        PMAIP1  BCL2
ZNF516  ABCA7   KLF16   FAM108A1        TIMM44  CYP4F22 CRLF1   RELB    BBC3
SPHK2   TGM3    VSX1    NNAT    B4GALT5 MIR133A2        TIMP3   KAL1    EGFL6
MTMR1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0046902      1.61334629839148e-06    66.3472222222222        0.0930039443637119
4       12      regulation of mitochondrial membrane permeability
Tissue: Whole_Blood=>Muscle_Skeletal    Type:   asymmetric
SourceGene:     PTN(ENSG00000105894.7)
TargetGeneSet:  CACNA1A RP4     ERMN    SLC16A14        SOWAHA  CPLX2   TMEM130 RP11
NEFL    GRIN1   INA     SLC1A2  SYT1    KLHDC1  RPL5P3  RUNDC3A ZNF615  TTYH1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0060052      1.56486111333871e-05    524.836363636364        0.00629714206629299
2       7       neurofilament cytoskeleton organization
Tissue: Muscle_Skeletal=>Whole_Blood    Type:   asymmetric
SourceGene:     REM1(ENSG00000088320.3)
TargetGeneSet:  SYT12   PPP1R12B        RP11    PRKCD   RPN1    PAICS   DAPP1
RTN3P1  CDHR2   CANX    OGFRL1  CDK6    PDIA4   RNF32   ANXA1   RPL12P8 COMTD1
TRIM3   GDF3    ZNF592  STUB1   C16orf88        TP53    SCRN2   MIS18A-AS1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0090398      3.88690786963359e-06    128.660714285714        0.031762507784928
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3       27      cellular senescence
Tissue: Whole_Blood=>Muscle_Skeletal    Type:   asymmetric
SourceGene:     RP11-184M15.1(ENSG00000248187.1)
TargetGeneSet:  RP3     ERI3    TAL1    GADD45A RD3     LPGAT1  RP11    ROCK2
OXSR1   ANKRD23 CDCA7   EPHA4   FAM132B LAMB2   SLC41A3 DCUN1D1 BHMT    HUS1B
TCF21   ELMO1   CA1     KDM4C   FTH1P12 BICC1   METTL7A BRI3BP  SOCS6   CHRNA7
GCHFR   DYX1C1-CCPG1    SOCS1   FBXL19  ABR     NLE1    MED13   SLC25A19
ARHGAP28        SOGA2   GALNT1  ELAVL1  BBC3    BMP2    BCR     TOM1    CASK
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0048708      2.23270655358904e-06    53.0175115207373        0.0944571309943949
4       39      astrocyte differentiation
Tissue: Muscle_Skeletal=>Whole_Blood    Type:   asymmetric
SourceGene:     RP11-36C20.1(ENSG00000240376.1)
TargetGeneSet:  CELA2A  CELA3B  CELA3A  LAMP3   MUC21   CPA2    CPA1    PRSS1
PRSS3P2 PNLIP   PNLIPRP2        TEX12   RP11    SNHG9   KREMEN2 CTRB2   POLR2A  SYCN
OTUD5   PIN4
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0007586      1.28159346036606e-07    57.411858974359 0.128226420316933       5
109     digestion
Tissue: Muscle_Skeletal=>Whole_Blood    Type:   asymmetric
SourceGene:     RP11-543B16.1(ENSG00000234004.2)
TargetGeneSet:  RP11    MYT1L   VSNL1   SCN2A   DNER    KIF1A   SLC6A1  TAGLN3
TECRL   GRIA2   CTNND2  GABRB2  GABRA1  GABRG2  ODZ2    SNCB    NRSN1   BEND6
SNAP91  FABP7   MLLT4   STMN2   SH3GL2  DIRAS2  OPALIN  BAD     OPCML   PRMT8
FAIM2   CTD     CKMT1B  ASPHD1  CBLN1   NPTX1   SYT4    ST8SIA3 HSBP1L1 TUBB4A
ELAVL3  UNC13A  TCF15   SNAP25  GAL3ST1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0051932      7.95299767355556e-07    70.5343137254902        0.0736281226212719
4       28      synaptic transmission, GABAergic
GO:0007270      3.19865250630032e-06    26.1591821832786        0.231402671095426
5       88      neuron-neuron synaptic transmission
GO:0007214      1.33208946821051e-05    82.2742857142857        0.0473323645422462
3       18      gamma-aminobutyric acid signaling pathway
Tissue: Whole_Blood=>Muscle_Skeletal    Type:   asymmetric
SourceGene:     SLC6A1(ENSG00000157103.6)
TargetGeneSet:  CACNA1A KCNJ9   CNTN2   RP11    MYT1L   VSNL1   PTPRN   ASB1    MOBP
CAMKV   CTD     SYNPR   TAGLN3  GUF1    GRIA2   GPM6A   SOWAHA  CTB     CPLX2
NRSN1   CTA     MOG     HCG17   7SK     TMEM130 SDSL    NEFL    STMN2   DIRAS2
GRIN1   VPS26A  OPALIN  INA     SLC1A2  NRGN    KIF5A   SYT1    GABRB3  FBXL16
LONP2   NEUROD2 RUNDC3A GFAP    PNPO    SYT4    SCARNA17        MAST1   PSMF1
SNAP25  SLC12A5 CBX6    APOBEC3H        MLC1    ZCCHC12
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006836      1.30577705071748e-06    20.5142310452045        0.35409314234309
6       119     neurotransmitter transport
GO:0001505      1.58500294118228e-06    19.8073458073458        0.365995432842018
6       123     regulation of neurotransmitter levels
GO:0007269      5.34763290410581e-06    23.2732293697206        0.255899245726939
5       86      neurotransmitter secretion
Tissue: Whole_Blood=>Muscle_Skeletal    Type:   asymmetric
SourceGene:     SNAP91(ENSG00000065609.8)
TargetGeneSet:  VPS13D  STMN1   CACNA1A CELF3   RP11    MYT1L   VSNL1   MZT2A   ERMN
SCN2A   PTPRN   SLC16A14        ASB1    MOBP    CTD     TAGLN3  GUF1    GRIA2
CPLX2   CTA     MOG     RP1     TMEM130 NEFL    STMN2   GRIN1   VPS26A  OPALIN  INA
NRAP    CALY    CEND1   SLC1A2  PRMT8   USP5    FAM186B SYT1    C14orf21
KLHDC1  SYNDIG1L        TMEM179 SCG5    RPL5P3  GABARAPL3       FBXL16  TOM1L2  BLMH
NEUROD2 DUSP3   RUNDC3A GFAP    C18orf34        SYT4    MAST1   TTYH1   SNAP25
SLC12A5 POLR3H  SEPT3   LDOC1L
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006836      1.72131677403843e-06    19.4594962559564        0.370562590824164
6       119     neurotransmitter transport
GO:0001505      2.08841173625885e-06    18.7889546351085        0.383018476230019
6       123     regulation of neurotransmitter levels
GO:0007269      6.72428868269139e-06    22.1064814814815        0.267801536225867
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5       86      neurotransmitter secretion
Tissue: Whole_Blood=>Muscle_Skeletal    Type:   asymmetric
SourceGene:     ZNF276(ENSG00000158805.7)
TargetGeneSet:  PAFAH2  CERS2   PYGO2   SLAMF7  FCGR2A  PTPRC   PLEK    MGAT5
TMEFF2  RP11    GJA1    GIMAP2  RNF141  SPI1    CD3E    REP15   ARHGAP9 LCP1
LINC00441       RCBTB2  MCTP2   SPN     C16orf54        CORO1A  DUSP14  SOCS3
HMHA1   JAK3    TYROBP  SERTAD3 BCL3    C19orf76        ZNF628  HCK     ITGB2   RAC2
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0042102      1.54330267381976e-07    51.1831789023521        0.127880423500104
5       66      positive regulation of T cell proliferation
GO:0002252      4.68992648981497e-07    14.8624338624339        0.747906719258183
8       386     immune effector process
GO:0050671      1.01426167023644e-06    34.2379359770664        0.186007888727424
5       96      positive regulation of lymphocyte proliferation
GO:0032946      1.06796307774564e-06    33.8634215500945        0.187945470901668
5       97      positive regulation of mononuclear cell proliferation
GO:0046649      1.11743181211452e-06    13.1745882352941        0.838973081447651
8       433     lymphocyte activation
GO:0070665      1.24265332334512e-06    32.7871853546911        0.1937582174244 5
100     positive regulation of leukocyte proliferation
GO:0042129      1.30563684756582e-06    32.4433876811594        0.195695799598644
5       101     regulation of T cell proliferation
GO:0042110      1.90053653913798e-06    15.0758547008547        0.618088713583835
7       319     T cell activation
GO:0042098      2.81950870580034e-06    27.5298191612159        0.228634696560792
5       118     T cell proliferation
GO:0050865      3.07598683139619e-06    13.9751984126984        0.664590685765691
7       343     regulation of cell activation
GO:0050867      5.46715383363551e-06    16.537296037296 0.465019721818559       6
240     positive regulation of cell activation
GO:0050670      7.48770937435757e-06    22.3396934626212        0.279011833091136
5       144     regulation of lymphocyte proliferation
GO:0032944      7.74480916145515e-06    22.1785714285714        0.28094941526538
5       145     regulation of mononuclear cell proliferation
GO:0007229      8.43117066891122e-06    37.3932291666667        0.131755587848592
4       68      integrin-mediated signaling pathway
GO:0070663      9.13597438646053e-06    21.4062968515742        0.2906373261366 5
150     regulation of leukocyte proliferation
GO:0030217      1.10557334963855e-05    20.5470774546502        0.302262819182064
5       156     T cell differentiation
GO:0051249      1.40216944209456e-05    13.927797833935 0.548335755311051       6
283     regulation of lymphocyte activation
GO:0050870      1.72487052878309e-05    18.6707700366684        0.331326551795723
5       171     positive regulation of T cell activation
GO:0046651      1.77414845089915e-05    18.5576672741474        0.333264133969967
5       172     lymphocyte proliferation
GO:0032943      1.87599746165927e-05    18.3354772317983        0.337139298318455
5       174     mononuclear cell proliferation
Tissue: Skin_Sun_Exposed_Lower_leg=>Nerve_Tibial        Type:   asymmetric
SourceGene:     C11orf51(ENSG00000110200.4)
TargetGeneSet:  CROCCP3 RPL11   TMEM57  NASP    RPL5    TOMM20  RPL31   RPL15
RPL14   RPL24   RP11    ZNF718  GALNT7  FAM149A KLKB1   EEF1A1P19       CAMLG
RPS14   EEF1A1  BCKDHB  MKRN1   SSPO    RPS20   RPL30   EIF3H   EEF1D   SCRIB   RPS6
TCEA1P1 CCL21   RPL12   LDB1    RPLP2   RPL27A  FAU     RPS25   TMEM136 ATP5G2
RPL41   RPL14P1 U8      RPL4    ALDH3A1 RPL23A  RPL17   RPL19   KPNA2   MUM1
CEP89   PTOV1   EIF3L   RANGAP1 TTLL12  RPS4X   RPL10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      3.93523516651412e-40    184.515297906602        0.341498858210504
24      105     translational elongation
GO:0006415      3.22333858429592e-37    182.823188405797        0.295965677115771
22      91      translational termination
GO:0006413      6.67234534614046e-36    116.380434782609        0.494360251885683
24      152     translational initiation
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GO:0006614	1.09240280307253e-35	151.837108433735	0.341498858210504
22	105	SRP-dependent cotranslational protein targeting to membrane
GO:0006613	1.37621165623957e-35	150.019047619048	0.3447512282887	22
106	cotranslational protein targeting to membrane
GO:0045047	1.37621165623957e-35	150.019047619048	0.3447512282887	22
106	protein targeting to ER
GO:0072599	1.37621165623957e-35	150.019047619048	0.3447512282887	22
106	establishment of protein localization to endoplasmic reticulum
GO:0070972	1.84238264441215e-34	131.156666666667	0.383779669227043
22	118	protein localization to endoplasmic reticulum
GO:0000184	2.25647386992946e-34	129.795463917526	0.387032039305238
22	119	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080	6.40124123854654e-32	97.3798449612403	0.491107881807487
22	151	viral genome expression
GO:0019083	6.40124123854654e-32	97.3798449612403	0.491107881807487
22	151	viral transcription
GO:0006612	8.71228281547153e-32	95.8796946564886	0.497612621963878
22	153	protein targeting to membrane
GO:0043624	8.71228281547153e-32	95.8796946564886	0.497612621963878
22	153	cellular protein complex disassembly
GO:0043241	1.84769533836988e-31	92.3223529411765	0.513874472354854
22	158	protein complex disassembly
GO:0000956	8.85202173874874e-31	85.3480272108844	0.549650543215002
22	169	nuclear-transcribed mRNA catabolic process
GO:0072594	9.40156975132788e-31	75.3059392265193	0.663483495951837
23	204	establishment of protein localization to organelle
GO:0034623	1.7402654742189e-30	82.5115789473684	0.565912393605979
22	174	cellular macromolecular complex disassembly
GO:0006402	2.94429546497264e-30	80.3733333333333	0.57892187391876
22	178	mRNA catabolic process
GO:0032984	3.3512531851011e-30	79.855796178344	0.582174243996955	22
179	macromolecular complex disassembly
GO:0006401	7.56836305532536e-29	68.3851366120219	0.666735866030033
22	205	RNA catabolic process
GO:0019058	1.14795816151814e-27	59.7684210526316	0.75129748806311
22	231	viral infectious cycle
GO:0071845	2.42024313434875e-27	51.9299169859515	0.92367310220746
23	284	cellular component disassembly at cellular level
GO:0022411	3.36061533517501e-27	51.1316037735849	0.936682582520241
23	288	cellular component disassembly
GO:0022415	1.66022616153413e-26	52.378487394958	0.845616220330773	22
260	viral reproductive process
GO:0006605	3.2150454592583e-25	35.3183842883175	1.54162341706456
25	474	protein targeting
GO:0033365	1.03305378704065e-23	32.4314902682289	1.53837104698637
24	473	protein localization to organelle
GO:0016032	3.25821142747066e-21	28.6666666666667	1.46681890526607
22	451	viral reproduction
GO:0000028	6.40494922747351e-07	327.295454545455	0.0195142204691717
3	6	ribosomal small subunit assembly
GO:0042273	6.94949201671952e-06	109.05303030303	0.0390284409383434	3
12	ribosomal large subunit biogenesis
GO:0022613	7.48271332996681e-06	11.3878440366972	0.731783267593938
7	225	ribonucleoprotein complex biogenesis
GO:0042254	8.23103658715123e-06	14.5942350332594	0.484603141651097
6	149	ribosome biogenesis
GO:0071843	1.10960357636727e-05	10.6900862068966	0.777316448688672
7	239	cellular component biogenesis at cellular level
GO:0042255	1.75287177006372e-05	75.4772727272727	0.0520379212511245
3	16	ribosome assembly
Tissue: Skin_Sun_Exposed_Lower_leg=>Nerve_Tibial	Type:	asymmetric
SourceGene:	CIB2(ENSG00000136425.8)
TargetGeneSet:	RPL22	RPL11	RPS27	GAS5	ASTN1	UBC	RPL31	MLPH	XPC
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RPL14   KPNA1   RP11    PLD1    RPL34   RPS3A   HOMER1  EIF4EBP3        EFCAB9
RPL10A  VN1R42P RPS20   RPL30   RPL27A  DDB2    PITPNM1 RPS25   NCKAP5L PFDN5
RPL41   NACA    CYP27B1 SSH1    RPS3AP6 SEC11A  RPS15A  NFAT5   RPL26   C17orf48
RPL23A  RPL17   RPL19   WIZ     UBA52   FTL     RPS4X   HAUS7   RPL10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006614      3.93238183764693e-40    236.418220946915        0.2906373261366 23
105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      5.01637705209728e-40    233.553508150248        0.293405300671234
23      106     cotranslational protein targeting to membrane
GO:0045047      5.01637705209728e-40    233.553508150248        0.293405300671234
23      106     protein targeting to ER
GO:0072599      5.01637705209728e-40    233.553508150248        0.293405300671234
23      106     establishment of protein localization to endoplasmic reticulum
GO:0006415      2.54414903770958e-39    254.045088566828        0.25188568265172
22      91      translational termination
GO:0070972      7.72410679129691e-39    203.881114551084        0.326620995086845
23      118     protein localization to endoplasmic reticulum
GO:0006414      8.67876567754578e-38    210.987951807229        0.2906373261366 22
105     translational elongation
GO:0000184      1.80445658011118e-36    180.359679266896        0.329388969621479
22      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006413      4.31958891118867e-36    149.788417692658        0.420732129264411
23      152     translational initiation
GO:0006612      5.07803517317897e-36    148.625791855204        0.423500103799045
23      153     protein targeting to membrane
GO:0019080      5.19616739139964e-34    135.316106804479        0.417964154729776
22      151     viral genome expression
GO:0019083      5.19616739139964e-34    135.316106804479        0.417964154729776
22      151     viral transcription
GO:0043624      7.07876921231269e-34    133.23155216285 0.423500103799045       22
153     cellular protein complex disassembly
GO:0043241      1.50478167661709e-33    128.28839869281 0.437339976472216       22
158     protein complex disassembly
GO:0072594      5.6314287424571e-33     106.366590835229        0.564666805065393
23      204     establishment of protein localization to organelle
GO:0000956      7.24644259793017e-33    118.597127739985        0.467787696353194
22      169     nuclear-transcribed mRNA catabolic process
GO:0034623      1.42796062147389e-32    114.655701754386        0.481627569026365
22      174     cellular macromolecular complex disassembly
GO:0006402      2.42045501881131e-32    111.684472934473        0.492699467164902
22      178     mRNA catabolic process
GO:0032984      2.75630086898174e-32    110.965322009908        0.495467441699536
22      179     macromolecular complex disassembly
GO:0019058      1.1129298490132e-31     92.3837669683258        0.639402117500519
23      231     viral infectious cycle
GO:0006401      6.30120187678486e-31    95.0261080752884        0.567434779600028
22      205     RNA catabolic process
GO:0022415      1.86162517444779e-30    80.9138744105237        0.719673379004913
23      260     viral reproductive process
GO:0071845      1.50548546374765e-29    73.3491097588461        0.786104767836136
23      284     cellular component disassembly at cellular level
GO:0022411      2.09439452941768e-29    72.2215316315205        0.797176665974673
23      288     cellular component disassembly
GO:0006605      1.07853780536434e-27    51.826280623608 1.31201992941665        25
474     protein targeting
GO:0033365      4.97986219813e-26       46.6436525612472        1.30925195488202
24      473     protein localization to organelle
GO:0016032      7.30060770849561e-25    44.2013468938977        1.24835651512006
23      451     viral reproduction
GO:0042273      4.24829873259561e-06    129.747747747748        0.0332156944156114
3       12      ribosomal large subunit biogenesis
Tissue: Nerve_Tibial=>Skin_Sun_Exposed_Lower_leg        Type:   asymmetric
SourceGene:     EIF3M(ENSG00000149100.8)
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TargetGeneSet:  LAMTOR2 ACBD6   GLT25D2 KLHL12  RP11    ADCK3   NUP133  TOMM20  UBC
MZT2B   WDR75   GTF3C3  CNPPD1  TMEM111 HDAC11  FNDC3B  HAUS3   LIAS    NOA1
NUP54   ZNF622  BTF3    RPS14   HNRNPC  RPL10A  C6orf130        PSMB1   MRPS24
BUD31   MKRN1   HOOK3   C9orf123        RPS6    FAM95B1 AKR1C1  MGEA5   POLR2G  FAU
THYN1   C12orf57        PRKAG1  PWP1    SAP18   C14orf183       SPTB    C14orf2
GCHFR   LYSMD2  ANP32A  RPS2    RPS15A  NUPR1   BCKDK   GGNBP2  FN3KRP  ELP2
PRKCSH  ZNF826P SNRPD2  RPL13A  RPS5    NSFL1C  CRYZL1  SAMM50  EDA     IL13RA2
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006612      1.28973883831421e-11    24.5356807511737        0.592900145318663
11      153     protein targeting to membrane
GO:0043241      1.8325166667218e-11     23.6928193499622        0.612275967061103
11      158     protein complex disassembly
GO:0006415      6.1771917725899e-11     33.4242345614946        0.352639955712407
9       91      translational termination
GO:0032984      7.10308950550242e-11    20.7006613756614        0.693654418379351
11      179     macromolecular complex disassembly
GO:0006414      2.27284005861797e-10    28.5219414893617        0.406892256591239
9       105     translational elongation
GO:0006614      2.27284005861797e-10    28.5219414893617        0.406892256591239
9       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      2.47642470537799e-10    28.2259267383198        0.410767420939727
9       106     cotranslational protein targeting to membrane
GO:0045047      2.47642470537799e-10    28.2259267383198        0.410767420939727
9       106     protein targeting to ER
GO:0072599      2.47642470537799e-10    28.2259267383198        0.410767420939727
9       106     establishment of protein localization to endoplasmic reticulum
GO:0019080      2.71259836378899e-10    21.9765649090348        0.585149816621687
10      151     viral genome expression
GO:0019083      2.71259836378899e-10    21.9765649090348        0.585149816621687
10      151     viral transcription
GO:0072594      2.89516314673346e-10    17.9875647668394        0.790533527091551
11      204     establishment of protein localization to organelle
GO:0043624      3.08861291364601e-10    21.6661599270295        0.592900145318663
10      153     cellular protein complex disassembly
GO:0070972      6.50848000839002e-10    25.0974038649229        0.457269393121583
9       118     protein localization to endoplasmic reticulum
GO:0000184      7.02029640361192e-10    24.8675048355899        0.461144557470071
9       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0034623      1.0908891756791e-09     18.8639978791092        0.674278596636911
10      174     cellular macromolecular complex disassembly
GO:0006605      2.26412594476969e-09    10.0978260869565        1.83682790118331
14      474     protein targeting
GO:0006413      6.1746345430566e-09     19.0846600208302        0.589024980970175
9       152     translational initiation
GO:0022411      1.09352464497453e-08    12.4587244283995        1.11604733236454
11      288     cellular component disassembly
GO:0016032      1.24746289364511e-08    9.63369438249974        1.74769912116809
13      451     viral reproduction
GO:0000956      1.56302678744595e-08    17.0365691489362        0.654902774894471
9       169     nuclear-transcribed mRNA catabolic process
GO:0019058      1.67773738420351e-08    13.9425536100728        0.895162964500727
10      231     viral infectious cycle
GO:0033365      2.19498901115659e-08    9.15849342770475        1.83295273683482
13      473     protein localization to organelle
GO:0006402      2.45514522992741e-08    16.1190985773637        0.689779254030863
9       178     mRNA catabolic process
GO:0022415      5.14251305473823e-08    12.3    1.00754273060688        10      260
viral reproductive process
GO:0006401      8.30638180347452e-08    13.872231871472 0.794408691440039       9
205     RNA catabolic process
GO:0071845      1.17653160995401e-07    11.2035861631228        1.10054667497059
10      284     cellular component disassembly at cellular level
Tissue: Skin_Sun_Exposed_Lower_leg=>Nerve_Tibial        Type:   asymmetric
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SourceGene:     MMP27(ENSG00000137675.4)
TargetGeneSet:  TMEM201 RPL11   CDC42SE1        CCT3    RP11    URB2    CDC42EP3
RTKN    C2orf55 RPL31   RFX8    R3HDM1  HOXD8   RPL37A  OTOS    RPL32   CRTAP
RPL14   IFRD2   CCDC48  GPR160  PLD1    EIF4G1  RPL35A  LETM1   SOD3    UBA6
RPL34   CCT5    RPL37   EPB41L4A        EPB41L4A-AS1    CTD     LYRM4   HLA-C
PAQR8   CD109   ICA1    RPS20   SCRIB   LRRC14  KCNV2   RPS6    QSOX2   EGFL7
SNHG7   ABCA2   RPL13AP5        PTDSS2  RPLP2   RPS13   FAU     CCL13   C2CD3   RPS3
CAPRIN2 KIF21A  FMNL3   NCKAP5L MARS    RPL14P1 GPR137C C14orf135       RPL3P4
TP53BP1 RPLP1   TMC7    U6      RPL17   RPL19   ACLY    PRPSAP1 RPL18   RPS9
RPS21   NPTXR   PPARA   PIM2    NLGN3   RPL10   PLXNA3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      2.18531216577091e-32    113.068421052632        0.371531381911286
21      91      translational termination
GO:0000184      1.26188456293878e-31    87.6260796879354        0.485848730191682
22      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006414      6.09772356402699e-31    94.1315789473684        0.428690056051484
21      105     translational elongation
GO:0006614      6.09772356402699e-31    94.1315789473684        0.428690056051484
21      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      7.58500679264764e-31    93.0176470588235        0.43277281849007
21      106     cotranslational protein targeting to membrane
GO:0045047      7.58500679264764e-31    93.0176470588235        0.43277281849007
21      106     protein targeting to ER
GO:0072599      7.58500679264764e-31    93.0176470588235        0.43277281849007
21      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      8.80646416025724e-30    81.4419424850787        0.481765967753097
21      118     protein localization to endoplasmic reticulum
GO:0006413      4.06936847496523e-29    65.2316008316008        0.620579890665006
22      152     translational initiation
GO:0000956      4.75552145898171e-28    57.6190476190476        0.68998685212096
22      169     nuclear-transcribed mRNA catabolic process
GO:0006402      1.57033952636964e-27    54.2605682605683        0.726731714068231
22      178     mRNA catabolic process
GO:0019080      2.21888062683604e-27    60.6279352226721        0.61649712822642
21      151     viral genome expression
GO:0019083      2.21888062683604e-27    60.6279352226721        0.61649712822642
21      151     viral transcription
GO:0006612      2.9690674028572e-27     59.700956937799 0.624662653103591       21
153     protein targeting to membrane
GO:0043624      2.9690674028572e-27     59.700956937799 0.624662653103591       21
153     cellular protein complex disassembly
GO:0043241      6.04079034146103e-27    57.5019208605455        0.645076465296519
21      158     protein complex disassembly
GO:0006401      3.9497866500228e-26     46.1671835770196        0.836966299910041
22      205     RNA catabolic process
GO:0034623      5.02452105141684e-26    51.4308565531476        0.710400664313888
21      174     cellular macromolecular complex disassembly
GO:0032984      9.32911505383716e-26    49.7858094603598        0.730814476506816
21      179     macromolecular complex disassembly
GO:0072594      1.59168676835374e-24    42.9089732528041        0.832883537471455
21      204     establishment of protein localization to organelle
GO:0019058      2.29831854276085e-23    37.321052631579 0.943118123313265       21
231     viral infectious cycle
GO:0022415      2.84789655475449e-22    32.7255009909711        1.06151823403225
21      260     viral reproductive process
GO:0071845      1.83803761985036e-21    29.6887132279368        1.1595045325583 21
284     cellular component disassembly at cellular level
GO:0022411      2.46690905591522e-21    29.235659373152 1.17583558231264        21
288     cellular component disassembly
GO:0016032      2.62847622369186e-17    17.9438188494492        1.84132585980209
21      451     viral reproduction
GO:0033365      6.90344421122322e-17    17.0435491383326        1.93114663345097
21      473     protein localization to organelle
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GO:0006605      7.20480194752119e-17    17.00470547229  1.93522939588956        21
474     protein targeting
GO:0042273      1.38548381246585e-05    85.6130952380952        0.0489931492630268
3       12      ribosomal large subunit biogenesis
Tissue: Skin_Sun_Exposed_Lower_leg=>Nerve_Tibial        Type:   asymmetric
SourceGene:     PRG4(ENSG00000116690.7)
TargetGeneSet:  RPL22   SLC45A1 RP4     CROCCP3 RPL11   GTF2B   RPL5    VPS45
PLXNA2  RP11    FAM179A PPM1B   THSD7B  STK39   SATB2   RPL32   RPL15   SPICE1
RPL34   CTD     EEF1A1P19       ARSK    CAMLG   SLU7    RPL10A  EEF1A1  BCKDHB  ELN
GNAI1   CPSF4   U6      RPL30   EIF3E   EIF3H   RPS6    RPL12   NUDT5   OR13A1
RPS13   FAU     RPS25   LGR5    RPS2P5  ZNF605  GPR137C RSL24D1 RPS3AP6 RPL4
HEATR3  WSCD1   MAPK7   RNF112  FAM106B RPL23A  RPL17   RPL19   TMEM104 SOCS6
SAMD1   ZNF233  FTL     GYS1    FER1L4  LSS     EIF3L   RPS4X   RPL10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006413      4.35570908347227e-31    86.2532967032967        0.525915161580513
22      152     translational initiation
GO:0006414      9.81471333792888e-31    112.282352941176        0.363296657670749
20      105     translational elongation
GO:0006415      5.3704315342553e-30     121.976254480287        0.31485710331465
19      91      translational termination
GO:0000184      1.48520467396305e-29    96.3097643097643        0.411736212026849
20      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006614      1.0549507204945e-28     102.019879969993        0.363296657670749
19      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.28270559702417e-28    100.840192806822        0.366756625839042
19      106     cotranslational protein targeting to membrane
GO:0045047      1.28270559702417e-28    100.840192806822        0.366756625839042
19      106     protein targeting to ER
GO:0072599      1.28270559702417e-28    100.840192806822        0.366756625839042
19      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      1.15508207417614e-27    88.5428478331704        0.408276243858556
19      118     protein localization to endoplasmic reticulum
GO:0000956      2.52199054182393e-26    63.7673378076063        0.584734620441492
20      169     nuclear-transcribed mRNA catabolic process
GO:0006402      7.43531417677252e-26    60.0970464135021        0.615874333956128
20      178     mRNA catabolic process
GO:0019080      1.65882790846359e-25    66.2539100684262        0.522455193412221
19      151     viral genome expression
GO:0019083      1.65882790846359e-25    66.2539100684262        0.522455193412221
19      151     viral transcription
GO:0006612      2.15571449226425e-25    65.2558979297063        0.529375129748806
19      153     protein targeting to membrane
GO:0043624      2.15571449226425e-25    65.2558979297063        0.529375129748806
19      153     cellular protein complex disassembly
GO:0043241      4.08474764064686e-25    62.8865165931771        0.546674970590271
19      158     protein complex disassembly
GO:0006401      1.3805767162083e-24     51.2288288288288        0.709293474500035
20      205     RNA catabolic process
GO:0034623      2.75125290830841e-24    56.331737773153 0.602034461282956       19
174     cellular macromolecular complex disassembly
GO:0032984      4.80452761347157e-24    54.5522177419355        0.61933430212442
19      179     macromolecular complex disassembly
GO:0019058      1.59507992332374e-23    44.8341232227488        0.799252646875649
20      231     viral infectious cycle
GO:0072594      6.2000572913919e-23     47.0974716652136        0.705833506331742
19      204     establishment of protein localization to organelle
GO:0022415      1.76520224049109e-22    39.3361111111111        0.899591723756141
20      260     viral reproductive process
GO:0071845      3.62015978859154e-20    32.6943396226415        0.98263095979517
19      284     cellular component disassembly at cellular level
GO:0022411      4.7241771343403e-20     32.1990646360475        0.996470832468341
19      288     cellular component disassembly
GO:0016032      4.42119662935522e-19    23.5277465918204        1.56044564390008
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21      451     viral reproduction
GO:0033365      2.54654235090876e-17    20.5268579838116        1.63656494360252
20      473     protein localization to organelle
GO:0006605      2.65331051473204e-17    20.4801762114537        1.64002491177081
20      474     protein targeting
GO:0022613      1.14224741638247e-05    10.5911030509921        0.778492837865892
7       225     ribonucleoprotein complex biogenesis
GO:0071843      1.68953775952073e-05    9.94216118684844        0.826932392221992
7       239     cellular component biogenesis at cellular level
Tissue: Nerve_Tibial=>Skin_Sun_Exposed_Lower_leg        Type:   asymmetric
SourceGene:     RP11-134P9.1(ENSG00000233791.1)
TargetGeneSet:  PADI3   PTGFRN  RP11    TCHH    S100A3  C1orf204        VSIG8
MYCNOS  LYG2    ALS2CL  RAP2B   RP1     TTYH3   LRRC4   CUL1    RP4     LZTS1   BNC2
KRTAP5-3        TMPRSS5 CCND2   GPRC5D  KRT81   KRT83   KRT85   KRT82   KRT71
BEST3   RARA    KRT25   KRT26   KRT27   KRT28   KRTAP3-3        KRTAP3-1
KRTAP1-3        KRTAP2-2        KRTAP4-9        KRTAP4-12       KRTAP4-6
KRTAP4-5        KRTAP4-3        KRTAP9-2        KRTAP9-3        KRTAP9-8
KRTAP16-1       KRTAP17-1       KRT33A  KRT34   KRT38   KRT32   KRT35   KRT36
TIMM21  TGM6    CST1    KRTAP24-1       KRTAP26-1       KRTAP13-2       KRTAP13-1
KRTAP19-1       KRTAP19-3       KRTAP19-5       KRTAP11-1       KRTAP10-1
KRTAP10-3       KRTAP10-5       KRTAP10-6       KRTAP10-7       KRTAP10-8
KRTAP10-9       KRTAP10-10      KRTAP12-3       KRTAP12-2       KRTAP12-1
KRTAP10-12      APOBEC3C
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0008544      1.21542717159529e-10    26.0802355539198        0.569095564320808
10      257     epidermis development
Tissue: Nerve_Tibial=>Skin_Sun_Exposed_Lower_leg        Type:   cluster
SourceGene:     RP11-134P9.1(ENSG00000233791.1)
TargetGeneSet:  PADI3   PTGFRN  RP11    TCHH    S100A3  C1orf204        VSIG8
MYCNOS  LYG2    ALS2CL  RAP2B   RP1     TTYH3   LRRC4   CUL1    RP4     LZTS1   BNC2
KRTAP5-3        TMPRSS5 CCND2   GPRC5D  KRT81   KRT83   KRT85   KRT82   KRT71
BEST3   RARA    KRT25   KRT26   KRT27   KRT28   KRTAP3-3        KRTAP3-1
KRTAP1-3        KRTAP2-2        KRTAP4-9        KRTAP4-12       KRTAP4-6
KRTAP4-5        KRTAP4-3        KRTAP9-2        KRTAP9-3        KRTAP9-8
KRTAP16-1       KRTAP17-1       KRT33A  KRT34   KRT38   KRT32   KRT35   KRT36
TIMM21  TGM6    CST1    KRTAP24-1       KRTAP26-1       KRTAP13-2       KRTAP13-1
KRTAP19-1       KRTAP19-3       KRTAP19-5       KRTAP11-1       KRTAP10-1
KRTAP10-3       KRTAP10-5       KRTAP10-6       KRTAP10-7       KRTAP10-8
KRTAP10-9       KRTAP10-10      KRTAP12-3       KRTAP12-2       KRTAP12-1
KRTAP10-12      APOBEC3C
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0008544      1.21542717159529e-10    26.0802355539198        0.569095564320808
10      257     epidermis development
Tissue: Skin_Sun_Exposed_Lower_leg=>Nerve_Tibial        Type:   asymmetric
SourceGene:     RP11-359P5.1(ENSG00000249996.1)
TargetGeneSet:  PLA2G2A RP11    SORT1   C1orf9  TTC32   RPLP0P6 RPL15   GPR160
EIF4G1  HSD17B11        ADH1C   IL6ST   CTD     GNB2L1  PACSIN1 RPL10A  CTB
PNPLA8  SSPO    EIF3E   RPL7A   FAM208B C10orf95        MICAL2  MICALCL ABTB2
KLRF1   FAM19A2 RPL18AP3        PPTC7   RPLP0   OXA1L   ARID4A  TBC1D2B GOLGA6L4
OR2C1   C16orf46        RPL26   RPL23A  COX11   TEX2    RPL13A  ZNF28   RPS5
CBR3-AS1        RPL10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0000184      1.79752529619068e-15    63.3651368760064        0.279980624178258
11      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006413      2.81102848889924e-14    48.4230650632131        0.357622309874749
11      152     translational initiation
GO:0006414      3.00209303319272e-14    62.8157894736842        0.24704172721611
10      105     translational elongation
GO:0000956      9.14113499326756e-14    43.1615299944964        0.397619541900215
11      169     nuclear-transcribed mRNA catabolic process
GO:0006402      1.62388034869741e-13    40.8096849778703        0.418794547090167
11      178     mRNA catabolic process
GO:0006415      4.78713812070416e-13    62.9341463414634        0.214102830253962
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9       91      translational termination
GO:0006401      7.69623482128468e-13    35.0634244733303        0.482319562660024
11      205     RNA catabolic process
GO:0043624      1.38765298793194e-12    41.5909090909091        0.359975088229188
10      153     cellular protein complex disassembly
GO:0006614      1.79564410525806e-12    53.70375        0.24704172721611        9
105     SRP-dependent cotranslational protein targeting to membrane
GO:0043241      1.91798284449093e-12    40.1717342342342        0.371738980001384
10      158     protein complex disassembly
GO:0006613      1.95917933070476e-12    53.1463917525773        0.249394505570549
9       106     cotranslational protein targeting to membrane
GO:0045047      1.95917933070476e-12    53.1463917525773        0.249394505570549
9       106     protein targeting to ER
GO:0072599      1.95917933070476e-12    53.1463917525773        0.249394505570549
9       106     establishment of protein localization to endoplasmic reticulum
GO:0034623      5.04667242327994e-12    36.2118902439024        0.40938343367241
10      174     cellular macromolecular complex disassembly
GO:0070972      5.23481552223919e-12    47.2557798165138        0.277627845823818
9       118     protein localization to endoplasmic reticulum
GO:0032984      6.69863956678448e-12    35.1282051282051        0.421147325444606
10      179     macromolecular complex disassembly
GO:0019080      4.90384069790226e-11    36.1901408450704        0.35526953152031
9       151     viral genome expression
GO:0019083      4.90384069790226e-11    36.1901408450704        0.35526953152031
9       151     viral transcription
GO:0006612      5.5208947747555e-11     35.6825 0.359975088229188       9       153
protein targeting to membrane
GO:0071845      6.34576895101125e-10    21.50699513382  0.668189052660715       10
284     cellular component disassembly at cellular level
GO:0072594      7.21199214575709e-10    26.256  0.479966784305584       9       204
establishment of protein localization to organelle
GO:0022411      7.27008819346467e-10    21.1915467625899        0.677600166078472
10      288     cellular component disassembly
GO:0019058      2.16087239176098e-09    23.0189189189189        0.543491799875441
9       231     viral infectious cycle
GO:0022415      6.09193218574354e-09    20.3177689243028        0.611722372154176
9       260     viral reproductive process
GO:0016032      6.79301792375875e-07    11.3823529411765        1.06110303785205
9       451     viral reproduction
GO:0033365      1.01075029464476e-06    10.8256034482759        1.11286416164971
9       473     protein localization to organelle
GO:0006605      1.02867318047624e-06    10.8015483870968        1.11521694000415
9       474     protein targeting
GO:0071843      1.7535784145997e-05     13.04475781729  0.562314026710954       6
239     cellular component biogenesis at cellular level
Tissue: Skin_Sun_Exposed_Lower_leg=>Nerve_Tibial        Type:   asymmetric
SourceGene:     RP11-456P18.2(ENSG00000229808.1)
TargetGeneSet:  RP3     C1QC    C1QB    HMGCL   LAPTM5  CTSS    SLAMF8  CD84    CD48
ARHGAP30        CHIT1   TLR5    U4      GPX1    TRAT1   CD96    HCLS1   LRRC33
C4orf19 RBM47   MRPL1   CTD     FYB     EMB     ERBB2IP CCDC112 ABLIM3  ARHGEF37
CD74    GAPDHP71        LY86    HLA-H   HLA-DRA HLA-DMA HLA-DOA COL11A2 DEFA6   FGD2
BVES-AS1        AOAH    GUSB    NCF1C   TFEC    TBXAS1  RP11    EPB49   MYBL1
LRRCC1  SLA     SYK     FGD3    NKX2-1  FCN1    WDFY4   PRF1    PAN3    OR52N4
PLEKHA7 MS4A6A  MS4A7   SLCO2B1 IL10RA  SIAE    CACNA2D4        PTPN6   C3AR1
C12orf35        IRAK4   BIN2    NCKAP1L YEATS4  P2RX4   ERCC5   GZMH    SERPINA1
SPG11   ITGAL   ACSF3   ZFP3    EVI2B   EVI2A   GHDC    HMHA1   C19orf35
TMPRSS9 TMIGD2  STXBP2  SUGP1   ZNF546  CEACAM21        NKG7    SIGLEC10
LAIR1   FCAR    MAFB    PLTP    RGS19   BRWD1-IT2       ITGB2   CECR6   APOBEC3G
GPR34   WAS     BTK     GAB3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0002253      5.51180325839901e-09    10.0056818181818        1.59317694277213
13      299     activation of immune response
GO:0050778      6.43565678999881e-09    8.90412698412698        1.93951975641824
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14      364     positive regulation of immune response
GO:0050851      1.7307211487588e-08     16.5557275541796        0.655387170438032
9       123     antigen receptor-mediated signaling pathway
GO:0002429      3.42978619868544e-08    15.2099146110057        0.708670680229742
9       133     immune response-activating cell surface receptor signaling pathway
GO:0002757      4.32779456435286e-08    10.5282738095238        1.25216248010518
11      235     immune response-activating signal transduction
GO:0002768      6.83749069799591e-08    13.9598039215686        0.767282541000623
9       144     immune response-regulating cell surface receptor signaling pathway
GO:0002764      7.50060801641483e-08    9.94163150492264        1.32143104283441
11      248     immune response-regulating signaling pathway
GO:0051251      2.0292658794333e-06     9.10279840091376        1.14559546052176
9       215     positive regulation of lymphocyte activation
GO:0019886      2.87593169441638e-06    194.202702702703        0.031970105875026
3       6       antigen processing and presentation of exogenous peptide antigen via
MHC class II
GO:0050870      3.42869900239267e-06    10.1082955454788        0.91114801743824
8       171     positive regulation of T cell activation
GO:0030593      3.47657926738284e-06    25.5252849002849        0.234447443083524
5       44      neutrophil chemotaxis
GO:0002696      3.92689344981484e-06    8.36068802521008        1.24150577814684
9       233     positive regulation of leukocyte activation
GO:0050867      4.99799814425011e-06    8.1033231474408 1.27880423500104        9
240     positive regulation of cell activation
GO:0002504      5.06717964097792e-06    43.7016742770167        0.117223721541762
4       22      antigen processing and presentation of peptide or polysaccharide
antigen via MHC class II
GO:0050900      5.16980516194615e-06    8.06782454361055        1.28413258598021
9       241     leukocyte migration
GO:0002252      5.8858160284775e-06     6.22177777777778        2.05674347796   11
386     immune effector process
GO:0042110      7.06599692442657e-06    6.79370139593296        1.69974396235555
10      319     T cell activation
GO:0050850      7.30147993351765e-06    39.3260273972603        0.127880423500104
4       24      positive regulation of calcium-mediated signaling
GO:0002694      7.46462572720965e-06    6.74905216681864        1.71040066431389
10      321     regulation of leukocyte activation
GO:0002495      7.99090519834147e-06    116.505405405405        0.0426268078333679
3       8       antigen processing and presentation of peptide antigen via MHC class
II
GO:0002250      1.01043864714539e-05    8.65537757437071        1.05501349387586
8       198     adaptive immune response
GO:0045579      1.19403604403125e-05    97.0810810810811        0.0479551588125389
3       9       positive regulation of B cell differentiation
GO:0050865      1.33103492590027e-05    6.29330823360674        1.82762438585565
10      343     regulation of cell activation
GO:0045619      1.42055282453058e-05    12.9768287142208        0.527506746937928
6       99      regulation of lymphocyte differentiation
GO:0050852      1.42055282453058e-05    12.9768287142208        0.527506746937928
6       99      T cell receptor signaling pathway
GO:0046649      1.73307415273254e-05    5.51026856240126        2.30717597398104
11      433     lymphocyte activation
GO:0051249      1.87708302529189e-05    6.81086303134392        1.50792332710539
9       283     regulation of lymphocyte activation
GO:0045621      1.92243727644204e-05    17.442738791423 0.330357760708601       5
62      positive regulation of lymphocyte differentiation
Tissue: Nerve_Tibial=>Skin_Sun_Exposed_Lower_leg        Type:   asymmetric
SourceGene:     RP11-626E13.1(ENSG00000235902.1)
TargetGeneSet:  RPL11   RPS8    RPL5    NBPF10  MIR765  JMJD4   RN5S18  RPL23AP23
SH3YL1  RPS7    RPL31   THUMPD3 RPL32   RPL15   RPL14   RPL24   RPL32P3 RP11
RPL35A  CAMLG   RPS6    EXOSC2  CTSD    C11orf9 RNF169  CASP4   RPS25   POU6F1
PFDN5   RPL14P1 RPL6    RSL24D1 RPS3AP6 RPS17L  FAM103A1        RPS15A  CTD     CTC1
RPL26   RPS7P1  RPL23A  RPL19   RPL27   ZNF529  PSG7    RPS11   KCNS1   FAM209B
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CECR7   RP4     RBMX2
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      6.92165224449662e-36    252.535211267606        0.226697114386548
20      91      translational termination
GO:0006414      1.64673108293849e-34    210.735294117647        0.26157359352294
20      105     translational elongation
GO:0006614      1.64673108293849e-34    210.735294117647        0.26157359352294
20      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      2.02753692052414e-34    208.270348837209        0.26406477060411
20      106     cotranslational protein targeting to membrane
GO:0045047      2.02753692052414e-34    208.270348837209        0.26406477060411
20      106     protein targeting to ER
GO:0072599      2.02753692052414e-34    208.270348837209        0.26406477060411
20      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      2.10251040588688e-33    182.614795918367        0.293958895578161
20      118     protein localization to endoplasmic reticulum
GO:0000184      2.5245746104842e-33     180.757575757576        0.296450072659332
20      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0000956      3.57071027686695e-32    134.958108108108        0.421008926717874
21      169     nuclear-transcribed mRNA catabolic process
GO:0006402      1.12637427027264e-31    127.141401273885        0.443429520448412
21      178     mRNA catabolic process
GO:0019080      4.16001389418109e-31    136.297709923664        0.376167739256799
20      151     viral genome expression
GO:0019083      4.16001389418109e-31    136.297709923664        0.376167739256799
20      151     viral transcription
GO:0006413      4.78521822791732e-31    135.255681818182        0.37865891633797
20      152     translational initiation
GO:0006612      5.4989379484775e-31     134.229323308271        0.381150093419141
20      153     protein targeting to membrane
GO:0043624      5.4989379484775e-31     134.229323308271        0.381150093419141
20      153     cellular protein complex disassembly
GO:0043241      1.08622902858703e-30    129.320652173913        0.393605978824995
20      158     protein complex disassembly
GO:0006401      2.51579554452287e-30    108.279347826087        0.510691301640025
21      205     RNA catabolic process
GO:0034623      8.28925107923251e-30    115.75487012987 0.433464812123728       20
174     cellular macromolecular complex disassembly
GO:0032984      1.50170622681188e-29    112.075471698113        0.445920697529583
20      179     macromolecular complex disassembly
GO:0072594      2.29719178236226e-28    96.6779891304348        0.508200124558854
20      204     establishment of protein localization to organelle
GO:0019058      3.01029488319043e-27    84.1469194312796        0.575461905750467
20      231     viral infectious cycle
GO:0022415      3.42319991022414e-26    73.828125       0.647706041104422       20
260     viral reproductive process
GO:0071845      2.08122307600338e-25    67.0028409090909        0.707494291052522
20      284     cellular component disassembly at cellular level
GO:0022411      2.7679832832455e-25     65.9841417910448        0.717458999377206
20      288     cellular component disassembly
GO:0016032      2.33832989655251e-21    40.5568445475638        1.12352086360805
20      451     viral reproduction
GO:0033365      6.03905485999849e-21    38.5264900662252        1.17832675939381
20      473     protein localization to organelle
GO:0006605      6.29823720749117e-21    38.4388766519824        1.18081793647498
20      474     protein targeting
GO:0022613      9.19556629956182e-17    42.8384317104696        0.560514843263442
14      225     ribonucleoprotein complex biogenesis
GO:0071843      2.15048052944305e-16    40.1333333333333        0.595391322399834
14      239     cellular component biogenesis at cellular level
GO:0042254      9.32638157733248e-16    52.1094890510949        0.371185385094457
12      149     ribosome biogenesis
GO:0006364      5.21097056447939e-14    58.5965630114566        0.259082416441769
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10      104     rRNA processing
GO:0016072      9.2709369723543e-14     55.0576923076923        0.274029478928794
10      110     rRNA metabolic process
GO:0034470      3.8257783274865e-11     28.7955465587045        0.498235416234171
10      200     ncRNA processing
GO:0042273      5.6183419832097e-11     331.981566820276        0.0298941249740502
5       12      ribosomal large subunit biogenesis
GO:0042274      6.01309559398377e-10    178.684863523573        0.0448411874610754
5       18      ribosomal small subunit biogenesis
GO:0034660      1.22928431002903e-09    19.7762237762238        0.709985468133693
10      285     ncRNA metabolic process
GO:0000028      2.82515477576935e-07    436.727272727273        0.0149470624870251
3       6       ribosomal small subunit assembly
GO:0022618      3.54261731008932e-06    25.6720430107527        0.236661822711231
5       95      ribonucleoprotein complex assembly
GO:0071826      4.56221489971051e-06    24.3123938879457        0.249117708117085
5       100     ribonucleoprotein complex subunit organization
GO:0042255      7.77602369431775e-06    100.713286713287        0.0398588332987337
3       16      ribosome assembly
Tissue: Skin_Sun_Exposed_Lower_leg=>Nerve_Tibial        Type:   asymmetric
SourceGene:     RP11-727A23.4(ENSG00000254676.1)
TargetGeneSet:  RPS6KA1 TMEM81  UXS1    CDK15   EPM2AIP1        GAP43   CLDN18  RP11
RBM47   BTC     SLC1A3  ERBB2IP CD74    HLA-H   HLA-DRA HLA-DMB HLA-DMA HLA-DOA
HLA-DPB1        KCNQ5   SNORD50A        FTSJ2   CLDN12  HR      SYK     C9orf152
WDFY4   KIAA1274        FGF8    KNDC1   RARRES3 ALKBH8  PTPRO   MED21   LACC1
ARL11   APBA2   KLHDC4  NUFIP2  IMPACT  HMHA1   TMIGD2  FSD1    TMEM59L NUMBL   BCL3
BRWD1-IT2       SSR4P1  TMEM27  GPR34
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0002504      9.3239907501338e-12     186.206896551724        0.0532835097917099
6       22      antigen processing and presentation of peptide or polysaccharide
antigen via MHC class II
GO:0019882      6.51431909511458e-08    24.6051724137931        0.368140613106359
7       152     antigen processing and presentation
GO:0050867      8.23210804775444e-08    18.1149425287356        0.581274652273199
8       240     positive regulation of cell activation
GO:0050870      1.46119192084503e-07    21.7256097560976        0.414158189744654
7       171     positive regulation of T cell activation
GO:0019886      2.59012915558126e-07    450.40625       0.01453186630683        3
6       antigen processing and presentation of exogenous peptide antigen via MHC
class II
GO:0050851      4.46117382246977e-07    25.2855879752431        0.297903259290015
6       123     antigen receptor-mediated signaling pathway
GO:0051251      6.90765278446614e-07    17.0769230769231        0.520725209328074
7       215     positive regulation of lymphocyte activation
GO:0002429      7.0750114798147e-07     23.2783057290253        0.322123036468065
6       133     immune response-activating cell surface receptor signaling pathway
GO:0002495      7.22829210925623e-07    270.20625       0.01937582174244        3
8       antigen processing and presentation of peptide antigen via MHC class II
GO:0042110      7.23165851965889e-07    13.4381326664285        0.772610891979794
8       319     T cell activation
GO:0050863      8.31241752709878e-07    16.5911214953271        0.535257075634904
7       221     regulation of T cell activation
GO:0031294      9.45662089990647e-07    34.1571428571429        0.181648328835375
5       75      lymphocyte costimulation
GO:0031295      9.45662089990647e-07    34.1571428571429        0.181648328835375
5       75      T cell costimulation
GO:0002768      1.12819095447537e-06    21.4062968515742        0.348764791363919
6       144     immune response-regulating cell surface receptor signaling pathway
GO:0002696      1.18502447723853e-06    15.6969026548673        0.564320808248564
7       233     positive regulation of leukocyte activation
GO:0060333      1.22632538943352e-06    32.3018018018018        0.191336239706595
5       79      interferon-gamma-mediated signaling pathway
GO:0050865      1.24856728025995e-06    12.4541735765616        0.830738357207114
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8       343     regulation of cell activation
GO:0002757      1.25477136142623e-06    15.5570175438596        0.569164763684174
7       235     immune response-activating signal transduction
GO:0002764      1.79747702408908e-06    14.704356846473 0.600650474015639       7
248     immune response-regulating signaling pathway
GO:0050778      1.94789146810557e-06    11.7020391177695        0.881599889281019
8       364     positive regulation of immune response
GO:0071346      2.91011042818244e-06    26.8295880149813        0.22766590547367
5       94      cellular response to interferon-gamma
GO:0050852      3.7591586958813e-06     25.3936170212766        0.239775794062695
5       99      T cell receptor signaling pathway
GO:0051249      4.31125997728482e-06    12.8079710144928        0.685419694138814
7       283     regulation of lymphocyte activation
GO:0002253      6.1892885825452e-06     12.0924657534247        0.724171337623694
7       299     activation of immune response
GO:0034341      6.59747971644911e-06    22.5    0.268839526676355       5       111
response to interferon-gamma
GO:0046649      7.03762282738726e-06    9.75407407407407        1.04871635180956
8       433     lymphocyte activation
GO:0002694      9.84499468954118e-06    11.2277070063694        0.777454847415404
7       321     regulation of leukocyte activation
GO:0019221      1.45796365421009e-05    10.5404191616766        0.825894401771504
7       341     cytokine-mediated signaling pathway
Tissue: Skin_Sun_Exposed_Lower_leg=>Nerve_Tibial        Type:   asymmetric
SourceGene:     RP11-83A16.1(ENSG00000235096.1)
TargetGeneSet:  C1QC    C1QB    LAPTM5  CD53    FCGR1A  CTSS    FCER1G  FCGR3A
ARL4C   MIR135A1        RP11    SIDT1   HCLS1   FYB     CSF1R   HAVCR2  LY86
GPSM3   TREM2   FAM26F  TRMT11  VNN2    TBXAS1  CTSB    MRC1    FAM86GP LDHAL6A
MS4A7   FOLR2   KCNE3   SLCO2B1 PTPN6   C3AR1   P2RX4   LCP1    ARL11   GPR183
SERPINA1        GOLGA8J DPEP3   DPEP2   ARRB2   CD300A  RHBDF2  DSC2    VAV1    EMR1
STXBP2  IL12RB1 IFI30   PDE4C   LRRC25  HCST    SIGLEC9 FPR3    SIRPB1  HCK
RPS3P2  ITGB2   NFAM1   TLR8    RP1     WAS
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0050778      9.68765605504039e-07    8.81481481481481        1.38537125458446
10      364     positive regulation of immune response
GO:0002252      1.64707071475623e-06    8.28605200945626        1.46910248425714
10      386     immune effector process
GO:0002250      9.48230441307929e-06    10.8458769633508        0.753581067054183
7       198     adaptive immune response
GO:0002443      1.43434834545748e-05    10.1454248366013        0.803058611860771
7       211     leukocyte mediated immunity
GO:0002253      1.60009015720984e-05    8.25034729838415        1.13798353055152
8       299     activation of immune response
Tissue: Skin_Sun_Exposed_Lower_leg=>Nerve_Tibial        Type:   asymmetric
SourceGene:     RP11-84C10.4(ENSG00000258471.1)
TargetGeneSet:  RPL11   GPR161  KRT18P12        C2orf63 RPL31   RPL32   RHOA
FAM162A RPL37   IL6ST   CAMLG   PCDHB5  RPL10A  RPL39P3 SSPO    RPS20   RPL30   RP11
S1PR3   RPL12   ARFIP2  RPS25   PFDN5   RPL41   PARP2   DLST    RPS15A  RPL17
RPL19   ACLY    CTD     UBA52   IGBP1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      3.89347974264337e-24    173.878787878788        0.182617119922497
14      91      translational termination
GO:0006414      3.29879799035074e-23    146.984615384615        0.210712061449035
14      105     translational elongation
GO:0006614      3.29879799035074e-23    146.984615384615        0.210712061449035
14      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      3.79708282379369e-23    145.376811594203        0.212718842986645
14      106     cotranslational protein targeting to membrane
GO:0045047      3.79708282379369e-23    145.376811594203        0.212718842986645
14      106     protein targeting to ER
GO:0072599      3.79708282379369e-23    145.376811594203        0.212718842986645
14      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      1.85228473059208e-22    128.494871794872        0.236800221437963
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14      118     protein localization to endoplasmic reticulum
GO:0000184      2.09720741435729e-22    127.262222222222        0.238807002975573
14      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      6.78599757980201e-21    97.3187347931873        0.303024012179088
14      151     viral genome expression
GO:0019083      6.78599757980201e-21    97.3187347931873        0.303024012179088
14      151     viral transcription
GO:0006413      7.46712331646782e-21    96.6067632850242        0.305030793716698
14      152     translational initiation
GO:0006612      8.21117011725791e-21    95.905035971223 0.307037575254308       14
153     protein targeting to membrane
GO:0043624      8.21117011725791e-21    95.905035971223 0.307037575254308       14
153     cellular protein complex disassembly
GO:0043241      1.30761493981802e-20    92.5425925925926        0.317071482942357
14      158     protein complex disassembly
GO:0000956      3.45346379146708e-20    85.9088172043011        0.339146079856065
14      169     nuclear-transcribed mRNA catabolic process
GO:0034623      5.25409965248226e-20    83.195  0.349179987544115       14      174
cellular macromolecular complex disassembly
GO:0006402      7.28396567836956e-20    81.1430894308943        0.357207113694554
14      178     mRNA catabolic process
GO:0032984      7.89425949776488e-20    80.6456565656566        0.359213895232164
14      179     macromolecular complex disassembly
GO:0072594      5.12801761457407e-19    69.9115789473684        0.40938343367241
14      204     establishment of protein localization to organelle
GO:0006401      5.49849388107925e-19    69.5406631762653        0.41139021521002
14      205     RNA catabolic process
GO:0019058      3.00474331921092e-18    61.0967741935484        0.463566535187876
14      231     viral infectious cycle
GO:0022415      1.60062313346179e-17    53.7842818428184        0.521763199778562
14      260     viral reproductive process
GO:0071845      5.54797086712677e-17    48.9204938271605        0.569925956681198
14      284     cellular component disassembly at cellular level
GO:0022411      6.75234286321892e-17    48.192700729927 0.577953082831638       14
288     cellular component disassembly
GO:0033365      2.16924871329741e-15    32.666874610106 0.949207667289461       15
473     protein localization to organelle
GO:0006605      2.23804350974266e-15    32.593370681606 0.951214448827071       15
474     protein targeting
GO:0016032      3.44467018415915e-14    29.8688024408848        0.905058473462044
14      451     viral reproduction
Tissue: Nerve_Tibial=>Skin_Sun_Exposed_Lower_leg        Type:   cluster
SourceGene:     SPATA25(ENSG00000149634.4)
TargetGeneSet:  RP4     C1orf170        CDC20   KIF2C   ORC1    DEPDC1  FAM72D  MTX1
IQGAP3  NUF2    ASPM    CENPF   DPYSL5  NCAPH   BUB1    TUBA4A  SPHKAP  HJURP
ITPR1   CRELD1  KIF15   WNT5A   SETP14  EIF4A2  TACC3   NCAPG   CCNA2   PCDH10
HMGB2   BRCC3   CCNB1   ZFYVE16 FAM13B  KIF20A  CDC25C  KIAA1191        PBK
ZBTB34  ZWINT   CDK1    HNRNPH3 KIF11   FAM160B1        C10orf46        MKI67   E2F8
STIP1   CDCA5   YAP1    CACNA2D4        FKBP4   TROAP   MBD6    E2F7    ZNF891
DIAPH3  DLGAP5  SLC8A3  AHSA1   BUB1B   CASC5   NUSAP1  CCNB2   KIF23   NPTN
C15orf42        UNC45A  PRC1    SYNM    RP11    HBA2    HBA1    PLK1    AARS
AURKB   CDC6    NKIRAS2 PRPSAP1 BIRC5   RP13    NDC80   SKA1    GNG7    CADM4   TPX2
UBE2C   AURKA   C21orf58        GTSE1   KIF4A
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0000087      5.0847274738295e-32     29.5246559633028        2.01785343574839
33      360     M phase of mitotic cell cycle
GO:0000280      5.91476317426276e-31    28.8579129765114        1.96180195142205
32      350     nuclear division
GO:0007067      5.91476317426276e-31    28.8579129765114        1.96180195142205
32      350     mitosis
GO:0048285      3.55039377299656e-30    27.1117014853279        2.07390492007474
32      370     organelle fission
GO:0051301      4.47473727085696e-26    20.5424703087886        2.53352709155076
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31      452     cell division
GO:0010564      9.39408493606754e-21    17.0352389878163        2.32053145111065
26      414     regulation of cell cycle process
GO:0007017      4.45654204773914e-20    16.9861218944099        2.20282333402533
25      393     microtubule-based process
GO:0007059      5.01608028890097e-20    33.367681498829 0.784720780568819       18
140     chromosome segregation
GO:0000226      2.09231203884606e-17    18.5937191388505        1.50778492837866
20      269     microtubule cytoskeleton organization
GO:0000236      2.5768957809755e-17     42.0824048770233        0.476437616773926
14      85      mitotic prometaphase
GO:0000075      1.01798615418588e-15    18.0433673469388        1.35644592069753
18      242     cell cycle checkpoint
GO:0007346      3.43616833472551e-15    15.19956837801  1.69835997508823        19
303     regulation of mitotic cell cycle
GO:0071156      4.69716445293593e-15    16.404181184669 1.47975918621549        18
264     regulation of cell cycle arrest
GO:0007051      1.82947026663233e-14    36.5780051150895        0.448411874610754
12      80      spindle organization
GO:0007050      1.48551154839294e-12    11.4114774114774        2.0682997716421 18
369     cell cycle arrest
GO:0007088      1.92177534431201e-12    29.169387755102 0.493253062071829       11
88      regulation of mitosis
GO:0051783      1.92177534431201e-12    29.169387755102 0.493253062071829       11
88      regulation of nuclear division
GO:0045786      2.50036875731423e-11    9.51312649164678        2.44944986506124
18      437     negative regulation of cell cycle
GO:0031577      6.91910766519952e-11    46.2078968573731        0.235416234170646
8       42      spindle checkpoint
GO:0000070      2.56165649153333e-10    38.300033411293 0.274652273199087       8
49      mitotic sister chromatid segregation
GO:0051329      2.5981955340301e-10     9.49828353464717        2.12435125596844
16      379     interphase of mitotic cell cycle
GO:0007093      2.98659727102064e-10    17.4845982142857        0.779115632136184
11      139     mitotic cell cycle checkpoint
GO:0051325      3.52951857411441e-10    9.28816089570807        2.16919244342952
16      387     interphase
GO:0000819      4.21721831072271e-10    35.681195516812 0.29146771849699        8
52      sister chromatid segregation
GO:0000086      4.37089679068325e-10    16.8213748657358        0.807141374299356
11      144     G2/M transition of mitotic cell cycle
GO:0007052      5.06895725025873e-10    52.1871101871102        0.184969898276936
7       33      mitotic spindle organization
GO:0090068      7.27458579217874e-10    15.9724489795918        0.846377413327797
11      151     positive regulation of cell cycle process
GO:0033043      2.34798653977427e-09    8.07674208144796        2.47187045879178
16      441     regulation of organelle organization
GO:0051983      3.19035394030749e-09    63.7866666666667        0.134523562383226
6       24      regulation of chromosome segregation
GO:0030071      3.6555912191931e-09     37.6644144144144        0.24102138260328
7       43      regulation of mitotic metaphase/anaphase transition
GO:0007091      5.10195485306002e-09    35.6770981507824        0.252231679468549
7       45      mitotic metaphase/anaphase transition
GO:0030261      1.37029512037098e-08    47.82   0.168154452979033       6       30
chromosome condensation
GO:0031145      1.9223468939349e-08     20.8876712328767        0.465227319908657
8       83      anaphase-promoting complex-dependent proteasomal ubiquitin-dependent
protein catabolic process
GO:0071173      3.04889055198969e-08    40.9771428571429        0.19057504670957
6       34      spindle assembly checkpoint
GO:0071174      4.37645745520425e-08    38.24   0.201785343574839       6       36
mitotic cell cycle spindle checkpoint
GO:0000910      5.16292071265058e-08    18.2019751513221        0.526883952667635
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8       94      cytokinesis
GO:0050000      9.26031690678646e-08    59.0213815789474        0.117708117085323
5       21      chromosome localization
GO:0051303      9.26031690678646e-08    59.0213815789474        0.117708117085323
5       21      establishment of chromosome localization
GO:0034502      1.51789880148426e-07    52.4561403508772        0.128918413950592
5       23      protein localization to chromosome
GO:0051640      1.51824571807191e-07    12.6143617021277        0.840772264895163
9       150     organelle localization
GO:0006323      1.79885415492457e-07    12.3489583333333        0.857587710193066
9       153     DNA packaging
GO:0033205      5.21782332135302e-07    39.3256578947368        0.162549304546398
5       29      cell cycle cytokinesis
GO:0010389      6.23398208321624e-07    37.75   0.168154452979033       5       30
regulation of G2/M transition of mitotic cell cycle
GO:0007076      6.30228466653901e-07    82.8917748917749        0.0728669296242475
4       13      mitotic chromosome condensation
GO:0007094      1.02466434659373e-06    33.6983082706767        0.184969898276936
5       33      mitotic cell cycle spindle assembly checkpoint
GO:0010948      1.06582718270912e-06    15.1787124202855        0.538094249532904
7       96      negative regulation of cell cycle process
GO:0071103      1.07300540491188e-06    9.85416666666667        1.05937305376791
9       189     DNA conformation change
GO:0007018      1.25327483367243e-06    11.642608873441 0.795931077434088       8
142     microtubule-based movement
GO:0045841      1.38931399792082e-06    31.4473684210526        0.196180195142205
5       35      negative regulation of mitotic metaphase/anaphase transition
GO:0051656      1.5038836713339e-06     14.3663024726855        0.566119991696076
7       101     establishment of organelle localization
GO:0045787      1.60746686796036e-06    14.2140825035562        0.571725140128711
7       102     positive regulation of cell cycle
GO:0008608      2.06231748342511e-06    57.3706293706294        0.0952875233547851
4       17      attachment of spindle microtubules to kinetochore
GO:0045839      2.75499188362075e-06    26.9454887218045        0.224205937305377
5       40      negative regulation of mitosis
GO:0051784      2.75499188362075e-06    26.9454887218045        0.224205937305377
5       40      negative regulation of nuclear division
GO:0051313      3.33009793296381e-06    49.7142857142857        0.106497820220054
4       19      attachment of spindle microtubules to chromosome
GO:0034501      3.35230564627903e-06    184.192307692308        0.0336308905958065
3       6       protein localization to kinetochore
GO:0051439      4.78685095042972e-06    15.8866666666667        0.437201577745485
6       78      regulation of ubiquitin-protein ligase activity involved in mitotic
cell cycle
GO:0051488      5.84279665726836e-06    138.134615384615        0.0392360390284409
3       7       activation of anaphase-promoting complex activity
GO:0000079      6.87961998116735e-06    14.8498701298701        0.465227319908657
6       83      regulation of cyclin-dependent protein kinase activity
GO:0032886      1.17246328134062e-05    13.4447058823529        0.510068507369732
6       91      regulation of microtubule-based process
GO:0051438      1.5947979052682e-05     12.6933333333333        0.538094249532904
6       96      regulation of ubiquitin-protein ligase activity
Tissue: Skin_Sun_Exposed_Lower_leg=>Nerve_Tibial        Type:   asymmetric
SourceGene:     TSC1(ENSG00000165699.6)
TargetGeneSet:  C1QC    C1QB    RPS6KA1 PPCS    FCGR1B  FAM72D  SEMA4A  C1orf85
SLAMF8  CD84    ARHGAP30        TMEM81  OR2L3   GPN1    PKDCC   ARHGAP25        GPX1
UBA7    STX18   TLR1    TLR6    LIAS    DAPP1   ANKDD1B XRCC4   SLC25A46        SNX2
SLU7    RP11    DDX41   F13A1   LST1    AIF1    GPANK1  HSPA1B  GPSM3   FGD2
CYB5R4  ZC3H12D C6orf97 MKRN1   MRPS33  DOK2    FAM49B  SYK     TRIM14  NDUFA8
FAM78A  FCN1    ACBD5   PIK3AP1 COMMD9  MS4A6A  LAMTOR1 SLCO2B1 VPS11   PTPN6
ARHGDIB PTPRO   LRMP    NR4A1   NCKAP1L TMEM194A        ERP29   DENR    LCP1
ARL11   NLRC3   NAGPA   CORO1A  DUS2L   FANCA   DBIL5P  ADAP2   CDR2L   TNFRSF11A
VPS4B   EBI3    VAV1    STXBP2  C19orf40        POU2F2  SIGLEC10        CTD
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LAIR1   SIRPG   GINS1   HCK     PLTP    ITGB2   TXNRD2  C22orf25        BCR
SLC2A11 RAC2    C22orf40        TLR7    CYBB    GPR34   WAS     ARHGAP4
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006909      1.56187313052746e-09    22.2701298701299        0.499896200954951
9       86      phagocytosis
GO:0050900      1.37690707673575e-08    10.2896652110626        1.40087191197841
12      241     leukocyte migration
GO:0042110      3.54707280255418e-08    8.41355979011323        1.85426614075151
13      319     T cell activation
GO:0002252      4.32196566570316e-08    7.5241935483871 2.24372015777455        14
386     immune effector process
GO:0046649      1.78450638055667e-07    6.65775656324582        2.51691924434295
14      433     lymphocyte activation
GO:0002250      2.12684226820067e-07    10.1919206440483        1.15092381150093
10      198     adaptive immune response
GO:0002263      5.56195940913319e-07    13.0453089244851        0.714967822296035
8       123     cell activation involved in immune response
GO:0002366      5.56195940913319e-07    13.0453089244851        0.714967822296035
8       123     leukocyte activation involved in immune response
GO:0060326      1.19580713977144e-06    11.7097039473684        0.790533527091551
8       136     cell chemotaxis
GO:0002253      1.20183616994373e-06    7.36629566210046        1.73801121029687
11      299     activation of immune response
GO:0050778      1.20317321759012e-06    6.63589015151515        2.11583973427444
12      364     positive regulation of immune response
GO:0002764      1.67589937093668e-06    8.02237111060641        1.44156113763753
10      248     immune response-regulating signaling pathway
GO:0050764      2.53995359159108e-06    27.4913693901036        0.220884367863816
5       38      regulation of phagocytosis
GO:0030595      3.62929556025758e-06    12.4676573426573        0.645214864023251
7       111     leukocyte chemotaxis
GO:0050865      4.53592914436223e-06    6.37006931836937        1.99377205729707
11      343     regulation of cell activation
GO:0050870      6.62202013862449e-06    9.17274782047142        0.99397965538717
8       171     positive regulation of T cell activation
GO:0002275      6.68814015747244e-06    22.1148502624267        0.267386340045672
5       46      myeloid cell activation involved in immune response
GO:0002886      8.64650380938989e-06    37.7578947368421        0.133693170022836
4       23      regulation of myeloid leukocyte mediated immunity
GO:0002757      8.70612819212225e-06    7.50849557522124        1.36599543284202
9       235     immune response-activating signal transduction
GO:0002460      1.00493545434512e-05    8.6364466078491 1.05210712061449        8
181     adaptive immune response based on somatic recombination of immune receptors
built from immunoglobulin superfamily domains
GO:0050867      1.03118971907143e-05    7.34337662337662        1.39505916545568
9       240     positive regulation of cell activation
GO:0006954      1.38329207528784e-05    5.15444444444444        2.68548889350218
12      462     inflammatory response
GO:0001774      1.55193509925864e-05    88.6481481481482        0.0523147187045879
3       9       microglial cell activation
GO:0043312      1.55193509925864e-05    88.6481481481482        0.0523147187045879
3       9       neutrophil degranulation
GO:0002694      1.63789020496631e-05    6.10758668636482        1.86589163379697
10      321     regulation of leukocyte activation
Tissue: Skin_Sun_Exposed_Lower_leg=>Nerve_Tibial        Type:   asymmetric
SourceGene:     WDR75(ENSG00000115368.5)
TargetGeneSet:  RPL11   RP11    UBC     RPL31   ASNSD1  RPL37A  SCARNA6 RPL32
EXOSC7  FAM162A IFT80   RPL34   ODZ1    CTD     RPL37   RPL10A  RPL39P3 MRPS12  SSPO
RPL30   RPS6    RPL12   LCN2    RPS24   MIR1307 RPS13   EIF3M   GANAB   C11orf67
RPS25   PFDN5   RPL41   NACA    RPS2P5  RPS29   RPL3P4  RPL4    CHD2    RPL17
RPL36   IFNGR2  C22orf32
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      1.5680139250674e-34     270.410714285714        0.207805688187669
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19      91      translational termination
GO:0006414      3.12909219563623e-33    226.169435215947        0.239775794062695
19      105     translational elongation
GO:0006614      3.12909219563623e-33    226.169435215947        0.239775794062695
19      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      3.80892439741973e-33    223.554187192118        0.242059373053768
19      106     cotranslational protein targeting to membrane
GO:0045047      3.80892439741973e-33    223.554187192118        0.242059373053768
19      106     protein targeting to ER
GO:0072599      3.80892439741973e-33    223.554187192118        0.242059373053768
19      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      3.47664674423231e-32    196.292207792208        0.269462320946647
19      118     protein localization to endoplasmic reticulum
GO:0006413      3.85299653365757e-32    166.503496503497        0.347104006643139
20      152     translational initiation
GO:0000184      4.13337274621525e-32    194.315714285714        0.271745899937721
19      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0000956      3.62877134318008e-31    147.330924109448        0.385924849491385
20      169     nuclear-transcribed mRNA catabolic process
GO:0006402      1.08080495844364e-30    138.851022395326        0.406477060411044
20      178     mRNA catabolic process
GO:0019080      5.18226236288466e-30    146.87987012987 0.344820427652066       19
151     viral genome expression
GO:0019083      5.18226236288466e-30    146.87987012987 0.344820427652066       19
151     viral transcription
GO:0006612      6.74979111260142e-30    144.667377398721        0.349387585634212
19      153     protein targeting to membrane
GO:0043624      6.74979111260142e-30    144.667377398721        0.349387585634212
19      153     cellular protein complex disassembly
GO:0043241      1.2862263367654e-29     139.414696813977        0.360805480589579
19      158     protein complex disassembly
GO:0006401      2.06927629276862e-29    118.361746361746        0.468133693170023
20      205     RNA catabolic process
GO:0034623      8.82139705076275e-29    124.883410138249        0.397342744446751
19      174     cellular macromolecular complex disassembly
GO:0032984      1.54922199540392e-28    120.938392857143        0.408760639402117
19      179     macromolecular complex disassembly
GO:0072594      2.05660090582034e-27    104.411969111969        0.46585011417895
19      204     establishment of protein localization to organelle
GO:0019058      2.36044711594199e-26    90.9413746630728        0.527506746937928
19      231     viral infectious cycle
GO:0022415      2.37057827528782e-25    79.834914048607 0.593730537679053       19
260     viral reproductive process
GO:0071845      1.31503124514101e-24    72.4816711590296        0.648536433464812
19      284     cellular component disassembly at cellular level
GO:0022411      1.72390005902751e-24    71.3836962294211        0.657670749429105
19      288     cellular component disassembly
GO:0016032      9.27379826671703e-21    43.9375 1.02989412497405        19      451
viral reproduction
GO:0033365      2.28597037358896e-20    41.7426054122089        1.08013286277766
19      473     protein localization to organelle
GO:0006605      2.37916861648841e-20    41.6478806907378        1.08241644176874
19      474     protein targeting
GO:0042274      8.6489391356826e-06     96.02   0.0411044218393191      3       18
ribosomal small subunit biogenesis
GO:0022613      1.03848533290597e-05    14.4079147640791        0.513805272991488
6       225     ribonucleoprotein complex biogenesis
GO:0071843      1.46423493164358e-05    13.5288507391512        0.545775378866514
6       239     cellular component biogenesis at cellular level
Tissue: Nerve_Tibial=>Skin_Sun_Exposed_Lower_leg        Type:   asymmetric
SourceGene:     ZNF426(ENSG00000130818.4)
TargetGeneSet:  WASF2   MAGOH   ENSA    BROX    GCC2    RPL37A  DCP1A   SEC62
SLC34A2 ADAMTS3 RP11    RPL39P3 TBP     GTF2IP1 RPS15AP24       ANP32B  FAU
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RAB6A   RPS3    SNRPF   RPS2P5  RPS29   RPL3P4  HMGN2P5 C15orf41        CTD
SUZ12   NLE1    RPS16   RPS21   TCP10L  NDUFB11 ZDHHC9
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0000184      3.10082702951292e-12    79.3846153846154        0.172929209051277
8       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0000956      5.2972725883944e-11     54.539894887721 0.245588540585427       8
169     nuclear-transcribed mRNA catabolic process
GO:0006402      8.03358941506834e-11    51.6199095022624        0.258667220261574
8       178     mRNA catabolic process
GO:0006613      9.99015863106583e-11    72.3787878787879        0.154037782852398
7       106     cotranslational protein targeting to membrane
GO:0072594      2.39006241070147e-10    44.690737833595 0.296450072659332       8
204     establishment of protein localization to organelle
GO:0006401      2.48511036922702e-10    44.4607575165951        0.297903259290015
8       205     RNA catabolic process
GO:0006612      1.33423773257923e-09    48.9178082191781        0.222337554494499
7       153     protein targeting to membrane
GO:0006415      2.65350413836654e-09    67.5058823529412        0.132239983392153
6       91      translational termination
GO:0006414      6.32691400295807e-09    57.9030303030303        0.152584596221715
6       105     translational elongation
GO:0006614      6.32691400295807e-09    57.9030303030303        0.152584596221715
6       105     SRP-dependent cotranslational protein targeting to membrane
GO:0045047      6.7005347479569e-09     57.32   0.154037782852398       6       106
protein targeting to ER
GO:0072599      6.7005347479569e-09     57.32   0.154037782852398       6       106
establishment of protein localization to endoplasmic reticulum
GO:0006605      8.43381150091961e-09    22.5241935483871        0.688810462943741
9       474     protein targeting
GO:0070972      1.28046562758319e-08    51.1357142857143        0.171476022420594
6       118     protein localization to endoplasmic reticulum
GO:0019080      5.61716063210416e-08    39.4068965517241        0.219431181233133
6       151     viral genome expression
GO:0019083      5.61716063210416e-08    39.4068965517241        0.219431181233133
6       151     viral transcription
GO:0006413      5.8427660726956e-08     39.1342465753425        0.220884367863816
6       152     translational initiation
GO:0043624      6.07580045226447e-08    38.865306122449 0.222337554494499       6
153     cellular protein complex disassembly
GO:0043241      7.35921978450444e-08    37.5736842105263        0.229603487647914
6       158     protein complex disassembly
GO:0034623      1.30566915846309e-07    33.9571428571429        0.252854473738842
6       174     cellular macromolecular complex disassembly
GO:0032984      1.54445931912642e-07    32.964161849711 0.260120406892257       6
179     macromolecular complex disassembly
GO:0033365      1.73630693240662e-07    18.4813895781638        0.687357276313058
8       473     protein localization to organelle
GO:0019058      6.9406123036348e-07     25.2533333333333        0.335686111687772
6       231     viral infectious cycle
GO:0022415      1.38494421022697e-06    22.3244094488189        0.377828523977579
6       260     viral reproductive process
GO:0016032      2.18983943464244e-06    15.75   0.655387170438032       7       451
viral reproduction
GO:0071845      2.31347185524326e-06    20.3625899280576        0.412705003113971
6       284     cellular component disassembly at cellular level
GO:0022411      2.50880477984474e-06    20.068085106383 0.418517749636703       6
288     cellular component disassembly
Tissue: Thyroid=>Adipose_Subcutaneous   Type:   asymmetric
SourceGene:     C11orf94(ENSG00000234776.1)
TargetGeneSet:  RPL11   RP4     RPS8    MAGOH   RPL5    RWDD3   RP11    ATP5F1
HSD3BP2 SNRPE   KIAA1383        IRF2BP2 RPS7    RPLP0P6 UBC     SNRPG   TPRKB
C2orf65 HAT1    EEF1B2  XRCC5   RPL37A  RPL15   RPSA    RPL14   LAMB2   RPL24   ATG3
RNF7    RPL22L1 DNAJC19 HNRPDL  OSTC    WDR70   CTD     CWC27   TAF9    BTF3
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HINT1   CTB     SYNPO   ZNF300  MRPL22  NUDCD2  RPL26L1 LYRM4   NOL7    TDP2
RPS10   RPL10A  RPL39P3 MRPS12  PSMB1   SLC29A4 CBX3    ECD     NAA38   SSBP1
RPS20   SNHG6   RPL7    C8orf59 RPL30   POLR2K  KANK1   RPS6    NDUFB6  XPA
SEC61B  FAM206A RPL12   RPL7A   CDC123  RPS24   RPL13AP5        GSTO1   POLR2G  FIBP
LAMTOR1 CLNS1A  TMEM126A        RPS25   PRR13   HNRNPA1 C12orf45        RPLP0
UNC119B HMGB1   F7      ERH     COX16   RPSAP4  RPS3AP6 ANKDD1A RPLP1   CES2
DDX19B  C17orf61-PLSCR3 PLSCR3  RPL26   RPS7P1  RPL23A  SLC6A4  RPL19   RPL27
PSMG2   HNRNPA1P7       RPL17   NFIX    RPS19   RPL13A  RPL28   CHMP2A  NAA20   DPM1
PFDN4   BRWD1-IT2       HIRA    PRDX4   PDZD11  RPS23P8 CXorf26 RPL39   HPRT1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      4.58188832262933e-49    100.549295774648        0.741125181648329
34      105     translational elongation
GO:0006415      1.77973484293038e-47    110.721549636804        0.642308490761885
32      91      translational termination
GO:0006614      4.479817834146e-47      94.8351449275362        0.741125181648329
33      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      6.47458769958061e-47    93.5294818344253        0.748183516711646
33      106     cotranslational protein targeting to membrane
GO:0045047      6.47458769958061e-47    93.5294818344253        0.748183516711646
33      106     protein targeting to ER
GO:0072599      6.47458769958061e-47    93.5294818344253        0.748183516711646
33      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      3.9693343567914e-45     80.2578005115089        0.832883537471455
33      118     protein localization to endoplasmic reticulum
GO:0000184      5.46680105828962e-45    79.3190091001011        0.839941872534773
33      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      6.33160869608941e-43    60.8205128205128        1.06580859456093
34      151     viral genome expression
GO:0019083      6.33160869608941e-43    60.8205128205128        1.06580859456093
34      151     viral transcription
GO:0006612      1.03896542454123e-42    59.7899159663866        1.07992526468756
34      153     protein targeting to membrane
GO:0000956      2.19268408537288e-39    49.9817774936061        1.19285862570064
33      169     nuclear-transcribed mRNA catabolic process
GO:0006413      2.67922162204485e-39    54.2057142857143        1.07286692962425
32      152     translational initiation
GO:0043624      3.3717066276433e-39     53.7539551357733        1.07992526468756
32      153     cellular protein complex disassembly
GO:0043241      1.03774293688346e-38    51.6027210884354        1.11521694000415
32      158     protein complex disassembly
GO:0006402      1.39576346096265e-38    46.8497751124438        1.2563836412705 33
178     mRNA catabolic process
GO:0072594      4.16417593864301e-38    41.7029411764706        1.43990035291675
34      204     establishment of protein localization to organelle
GO:0019058      9.72323431385238e-38    37.7212153518124        1.63047539962632
35      231     viral infectious cycle
GO:0034623      2.93436748613485e-37    45.7368209255533        1.22815030101723
32      174     cellular macromolecular complex disassembly
GO:0032984      7.76666320262037e-37    44.1655976676385        1.26344197633382
32      179     macromolecular complex disassembly
GO:0006401      2.02075855827984e-36    39.4203741152679        1.44695868798007
33      205     RNA catabolic process
GO:0022415      7.33747502724919e-36    32.792039800995 1.83516711646253        35
260     viral reproductive process
GO:0071845      1.43879461956619e-31    26.8626364108782        2.00456715798215
33      284     cellular component disassembly at cellular level
GO:0022411      2.30340311471369e-31    26.4337595907928        2.03280049823542
33      288     cellular component disassembly
GO:0016032      5.95522087315355e-30    19.159977703456 3.18330911355616        37
451     viral reproduction
GO:0006605      6.50904804752065e-28    17.3237858032379        3.34565082001246
36      474     protein targeting
GO:0033365      1.03401432052651e-26    16.5911878961358        3.33859248494914
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35      473     protein localization to organelle
GO:0022613      1.34282864689106e-15    15.7162826061528        1.58812538924642
19      225     ribonucleoprotein complex biogenesis
GO:0071843      4.10075410879317e-15    14.7015881708653        1.68694208013286
19      239     cellular component biogenesis at cellular level
GO:0042254      1.25296005045935e-13    18.2900154400412        1.0516919244343 15
149     ribosome biogenesis
GO:0042274      2.11523361997678e-11    96.044019138756 0.127050031139714       7
18      ribosomal small subunit biogenesis
GO:0006364      1.61763612700701e-10    18.5295994328252        0.734066846585011
11      104     rRNA processing
GO:0016072      2.98620379108735e-10    17.3992673992674        0.776416856964916
11      110     rRNA metabolic process
GO:0042273      1.20855297190459e-08    105.611192930781        0.084700020759809
5       12      ribosomal large subunit biogenesis
GO:0034660      1.23136219132765e-08    8.26450855417645        2.01162549304546
14      285     ncRNA metabolic process
GO:0034470      1.61007550097505e-07    9.05634048491191        1.41166701266348
11      200     ncRNA processing
GO:0000377      1.73708903383027e-06    7.93086060062752        1.43990035291675
10      204     RNA splicing, via transesterification reactions with bulged
adenosine as nucleophile
GO:0000398      1.73708903383027e-06    7.93086060062752        1.43990035291675
10      204     nuclear mRNA splicing, via spliceosome
GO:0000375      2.16127954638703e-06    7.72886169980336        1.47519202823334
10      209     RNA splicing, via transesterification reactions
GO:0022618      4.71284595855416e-06    11.941028708134 0.670541831015155       7
95      ribonucleoprotein complex assembly
GO:0071826      6.63361502968288e-06    11.2950764006791        0.705833506331742
7       100     ribonucleoprotein complex subunit organization
GO:0000028      6.72414408354161e-06    144.909090909091        0.0423500103799045
3       6       ribosomal small subunit assembly
GO:0000462      6.72414408354161e-06    144.909090909091        0.0423500103799045
3       6       maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA,
5.8S rRNA, LSU-rRNA)
GO:0030490      1.17068313659372e-05    108.674242424242        0.0494083454432219
3       7       maturation of SSU-rRNA
Tissue: Thyroid=>Adipose_Subcutaneous   Type:   asymmetric
SourceGene:     C19orf43(ENSG00000123144.5)
TargetGeneSet:  PLEKHN1 PRKCZ   RP4     RP1     RPS8    CTB     ABCA4   RPS27
MEF2D   ZC3H11B UBC     EEF1B2  KCNE4   RPL29   GPR87   RP11    TP63    H3F3AP6
RPS3A   CTD     SKP1    RPS14   ZNF300  DSP     UBD     FTH1P5  SENP6   FOXK1   BZW2
IGFBP3  SLC26A4 EEF1D   RPL8    RPS6    RPL7A   BCCIP   RPL27A  SDHD    DDX6    NACA
RPL18AP3        RPL6    ZDHHC20 RPL21   EXOSC8  DNAJC3  RPL4    RPS15A  ESRP2
RPL13   GGT6    RPL26   RPL19   KRT35   NT5C    RPL36   HNRNPA1P10      NCCRP1
ZNF600  RPS5    SOGA1   TSHZ2   PLA2G3  RPL3    TNRC6B  WDR13   WDR45   POF1B
RPL39
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      3.53396181174091e-35    114.687456445993        0.421424122898069
23      105     translational elongation
GO:0006415      1.41405068971443e-32    116.132432432432        0.365234239844993
21      91      translational termination
GO:0006614      3.94933669285342e-31    96.6824324324324        0.421424122898069
21      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      4.91293861919361e-31    95.5383147853736        0.425437685973289
21      106     cotranslational protein targeting to membrane
GO:0045047      4.91293861919361e-31    95.5383147853736        0.425437685973289
21      106     protein targeting to ER
GO:0072599      4.91293861919361e-31    95.5383147853736        0.425437685973289
21      106     establishment of protein localization to endoplasmic reticulum
GO:0000956      4.85786966626846e-30    64.1254403131115        0.678292159712131
23      169     nuclear-transcribed mRNA catabolic process
GO:0070972      5.70866153285636e-30    83.6489272777933        0.473600442875926
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21      118     protein localization to endoplasmic reticulum
GO:0000184      6.91487865576159e-30    82.7895752895753        0.477614005951145
21      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006402      1.7043328369606e-29     60.3638709677419        0.714414227389108
23      178     mRNA catabolic process
GO:0006401      5.04637953237574e-28    51.3113029827316        0.82278043042004
23      205     RNA catabolic process
GO:0019080      1.44152805700065e-27    62.270893970894 0.606048024358176       21
151     viral genome expression
GO:0019083      1.44152805700065e-27    62.270893970894 0.606048024358176       21
151     viral transcription
GO:0006413      1.6684861258793e-27     61.7912110583866        0.610061587433396
21      152     translational initiation
GO:0006612      1.9291555246234e-27     61.3187960687961        0.614075150508615
21      153     protein targeting to membrane
GO:0043624      1.9291555246234e-27     61.3187960687961        0.614075150508615
21      153     cellular protein complex disassembly
GO:0043241      3.92632307364915e-27    59.0601696587098        0.634142965884714
21      158     protein complex disassembly
GO:0034623      3.26927523770176e-26    52.8245892951775        0.698359975088229
21      174     cellular macromolecular complex disassembly
GO:0032984      6.07215039653247e-26    51.134964078002 0.718427790464328       21
179     macromolecular complex disassembly
GO:0072594      1.03773523730116e-24    44.0717766947275        0.81876686734482
21      204     establishment of protein localization to organelle
GO:0019058      1.50115437852748e-23    38.3324324324324        0.927133070375753
21      231     viral infectious cycle
GO:0071845      3.762365063634e-23      32.9603477523325        1.1398519133624 22
284     cellular component disassembly at cellular level
GO:0022411      5.12908182491589e-23    32.4555137844612        1.15590616566328
22      288     cellular component disassembly
GO:0022415      1.86373894425895e-22    33.6123487504241        1.04352639955712
21      260     viral reproductive process
GO:0016032      8.98932556008988e-19    19.8917378917379        1.81011694692409
22      451     viral reproduction
GO:0033365      4.58332234219373e-17    17.50544128199  1.89841533457892        21
473     protein localization to organelle
GO:0006605      4.78372454065249e-17    17.4655450152139        1.90242889765414
21      474     protein targeting
GO:0022613      2.9915768230483e-06     10.4523502304147        0.903051691924434
8       225     ribonucleoprotein complex biogenesis
GO:0071843      4.67770726164057e-06    9.80917748917749        0.95924157497751
8       239     cellular component biogenesis at cellular level
GO:0007603      9.89560402546092e-06    98.0795454545455        0.0441491938274168
3       11      phototransduction, visible light
Tissue: Thyroid=>Adipose_Subcutaneous   Type:   asymmetric
SourceGene:     C6orf108(ENSG00000112667.8)
TargetGeneSet:  CLSTN1  HSPG2   PEF1    RPS8    RP4     CRYZ    CCBL2   RPL5    RP11
SRGAP2P2        JTB     RPS27   TKT     GORAB   PRRC2C  TPR     ZBTB41  FAM108A4P
RPS7    UBC     PRORSD1P        UGGT1   KLF7    BRK1    WDR48   LAMB2   APPL1
KCTD6   CCDC80  PHC3    DNAJC19 PPP1R2  BOD1L   MTHFD2L WDFY3-AS1       RPL34
RPS3A   CTD     SKP1    RPS14   HMGN4   HCG16   WDR11   IGF2R   STARD3NL
RPS3AP26        MTPN    LSM1    PPAPDC1B        HOOK3   PAG1    RNF19A  SMARCA2 RPS6
CDC26   RPL12   RPL7A   NUDT5   ANAPC16 RPS24   RPS3AP5 ARL3    EIF6    RPL27A
CKAP5   AHNAK   SLC22A25        NUMA1   TMEM126B        BACE1   UBE4A   CD163L1
SCAF11  LRP1    EEA1    ISCU    DNAJC3  CCNB1IP1        RPS27L  RPL4    IFT140
RPS15A  TERF2   RPL26   RPS7P1  RPL23A  TAOK1   RPL17   RPL27   RPS7P11 TNRC6C
CEP192  RPL12P4 EP300   C22orf32        MXRA5   RPS4X   RPL39
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      2.10803275797202e-29    75.2789473684211        0.491177081170853
21      91      translational termination
GO:0006414      5.77875692373691e-28    62.6710526315789        0.566742785966369
21      105     translational elongation
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GO:0006614      5.77875692373691e-28    62.6710526315789        0.566742785966369
21      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      7.17914378665368e-28    61.9294117647059        0.572140336308906
21      106     cotranslational protein targeting to membrane
GO:0045047      7.17914378665368e-28    61.9294117647059        0.572140336308906
21      106     protein targeting to ER
GO:0072599      7.17914378665368e-28    61.9294117647059        0.572140336308906
21      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      8.20948226222399e-27    54.2224633749322        0.636910940419348
21      118     protein localization to endoplasmic reticulum
GO:0000184      9.93085599893116e-27    53.6654135338346        0.642308490761885
21      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      4.68301832880547e-26    43.3787375415282        0.815030101723064
22      151     viral genome expression
GO:0019083      4.68301832880547e-26    43.3787375415282        0.815030101723064
22      151     viral transcription
GO:0000956      6.23836773568815e-25    38.0189504373178        0.912186007888727
22      169     nuclear-transcribed mRNA catabolic process
GO:0006402      2.03651287174155e-24    35.8028846153846        0.960763960971559
22      178     mRNA catabolic process
GO:0006413      2.29291946577241e-24    40.053836882282 0.820427652065601       21
152     translational initiation
GO:0006612      2.647604090615e-24      39.7476076555024        0.825825202408138
21      153     protein targeting to membrane
GO:0043624      2.647604090615e-24      39.7476076555024        0.825825202408138
21      153     cellular protein complex disassembly
GO:0043241      5.3526565448962e-24     38.2835190165194        0.852812954120822
21      158     protein complex disassembly
GO:0034623      4.36256393431683e-23    34.2414860681115        0.939173759601412
21      174     cellular macromolecular complex disassembly
GO:0072594      4.43450340207823e-23    30.6320643642072        1.1011002698752
22      204     establishment of protein localization to organelle
GO:0006401      4.94897124682394e-23    30.4625292740047        1.10649782022005
22      205     RNA catabolic process
GO:0032984      8.04872623616844e-23    33.1462358427715        0.966161511314096
21      179     macromolecular complex disassembly
GO:0019058      7.11073970455692e-22    26.6240601503759        1.24683412912601
22      231     viral infectious cycle
GO:0033365      5.51543519836817e-21    16.5316539171722        2.55304131201993
27      473     protein localization to organelle
GO:0022415      9.68003615885008e-21    23.3320828331333        1.40336308905958
22      260     viral reproductive process
GO:0071845      6.67665909730729e-20    21.1588058887677        1.53290429728046
22      284     cellular component disassembly at cellular level
GO:0022411      9.0530347428169e-20     20.8347207303974        1.55449449865061
22      288     cellular component disassembly
GO:0006605      1.44216818696266e-18    14.6278942723873        2.55843886236247
25      474     protein targeting
GO:0016032      6.63950148420574e-18    14.5157429091855        2.43429520448412
24      451     viral reproduction
GO:0022613      3.17925908695173e-08    10.8626726182173        1.21444882707079
11      225     ribonucleoprotein complex biogenesis
GO:0042274      3.26261657760861e-08    75.6585879873551        0.0971559061656633
5       18      ribosomal small subunit biogenesis
GO:0071843      5.90216155929363e-08    10.1855852317361        1.29001453186631
11      239     cellular component biogenesis at cellular level
GO:0042254      1.0287403911049e-07     13.2605590062112        0.804235001037991
9       149     ribosome biogenesis
GO:0006364      1.4171483529461e-06     14.5102366777988        0.561345235623832
7       104     rRNA processing
GO:0016072      2.06869764851902e-06    13.6592369752496        0.593730537679053
7       110     rRNA metabolic process
GO:0030490      5.21301543614226e-06    143.69  0.0377828523977579      3       7
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maturation of SSU-rRNA
Tissue: Thyroid=>Adipose_Subcutaneous   Type:   asymmetric
SourceGene:     CTD-2034L19.1(ENSG00000248394.1)
TargetGeneSet:  MTND1P23        MTND2P28        NMNAT1  DFFA    AIM1L   DNAJC8  RP11
RPS8    HBXIP   SPRR2D  RPS27   CADM3   PFN1P1  GAS5    HMGN1P4 ST13P19 XDH
DGUOK-AS1       EIF5B   UGGT1   RHOQP3  HAT1    H3F3AP4 CASP10  TRANK1  RPL29
METTL15P1       SETD7   H3F3AP6 RPS3A   C5orf15 SKP1    CTB     MTND5P11
RPL15P3 PPIAP29 AGPAT1  FTH1P5  MTRNR2L9        KIAA1919        FOXK1   EEF1A1P6
RPS3AP26        POLR2J  ARF5    CTAGE8  HMBOX1  HOOK3   GS1     ATP6V1G1
RPL7A   FUT11   EIF2S2P3        MRPL43  GLRX3   MTRNR2L8        TSG101  C11orf94
ALDH3B2 DDX6    BARX2   KRT6B   NACA    RPL6    COX6A1  SBNO1   GOLGA3  MED4-AS1
NDFIP2  PSMA6   TJP1    HERC2P10        C15orf40        CTD     MPG     HBQ1
SPSB3   RPS15A  SULT1A4 NFATC3  VPS53   TLCD2   RPL26   C17orf48        TAF15
RPL19   RPS7P11 PRR15L  RPS2P48 ROCK1P1 MYL12B  RPL17   HMSD    HNRNPA1P10
SLC35E1 LGALS7  RPL18   RPL13A  KLK7    RPS5    RPL41P1 KIF3B   RP4     RPL12P4
HMGB1P10        PRR14L  RPL3    RBX1    USP9X   RP6     RPS4X   TTC3P1  RP1
HCFC1   RPL10   MT
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      4.75045189170174e-21    54.4914285714286        0.453394228773095
16      91      translational termination
GO:0006414      5.42406537022357e-20    45.8747993579454        0.523147187045879
16      105     translational elongation
GO:0006614      5.42406537022357e-20    45.8747993579454        0.523147187045879
16      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      6.36490887575167e-20    45.3619047619048        0.528129541208221
16      106     cotranslational protein targeting to membrane
GO:0045047      6.36490887575167e-20    45.3619047619048        0.528129541208221
16      106     protein targeting to ER
GO:0072599      6.36490887575167e-20    45.3619047619048        0.528129541208221
16      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      3.84607719690325e-19    39.9915966386555        0.587917791156321
16      118     protein localization to endoplasmic reticulum
GO:0000184      4.42721450880039e-19    39.6005547850208        0.592900145318663
16      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      6.98033579785191e-19    32.8582089552239        0.752335478513598
17      151     viral genome expression
GO:0019083      6.98033579785191e-19    32.8582089552239        0.752335478513598
17      151     viral transcription
GO:0006413      7.83085074124861e-19    32.6125252525253        0.757317832675939
17      152     translational initiation
GO:0022415      8.22254859659035e-19    22.6586538461538        1.29541208220884
20      260     viral reproductive process
GO:0019058      1.96121604843618e-18    23.9563011747953        1.15092381150093
19      231     viral infectious cycle
GO:0000956      4.9171950353796e-18     28.9305023923445        0.842017853435748
17      169     nuclear-transcribed mRNA catabolic process
GO:0006402      1.20074409114895e-17    27.2959909655562        0.886859040896824
17      178     mRNA catabolic process
GO:0016032      1.27258931473331e-17    15.3000667556742        2.24704172721611
23      451     viral reproduction
GO:0006612      2.7774367925768e-17     29.7017726798749        0.762300186838281
16      153     protein targeting to membrane
GO:0043624      2.7774367925768e-17     29.7017726798749        0.762300186838281
16      153     cellular protein complex disassembly
GO:0043241      4.68432741617164e-17    28.6458752515091        0.78721195764999
16      158     protein complex disassembly
GO:0006401      1.33614007288617e-16    23.3314313346228        1.02138260328005
17      205     RNA catabolic process
GO:0034623      2.22674282394987e-16    25.7160940325497        0.866929624247457
16      174     cellular macromolecular complex disassembly
GO:0032984      3.510842773563e-16      24.9184925503944        0.891841395059165
16      179     macromolecular complex disassembly
GO:0071845      1.78371966509068e-15    17.6854636591479        1.41498858210504
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18      284     cellular component disassembly at cellular level
GO:0022411      2.27923242445049e-15    17.4185185185185        1.43491799875441
18      288     cellular component disassembly
GO:0072594      2.82815523203863e-15    21.5668693009119        1.01640024911771
16      204     establishment of protein localization to organelle
GO:0033365      1.10032896569639e-10    9.43744019138756        2.35665351878763
17      473     protein localization to organelle
GO:0006605      1.05853921576791e-09    8.68434185901435        2.36163587294997
16      474     protein targeting
Tissue: Adipose_Subcutaneous=>Thyroid   Type:   asymmetric
SourceGene:     ENSG00000179935.5
TargetGeneSet:  NOL9    DNAJC11 DNAJC16 TCEB3   ARID1A  NUDC    SNRNP40 TXLNA
ADPRHL2 GNL2    RP11    IPO13   POMGNT1 C1orf123        WDR3    GOLPH3L ADAR
PYGO2   FLAD1   CCT3    METTL13 STX6    DHX9    RBBP5   FBXO28  ACBD3   LIN9    URB2
HEATR1  HNRNPU  TAF1B   PREB    SLC5A6  EIF2B4  PPM1G   ASS1P2  PNPT1   PAPOLG  CCT7
POLR1A  RPIA    LMAN2L  POLR1B  AMMECR1L        CREB1   ATIC    CLN5    ANO7
ZDHHC3  SCAP    SLC52A1 ACTR8   SHQ1    QTRTD1  TSC22D2 ACTL6A  ABCF3   ALG3
PSMD2   LETM1   FAM193A GRPEL1  ANKRD17 SDAD1   CCT5    MARCH6  NUP155  SKIV2L2
MIER3   IPO11   C5orf48 HARS    TSPAN17 ZSCAN12P1       TRIM27  C6orf25 VARS
ZBTB9   BYSL    PPP2R5D MCM3    RP3     LATS1   MRPL18  EIF3B   C7orf26 BAZ1B
MEPCE   METTL2A TNPO3   CASP2   ZNF398  ABCF2   NEIL2   POLR3D  ELP3    INTS9   TTI2
TMEM68  SMU1    NOL6    ALG2    PAPPA   NUP188  EXOSC2  TPRN    NGB     BMS1
HNRNPF  ZFAND4  SEC24C  POLR3A  PDCD11  CTR9    NAT10   SSRP1   CCDC86  MTA2
GANAB   C11orf84        MARK2   STIP1   MRPL11  ANKRD42 DDX10   ZNF259  DDX6
TRAPPC4 FKBP4   RP4     DDX23   TARBP2  SUOX    OBFC2B  CCT2    UTP20   RNF34
DDX55   PUS1    PRMT5-AS1       PRMT5   AHSA1   PPP1R14D        TUBGCP4 GABPB1
RNF111  DIS3L   ASB7    SOLH    DNAJA3  GLYR1   CTD     CD2BP2  TBC1D10B
SALL1   TMCO7   CIRH1A  EXOSC6  SF3B3   DHODH   ZNF778  TSR1    TP53    ELAC2
TMEM11  TMEM199 ERAL1   UTP6    PSME3   TMEM101 EFTUD2  UBE2Z   DLX3    PPP1R9B
APPBP2  TACO1   FTSJ3   SRP68   CANT1   EIF4A3  MBD1    MOB3A   ELAVL1  HNRNPM
SYCE2   DNAJB1  MPV17L2 ZNF526  GRWD1   PRMT1   FIZ1    ZNF264  ZNF749  ZNF549
ZNF586  ZSCAN22 FAM110A NOP56   CSRP2BP SYS1    NCOA5   ZFP64   URB1    GART    CRKL
MORC2   PRR14L  ADSL    XPNPEP3 L3MBTL2 RRP7A   BCOR    GPKOW   SMC1A   FAM123B
TCEAL3-AS1      UTP14A
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0071843      1.73703127267487e-19    12.1937862032649        2.99349525984361
28      239     cellular component biogenesis at cellular level
GO:0022613      4.32132962375617e-19    12.4604486422668        2.81814407307453
27      225     ribonucleoprotein complex biogenesis
GO:0042254      1.69362791843912e-16    14.50107421875  1.8662376306138 21      149
ribosome biogenesis
GO:0034660      1.42909505026306e-13    8.20499304487883        3.56964915922774
24      285     ncRNA metabolic process
GO:0016072      6.8172733156039e-12     13.4828788839569        1.37775932461421
15      110     rRNA metabolic process
GO:0034470      6.97407048258037e-12    9.12935679694427        2.50501695384402
19      200     ncRNA processing
GO:0006364      4.20316621408951e-11    13.208250166334 1.30260881599889        14
104     rRNA processing
GO:0000377      2.80058731469138e-07    6.21241727072171        2.5551172929209 14
204     RNA splicing, via transesterification reactions with bulged adenosine as
nucleophile
GO:0000398      2.80058731469138e-07    6.21241727072171        2.5551172929209 14
204     nuclear mRNA splicing, via spliceosome
GO:0022618      2.98387086649268e-07    9.75920192638459        1.18988305307591
10      95      ribonucleoprotein complex assembly
GO:0000375      3.76452682895004e-07    6.05097497313066        2.61774271676701
14      209     RNA splicing, via transesterification reactions
GO:0071826      4.84306528829035e-07    9.21377517868746        1.25250847692201
10      100     ribonucleoprotein complex subunit organization
GO:0006397      2.73444066408918e-06    4.02560262789237        4.99750882291883
18      399     mRNA processing
GO:0006457      3.29274085052668e-06    5.36215693173821        2.70541831015155
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13      216     protein folding
GO:0006354      8.38605689660854e-06    7.4899577167019 1.35270915507577        9
108     DNA-dependent transcription, elongation
GO:0008380      1.36693574880991e-05    4.09618995462369        4.0456023804581 15
323     RNA splicing
Tissue: Thyroid=>Adipose_Subcutaneous   Type:   asymmetric
SourceGene:     ENSG00000239948.1
TargetGeneSet:  MTND2P28        RPL22   RPL11   ARID1A  KPNA7   RP1     RPS8
RPS15AP10       GTF2B   RPL5    RP11    RPS27   MTX1    UBC     EIF5B   MZT2B   BRK1
RPL15   RNF123  RPL29   DCP1A   PCNP    RPL24   FAM162A DNAJC19 ZBTB12B RPL34
RPS3A   FAM160A1        SKP1    CTB     SLC25A2 RPS14   RPL15P3 NOL7    RPS10
RPL10A  YIPF3   MTRNR2L9        RPL39P3 HSF2    MRPS12  EEF1A1P6        BAZ1B
RPS3AP26        TRIM56  HMBOX1  RPS20   MED30   RPS6    DCTN3   SETX    RPL7A
RPS24   PGAM1   RPL27A  BARX2   SLC38A4 PFDN5   NACA    STAT6   MRS2P2  RPL18AP3
MLXIP   ZC3H13  MBIP    SIVA1   RPL9P25 RPL4    C15orf40        SEC11A  RPS15A
RPL26   RPL23A  RPL17   RPL19   RPL27   SNORA76 ATF4P3  ROCK1P1 C18orf32
RPS15   ZBTB7A  RPL36   CTD     BRD4    RPSAP58 BCKDHA  RPL18   RPS5    RPL41P1
SOGA1   DPM1    HMGB1P10        RPL3    RP4     RP6     UXT     RPS4X   RPL10   MT
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      1.67042444738663e-54    185.120689655172        0.48487993910456
33      91      translational termination
GO:0006614      3.20328827974753e-54    159.286603340976        0.559476852812954
34      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      4.70222493290163e-54    157.06330749354 0.564805203792125       34
106     cotranslational protein targeting to membrane
GO:0045047      4.70222493290163e-54    157.06330749354 0.564805203792125       34
106     protein targeting to ER
GO:0072599      4.70222493290163e-54    157.06330749354 0.564805203792125       34
106     establishment of protein localization to endoplasmic reticulum
GO:0070972      3.428401168231e-52      134.512735326689        0.628745415542177
34      118     protein localization to endoplasmic reticulum
GO:0000184      4.78577855377913e-52    132.920930232558        0.634073766521348
34      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006414      4.91924770692221e-52    148.979166666667        0.559476852812954
33      105     translational elongation
GO:0006413      6.14796341299922e-48    95.5270003941663        0.809909348833991
34      152     translational initiation
GO:0006612      7.88144496579286e-48    94.7176079734219        0.815237699813162
34      153     protein targeting to membrane
GO:0034623      1.18682145954065e-47    85.341726618705 0.927133070375753       35
174     cellular macromolecular complex disassembly
GO:0032984      3.52072157385659e-47    82.349537037037 0.953774825271608       35
179     macromolecular complex disassembly
GO:0072594      7.0207651895783e-47     74.2473867595819        1.08698359975088
36      204     establishment of protein localization to organelle
GO:0000956      3.31579657706314e-46    83.398105081826 0.900491315479898       34
169     nuclear-transcribed mRNA catabolic process
GO:0019080      4.47185534298828e-46    90.6101694915254        0.80458099785482
33      151     viral genome expression
GO:0019083      4.47185534298828e-46    90.6101694915254        0.80458099785482
33      151     viral transcription
GO:0043624      7.23932442857183e-46    89.0875 0.815237699813162       33      153
cellular protein complex disassembly
GO:0006402      2.28648566589893e-45    78.1363049095607        0.948446474292437
34      178     mRNA catabolic process
GO:0043241      2.34076064577948e-45    85.494  0.841879454709017       33      158
protein complex disassembly
GO:0006401      4.11909201221411e-43    65.6741466068272        1.09231195073005
34      205     RNA catabolic process
GO:0071845      1.06961756697119e-39    47.2724230254351        1.51325167808456
35      284     cellular component disassembly at cellular level
GO:0019058      1.7280090696582e-39     53.6969696969697        1.2308490761885 33
231     viral infectious cycle
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GO:0022411      1.78061290578568e-39    46.5118577075099        1.53456508200125
35      288     cellular component disassembly
GO:0022415      1.03803681237724e-37    46.7411894273128        1.38537125458446
33      260     viral reproductive process
GO:0033365      1.09028316365855e-34    29.5702981651376        2.52031001314788
37      473     protein localization to organelle
GO:0006605      1.17930594278941e-34    29.5005148741419        2.52563836412705
37      474     protein targeting
GO:0016032      1.62166457839337e-32    27.9607371794872        2.40308629160612
35      451     viral reproduction
GO:0042274      3.05577230658442e-08    76.7147435897436        0.0959103176250778
5       18      ribosomal small subunit biogenesis
GO:0006364      7.65036914976698e-08    17.243961352657 0.554148501833783       8
104     rRNA processing
GO:0042254      9.18032191699592e-08    13.456512605042 0.793924295896478       9
149     ribosome biogenesis
GO:0016072      1.18618743017287e-07    16.2227905655016        0.586118607708809
8       110     rRNA metabolic process
GO:0022613      3.02358418324044e-07    9.82922596320722        1.19887897031347
10      225     ribonucleoprotein complex biogenesis
GO:0071843      5.27308797462763e-07    9.21918790327837        1.27347588402187
10      239     cellular component biogenesis at cellular level
GO:0030490      5.01355906814168e-06    145.641891891892        0.0372984568541969
3       7       maturation of SSU-rRNA
GO:0034470      1.08732419864739e-05    8.56400966183575        1.0656701958342 8
200     ncRNA processing
Tissue: Thyroid=>Adipose_Subcutaneous   Type:   asymmetric
SourceGene:     FSCN3(ENSG00000106328.8)
TargetGeneSet:  NMNAT1  DFFA    SPEN    RPL11   KPNA7   TXLNA   RP3     RP1
RABGGTB RP4     RP11    HBXIP   ATP5F1  HMGCS2  SRGAP2P1        RPRD2   LCE2B
RPS27   PYGO2   MEF2D   ISG20L2 GORAB   TTC32   RHOQ    GPR75   UBC     TIA1
DGUOK   COX5B   SLC9A2  SPOPL   KCNE4   MAP4    RPL29   APPL1   PDCD10  RPL22L1
DNAJC19 RPL34   SETD7   WWC2    FRG1    RICTOR  GRAMD3  HINT1   CTB     RPS14
SYNPO   ZNF300  C5orf25 GPLD1   PPP1R18 RPS10   C6orf162        TRMT11  URGCP
BAZ1B   CLDN3   GTPBP10 TRIM56  NAA38   ZNF862  DCTN6   RPS20   SNHG6   RPL30
POLR2K  MED30   TG      LY6D    EEF1D   RPL8    RPS6    TUSC1   NDUFB6  CALML5
VDAC2   RPS24   SNCG    AS3MT   C10orf118       PIDD    EIF3F   RPL27A  SPTY2D1 EXT2
NDUFS3  MRPL16  ALDH3B2 RSF1    TMEM126A        SDHD    BACE1   DDX6    KRT80
PFDN5   NACA    AVIL    SSH1    RPL21   MED4-AS1        PHF11   METTL17 PSME1
PSME2   OIP5-AS1        RPS3AP6 C15orf40        ECI1    RPS15A  CES2    APRT
VPS53   TLCD2   KDM6B   TMEM107 RPL26   TOM1L2  SUPT6H  NUFIP2  RPL19   WIPF2   RARA
RPL27   UBTF    ERN1    TNRC6C  STRA13  CTD     RPS15   OAZ1    RPL36   BRD4
UQCRFS1 KCNK6   RPL18   ZNF264  ZSCAN22 PCNA    KIF3B   SOGA1   ZNFX1   B4GALT5
PFDN4   ATP5O   ICOSLG  MPST    STS     BCOR    NDUFB11 UXT     RPS4X   RPL39
BCORL1  MT
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      1.72261507924495e-27    39.429560401523 0.951837243097364       24
105     translational elongation
GO:0006415      1.76542062947188e-27    44.6345315904139        0.824925610684382
23      91      translational termination
GO:0006614      6.65790942945432e-26    36.9776422764228        0.951837243097364
23      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      8.44160722142093e-26    36.5295626952253        0.960902359698291
23      106     cotranslational protein targeting to membrane
GO:0045047      8.44160722142093e-26    36.5295626952253        0.960902359698291
23      106     protein targeting to ER
GO:0072599      8.44160722142093e-26    36.5295626952253        0.960902359698291
23      106     establishment of protein localization to endoplasmic reticulum
GO:0019080      7.26053316034125e-25    26.568583408206 1.36883260674002        25
151     viral genome expression
GO:0019083      7.26053316034125e-25    26.568583408206 1.36883260674002        25
151     viral transcription
GO:0006413      8.62794227092081e-25    26.3575248848611        1.37789772334095
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25      152     translational initiation
GO:0070972      1.20810811690048e-24    31.8884015594542        1.06968375890942
23      118     protein localization to endoplasmic reticulum
GO:0000184      1.4867530081339e-24     31.554012345679 1.07874887551035        23
119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0043624      2.63788859273469e-23    24.6746359487068        1.38696283994187
24      153     cellular protein complex disassembly
GO:0034623      2.85741956529368e-23    22.4309864505508        1.57733028856135
25      174     cellular macromolecular complex disassembly
GO:0043241      5.86700946048458e-23    23.7455712093737        1.43228842294651
24      158     protein complex disassembly
GO:0032984      5.90363735413787e-23    21.6950502327861        1.62265587156598
25      179     macromolecular complex disassembly
GO:0000956      3.09189014661989e-22    21.9271672574927        1.53200470555671
24      169     nuclear-transcribed mRNA catabolic process
GO:0006612      6.41441462649512e-22    23.2457264957265        1.38696283994187
23      153     protein targeting to membrane
GO:0006402      1.10239174416829e-21    20.632601043816 1.61359075496505        24
178     mRNA catabolic process
GO:0019058      2.13772651322195e-21    17.0494773519164        2.0940419348142 26
231     viral infectious cycle
GO:0072594      2.98938399073077e-20    17.619937694704 1.84928378658916        24
204     establishment of protein localization to organelle
GO:0006401      3.36142128074374e-20    17.5213507512779        1.85834890319009
24      205     RNA catabolic process
GO:0022415      4.45590464750292e-20    14.9058201058201        2.35693031624109
26      260     viral reproductive process
GO:0071845      4.17372903084162e-19    13.4961978589886        2.57449311466334
26      284     cellular component disassembly at cellular level
GO:0022411      5.93462448425613e-19    13.2863685932388        2.61075358106705
26      288     cellular component disassembly
GO:0016032      4.70061871788295e-17    9.36348852337143        4.0883675870182 29
451     viral reproduction
GO:0033365      7.65497108572481e-13    7.30289757412399        4.2878001522386 25
473     protein localization to organelle
GO:0006605      8.02267033340791e-13    7.28610749254108        4.29686526883953
25      474     protein targeting
GO:0022904      2.499126848136e-06      10.5188470066519        0.870251193689018
8       96      respiratory electron transport chain
GO:0022613      6.29876814588043e-06    6.04228971962617        2.03965123520864
11      225     ribonucleoprotein complex biogenesis
GO:0042254      8.39393584807817e-06    7.47189695550351        1.35070237353816
9       149     ribosome biogenesis
GO:0071843      1.11563267010338e-05    5.6656432748538 2.16656286762162        11
239     cellular component biogenesis at cellular level
GO:0042274      1.7884689744967e-05     32.1844769403825        0.163172098816691
4       18      ribosomal small subunit biogenesis
Tissue: Adipose_Subcutaneous=>Thyroid   Type:   asymmetric
SourceGene:     OSBP(ENSG00000110048.6)
TargetGeneSet:  NOL9    DFFA    DNAJC16 SPEN    KIAA0090        ALPL    TCEB3   NUDC
GPR3    EYA3    GMEB1   SNRNP40 KPNA7   TMEM234 TXLNA   EIF2C3  THRAP3  FHL3
IPO13   DPH2    TOE1    CCDC17  RPS15AP10       RP11    ST7L    WDR3    PIAS3
GOLPH3L ADAR    PYGO2   CCT3    METTL13 URB2    HEATR1  KIF3C   EIF2B4  WDR43   MSH6
CCT4    TCEB1P21        POLR1A  ZNF2    LMAN2L  POU3F3  POLR1B  MYO7B   RBP4
AMMECR1L        CLN5    C3orf19 CMC1    MYD88   SCN5A   IP6K1   RRP9    ACTR8   GMPS
SH3BP2  NOP14   SRP72   NUP155  SKIV2L2 HSPA4   HARS    MFAP3   HRH2    NOP16   C4B
PFDN6   ZBTB9   BYSL    TAF8    RPL7L1  POLR1C  TRAM2   EIF3B   C7orf26 CCT6A   TBL2
POM121C ZKSCAN5 ZKSCAN1 MEPCE   AGFG2   KLHDC10 CNOT4   ABCF2   NOM1    NEIL2   XPO7
POLR3D  ELP3    EXTL3   LSM12P1 PRKDC   SULF1   ZNF706  BAALC   PLAA    DNAJA1  NOL6
STOML2  TBC1D13 NUP188  EXOSC2  GTF3C4  QSOX2   NGB     BMS1    HNRNPF  FAM35B
POLR3A  SFTPD   ENTPD7  CHUK    C10orf2 BTRC    PPRC1   NOLC1   PDCD11  CTR9
SPTY2D1 CAPRIN1 NAT10   CTD     HARBI1  OSBP    MTA2    GNG3    STX5    WDR74
C11orf95        MARK2   STIP1   DPF2    U4      IL18BP  ANKRD42 MRE11A  ZNF259  DDX6
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ZNF202  FKBP4   ZCRB1   SCAF11  DDX23   PA2G4   OBFC2B  KIF5A   CAND1   KRT8P22
SART3   ATXN2   GCN1L1  HSPH1   NUFIP1  RBM23   PRMT5-AS1       PRMT5   RNF31   RP4
NEK9    CYP46A1 C15orf57        TUBGCP4 MFAP1   DUOXA1  DUOX1   PIGB    CSNK1G1 ULK3
CHRNA5  C16orf73        THUMPD1 PPP4C   CD2BP2  ZNF785  ZNF629  DNAJA2  GFOD2
CIRH1A  DHODH   VPS53   TSR1    TP53    TMEM199 CTB     TP53I13 GOSR1   UTP6    NLE1
PSME3   AOC2    DHX8    EFTUD2  GFAP    SNX11   UBE2Z   VEZF1   APPBP2  FTSJ3
PSMC5   CEP76   ZNF24   FAM108A1        ZNF77   TNFSF14 ZNF121  ZNF562  SYCE2
DNAJB1  ZNF790  ZNF585B FBL     KCNJ14  JOSD2   ZNF613  ZNF614  ZNF347  ZNF542
ZNF582  ZNF543  ZNF17   ZNF749  ZNF587  ZNF417  ZNF8    NOP56   AHCY    SRSF6
RIMS4   NCOA5   GTPBP5  C20orf11        GART    COL18A1 ZNF70   BCRP3   TFIP11
TTC28   NF2     PES1    C22orf23        ADSL    XPNPEP3 ZNF81   PQBP1   GNL3L
FRMPD3  UTP14A
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0071843      3.85252355044714e-22    12.39983436853  3.42350010379905        32
239     cellular component biogenesis at cellular level
GO:0022613      7.56635125155855e-22    12.7562675726336        3.22296034876479
31      225     ribonucleoprotein complex biogenesis
GO:0042254      2.02701796015587e-16    13.2187273888061        2.13431596429313
22      149     ribosome biogenesis
GO:0006364      1.53815483121709e-12    13.4754878629224        1.48972389454017
16      104     rRNA processing
GO:0016072      3.75266354500608e-12    12.6100033418737        1.57566950384056
16      110     rRNA metabolic process
GO:0034470      2.93591071729606e-08    6.40109264739358        2.86485364334648
16      200     ncRNA processing
GO:0022618      1.08997984511789e-07    9.46064139941691        1.36080548058958
11      95      ribonucleoprotein complex assembly
GO:0034660      1.49143407056048e-07    4.98555377207063        4.08241644176874
18      285     ncRNA metabolic process
GO:0071826      1.85738005062477e-07    8.92599174501261        1.43242682167324
11      100     ribonucleoprotein complex subunit organization
GO:0006397      4.77018739622153e-06    3.68723404255319        5.71538301847623
19      399     mRNA processing
GO:0000377      7.67200425713932e-06    4.93034490203487        2.92215071621341
13      204     RNA splicing, via transesterification reactions with bulged
adenosine as nucleophile
GO:0000398      7.67200425713932e-06    4.93034490203487        2.92215071621341
13      204     nuclear mRNA splicing, via spliceosome
GO:0000375      9.96691757170118e-06    4.80286135072586        2.99377205729707
13      209     RNA splicing, via transesterification reactions
GO:0000460      1.85010637569267e-05    35.064039408867 0.171891218600789       4
12      maturation of 5.8S rRNA
Tissue: Thyroid=>Adipose_Subcutaneous   Type:   asymmetric
SourceGene:     PRINS(ENSG00000238115.1)
TargetGeneSet:  MTND1P23        MTND2P28        RPL22   NMNAT1  UBE4B   DFFA    SPEN
LDLRAD2 HSPG2   RPL11   ARID1A  WASF2   DNAJC8  EIF2C1  THRAP3  MFI2    RPS8
NEDD4   RP11    RPL5    HBXIP   NUDT4P1 HIST2H2AC       RPRD2   JTB     RPS27
ASH1L   MIR555  PIGM    TKT     PRRC2C  ZBTB37  CEP350  ARPC5   PTPN14  ZC3H11B ADI1
RPS7    ASXL2   C2orf18 CALM2   RPL36AP15       UBC     USP34   COMMD1  C1D     AAK1
DGUOK-AS1       TET3    DCTN1   VAMP5   TMEM131 EIF5B   UGGT1   MZT2B   RHOQP3
H3F3AP4 ANKRD44 RAPH1   TRIP12  PSMD1   GIGYF2  HDLBP   NR2C2   UBE2E2  RPL15
TRANK1  WDR48   HIGD1A  MAP4    RAD54L2 RPL29   DCP1A   NIT2    PCNP    RPL24
FAM162A NME9    COMMD2  PDCD10  PHC3    PEX5L   DNAJC19 HTT     BOD1L   RELL1
DANCR   LAMTOR3 RPL34   SETD7   H3F3AP6 RPS3A   MARCH6  NIPBL   CTD     SREK1IP1
MRPS36  TAF9    SERINC5 ERAP1   HINT1   C5orf15 SKP1    CTB     MTND5P11
CDC23   RPS14   ATP6V0E1        GNB2L1  TXNDC5  TMEM14C RPL15P3 NOL7    PPIAP29
ZSCAN23 SYNGAP1 MNF1    RP1     UHRF1BP1        RPL10A  MTRNR2L9        WDR11
BCKDHB  C6orf162        KIAA1919        PHACTR2 IGF2R   SFT2D1  FOXK1   EEF1A1P6
MPLKIP  CHCHD2  DPY19L2P4       RPS3AP26        TRIM56  PIK3CG  COG5    CAPZA2
METTL2A ZC3HAV1L        HIPK2   MLL3    DRP2    HMBOX1  DCTN6   LSM1    HOOK3
RPS20   POLR2K  UBR5    EIF3E   MED30   TG      RGP1    CLTA    CBWD6   CBWD3
ATP6V1G1        GAPVD1  RPL12   NUP214  PRRC2B  SETX    RPL7A   PRINS   FUT11
RPS24   RPS3AP5 EIF6    RPL27A  MTRNR2L8        TSG101  TRIM44  CKAP5   TMEM126B
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SDHD	BACE1	UBE4A	DDX6	EEF1A1P33	SCAF11	MLL4	PFDN5	CBX5	NACA
LRP1	GNS	EEA1	USP44	GIT2	RPL6	PEBP1	COX6A1	MLXIP	SBNO1
GOLGA3	RPSAP54	MZT1	COMMD6	COL4A2	CCNB1IP1	C14orf21	ACTR10
MNAT1	C14orf142	CCNK	TJP1	HERC2P10	SNAP23	B2M	GTF2A2	RPL4
MYO9A	C15orf40	SEC11A	MPG	SPSB3	NDUFB10	RPS15A	SULT1A3	SRCAP
NFATC3	ATXN1L	HSBP1	MNT	RPL26	TOM1L2	USP22	RPL23A	TAOK1	CPD	RFFL
TAF15	RPL19	CDK12	WIPF2	RPL27	RPS7P11	RPS2P48	CLTC	SUMO2	TNRC6C
ROCK1P1	MYL12A	MYL12B	ANKRD12	C18orf32	RPL17	NFIC	NDUFA11	BRD4
SLC35E1	SDHAF1	ZNF585A	KCNK6	RPL18	BCAT2	NUCB1-AS1	RPL13A	KLK7
ZNF264	ZNF587	RPS5	TMEM230	KIF3B	RP4	NCOA3	ADNP	TSHZ2	RPL12P4	SON
VWFP1	THAP7	HMGB1P10	NF2	APOL6	RPL3	EP300	TCF20	RNU12-2P
USP9X	RP6	HSD17B10	HUWE1	GNL3L	RPS4X	TTC3P1	COX7B	PGAM4
ITM2A	APOOL	RPL39	HCFC1	RPL10	FUNDC2	MT
GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0006415	7.33765796271195e-39	45.2089314194577	1.39166839665075
34	91	translational termination
GO:0006614	6.26152776488408e-38	38.0645161290323	1.60577122690471
35	105	SRP-dependent cotranslational protein targeting to membrane
GO:0006613	9.23046030882955e-38	37.525745873088	1.62106428620857	35
106	cotranslational protein targeting to membrane
GO:0045047	9.23046030882955e-38	37.525745873088	1.62106428620857	35
106	protein targeting to ER
GO:0072599	9.23046030882955e-38	37.525745873088	1.62106428620857	35
106	establishment of protein localization to endoplasmic reticulum
GO:0000184	2.99269513480796e-37	33.1678280690329	1.81987405715867
36	119	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006414	2.34027871483817e-36	36.258642765685	1.60577122690471	34
105	translational elongation
GO:0070972	6.98358439932385e-36	32.0731312346159	1.80458099785482
35	118	protein localization to endoplasmic reticulum
GO:0000956	2.99556436540263e-35	23.2417582417582	2.58452702235139
39	169	nuclear-transcribed mRNA catabolic process
GO:0019080	1.69538391784688e-34	24.8995041952708	2.30925195488201
37	151	viral genome expression
GO:0019083	1.69538391784688e-34	24.8995041952708	2.30925195488201
37	151	viral transcription
GO:0006402	2.62958091883432e-34	21.7230215827338	2.72216455608608
39	178	mRNA catabolic process
GO:0006413	5.39434674311892e-33	23.6767940354147	2.32454501418587
36	152	translational initiation
GO:0006401	8.735982473712e-32	18.1549053356282	3.13507715729015
39	205	RNA catabolic process
GO:0006612	1.615353405929e-31	22.5041006014215	2.33983807348972
35	153	protein targeting to membrane
GO:0043624	1.615353405929e-31	22.5041006014215	2.33983807348972
35	153	cellular protein complex disassembly
GO:0022415	3.6452905487949e-31	15.0813387319973	3.97619541900215
42	260	viral reproductive process
GO:0043241	5.40034035051794e-31	21.5816504939243	2.416303370009	35
158	protein complex disassembly
GO:0034623	9.81317478602205e-31	19.8712103407756	2.66099231887067
36	174	cellular macromolecular complex disassembly
GO:0072594	1.29617062208105e-30	17.592731582066	3.1197840979863	38	204
establishment of protein localization to organelle
GO:0032984	2.8715111329249e-30	19.1696087696088	2.73745761538994
36	179	macromolecular complex disassembly
GO:0019058	1.05483846835524e-29	15.6674107142857	3.53269669919037
39	231	viral infectious cycle
GO:0016032	3.86713719436514e-28	9.79943306722203	6.89716974603834
49	451	viral reproduction
GO:0071845	3.32954327223926e-26	12.231778425656	4.34322884229465	39
284	cellular component disassembly at cellular level
GO:0022411	5.68518374756703e-26	12.0318416523236	4.40440107951007
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39      288     cellular component disassembly
GO:0033365      1.74772767289841e-22    7.99710270896712        7.23361705072313
44      473     protein localization to organelle
GO:0006605      1.51247769006523e-21    7.7342605385959 7.24891011002699        43
474     protein targeting
GO:0006511      8.13314886944853e-07    4.01654518107139        5.566673586603  20
364     ubiquitin-dependent protein catabolic process
GO:0019941      1.09436102136724e-06    3.93445876032941        5.67372500172998
20      371     modification-dependent protein catabolic process
GO:0043632      1.23993118404523e-06    3.90027264805914        5.71960417964155
20      374     modification-dependent macromolecule catabolic process
GO:0051603      2.26947503386426e-06    3.73768016287128        5.94900006919936
20      389     proteolysis involved in cellular protein catabolic process
GO:0044257      3.73596844110694e-06    3.60709541298742        6.14780984014947
20      402     cellular protein catabolic process
GO:0022613      9.54713578926652e-06    4.49357785562195        3.44093834336724
14      225     ribonucleoprotein complex biogenesis
GO:0042254      1.81476997840804e-05    5.34893029675638        2.27866583627431
11      149     ribosome biogenesis
GO:0071843      1.88730436687949e-05    4.20976918947933        3.6550411736212 14
239     cellular component biogenesis at cellular level
Tissue: Thyroid=>Adipose_Subcutaneous   Type:   cluster
SourceGene:     PRINS(ENSG00000238115.1)
TargetGeneSet:  MTND1P23        MTND2P28        RPL22   NMNAT1  UBE4B   DFFA    SPEN
LDLRAD2 HSPG2   RPL11   ARID1A  WASF2   DNAJC8  EIF2C1  THRAP3  MFI2    RPS8
NEDD4   RP11    RPL5    HBXIP   NUDT4P1 HIST2H2AC       RPRD2   JTB     RPS27
ASH1L   MIR555  PIGM    TKT     PRRC2C  ZBTB37  CEP350  ARPC5   PTPN14  ZC3H11B ADI1
RPS7    ASXL2   C2orf18 CALM2   RPL36AP15       UBC     USP34   COMMD1  C1D     AAK1
DGUOK-AS1       TET3    DCTN1   VAMP5   TMEM131 EIF5B   UGGT1   MZT2B   RHOQP3
H3F3AP4 ANKRD44 RAPH1   TRIP12  PSMD1   GIGYF2  HDLBP   NR2C2   UBE2E2  RPL15
TRANK1  WDR48   HIGD1A  MAP4    RAD54L2 RPL29   DCP1A   NIT2    PCNP    RPL24
FAM162A NME9    COMMD2  PDCD10  PHC3    PEX5L   DNAJC19 HTT     BOD1L   RELL1
DANCR   LAMTOR3 RPL34   SETD7   H3F3AP6 RPS3A   MARCH6  NIPBL   CTD     SREK1IP1
MRPS36  TAF9    SERINC5 ERAP1   HINT1   C5orf15 SKP1    CTB     MTND5P11
CDC23   RPS14   ATP6V0E1        GNB2L1  TXNDC5  TMEM14C RPL15P3 NOL7    PPIAP29
ZSCAN23 SYNGAP1 MNF1    RP1     UHRF1BP1        RPL10A  MTRNR2L9        WDR11
BCKDHB  C6orf162        KIAA1919        PHACTR2 IGF2R   SFT2D1  FOXK1   EEF1A1P6
MPLKIP  CHCHD2  DPY19L2P4       RPS3AP26        TRIM56  PIK3CG  COG5    CAPZA2
METTL2A ZC3HAV1L        HIPK2   MLL3    DRP2    HMBOX1  DCTN6   LSM1    HOOK3
RPS20   POLR2K  UBR5    EIF3E   MED30   TG      RGP1    CLTA    CBWD6   CBWD3
ATP6V1G1        GAPVD1  RPL12   NUP214  PRRC2B  SETX    RPL7A   PRINS   FUT11
RPS24   RPS3AP5 EIF6    RPL27A  MTRNR2L8        TSG101  TRIM44  CKAP5   TMEM126B
SDHD    BACE1   UBE4A   DDX6    EEF1A1P33       SCAF11  MLL4    PFDN5   CBX5    NACA
LRP1    GNS     EEA1    USP44   GIT2    RPL6    PEBP1   COX6A1  MLXIP   SBNO1
GOLGA3  RPSAP54 MZT1    COMMD6  COL4A2  CCNB1IP1        C14orf21        ACTR10
MNAT1   C14orf142       CCNK    TJP1    HERC2P10        SNAP23  B2M     GTF2A2  RPL4
MYO9A   C15orf40        SEC11A  MPG     SPSB3   NDUFB10 RPS15A  SULT1A3 SRCAP
NFATC3  ATXN1L  HSBP1   MNT     RPL26   TOM1L2  USP22   RPL23A  TAOK1   CPD     RFFL
TAF15   RPL19   CDK12   WIPF2   RPL27   RPS7P11 RPS2P48 CLTC    SUMO2   TNRC6C
ROCK1P1 MYL12A  MYL12B  ANKRD12 C18orf32        RPL17   NFIC    NDUFA11 BRD4
SLC35E1 SDHAF1  ZNF585A KCNK6   RPL18   BCAT2   NUCB1-AS1       RPL13A  KLK7
ZNF264  ZNF587  RPS5    TMEM230 KIF3B   RP4     NCOA3   ADNP    TSHZ2   RPL12P4 SON
VWFP1   THAP7   HMGB1P10        NF2     APOL6   RPL3    EP300   TCF20   RNU12-2P
USP9X   RP6     HSD17B10        HUWE1   GNL3L   RPS4X   TTC3P1  COX7B   PGAM4
ITM2A   APOOL   RPL39   HCFC1   RPL10   FUNDC2  MT
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      7.33765796271195e-39    45.2089314194577        1.39166839665075
34      91      translational termination
GO:0006614      6.26152776488408e-38    38.0645161290323        1.60577122690471
35      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      9.23046030882955e-38    37.525745873088 1.62106428620857        35
106     cotranslational protein targeting to membrane
GO:0045047      9.23046030882955e-38    37.525745873088 1.62106428620857        35
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106     protein targeting to ER
GO:0072599      9.23046030882955e-38    37.525745873088 1.62106428620857        35
106     establishment of protein localization to endoplasmic reticulum
GO:0000184      2.99269513480796e-37    33.1678280690329        1.81987405715867
36      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006414      2.34027871483817e-36    36.258642765685 1.60577122690471        34
105     translational elongation
GO:0070972      6.98358439932385e-36    32.0731312346159        1.80458099785482
35      118     protein localization to endoplasmic reticulum
GO:0000956      2.99556436540263e-35    23.2417582417582        2.58452702235139
39      169     nuclear-transcribed mRNA catabolic process
GO:0019080      1.69538391784688e-34    24.8995041952708        2.30925195488201
37      151     viral genome expression
GO:0019083      1.69538391784688e-34    24.8995041952708        2.30925195488201
37      151     viral transcription
GO:0006402      2.62958091883432e-34    21.7230215827338        2.72216455608608
39      178     mRNA catabolic process
GO:0006413      5.39434674311892e-33    23.6767940354147        2.32454501418587
36      152     translational initiation
GO:0006401      8.735982473712e-32      18.1549053356282        3.13507715729015
39      205     RNA catabolic process
GO:0006612      1.615353405929e-31      22.5041006014215        2.33983807348972
35      153     protein targeting to membrane
GO:0043624      1.615353405929e-31      22.5041006014215        2.33983807348972
35      153     cellular protein complex disassembly
GO:0022415      3.6452905487949e-31     15.0813387319973        3.97619541900215
42      260     viral reproductive process
GO:0043241      5.40034035051794e-31    21.5816504939243        2.416303370009  35
158     protein complex disassembly
GO:0034623      9.81317478602205e-31    19.8712103407756        2.66099231887067
36      174     cellular macromolecular complex disassembly
GO:0072594      1.29617062208105e-30    17.592731582066 3.1197840979863 38      204
establishment of protein localization to organelle
GO:0032984      2.8715111329249e-30     19.1696087696088        2.73745761538994
36      179     macromolecular complex disassembly
GO:0019058      1.05483846835524e-29    15.6674107142857        3.53269669919037
39      231     viral infectious cycle
GO:0016032      3.86713719436514e-28    9.79943306722203        6.89716974603834
49      451     viral reproduction
GO:0071845      3.32954327223926e-26    12.231778425656 4.34322884229465        39
284     cellular component disassembly at cellular level
GO:0022411      5.68518374756703e-26    12.0318416523236        4.40440107951007
39      288     cellular component disassembly
GO:0033365      1.74772767289841e-22    7.99710270896712        7.23361705072313
44      473     protein localization to organelle
GO:0006605      1.51247769006523e-21    7.7342605385959 7.24891011002699        43
474     protein targeting
GO:0006511      8.13314886944853e-07    4.01654518107139        5.566673586603  20
364     ubiquitin-dependent protein catabolic process
GO:0019941      1.09436102136724e-06    3.93445876032941        5.67372500172998
20      371     modification-dependent protein catabolic process
GO:0043632      1.23993118404523e-06    3.90027264805914        5.71960417964155
20      374     modification-dependent macromolecule catabolic process
GO:0051603      2.26947503386426e-06    3.73768016287128        5.94900006919936
20      389     proteolysis involved in cellular protein catabolic process
GO:0044257      3.73596844110694e-06    3.60709541298742        6.14780984014947
20      402     cellular protein catabolic process
GO:0022613      9.54713578926652e-06    4.49357785562195        3.44093834336724
14      225     ribonucleoprotein complex biogenesis
GO:0042254      1.81476997840804e-05    5.34893029675638        2.27866583627431
11      149     ribosome biogenesis
GO:0071843      1.88730436687949e-05    4.20976918947933        3.6550411736212 14
239     cellular component biogenesis at cellular level
```

```
Tissue: Adipose_Subcutaneous=>Thyroid   Type:   asymmetric
SourceGene:     RNU5B-3P(ENSG00000252410.1)
TargetGeneSet:  GBP5    GAPDHP23        FCRL5   LAX1    IGKJ5   IGKC    IGKJ4
IGKJ3   IGKJ2   IGKJ1   IGKV4-1 IGKV1-5 IGKV1-9 IGKV3-11        IGKV3-15
IGKV1-16        IGKV2-28        IGKV1-39        SP140   IGJ     RP11    CPQ
TSPAN32 POU2AF1 PPIHP1  IGHG2   IGHGP   IGHG1   IGHG3   KIAA0125        IGHV4-39
CHRFAM7A        U6      FER1L4  IGLV1-47        IGLV3-19        IGLV2-14
IGLV3-10        IGLV3-1 IGLL5   IGLC1   IGLC3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006958      1.43760734354932e-16    342.690476190476        0.0553594906926856
8       50      complement activation, classical pathway
GO:0006956      1.03041429986511e-15    261.454545454545        0.0697529582727839
8       63      complement activation
GO:0002455      1.34156965685537e-15    252.245614035088        0.0719673379004913
8       65      humoral immune response mediated by circulating immunoglobulin
GO:0006959      1.75770439496887e-15    162.955752212389        0.135077157290153
9       122     humoral immune response
GO:0072376      9.39406184566582e-15    194.067567567568        0.0907895647360044
8       82      protein activation cascade
GO:0016064      1.14715514870305e-13    139.145631067961        0.122898069337762
8       111     immunoglobulin mediated immune response
GO:0019724      1.42774143786272e-13    135.179245283019        0.126219638779323
8       114     B cell mediated immunity
GO:0002449      3.1980049917134e-12     89.7861635220126        0.18490069891357
8       167     lymphocyte mediated immunity
GO:0002460      6.12848705203208e-12    82.4393063583815        0.200401356307522
8       181     adaptive immune response based on somatic recombination of immune
receptors built from immunoglobulin superfamily domains
GO:0002250      1.26327648627516e-11    74.9736842105263        0.219223583143035
8       198     adaptive immune response
GO:0002443      2.10622277151748e-11    70.1083743842365        0.233617050723133
8       211     leukocyte mediated immunity
GO:0002253      3.41068508676345e-10    48.6048109965636        0.33104975434226
8       299     activation of immune response
GO:0050778      1.61994340149145e-09    39.5477528089888        0.403017092242751
8       364     positive regulation of immune response
GO:0002252      2.57343455361979e-09    37.1878306878307        0.427375268147533
8       386     immune effector process
Tissue: Thyroid=>Adipose_Subcutaneous   Type:   asymmetric
SourceGene:     RP11-165M1.3(ENSG00000261394.1)
TargetGeneSet:  RPL22   NMNAT1  ZMYM4   RPS8    GTF2B   RPL5    RPS27   GAS5
ZBTB37  RP11    ZC3H11B RPS7    SNX17   CCT7    H3F3AP4 BRK1    RPL15   RPL14
LIMD1   PCNP    RPL24   C3orf33 RPL7L1P8        KIAA1530        LAMTOR3 EEF1A1P9
H3F3AP6 RPS3A   RWDD4   PDCD6   CTD     SMN1    SKP1    CTB     RPL15P3 PPIAP29 ABT1
RPS10   RPL10A  YIPF3   FTH1P5  EEF1A1P6        RPS3AP26        TRIM56  CLTA
ATP6V1G1        RPL7A   ADRA2A  RPS3AP5 BCCIP   RPL27A  TSG101  MRE11A  COPZ1   LRP1
RPL6    RPSAP54 COL4A2-AS1      SIVA1   RAB11A  MYO9A   RPS15A  TUFM
SLX1B-SULT1A4   SULT1A4 HSBP1   TAOK1   RPS7P11 PPM1E   SUMO2   RPL17   NFIC
RPL18A  RPSAP58 RPL18   RPL13A  RPL41P1 DPM1    RPL12P4 RP1     ZNF70   RP6
WASF4P  RPS23P8 HK2P1   MT
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      5.5318913889203e-29     86.316742081448 0.428690056051484       20
105     translational elongation
GO:0006415      2.36445172426491e-28    94.4722222222222        0.371531381911286
19      91      translational termination
GO:0006614      4.60603802964364e-27    79.0156976744186        0.428690056051484
19      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      5.59710219405467e-27    78.1020114942529        0.43277281849007
19      106     cotranslational protein targeting to membrane
GO:0045047      5.59710219405467e-27    78.1020114942529        0.43277281849007
19      106     protein targeting to ER
GO:0072599      5.59710219405467e-27    78.1020114942529        0.43277281849007
19      106     establishment of protein localization to endoplasmic reticulum
```

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GO:0070972      5.00424773490483e-26    68.5775252525252        0.481765967753097
19      118     protein localization to endoplasmic reticulum
GO:0000184      5.9392824035809e-26     67.887  0.485848730191682       19      119
nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      7.04633966105414e-24    51.3143939393939        0.61649712822642
19      151     viral genome expression
GO:0019083      7.04633966105414e-24    51.3143939393939        0.61649712822642
19      151     viral transcription
GO:0006413      8.0315888380199e-24     50.925  0.620579890665006       19      152
translational initiation
GO:0006612      9.14605855784254e-24    50.5414179104478        0.624662653103591
19      153     protein targeting to membrane
GO:0043624      9.14605855784254e-24    50.5414179104478        0.624662653103591
19      153     cellular protein complex disassembly
GO:0043241      1.72786162919261e-23    48.7062949640288        0.645076465296519
19      158     protein complex disassembly
GO:0000956      6.50560619729064e-23    45.0996666666667        0.68998685212096
19      169     nuclear-transcribed mRNA catabolic process
GO:0034623      1.15269674110565e-22    43.6295161290323        0.710400664313888
19      174     cellular macromolecular complex disassembly
GO:0006402      1.79869541711764e-22    42.5199685534591        0.726731714068231
19      178     mRNA catabolic process
GO:0032984      2.0069417338134e-22     42.25125        0.730814476506816       19
179     macromolecular complex disassembly
GO:0019058      8.33552572293967e-22    34.4659132336857        0.943118123313265
20      231     viral infectious cycle
GO:0072594      2.55136214309036e-21    36.4774324324324        0.832883537471455
19      204     establishment of protein localization to organelle
GO:0006401      2.80449918466187e-21    36.2787634408602        0.836966299910041
19      205     RNA catabolic process
GO:0022415      9.06468470910005e-21    30.2393162393162        1.06151823403225
20      260     viral reproductive process
GO:0016032      1.39265510665852e-18    19.3527373527374        1.84132585980209
22      451     viral reproduction
GO:0071845      1.41977872101893e-18    25.3219811320755        1.1595045325583 19
284     cellular component disassembly at cellular level
GO:0022411      1.84830042862882e-18    24.9383828996283        1.17583558231264
19      288     cellular component disassembly
GO:0033365      1.77300484115557e-14    14.5827092511013        1.93114663345097
19      473     protein localization to organelle
GO:0006605      1.84204569789139e-14    14.5496153846154        1.93522939588956
19      474     protein targeting
Tissue: Adipose_Subcutaneous=>Thyroid   Type:   cluster
SourceGene:     RP11-416A17.1(ENSG00000244540.1)
TargetGeneSet:  RP11    FCRL3   FCRL2   IGKJ5   IGKC    IGKJ4   IGKJ3   IGKJ2
IGKJ1   IGKV4-1 IGKV1-5 IGKV1-6 IGKV1-8 IGKV3-15        IGKV3D-15       EOMES
KLHL7   IGJ     GALNTL6 BLK     POU2AF1 GS1     GJB6    IGHA2   IGHG2   IGHGP
IGHA1   IGHG1   IGHG3   IGHM    IGHJ5   IGHV6-1 IGHV2-5 IGHV1-18        IGHV3-30
IGHV3-33        IGHV3-48        IGHV5-51        IGHV4-59        TNFRSF17
TBC1D27 IGLV4-69        IGLV1-47        IGLV5-45        IGLV1-44        IGLV1-40
ZNF280A IGLV3-25        IGLV2-11        IGLV3-1 IGLC1   IGLC2   IGLC3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006958      4.17272448412705e-17    210.526829268293        0.0830392360390284
9       50      complement activation, classical pathway
GO:0006956      3.89403027699151e-16    159.7   0.104629437409176       9       63
complement activation
GO:0002455      5.24961254567502e-16    153.975 0.107951006850737       9       65
humoral immune response mediated by circulating immunoglobulin
GO:0006959      2.24370981243159e-15    91.2946428571429        0.202615735935229
10      122     humoral immune response
GO:0072376      4.73636565626121e-15    117.978082191781        0.136184347104007
9       82      protein activation cascade
GO:0016064      7.94729347232045e-14    84.2647058823529        0.184347104006643
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9       111     immunoglobulin mediated immune response
GO:0019724      1.01656580271012e-13    81.84   0.189329458168985       9       114
B cell mediated immunity
GO:0002449      3.33579003599497e-12    54.1860759493671        0.277351048370355
9       167     lymphocyte mediated immunity
GO:0002460      6.91206296908552e-12    49.7267441860465        0.300602034461283
9       181     adaptive immune response based on somatic recombination of immune
receptors built from immunoglobulin superfamily domains
GO:0002250      1.55296624225031e-11    45.2    0.328835374714553       9       198
adaptive immune response
GO:0002253      1.87926130523349e-11    34.9431537320811        0.49657463151339
10      299     activation of immune response
GO:0002443      2.75033885290613e-11    42.2524752475247        0.3504255760847 9
211     leukocyte mediated immunity
GO:0050778      1.3027059467683e-10     28.3958837772397        0.604525638364127
10      364     positive regulation of immune response
GO:0002252      2.31323124500339e-10    26.6926291793313        0.6410629022213 10
386     immune effector process
Tissue: Thyroid=>Adipose_Subcutaneous   Type:   asymmetric
SourceGene:     RP11-95P2.3(ENSG00000263105.1)
TargetGeneSet:  FAM213B CEP104  DFFA    LUZP1   RPL11   RP4     RP1     RPS8    RPL5
MTF2    RWDD3   RP11    HBXIP   RPRD2   PI4KB   KIRREL  GORAB   ACBD6   UBC
PRORSD1P        CCDC104 COMMD1  TPRKB   DGUOK   ZEB2-AS1        ZNF662  SETD2
IP6K2   RPL10AP6        NIT2    RPL24   HEG1    TRIM42  RPL22L1 DNAJC19 HNRPDL
RPL34   SETD7   FRG1    C5orf55 NDUFAF2 TAF9    GRAMD3  CTB     NDST1   EHMT2
AGPAT1  MNF1    RPL10A  LINC00472       RPL39P3 COX7A2  SENP6   C6orf162
TRMT11  MRPS12  C7orf44 BAZ1B   FIS1    ST7-AS1 MRPS33  SSBP1   ZNF862  MLL3
KCTD9   DCTN6   RPS20   CHCHD7  C8orf59 RPL30   NDUFB9  ZNF572  RPS6    RPL12
PRRC2B  ARHGAP12        RPS24   SFR1    CYB5R2  RPL27A  FIBIN   INCENP  MRPL11
CLNS1A  TMEM126B        TMEM126A        SDHD    RPS25   CBL     PFDN5   SSH1    MMAB
RILPL1  MED4-AS1        NIN     MNAT1   EXD2    COX16   RPL15P2 PPP1R13B
ATPBD4  RN5S395 RPS27L  LRRC49  C15orf39        WDR61   MORF4L1 C15orf40
RPS15A  NFATC3  APRT    RPL26   C17orf48        NCOR1   RPL23A  RFFL    RPL17
RPL19   RPL27   SSTR2   CDC42EP4        TNRC6C  CTD     NDUFV2  C18orf32
RPS15   ZBTB7A  SLC35E1 ZNF224  SNRPD2  ARHGAP35        RPL18   ZNF264  SNRPB2
SOGA1   SNHG11  B4GALT5 SPATA2  DPM1    TSHZ2   PFDN4   ATP5O   KRTAP10-5
MRPL40  FAM211B EP300   FTLP2   RPS2P55 CXorf36 UXT     IQSEC2  COX7B   MID2
RPL39   CCDC160 MECP2   FUNDC2  MT
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      3.6001244660263e-29     54.2354593522802        0.705279911424815
23      91      translational termination
GO:0006414      1.38215202205398e-27    44.9316251027679        0.813784513182479
23      105     translational elongation
GO:0006614      1.38215202205398e-27    44.9316251027679        0.813784513182479
23      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.75467512630116e-27    44.3871666441045        0.821534841879455
23      106     cotranslational protein targeting to membrane
GO:0045047      1.75467512630116e-27    44.3871666441045        0.821534841879455
23      106     protein targeting to ER
GO:0072599      1.75467512630116e-27    44.3871666441045        0.821534841879455
23      106     establishment of protein localization to endoplasmic reticulum
GO:0019080      1.08115365886981e-26    32.4142492245941        1.17029963324337
25      151     viral genome expression
GO:0019083      1.08115365886981e-26    32.4142492245941        1.17029963324337
25      151     viral transcription
GO:0070972      2.54989901228049e-26    38.747723240686 0.914538786243167       23
118     protein localization to endoplasmic reticulum
GO:0000184      3.14202731221828e-26    38.34140917603  0.922289114940143       23
119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0034623      1.18028220087103e-23    25.7981818181818        1.34855719327382
24      174     cellular macromolecular complex disassembly
GO:0006413      1.21010173272858e-23    28.4670324884592        1.17804996194035
23      152     translational initiation
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GO:0006612      1.41571643707551e-23    28.2460674157303        1.18580029063733
23      153     protein targeting to membrane
GO:0043624      1.41571643707551e-23    28.2460674157303        1.18580029063733
23      153     cellular protein complex disassembly
GO:0032984      2.37440225082577e-23    24.9571847507331        1.3873088367587 24
179     macromolecular complex disassembly
GO:0019058      2.8929724382685e-23     20.8442427680091        1.79032592900145
26      231     viral infectious cycle
GO:0043241      3.05073149597029e-23    27.1903454015814        1.22455193412221
23      158     protein complex disassembly
GO:0000956      1.50675129089966e-22    25.1222872094813        1.30980554978894
23      169     nuclear-transcribed mRNA catabolic process
GO:0006402      5.11638036035902e-22    23.6485683218557        1.37955850806173
23      178     mRNA catabolic process
GO:0072594      5.79866532403971e-22    21.4530303030303        1.5810670541831 24
204     establishment of protein localization to organelle
GO:0022415      6.26001439040458e-22    18.2235142118863        2.01508546121376
26      260     viral reproductive process
GO:0006401      1.37336880572313e-20    20.1019261637239        1.58881738288008
23      205     RNA catabolic process
GO:0071845      9.85998518569059e-20    15.6215328629122        2.20109334994118
25      284     cellular component disassembly at cellular level
GO:0022411      1.38750251207979e-19    15.3795725711289        2.23209466472908
25      288     cellular component disassembly
GO:0016032      5.71737765680821e-17    10.424667036626 3.49539824233617        27
451     viral reproduction
GO:0033365      1.72757418304349e-14    8.90997023809524        3.66590547366964
25      473     protein localization to organelle
GO:0006605      1.81291181544045e-14    8.88948621457645        3.67365580236662
25      474     protein targeting
GO:0022613      1.69884318108812e-07    7.95830985915493        1.7438239568196 12
225     ribonucleoprotein complex biogenesis
GO:0042274      2.02089222131986e-07    51.4953271028037        0.139505916545568
5       18      ribosomal small subunit biogenesis
GO:0071843      3.26044016689171e-07    7.46008810572687        1.85232855857726
12      239     cellular component biogenesis at cellular level
GO:0006364      1.40535534033086e-06    11.4126602564103        0.806034184485503
8       104     rRNA processing
GO:0016072      2.15109764132722e-06    10.736802413273 0.852536156667359       8
110     rRNA metabolic process
GO:0042254      2.30284618741013e-06    8.8620665742025 1.15479897584942        9
149     ribosome biogenesis
GO:0018022      2.31647393217416e-06    58.9711934156379        0.100754273060688
4       13      peptidyl-lysine methylation
GO:0034660      1.30103427658037e-05    5.59062658090627        2.20884367863816
11      285     ncRNA metabolic process
Tissue: Thyroid=>Adipose_Subcutaneous   Type:   asymmetric
SourceGene:     SERPINB7(ENSG00000166396.8)
TargetGeneSet:  RP4     RPL11   SYNC    RP3     RPS8    PTGES3P1        RP11
RP11-165H20.1   SRGAP2P1        ISG20L2 C1orf9  UBC     COX5B   WDSUB1  RPL37A
PCOLCE2 NAALADL2        RPL34   NDUFC1  COX7C   CTD     HINT1   PAIP2   CTB
RPS14   GPLD1   PPP1R10 RPL24P4 RPL39P3 FILIP1  MRPS12  C7orf44 RPS20   EEF1D   RPL8
RPS6    ANKRD19P        SEC61B  RPL35   ITIH5   RPS24   NHP2P1  PIDD    RPLP2
STIM1   RPL27A  C11orf10        FAU     CDC42EP2        TMEM126A        RPS25
ZDHHC17 ACTR6   EIF4A1P7        RAD17P2 RPL7AP6 SNAP23  DUT     RPS3AP6 RPLP1
C16orf13        RPL13   RPL7AP64        RPL19   RPL27   BPTF    C18orf21
DAZAP1  RPS15   UQCR11  ZBTB7A  RPL36   RPS19   APOE    RPL18   SLC27A5 STS
EEF1B2P3        RPL39
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      3.91760352999628e-39    131.544117647059        0.428690056051484
25      105     translational elongation
GO:0006614      3.91760352999628e-39    131.544117647059        0.428690056051484
25      105     SRP-dependent cotranslational protein targeting to membrane
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GO:0006613      5.11506298933691e-39    129.91103848947 0.43277281849007        25
106     cotranslational protein targeting to membrane
GO:0045047      5.11506298933691e-39    129.91103848947 0.43277281849007        25
106     protein targeting to ER
GO:0072599      5.11506298933691e-39    129.91103848947 0.43277281849007        25
106     establishment of protein localization to endoplasmic reticulum
GO:0006415      1.01595607281427e-38    146.609808102345        0.371531381911286
24      91      translational termination
GO:0070972      1.01929864570169e-37    113.053447185326        0.481765967753097
25      118     protein localization to endoplasmic reticulum
GO:0000184      1.38503807196725e-35    103.196390977444        0.485848730191682
24      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006413      1.01370724578367e-34    82.5903195924039        0.620579890665006
25      152     translational initiation
GO:0006612      1.20892872418513e-34    81.9393382352941        0.624662653103591
25      153     protein targeting to membrane
GO:0019080      6.81769414030768e-33    77.0213723284589        0.61649712822642
24      151     viral genome expression
GO:0019083      6.81769414030768e-33    77.0213723284589        0.61649712822642
24      151     viral transcription
GO:0043624      9.55721164742459e-33    75.8166112956811        0.624662653103591
24      153     cellular protein complex disassembly
GO:0043241      2.17778342448324e-32    72.9620469083156        0.645076465296519
24      158     protein complex disassembly
GO:0000956      1.210548569293e-31      67.3749753694581        0.68998685212096
24      169     nuclear-transcribed mRNA catabolic process
GO:0072594      2.45626616808616e-31    58.3839960565232        0.832883537471455
25      204     establishment of protein localization to organelle
GO:0034623      2.53647848095198e-31    65.1062857142857        0.710400664313888
24      174     cellular macromolecular complex disassembly
GO:0006402      4.50871690182668e-31    63.3974025974026        0.726731714068231
24      178     mRNA catabolic process
GO:0032984      5.19459579490162e-31    62.9839631336406        0.730814476506816
24      179     macromolecular complex disassembly
GO:0006401      1.56735702897842e-29    53.8380426203631        0.836966299910041
24      205     RNA catabolic process
GO:0019058      3.04852624346059e-28    46.9896480331263        0.943118123313265
24      231     viral infectious cycle
GO:0022415      5.60861453497785e-27    41.1312348668281        1.06151823403225
24      260     viral reproductive process
GO:0071845      4.85079485677874e-26    37.2712087912088        1.1595045325583 24
284     cellular component disassembly at cellular level
GO:0022411      6.81833763565149e-26    36.6961038961039        1.17583558231264
24      288     cellular component disassembly
GO:0033365      1.81251467797619e-23    24.5793505525049        1.93114663345097
26      473     protein localization to organelle
GO:0006605      1.91335697240479e-23    24.5227272727273        1.93522939588956
26      474     protein targeting
GO:0016032      3.14244848263736e-21    22.4262295081967        1.84132585980209
24      451     viral reproduction
GO:0042274      4.02163361774794e-13    175.991258741259        0.0734897238945402
7       18      ribosomal small subunit biogenesis
GO:0042254      8.37006330389339e-09    18.324  0.608331603349249       9       149
ribosome biogenesis
GO:0022613      2.21126551623303e-08    13.4570479354533        0.918621548681752
10      225     ribonucleoprotein complex biogenesis
GO:0071843      3.9182406551914e-08     12.6218697085821        0.97578022282195
10      239     cellular component biogenesis at cellular level
GO:0006364      2.04628754142937e-07    19.838421887391 0.424607293612899       7
104     rRNA processing
GO:0016072      3.00773334138548e-07    18.6749439880508        0.449103868244412
7       110     rRNA metabolic process
GO:0000028      1.28170735981912e-06    256.946428571429        0.0244965746315134
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3       6       ribosomal small subunit assembly
GO:0030490      2.23647028926986e-06    192.696428571429        0.028579337070099
3       7       maturation of SSU-rRNA
GO:0034470      1.62448585712689e-05    9.90364687126345        0.816552487717113
7       200     ncRNA processing
Tissue: Thyroid=>Adipose_Subcutaneous   Type:   asymmetric
SourceGene:     STAC2(ENSG00000141750.5)
TargetGeneSet:  RPL11   SPATA1  GTF2B   RPL5    RP4     RP11    MRPL9   UFC1
GORAB   ZBTB37  RPS7    UBC     RPL37A  RPL14   RPL24   CD80    AADAC   ANKRD17
RPL34   EEF1A1P19       BTF3    CTB     RPS14   GTPBP10 BPGM    RPS20   RPL30   RPL8
RPS6    RPL35   GPSM1   RPS24   RPL13AP5        FAU     RPS3    RPL41   NACA
CSRP2   C12orf51        ST13P4  POU4F1  RPL7AP6 GANC    RPS3AP6 RPL4    GOLGA6L9
RPS15A  CES4A   RPL26   TOM1L2  RPS7P1  RPL23A  RPL17   RPL19   RPL27   CTD
RPS16   RPS19   SNRPD2  RPS11   RPS23P8 RPS4X
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      1.45136449418672e-52    304.840175953079        0.321154245380943
29      91      translational termination
GO:0006414      1.89776590058902e-50    248.442583732057        0.370562590824164
29      105     translational elongation
GO:0006614      1.89776590058902e-50    248.442583732057        0.370562590824164
29      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      2.60863724274437e-50    245.19893742621 0.374091758355823       29
106     cotranslational protein targeting to membrane
GO:0045047      2.60863724274437e-50    245.19893742621 0.374091758355823       29
106     protein targeting to ER
GO:0072599      2.60863724274437e-50    245.19893742621 0.374091758355823       29
106     establishment of protein localization to endoplasmic reticulum
GO:0070972      9.21040633400354e-49    211.960674157303        0.416441768735728
29      118     protein localization to endoplasmic reticulum
GO:0000184      1.21601407591743e-48    209.590909090909        0.419970936267386
29      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      2.69986575030717e-45    154.270491803279        0.532904297280465
29      151     viral genome expression
GO:0019083      2.69986575030717e-45    154.270491803279        0.532904297280465
29      151     viral transcription
GO:0006413      3.33145999118763e-45    153.005543237251        0.536433464812124
29      152     translational initiation
GO:0006612      4.1044811073224e-45     151.760997067449        0.539962632343782
29      153     protein targeting to membrane
GO:0043624      4.1044811073224e-45     151.760997067449        0.539962632343782
29      153     cellular protein complex disassembly
GO:0043241      1.13940202102058e-44    145.827695560254        0.557608470002076
29      158     protein complex disassembly
GO:0000956      9.54110386490306e-44    134.266233766234        0.596429312850322
29      169     nuclear-transcribed mRNA catabolic process
GO:0034623      2.38428944348493e-43    129.590909090909        0.614075150508615
29      174     cellular macromolecular complex disassembly
GO:0006402      4.85955415276291e-43    126.076571079927        0.62819182063525
29      178     mRNA catabolic process
GO:0032984      5.79043246756825e-43    125.227272727273        0.631720988166909
29      179     macromolecular complex disassembly
GO:0072594      3.36770442063706e-41    107.149350649351        0.719950176458377
29      204     establishment of protein localization to organelle
GO:0006401      3.91675899148825e-41    106.53305785124 0.723479343990035       29
205     RNA catabolic process
GO:0019058      1.53514968848981e-39    92.6512151215122        0.815237699813162
29      231     viral infectious cycle
GO:0022415      5.61262883182794e-38    80.8541912632822        0.917583558231264
29      260     viral reproductive process
GO:0071845      8.07621455431916e-37    73.120320855615 1.00228357899107        29
284     cellular component disassembly at cellular level
GO:0022411      1.23024967229617e-36    71.9706914706915        1.01640024911771
29      288     cellular component disassembly
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GO:0016032      1.62286670818752e-32    47.4346793349169        1.59165455677808
30      451     viral reproduction
GO:0033365      2.95274583043609e-30    41.4336609336609        1.66929624247457
29      473     protein localization to organelle
GO:0006605      3.14039544754146e-30    41.3375893769152        1.67282541000623
29      474     protein targeting
GO:0022613      6.30863781610371e-13    22.895233366435 0.794062694623209       13
225     ribonucleoprotein complex biogenesis
GO:0071843      1.36407422619961e-12    21.4557522123894        0.843471040066431
13      239     cellular component biogenesis at cellular level
GO:0006364      2.39628482267737e-12    37.1198754540737        0.367033423292506
10      104     rRNA processing
GO:0042254      3.22551214992942e-12    28.420652173913 0.525845962217148       11
149     ribosome biogenesis
GO:0016072      4.23907571398562e-12    34.8780487804878        0.388208428482458
10      110     rRNA metabolic process
GO:0042274      2.56231928117234e-11    159.866666666667        0.0635250155698568
6       18      ribosomal small subunit biogenesis
GO:0034470      1.60597167918263e-09    18.2413350449294        0.705833506331742
10      200     ncRNA processing
GO:0034660      3.42466960135217e-09    14.1775547445255        1.00581274652273
11      285     ncRNA metabolic process
GO:0042273      6.66989270388823e-08    153.106382978723        0.0423500103799045
4       12      ribosomal large subunit biogenesis
Tissue: Thyroid=>Adipose_Subcutaneous   Type:   asymmetric




SourceGene:     TNFRSF14(ENSG00000157873.11)





TargetGeneSet:  CEP104  UBR4    RP1     PPCS    RP11    RPS27   GUK1    UBC
TPRKB   ART4    EEF1B2  IL17RC  FLNB-AS1        THOC7   TMEM45A FAM55C  RPL22L1
WHSC1   BDH2    RPL34   RPS3A   CTD     TAF9    NDFIP1  CTB     ANKS1A  TRMT11
IGF2R   TMEM120A        FIS1    C7orf73 RPS20   RPL30   POLR2K  EEF1D   GPAA1   RPL8
RPS6    NOXA1   KIAA0913        RPS24   BTRC    TRIM44  C11orf55        FIBP    MLL
RPS25   B4GALNT3        ZNF384  NACA    POC1B   RPL18AP3        KIAA0247
ZC3H14  RPS3AP6 LRRC49  WDR61   APRT    TAX1BP3 RPL26   C17orf103       HSD17B1P1
RPL27   MAP3K3  NT5C    SEMA6B  RPL36   ERCC1   C19orf68        B4GALT5 RPS2P55 UXT
RPL39

GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term




GO:0006414      3.09E-22        67.69012419     0.39236039      16      105
translational elongation
```

GO:0070972	1.27E-19	53.37565347	0.440938343	15	118	protein localization to endoplasmic reticulum
GO:0006415	1.44E-19	65.09090909	0.340045672	14	91	translational termination
GO:0006614	1.19E-18	55.02307692	0.39236039	14	105	SRP-dependent cotranslational protein targeting to membrane
GO:0006613	1.37E-18	54.42119565	0.396097156	14	106	cotranslational protein targeting to membrane
GO:0045047	1.37E-18	54.42119565	0.396097156	14	106	protein targeting to ER
GO:0072599	1.37E-18	54.42119565	0.396097156	14	106	establishment of protein localization to endoplasmic reticulum
GO:0019080	5.81E-18	40.33088235	0.564251609	15	151	viral genome expression

GO:0019083	5.81E-18	40.33088235	0.564251609	15	151	viral transcription
GO:0000184	7.40E-18	47.64	0.444675109	14	119	"nuclear-transcribed mRNA catabolic process, nonsense-mediated decay"
GO:0006413	2.50E-16	36.16413043	0.567988375	14	152	translational initiation
GO:0006612	2.74E-16	35.90143885	0.57172514	14	153	protein targeting to membrane
GO:0043624	2.74E-16	35.90143885	0.57172514	14	153	cellular protein complex disassembly
GO:0043241	4.33E-16	34.64270833	0.590408968	14	158	protein complex disassembly
GO:0022415	8.70E-16	24.42277826	0.971559062	16	260	viral reproductive process

GO:0000956	1.12E-15	32.15935484	0.63151339	14	169	nuclear-transcribed mRNA catabolic process
GO:0034623	1.70E-15	31.1434375	0.650197218	14	174	cellular macromolecular complex disassembly
GO:0006402	2.33E-15	30.37530488	0.665144281	14	178	mRNA catabolic process
GO:0032984	2.53E-15	30.18909091	0.668881046	14	179	macromolecular complex disassembly
GO:0019058	3.59E-15	25.25106838	0.863192859	15	231	viral infectious cycle
GO:0072594	1.58E-14	26.17078947	0.762300187	14	204	establishment of protein localization to organelle
GO:0006401	1.69E-14	26.03193717	0.766036952	14	205	RNA catabolic process

GO:0016032	1.94E-14	16.12471132	1.685281295	18	451	viral reproduction
GO:0071845	1.50E-12	18.31277778	1.061241437	14	284	cellular component disassembly at cellular level
GO:0022411	1.81E-12	18.04032847	1.076188499	14	288	cellular component disassembly
GO:0033365	1.14E-10	11.70557608	1.767490139	15	473	protein localization to organelle
GO:0006605	1.34E-09	10.60423913	1.771226905	14	474	protein targeting

Tissue: Artery_Tibial=>Thyroid Type: asymmetric
SourceGene: AMPD3(ENSG00000133805.10)
TargetGeneSet: RPL22 ICMT RP11 RP3 WNT4 RPL11 KDM4A RPS8 IPP
PGM1 FPGT GNG5 EVI5 RPL5 ABCD3 PSMA5 RPS27 RGS8 NAV1
IPO9-AS1 CICP13 ACBD3 B3GALNT2 TRIM58 RPS7 DDX1 CIB4
KCNK3 DHX57 SRBD1 UBC AAK1 PAX8 MAP3K2 METTL8 OLA1 NBEAL1
CREB1 PSMD1 GRM7 ATP2B2 TMPPE DCLK3 RPL14 CTNNB1 RPL29 CRYBG3
RPL24 HGD ZNF148 COPG1 METTL15P1 PSMD2 C3orf70 MB21D2 MIR943
TAPT1 SCFD2 THAP6 SEC31A AGPAT9 RPS3A TMA16 STOX2 SORBS2 ANKRA2 CTD
PRRC1 CAMLG MTND5P11 PCDHA14 GNB2L1 RP1 MUTED PHACTR1 AGPAT1
CCND3 FAXC PDE7B IFNGR1 LATS1 TIAM2 TULP4 FAM120B ELFN1 FBXL18
TMEM60 RPS3AP26 CAV1 CEP41 RPS20 YTHDF3 FAM82B EIF3E FER1L6

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AK3P2   PUF60   RPS6    VCP     TSTD2   TGFBR1  CTNNAL1 RPL7A   SEC16A  CCNY
HKDC1   HK1     TSPAN15 C10orf35        VDAC2   RPS3AP5 ALDH18A1        ENTPD7  GBF1
MXI1    SEC23IP RPL27A  ST5     PLEKHA7 MUC15   METTL15 AMBRA1  ARHGAP1 CYBASC3
FADS2   U6      SNHG1   DRAP1   TSGA10IP        NDUFV1  CCND1   CAPN5   PAK1
ARHGAP20        RPS12P21        RPS25   PKNOX2  NRIP2   COPS7A  CYP27B1 CCDC65
PFDN5   CBX5    CAND1   NAP1L1  LTA4H   SLC9A7P1        SYCP3   KCTD10  RPL6
NOC4L   ANKRD26P4       N4BP2L1 TPT1    LMO7    GRK1    SALL2   CPNE6   TSSK6
LINC00517       MGAT2   GNPNAT1 VTI1B   FAM181A-AS1     FAM181A WDR25   SEC11A  DET1
GLYR1   BFAR    RPS15A  7SK     CHMP1A  POLR2A  RPL26   ZNF29P  TOM1L2  RPS7P1
RPL23A  RASL10B ZNHIT3  RPL17   RPL19   CNP     UBTF    RPS7P11 CD300C  TNRC6C
BAHCC1  MAPRE2  MYO5B   ADNP2   ZNF562  ZNF846  NOTCH3  SLC35E1 ARMC6   RPSAP58 OPA3
RSPH6A  FPR3    ZNF578  AP5S1   RRBP1   PYGB    COX4I2  FOXS1   PPIAP3  ZNFX1
SNAI1   ADNP    PMEPA1  GNAS    SLCO4A1 SOX18   WRB     ZNF70   TTC28   SH3BP1
SLC35A2 IGBP1   CXCR3   NHSL2   RPS4X   FGF16   LPAR4   FRMPD3  XIAP
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      5.49707574372244e-25    33.6272110242698        1.04532558300464
23      91      translational termination
GO:0006614      6.885869606049e-25      29.6379760041732        1.20614490346689
24      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      8.81679103035034e-25    29.2744761250429        1.21763199778562
24      106     cotranslational protein targeting to membrane
GO:0045047      8.81679103035034e-25    29.2744761250429        1.21763199778562
24      106     protein targeting to ER
GO:0072599      8.81679103035034e-25    29.2744761250429        1.21763199778562
24      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      1.4048713517324e-23     25.5157326940366        1.35547712961041
24      118     protein localization to endoplasmic reticulum
GO:0000184      1.74307841946451e-23    25.2453669384729        1.36696422392914
24      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006414      2.0059914759924e-23     27.8585195292512        1.20614490346689
23      105     translational elongation
GO:0006413      4.10438586134194e-22    19.7660132908918        1.7460383364473 25
152     translational initiation
GO:0006612      4.85961034177315e-22    19.6102061170213        1.75752543076604
25      153     protein targeting to membrane
GO:0019080      6.81456303131408e-21    18.8417433736276        1.73455124212857
24      151     viral genome expression
GO:0019083      6.81456303131408e-21    18.8417433736276        1.73455124212857
24      151     viral transcription
GO:0000956      1.06276498205865e-19    16.4817872753764        1.94131893986575
24      169     nuclear-transcribed mRNA catabolic process
GO:0043624      1.726210050884e-19      17.5129101667563        1.75752543076604
23      153     cellular protein complex disassembly
GO:0043241      3.65285913707503e-19    16.8583268583269        1.8149609023597 23
158     protein complex disassembly
GO:0006402      3.709521462815e-19      15.508688494604 2.04470278873434        24
178     mRNA catabolic process
GO:0034623      3.38665676251778e-18    15.0549715185477        1.99875441145941
23      174     cellular macromolecular complex disassembly
GO:0032984      6.47404941193852e-18    14.5672852788237        2.05618988305308
23      179     macromolecular complex disassembly
GO:0072594      9.45973896564975e-18    13.2441314553991        2.34336724102138
24      204     establishment of protein localization to organelle
GO:0006401      1.06119106486774e-17    13.1700256789355        2.35485433534011
24      205     RNA catabolic process
GO:0019058      1.71046442166792e-16    11.4945907328026        2.65351878762715
24      231     viral infectious cycle
GO:0022415      2.55124071533549e-15    10.0613511577942        2.98664452287039
24      260     viral reproductive process
GO:0071845      1.85440489406182e-14    9.11700975081257        3.26233478651996
24      284     cellular component disassembly at cellular level
GO:0022411      2.53208610317863e-14    8.97631241997439        3.30828316379489
24      288     cellular component disassembly
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GO:0016032      1.60963128202544e-12    6.3500576896973 5.18067953774825        27
451     viral reproduction
GO:0006605      5.14730290142517e-12    6.01332625175028        5.44488270707909
27      474     protein targeting
GO:0033365      2.95186882341796e-11    5.7492489613295 5.43339561276036        26
473     protein localization to organelle
GO:0042273      7.73650233766217e-06    44.0648148148148        0.137845131824787
4       12      ribosomal large subunit biogenesis
GO:0042254      8.44832163588241e-06    6.52370411363217        1.71157705349111
10      149     ribosome biogenesis
GO:0022613      1.11906352074409e-05    5.1479787817816 2.58459622171476        12
225     ribonucleoprotein complex biogenesis
Tissue: Artery_Tibial=>Thyroid  Type:   cluster
SourceGene:     AMPD3(ENSG00000133805.10)
TargetGeneSet:  RPL22   ICMT    RP11    RP3     WNT4    RPL11   KDM4A   RPS8    IPP
PGM1    FPGT    GNG5    EVI5    RPL5    ABCD3   PSMA5   RPS27   RGS8    NAV1
IPO9-AS1        CICP13  ACBD3   B3GALNT2        TRIM58  RPS7    DDX1    CIB4
KCNK3   DHX57   SRBD1   UBC     AAK1    PAX8    MAP3K2  METTL8  OLA1    NBEAL1
CREB1   PSMD1   GRM7    ATP2B2  TMPPE   DCLK3   RPL14   CTNNB1  RPL29   CRYBG3
RPL24   HGD     ZNF148  COPG1   METTL15P1       PSMD2   C3orf70 MB21D2  MIR943
TAPT1   SCFD2   THAP6   SEC31A  AGPAT9  RPS3A   TMA16   STOX2   SORBS2  ANKRA2  CTD
PRRC1   CAMLG   MTND5P11        PCDHA14 GNB2L1  RP1     MUTED   PHACTR1 AGPAT1
CCND3   FAXC    PDE7B   IFNGR1  LATS1   TIAM2   TULP4   FAM120B ELFN1   FBXL18
TMEM60  RPS3AP26        CAV1    CEP41   RPS20   YTHDF3  FAM82B  EIF3E   FER1L6
AK3P2   PUF60   RPS6    VCP     TSTD2   TGFBR1  CTNNAL1 RPL7A   SEC16A  CCNY
HKDC1   HK1     TSPAN15 C10orf35        VDAC2   RPS3AP5 ALDH18A1        ENTPD7  GBF1
MXI1    SEC23IP RPL27A  ST5     PLEKHA7 MUC15   METTL15 AMBRA1  ARHGAP1 CYBASC3
FADS2   U6      SNHG1   DRAP1   TSGA10IP        NDUFV1  CCND1   CAPN5   PAK1
ARHGAP20        RPS12P21        RPS25   PKNOX2  NRIP2   COPS7A  CYP27B1 CCDC65
PFDN5   CBX5    CAND1   NAP1L1  LTA4H   SLC9A7P1        SYCP3   KCTD10  RPL6
NOC4L   ANKRD26P4       N4BP2L1 TPT1    LMO7    GRK1    SALL2   CPNE6   TSSK6
LINC00517       MGAT2   GNPNAT1 VTI1B   FAM181A-AS1     FAM181A WDR25   SEC11A  DET1
GLYR1   BFAR    RPS15A  7SK     CHMP1A  POLR2A  RPL26   ZNF29P  TOM1L2  RPS7P1
RPL23A  RASL10B ZNHIT3  RPL17   RPL19   CNP     UBTF    RPS7P11 CD300C  TNRC6C
BAHCC1  MAPRE2  MYO5B   ADNP2   ZNF562  ZNF846  NOTCH3  SLC35E1 ARMC6   RPSAP58 OPA3
RSPH6A  FPR3    ZNF578  AP5S1   RRBP1   PYGB    COX4I2  FOXS1   PPIAP3  ZNFX1
SNAI1   ADNP    PMEPA1  GNAS    SLCO4A1 SOX18   WRB     ZNF70   TTC28   SH3BP1
SLC35A2 IGBP1   CXCR3   NHSL2   RPS4X   FGF16   LPAR4   FRMPD3  XIAP
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      5.49707574372244e-25    33.6272110242698        1.04532558300464
23      91      translational termination
GO:0006614      6.885869606049e-25      29.6379760041732        1.20614490346689
24      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      8.81679103035034e-25    29.2744761250429        1.21763199778562
24      106     cotranslational protein targeting to membrane
GO:0045047      8.81679103035034e-25    29.2744761250429        1.21763199778562
24      106     protein targeting to ER
GO:0072599      8.81679103035034e-25    29.2744761250429        1.21763199778562
24      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      1.4048713517324e-23     25.5157326940366        1.35547712961041
24      118     protein localization to endoplasmic reticulum
GO:0000184      1.74307841946451e-23    25.2453669384729        1.36696422392914
24      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006414      2.0059914759924e-23     27.8585195292512        1.20614490346689
23      105     translational elongation
GO:0006413      4.10438586134194e-22    19.7660132908918        1.7460383364473 25
152     translational initiation
GO:0006612      4.85961034177315e-22    19.6102061170213        1.75752543076604
25      153     protein targeting to membrane
GO:0019080      6.81456303131408e-21    18.8417433736276        1.73455124212857
24      151     viral genome expression
GO:0019083      6.81456303131408e-21    18.8417433736276        1.73455124212857
24      151     viral transcription
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GO:0000956      1.06276498205865e-19    16.4817872753764        1.94131893986575
24      169     nuclear-transcribed mRNA catabolic process
GO:0043624      1.726210050884e-19      17.5129101667563        1.75752543076604
23      153     cellular protein complex disassembly
GO:0043241      3.65285913707503e-19    16.8583268583269        1.8149609023597 23
158     protein complex disassembly
GO:0006402      3.709521462815e-19      15.508688494604 2.04470278873434        24
178     mRNA catabolic process
GO:0034623      3.38665676251778e-18    15.0549715185477        1.99875441145941
23      174     cellular macromolecular complex disassembly
GO:0032984      6.47404941193852e-18    14.5672852788237        2.05618988305308
23      179     macromolecular complex disassembly
GO:0072594      9.45973896564975e-18    13.2441314553991        2.34336724102138
24      204     establishment of protein localization to organelle
GO:0006401      1.06119106486774e-17    13.1700256789355        2.35485433534011
24      205     RNA catabolic process
GO:0019058      1.71046442166792e-16    11.4945907328026        2.65351878762715
24      231     viral infectious cycle
GO:0022415      2.55124071533549e-15    10.0613511577942        2.98664452287039
24      260     viral reproductive process
GO:0071845      1.85440489406182e-14    9.11700975081257        3.26233478651996
24      284     cellular component disassembly at cellular level
GO:0022411      2.53208610317863e-14    8.97631241997439        3.30828316379489
24      288     cellular component disassembly
GO:0016032      1.60963128202544e-12    6.3500576896973 5.18067953774825        27
451     viral reproduction
GO:0006605      5.14730290142517e-12    6.01332625175028        5.44488270707909
27      474     protein targeting
GO:0033365      2.95186882341796e-11    5.7492489613295 5.43339561276036        26
473     protein localization to organelle
GO:0042273      7.73650233766217e-06    44.0648148148148        0.137845131824787
4       12      ribosomal large subunit biogenesis
GO:0042254      8.44832163588241e-06    6.52370411363217        1.71157705349111
10      149     ribosome biogenesis
GO:0022613      1.11906352074409e-05    5.1479787817816 2.58459622171476        12
225     ribonucleoprotein complex biogenesis
Tissue: Artery_Tibial=>Thyroid  Type:   asymmetric
SourceGene:     C19orf66(ENSG00000130813.12)
TargetGeneSet:  RPL22   PNRC2   TMEM57  PTAFR   DNAJC8  TAF12   RPS8    NASP
CMPK1   ST6GALNAC3      NEDD4   GNG5    RPL5    RP11    JTB     RPS27   C1orf43
IVNS1ABP        SERTAD4 GGPS1   SH3YL1  SRSF7   UBC     CCDC104 CCT4    SSB     OLA1
HSPD1   CASP10  MFF     UBE2F   ING5    JAGN1   RPL15   RPL14   IFRD2   RPL29   NEK4
RPL24   SEMA5B  CNBP    PIK3CB  RPL22L1 LBP     MRFAP1  CC2D2A  CCNI    MAPK10
H2AFZ   ANK2    RPS3A   SORBS2  PLEKHG4B        NDUFAF2 SLC30A5 BTF3    NSA2
HINT1   PAIP2   CTB     BOD1    ZNF354B BPHL    DEK     HLA-H   HIST1H2BK
RPS10   C6orf106        RPL10A  BRPF3   EEF1A1  PNISR   AKD1    MRPS12  C6orf70
HOXA-AS3        FKBP9   C7orf23 CDK14   RPS3AP26        FAM185A HGSNAT  RPS20   E2F5
GS1     EIF3E   EIF3H   EEF1D   AK3     FREM1   RPS6    RFK     RBM18   RPL35
GARNL3  RPL12   SET     NKX2-1  EEF1A1P5        RPL7A   DCLRE1C WAC     P4HA1
VDAC2   RPS3AP5 MINPP1  MRPL43  KAZALD1 TIAL1   HTRA1   RASSF7  OLFML1  RPL27A  IPO7
C11orf58        SERGEF  SNHG1   SLC25A45        CAPN5   C11orf75        TAF1D
SCN4B   RPS25   FAM118B SLC6A12 SLC6A13 COPS7A  FGFR1OP2        MED21   MBD6
RPL14P1 NAP1L1  CHPT1   RPLP0   C12orf65        RP13    MRP63   C1QTNF9-AS1     TPT1
PIBF1   FAM155A LRRC16B BAZ1A   VTI1B   CDAN1   SLTM    RPS3AP6 FAM96A  RSL1D1
SNX29   BFAR    NPIP    RPS15A  BCKDK   KAT8    PLCG2   MNT     FXR2    RPL26
ZNF18   C17orf108       RPL23A  RPL19   ASB16   TMUB2   RPS7P11 UTP18   RPL17
ADNP2   RPS15   OAZ1    CAMSAP3 EIF3G   DHPS    RPL18   RPL13A  RPS9    RPS5
BFSP1   AHCY    C22orf39        SEPT5   EIF3L   PLXNB2  MED14   IGBP1   RPS4X
EIF4BP7 FAM3A
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      2.36050348003758e-40    53.8825757575758        1.11895370562591
33      105     translational elongation
GO:0006415      3.48190877685576e-39    59.8031165311653        0.96975987820912
```

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31      91      translational termination
GO:0006413      4.94510631537467e-39    37.2966101694915        1.61981869766798
36      152     translational initiation
GO:0000184      2.7413336646545e-38     45.0665961945032        1.2681475330427 33
119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006614      6.23447663693387e-37    48.4413315754779        1.11895370562591
31      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      8.73826405145199e-37    47.7920867208672        1.12961040758425
31      106     cotranslational protein targeting to membrane
GO:0045047      8.73826405145199e-37    47.7920867208672        1.12961040758425
31      106     protein targeting to ER
GO:0072599      8.73826405145199e-37    47.7920867208672        1.12961040758425
31      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      8.93874122208456e-37    43.3427373236752        1.25749083108435
32      118     protein localization to endoplasmic reticulum
GO:0000956      9.20926500736885e-33    28.3977272727273        1.8009826309598 33
169     nuclear-transcribed mRNA catabolic process
GO:0006402      5.67781830737457e-32    26.6181818181818        1.89689294858487
33      178     mRNA catabolic process
GO:0019080      1.67542810010713e-31    29.7755420054201        1.60916199570964
31      151     viral genome expression
GO:0019083      1.67542810010713e-31    29.7755420054201        1.60916199570964
31      151     viral transcription
GO:0006612      2.59571371316958e-31    29.2832866853259        1.63047539962632
31      153     protein targeting to membrane
GO:0043624      2.59571371316958e-31    29.2832866853259        1.63047539962632
31      153     cellular protein complex disassembly
GO:0034623      6.9257309933436e-31     26.1463865158162        1.85426614075151
32      174     cellular macromolecular complex disassembly
GO:0043241      7.53752324109567e-31    28.1204788425837        1.68375890941803
31      158     protein complex disassembly
GO:0032984      1.80086583217337e-30    25.2481320397011        1.90754965054322
32      179     macromolecular complex disassembly
GO:0072594      6.31783128145094e-30    22.5295055821372        2.17396719950176
33      204     establishment of protein localization to organelle
GO:0006401      7.46800371641796e-30    22.3969344608879        2.18462390146011
33      205     RNA catabolic process
GO:0019058      8.21654898857364e-27    18.5820907817777        2.461698152377  32
231     viral infectious cycle
GO:0022415      2.20499404397268e-26    16.9042851421706        2.77074250916892
33      260     viral reproductive process
GO:0071845      6.06660650136629e-24    14.6187874056727        3.02650335616912
32      284     cellular component disassembly at cellular level
GO:0022411      9.42250704533257e-24    14.3862704918033        3.06913016400249
32      288     cellular component disassembly
GO:0016032      9.6487085624725e-21     9.81405542986425        4.80617258321223
35      451     viral reproduction
GO:0033365      4.5441610743182e-20     9.30633897394574        5.04062002629576
35      473     protein localization to organelle
GO:0006605      4.49057635309671e-19    8.92306818181818        5.0512767282541 34
474     protein targeting
GO:0042254      5.49616685618282e-07    7.89241917502787        1.58784859179296
11      149     ribosome biogenesis
GO:0022613      5.18549968006423e-06    5.5877802023408 2.39775794062695        12
225     ribonucleoprotein complex biogenesis
GO:0071843      9.58602691291293e-06    5.2379475088416 2.54695176804373        12
239     cellular component biogenesis at cellular level
GO:0006364      1.50371048294149e-05    8.10559360730594        1.10829700366757
8       104     rRNA processing
Tissue: Artery_Tibial=>Thyroid  Type:   asymmetric
SourceGene:     C3orf37(ENSG00000183624.8)
TargetGeneSet:  ATAD3C  RPL22   RP11    C1orf100        CHMP3   MRPS25  NEK10
RPL10AP6        EIF4E3  SLC15A2 ATP13A4-AS1     WDR19   RAP1GDS1        CTB
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RPL10A  KLHDC3  MED23   RP1     INHBA   RPS20   RPL7    RPL30   RPL13AP5        SSH3
RPS12P21        CREBL2  SIPA1L1 ANP32BP1        ODF3L1  JMJD5   MT1G    ZDHHC1
C16orf7 RPL23A  RPL17   RPL19   SDK2    KIAA1328        RPL18A  RPS11   RPS5
C20orf196       ZC3H7B  SHROOM2 MCF2    VDAC1P6
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      8.40751245877888e-17    85.7103260869565        0.214102830253962
11      91      translational termination
GO:0006414      4.33612779750617e-16    72.8737280296022        0.24704172721611
11      105     translational elongation
GO:0006614      4.33612779750617e-16    72.8737280296022        0.24704172721611
11      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      4.83110592468598e-16    72.1016018306636        0.249394505570549
11      106     cotranslational protein targeting to membrane
GO:0045047      4.83110592468598e-16    72.1016018306636        0.249394505570549
11      106     protein targeting to ER
GO:0072599      4.83110592468598e-16    72.1016018306636        0.249394505570549
11      106     establishment of protein localization to endoplasmic reticulum
GO:0043624      5.75205039824041e-16    55.2263056092843        0.359975088229188
12      153     cellular protein complex disassembly
GO:0043241      8.52251785682823e-16    53.3163138231631        0.371738980001384
12      158     protein complex disassembly
GO:0070972      1.63376664072382e-15    63.9618041446566        0.277627845823818
11      118     protein localization to endoplasmic reticulum
GO:0000184      1.79752529619068e-15    63.3651368760064        0.279980624178258
11      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0034623      2.75998083956882e-15    47.996632996633 0.40938343367241        12
174     cellular macromolecular complex disassembly
GO:0032984      3.89294897056301e-15    46.5432770821992        0.421147325444606
12      179     macromolecular complex disassembly
GO:0019080      2.61144042545839e-14    48.7723602484472        0.35526953152031
11      151     viral genome expression
GO:0019083      2.61144042545839e-14    48.7723602484472        0.35526953152031
11      151     viral transcription
GO:0006413      2.81102848889924e-14    48.4230650632131        0.357622309874749
11      152     translational initiation
GO:0006612      3.02432840322377e-14    48.0786895284752        0.359975088229188
11      153     protein targeting to membrane
GO:0000956      9.14113499326756e-14    43.1615299944964        0.397619541900215
11      169     nuclear-transcribed mRNA catabolic process
GO:0006402      1.62388034869741e-13    40.8096849778703        0.418794547090167
11      178     mRNA catabolic process
GO:0072594      7.29402674082471e-13    35.2475782833972        0.479966784305584
11      204     establishment of protein localization to organelle
GO:0006401      7.69623482128468e-13    35.0634244733303        0.482319562660024
11      205     RNA catabolic process
GO:0071845      9.82304026513999e-13    28.3656417112299        0.668189052660715
12      284     cellular component disassembly at cellular level
GO:0022411      1.15902680630502e-12    27.9466403162055        0.677600166078472
12      288     cellular component disassembly
GO:0019058      2.84176510755388e-12    30.8630434782609        0.543491799875441
11      231     viral infectious cycle
GO:0022415      1.02754949058485e-11    27.2128514056225        0.611722372154176
11      260     viral reproductive process
GO:0016032      3.62519974997775e-09    15.1923913043478        1.06110303785205
11      451     viral reproduction
GO:0033365      5.95747487152447e-09    14.4461697722567        1.11286416164971
11      473     protein localization to organelle
GO:0006605      6.08988502832755e-09    14.4139355808057        1.11521694000415
11      474     protein targeting
Tissue: Thyroid=>Artery_Tibial  Type:   asymmetric
SourceGene:     CDC37P1(ENSG00000259982.1)
TargetGeneSet:  RNASEL  PPP1R15B        CNIH3   RPS7    MSH2    MZT2B   MZT2A
COL3A1  SATB2   ZNF860  CCR5    RPL29   ZNF721  BEND4   RPL34   RPS3A   FYB
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RPS14   EDN1    RPS18   RPS10   ZFAND2A COL1A2  RP11    ENY2    FAM69B  SNHG7
TSSC4   RPL27A  RPS13   CTD     FAU     CCDC85B CTSC    YEATS4  CCDC59  RPL18AP3
GIT2    ARL6IP4 COL4A2  TRAV18  CATSPERB        BNIP2   RPS3AP6 HMGN1P38
CDC37P1 ELMO3   ZFPM1   RPL13   RPL27   PLIN3   RPL36   ZNF358  C19orf43
FXYD1   ZNF567  DEDD2   RPS11   RRAS    CACNG6  RPS9    PPP1R12C        ZNF579
ZNF865  RPS5    MAP1LC3A        PKIG    PCIF1   NEFH
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      2.65957599051324e-23    80.4042105263158        0.340045671579821
16      91      translational termination
GO:0006414      3.08734828789197e-22    67.6901241868717        0.392360390284409
16      105     translational elongation
GO:0006614      3.08734828789197e-22    67.6901241868717        0.392360390284409
16      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      3.62715533822434e-22    66.9333333333333        0.396097155906166
16      106     cotranslational protein targeting to membrane
GO:0045047      3.62715533822434e-22    66.9333333333333        0.396097155906166
16      106     protein targeting to ER
GO:0072599      3.62715533822434e-22    66.9333333333333        0.396097155906166
16      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      2.22306795689632e-21    59.0092879256966        0.440938343367241
16      118     protein localization to endoplasmic reticulum
GO:0000184      2.5619983674375e-21     58.4322943280531        0.444675108988997
16      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      1.34729230239709e-19    44.4818713450292        0.564251608885198
16      151     viral genome expression
GO:0019083      1.34729230239709e-19    44.4818713450292        0.564251608885198
16      151     viral transcription
GO:0019058      1.38823242073223e-19    33.2957746478873        0.863192858625701
18      231     viral infectious cycle
GO:0006413      1.50203774440156e-19    44.1517027863777        0.567988374506954
16      152     translational initiation
GO:0006612      1.67326985126662e-19    43.8263542066846        0.571725140128711
16      153     protein targeting to membrane
GO:0043624      1.67326985126662e-19    43.8263542066846        0.571725140128711
16      153     cellular protein complex disassembly
GO:0043241      2.83883936612228e-19    42.2683469236471        0.590408968237492
16      158     protein complex disassembly
GO:0006401      5.8075238810556e-19     34.7258481886141        0.766036952460037
17      205     RNA catabolic process
GO:0000956      8.5466593718169e-19     39.1991744066047        0.631513390076811
16      169     nuclear-transcribed mRNA catabolic process
GO:0022415      1.1761615366002e-18     29.245867768595 0.971559061656633       18
260     viral reproductive process
GO:0034623      1.37529854420929e-18    37.9453697534977        0.650197218185593
16      174     cellular macromolecular complex disassembly
GO:0006402      1.99128888750454e-18    36.9980506822612        0.665144280672618
16      178     mRNA catabolic process
GO:0032984      2.18128476970743e-18    36.7684856312561        0.668881046294374
16      179     macromolecular complex disassembly
GO:0072594      1.81001713496122e-17    31.8230683090705        0.762300186838281
16      204     establishment of protein localization to organelle
GO:0071845      1.48037041826462e-16    24.315214090495 1.06124143657878        17
284     cellular component disassembly at cellular level
GO:0022411      1.87222646465371e-16    23.9495362521193        1.07618849906581
17      288     cellular component disassembly
GO:0016032      1.94146036038663e-14    16.1247113163972        1.68528129541208
18      451     viral reproduction
GO:0033365      4.40832093871633e-14    15.3208791208791        1.76749013909072
18      473     protein localization to organelle
GO:0006605      4.57120842919428e-14    15.2861842105263        1.77122690471248
18      474     protein targeting
Tissue: Thyroid=>Artery_Tibial  Type:   asymmetric
SourceGene:     ENSG00000161149.7
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TargetGeneSet:  RP11    ZNF683  MIR4426 U6      RPL7AP11        SEC62   RPL7AP31
RPL34   RPL37   RPS23   CTD     RPS14   RPS10   RP3     RPL24P4 RPL39P3 RP1
MRPS12  TOMM7   RP9     CTB     INSIG1  STMN4   UQCRB   LDHAP4  RPS6    EDF1    SNCG
NHP2P1  NDUFB8  USMG5   RPLP2   FAU     KCNJ5   CYP27B1 RPS11P5 SAP18   RPS7P10 LMO7
RPS29   RPL7AP6 NDUFB1  RPL3P4  MIR1282 EMP2    FHOD1   CCL3L1  RPL27   RPL38
SNRPEP4 RPL36   C19orf79        RPS16   RPS19   SNRPD2  RPS11   NDUFA3  RPL28   RPS5
TOMM22  EEF1B2P3        RP13
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006613      4.35162316180297e-28    117.163636363636        0.315410698221576
18      106     cotranslational protein targeting to membrane
GO:0006415      2.93000940157936e-27    126.651767151767        0.270777108850599
17      91      translational termination
GO:0006612      6.03872468444355e-27    84.330223880597 0.455262611583973       19
153     protein targeting to membrane
GO:0006414      4.08057203539776e-26    106.398601398601        0.312435125596844
17      105     translational elongation
GO:0006614      4.08057203539776e-26    106.398601398601        0.312435125596844
17      105     SRP-dependent cotranslational protein targeting to membrane
GO:0045047      4.85169505409732e-26    105.195764909248        0.315410698221576
17      106     protein targeting to ER
GO:0072599      4.85169505409732e-26    105.195764909248        0.315410698221576
17      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      3.40182530046741e-25    92.6195734958111        0.351117569718359
17      118     protein localization to endoplasmic reticulum
GO:0000184      3.96200299049282e-25    91.7051282051282        0.35409314234309
17      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0072594      1.77855423505988e-24    60.8641891891892        0.607016815445298
19      204     establishment of protein localization to organelle
GO:0019080      2.8000847532111e-23     69.6492537313433        0.44931146633451
17      151     viral genome expression
GO:0019083      2.8000847532111e-23     69.6492537313433        0.44931146633451
17      151     viral transcription
GO:0006413      3.14728091390126e-23    69.12849002849  0.452287038959242       17
152     translational initiation
GO:0043624      3.53461810008498e-23    68.6153846153846        0.455262611583973
17      153     cellular protein complex disassembly
GO:0043241      6.24002465385604e-23    66.1590289143481        0.470140474707633
17      158     protein complex disassembly
GO:0000956      2.04168648612479e-22    61.3238866396761        0.502871773579683
17      169     nuclear-transcribed mRNA catabolic process
GO:0034623      3.40610328996313e-22    59.3500734933856        0.517749636703342
17      174     cellular macromolecular complex disassembly
GO:0006402      5.07242152605792e-22    57.859292881032 0.52965192720227        17
178     mRNA catabolic process
GO:0032984      5.59508439791447e-22    57.4981006647673        0.532627499827002
17      179     macromolecular complex disassembly
GO:0006401      5.94451087059195e-21    49.4558101472995        0.60999238807003
17      205     RNA catabolic process
GO:0019058      4.6818076760367e-20     43.3677210639827        0.687357276313058
17      231     viral infectious cycle
GO:0022415      3.56191690710266e-19    38.1141183918962        0.773648882430282
17      260     viral reproductive process
GO:0006605      6.6909496371469e-19     26.7266807125072        1.4104214241229 20
474     protein targeting
GO:0071845      1.60523228930624e-18    34.6293575338519        0.845062625423846
17      284     cellular component disassembly at cellular level
GO:0022411      2.03608818542751e-18    34.1085722395686        0.856964915922773
17      288     cellular component disassembly
GO:0033365      1.65005985964397e-17    24.3324155653451        1.40744585149817
19      473     protein localization to organelle
GO:0016032      3.74552213027413e-15    21.0526409074796        1.34198325375407
17      451     viral reproduction
GO:0042274      2.01711012928941e-07    105.450549450549        0.0535603072451733
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4       18      ribosomal small subunit biogenesis
GO:0042773      1.10436984124632e-05    34.2635658914729        0.139851913362397
4       47      ATP synthesis coupled electron transport
GO:0042775      1.10436984124632e-05    34.2635658914729        0.139851913362397
4       47      mitochondrial ATP synthesis coupled electron transport
Tissue: Artery_Tibial=>Thyroid  Type:   asymmetric
SourceGene:     FAM198A(ENSG00000144649.4)
TargetGeneSet:  MRPL20  TMEM52  PEX10   RPL11   RP11    PSMB4   UBC     RPL37A
RPL32   MUSTN1  FAM19A1 ALG1L   RPS14   C6orf48 TCTE1   TOMM7   RPL30   RPL13AP5
EIF3M   FAU     CTD     PHB2    ATP5G2  WDR90   TCEB2   POLR2C  RPS12P27
CENPV   RPL17   RPL27   RPS15   XAB2    SNRPD2  RPS11   RP4     CRYZL1  MRPL40
MAGT1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0019080      6.1554212472483e-19     84.0996376811594        0.303024012179088
13      151     viral genome expression
GO:0019083      6.1554212472483e-19     84.0996376811594        0.303024012179088
13      151     viral transcription
GO:0006415      1.04293495901498e-17    109.556944444444        0.182617119922497
11      91      translational termination
GO:0072594      3.35013978170808e-17    60.5376308900524        0.40938343367241
13      204     establishment of protein localization to organelle
GO:0006413      5.25490439834157e-17    72.0100840336135        0.305030793716698
12      152     translational initiation
GO:0006414      5.40296037411533e-17    93.1489361702128        0.210712061449035
11      105     translational elongation
GO:0006614      5.40296037411533e-17    93.1489361702128        0.210712061449035
11      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      6.02164137774053e-17    92.1619883040936        0.212718842986645
11      106     cotranslational protein targeting to membrane
GO:0045047      6.02164137774053e-17    92.1619883040936        0.212718842986645
11      106     protein targeting to ER
GO:0072599      6.02164137774053e-17    92.1619883040936        0.212718842986645
11      106     establishment of protein localization to endoplasmic reticulum
GO:0019058      1.71709935812202e-16    52.9392201834862        0.463566535187876
13      231     viral infectious cycle
GO:0070972      2.04419473587998e-16    81.757528556594 0.236800221437963       11
118     protein localization to endoplasmic reticulum
GO:0000184      2.2498105684425e-16     80.9948559670782        0.238807002975573
11      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0022415      8.05900844682899e-16    46.6282894736842        0.521763199778562
13      260     viral reproductive process
GO:0006612      3.82665601067179e-15    61.4553990610329        0.307037575254308
11      153     protein targeting to membrane
GO:0043624      3.82665601067179e-15    61.4553990610329        0.307037575254308
11      153     cellular protein complex disassembly
GO:0043241      5.48420494375765e-15    59.3442932728647        0.317071482942357
11      158     protein complex disassembly
GO:0000956      1.16255646827721e-14    55.1701828410689        0.339146079856065
11      169     nuclear-transcribed mRNA catabolic process
GO:0034623      1.60854144364843e-14    53.459100204499 0.349179987544115       11
174     cellular macromolecular complex disassembly
GO:0006402      2.0711872234438e-14     52.164005322688 0.357207113694554       11
178     mRNA catabolic process
GO:0032984      2.20425535631333e-14    51.8498677248677        0.359213895232164
11      179     macromolecular complex disassembly
GO:0016032      3.44467018415915e-14    29.8688024408848        0.905058473462044
14      451     viral reproduction
GO:0006401      9.9014971193746e-14     44.8190148911798        0.41139021521002
11      205     RNA catabolic process
GO:0033365      1.76897757278393e-12    24.6611413043478        0.949207667289461
13      473     protein localization to organelle
GO:0006605      1.81693803399836e-12    24.6058839479393        0.951214448827071
13      474     protein targeting
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GO:0071845      3.5201848940134e-12     31.6725681725682        0.569925956681198
11      284     cellular component disassembly at cellular level
GO:0022411      4.09790316936296e-12    31.2063778580024        0.577953082831638
11      288     cellular component disassembly
Tissue: Thyroid=>Artery_Tibial  Type:   asymmetric
SourceGene:     HEBP2(ENSG00000051620.5)
TargetGeneSet:  TRNAU1AP        RPS8    RP11    HSPB11  RPS27   UBC     MZT2B
MZT2A   RPL15   DAG1    RPL29   CEP70   RPS3A   SAP30   CCNO    RPS14   RGL2
RPS10   FAM135A RPL7A   RPS13   EHD1    FAU     NDUFA4L2        NUDT4   RPL18AP3
SIVA1   MT2A    RPL13   SNORD3A RPL23A  RPL27   RPL17   RPL36   CTD     RPL18A
ZNF461  RPS16   ITPKC   RPS19   OPA3    RPS11   A1BG    RPS5    ZNF133  MICALL1
C22orf23        RPS19BP1        RPS23P8 RPS4X
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      1.68042319824457e-40    251.211890243902        0.283371392983185
23      105     translational elongation
GO:0006415      1.15013307802615e-39    269.007672634271        0.245588540585427
22      91      translational termination
GO:0006614      3.9270726550027e-38     223.41459957477 0.283371392983185       22
105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      4.94997699629574e-38    220.739495798319        0.286070168154453
22      106     cotranslational protein targeting to membrane
GO:0045047      4.94997699629574e-38    220.739495798319        0.286070168154453
22      106     protein targeting to ER
GO:0072599      4.94997699629574e-38    220.739495798319        0.286070168154453
22      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      6.66930706644978e-37    192.985294117647        0.318455470209674
22      118     protein localization to endoplasmic reticulum
GO:0000184      8.17265548794994e-37    190.98241358399 0.321154245380943       22
119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      2.3584611271864e-34     143.285909712722        0.407515050861532
22      151     viral genome expression
GO:0019083      2.3584611271864e-34     143.285909712722        0.407515050861532
22      151     viral transcription
GO:0006413      2.75445166416166e-34    142.173755656109        0.4102138260328 22
152     translational initiation
GO:0006612      3.21337533899315e-34    141.078581050741        0.412912601204069
22      153     protein targeting to membrane
GO:0043624      3.21337533899315e-34    141.078581050741        0.412912601204069
22      153     cellular protein complex disassembly
GO:0043241      6.83317452860222e-34    135.844290657439        0.426406477060411
22      158     protein complex disassembly
GO:0000956      3.29301516299787e-33    125.582232893157        0.456093003944364
22      169     nuclear-transcribed mRNA catabolic process
GO:0034623      6.49128334689652e-33    121.40866873065 0.469586879800706       22
174     cellular macromolecular complex disassembly
GO:0006402      1.10059555255609e-32    118.262443438914        0.48038198048578
22      178     mRNA catabolic process
GO:0032984      1.25339068946911e-32    117.500936680405        0.483080755657048
22      179     macromolecular complex disassembly
GO:0072594      2.56527150823439e-31    101.182934712346        0.550550134938759
22      204     establishment of protein localization to organelle
GO:0006401      2.87038799609198e-31    100.622950819672        0.553248910110027
22      205     RNA catabolic process
GO:0022415      8.03852694519248e-31    85.9770569620253        0.70168154452979
23      260     viral reproductive process
GO:0019058      4.41503190645081e-30    87.9442724458204        0.623417064563006
22      231     viral infectious cycle
GO:0071845      4.76474345512123e-28    69.892231701841 0.766452148640232       22
284     cellular component disassembly at cellular level
GO:0022411      6.52897562544952e-28    68.8217602830606        0.777247249325306
22      288     cellular component disassembly
GO:0016032      3.19356796554016e-25    46.9672897196262        1.21714760224206
23      451     viral reproduction
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GO:0033365      9.57811070796263e-25    44.6008333333333        1.27652065600996
23      473     protein localization to organelle
GO:0006605      1.00555545696715e-24    44.4987527716186        1.27921943118123
23      474     protein targeting
GO:0042274      1.34855588817041e-07    117.534693877551        0.0485779530828316
4       18      ribosomal small subunit biogenesis
Tissue: Artery_Tibial=>Thyroid  Type:   asymmetric
SourceGene:     HES1(ENSG00000114315.3)
TargetGeneSet:  UBE2J2  DFFB    ERRFI1  DNAJC16 EPHA2   ARHGEF19        ARHGEF19-AS1
NECAP2  UBXN10  SRRM1   CNKSR1  XKR8    PTAFR   SNRNP40 TMEM39B FAM167B HDAC1   PHC2
ZMYM1   LSM10   SLFNL1  CCDC24  RNF220  C1orf123        TTC22   SYDE2   RP4
PSMA5   ATXN7L2 CEPT1   DDX20   RP11    LIX1L   BOLA1   LYSMD1  CHTOP   DENND4B SHE
PYGO2   FLAD1   CLK2    CCT3    USP21   SELP    CACYBP  MRPS14  SMG7    BAP1
PTGS2   BTG2    SOX13   IRF6    RP3     RPS6KC1 MARC1   HLX     TP53BP2 PARP1
PYCR2   ZNF678  COG2    C1orf131        TOMM20  ARID4B  PGBD2   SLC5A6  PPM1G   EHD3
FAM98A  PAPOLG  RAB1A   PCBP1-AS1       ART4    MRPL15  MRPL35  ZNF2    ARID5A
C2orf29 POLR1B  SCTR    CHN1    CALCRL  MOB4    CREB1   IDH1    TMEM169 BCS1L
TTLL4   NHEJ1   SP100   PSMD1   EIF4E2  ASB1    DTYMK   DHX8    CHCHD4  C3orf19
METTL6  ACAA1   GORASP1 ZNF619  ZNF620  NME6    NPRL2   DUSP7   PBRM1   SCT
ARL4D   MINA    ABHD10  QTRTD1  ARHGAP31        POGLUT1 TIMMDC1 ADPRH   GTF2E1
PLXNA1  C3orf25 SRPRB   SLCO2A1 MSL2    SLC25A36        RNF13   C3orf55 MYNN
ACTL6A  ABCF3   ALG3    POLR2H  EPHB3   CRYGS   TBCCD1  LRRC33  LRCH3   TACC3   LYAR
MRFAP1L1        TBC1D1  NFXL1   SLC10A4 UTP3    COX18   IL8     FAM47E  RASGEF1B
CASP6   ANKRD50 MFAP3L  STOX2   KLKB1   BRIP1   CTD     C5orf51 SNX18   PTCD2
HMGCR   ZCCHC9  PHAX    HARS2   DIAPH1  MED7    DOK3    RP1     RPP40   TRIM27
PFDN6   ZBTB9   PPIL1   TAF8    CAPN11  AARS2   MTO1    SH3BGRL2        UBE2J1
C6orf203        GOPC    MCM9    MAP3K4  PSMG3   ELFN1   MIOS    GLCCI1  VOPP1
ZNF107  BAZ1B   RUNDC3B CNPY4   SLC12A9 CLDN15  CAV2    LRRC4   METTL2A TNPO3
TRIM24  PRSS37  OR9A3P  ZNF786  ZNF398  SMARCD3 CLN8    FUT10   TTI2    CHMP4C
INTS8   GRHL2   TRIB1   ZNF623  EXOSC4  ZNF250  RANBP6  SNAPC3  KLHL9   TEK     VCP
STOML2  FAM214B FXN     CEP78   BICD2   FOXE1   RNF20   CTNNAL1 C9orf80 ZFP37
TRIM32  DOLPP1  EXOSC2  SLC2A6  SDCCAG3 C9orf142        NPDC1   TUBB4B  NRARP
NUDT5   ZFAND4  SYT15   C10orf128       CSTF2T  TMEM26  MSS51   AP3M1   ENTPD7  BTRC
SUFU    MXI1    STK32C  ZNF511  ZNF195  CHRNA10 RRP8    MRPL17  ZNF143  CTR9
MPPED2  CELF1   TMEM216 TTC9C   ZBTB3   TMEM223 STIP1   PLCB3   RPS6KA4 MEN1    UCP3
PICALM  FAM76B  MSANTD4 RDX     ARHGAP20        C11orf93        RNF214  DPAGT1
C2CD2L  ZNF202  HYLS1   VPS26B  RAD52   FKBP4   GNB3    YARS2   BCDIN3D MFSD5
TARBP2  HOXC6   SUOX    TIMELESS        PPM1H   LEMD3   DYRK2   NT5DC3  C12orf34
ANAPC7  DYNLL1  SNRNP35 GOLGA3  SERTM1  KBTBD6  KBTBD7  ITM2B   ARL11   SPRYD7
THSD1   LMO7    PCID2   TTC5    RNASE1  DAD1    AJUBA   CDH24   ACIN1   MGAT2
SOCS6   BCRP2   DPF3    MLH3    POMT2   BTBD7   RP13    C15orf41        BUB1B
ZFYVE19 LCMT2   SLC24A5 AP4E1   RNF111  PARP16  PTPLAD1 DIS3L   SMAD6   CALML4
ANP32A  CSK     SCAMP2  CHD2    MRPS34  SLC9A3R2        NTHL1   PGPEP1  ERCC4
C16orf88        UBFD1   NDUFAB1 MAZ     TAOK2   GDPD3   SULT1A3 TBC1D10B
FBXL19  ZNF668  CNEP1R1 HEATR3  CAPNS2  C16orf57        EXOC3L1 E2F4    CTCF
ZNRF1   PLCG2   MAP1LC3B        ZC3H18  CBFA2T3 ZNF276  CENPBD1 RTN4RL1 DERL2
SLC16A13        ARHGEF15        KRBA2   SCO1    ZSWIM7  ALKBH5  LLGL1   TMEM11
C17orf51        CRLF3   CDK5R1  MYO1D   ZNF830  PEX12   DHRS11  PIP4K2B LEPREL4 ACLY
RUNDC1  UBTF    DLX3    PPP1R9B RSAD1   MBTD1   DGKE    TRIM25  SEPT4   DHX40
FAM104A ICT1    HN1     TRIM65  QRICH2  CBX8    SIRT7   LRRC45  ZNF397  MIER2
LMNB2   ZNF555  PIAS4   DPP9    CAPS    ELAVL1  DNMT1   ZNF627  ZNF440  ZNF443
ZNF490  WDR83   LYL1    IL27RA  SAMD1   SIN3B   NR2F6   ANO8    GLT25D1 PIK3R2
RAB3A   ZNF91   ANKRD27 KCTD15  LIN37   THAP8   ZFP82   ZNF571  ZNF781  MAP3K10
ZNF526  GEMIN7  OPA3    FBXO46  DMPK    MYPOP   BAX     ALDH16A1        LINC00085
U2AF2   ZNF264  ZNF543  ZNF547  ZNF549  ZNF586  ZSCAN22 ZCCHC3  SOX12   FAM110A
NOP56   PCNA    GZF1    C20orf160       COMMD7  DNMT3B  RBL1    FITM2   SDC4
ZSWIM3  ZSWIM1  NCOA5   ELMO2   TMEM189 ADNP    ZFP64   CSTF1   C20orf151
TCFL5   SOX18   RGS19   RBM11   SNORA81 DSTNP1  CECR5   DGCR8   ZNF74   CRKL    HIC2
UBE2L3  ZNF280B ZNF70   SGSM1   RNF215  FBXO7   MGAT3   L3MBTL2 EFCAB6  ZBED4   TLR7
ZNF41   PPP1R3F WNK3    RPL23AP83       FAM123B MAGEC2  BEX4    TCEAL8  AIFM1
NAA10   LAGE3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0031060      2.1966285289602e-06     22.2522427440633        0.426268078333679
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6       16      regulation of histone methylation
Tissue: Artery_Tibial=>Thyroid  Type:   asymmetric
SourceGene:     IGSF6(ENSG00000140749.7)
TargetGeneSet:  SDF4    RPL22   RPL11   RP11    U6      UQCRH   RPL5    TARS2   RPS7
RPL31   OLA1    RPL37A  KCNE4   RPL32   RPL15   RPL14   RPL24   SLC15A2 TBC1D1  CCNI
PRLR    BTF3    FSTL4   CTB     GNB2L1  RPL10A  ELFN1   RPS20   RPL7    C8orf38
RPL30   EIF3E   EIF3H   RPS6    FAM214B RPL7A   HK1     CLNS1A  ATP5G2  RPL14P1
NAP1L1  RPL6    CCNB1IP1        SEC11A  BFAR    RPS15A  INCA1   RPL26   RPL23A
RPL17   RPL19   RPS7P11 CTD     MAPRE2  RFX1    UBA52   RPSAP58 ALDH16A1
RPS11   SUV420H2        RPL28   ISOC2   GPX1P2  RPSAP9  PLXNB3  RPL10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006614      7.9668230342967e-45     183.576923076923        0.392360390284409
27      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.06702684336943e-44    181.240506329114        0.396097155906166
27      106     cotranslational protein targeting to membrane
GO:0045047      1.06702684336943e-44    181.240506329114        0.396097155906166
27      106     protein targeting to ER
GO:0072599      1.06702684336943e-44    181.240506329114        0.396097155906166
27      106     establishment of protein localization to endoplasmic reticulum
GO:0006415      1.93958496782957e-44    204.742857142857        0.340045671579821
26      91      translational termination
GO:0070972      2.82321154560104e-43    157.208791208791        0.440938343367241
27      118     protein localization to endoplasmic reticulum
GO:0000184      3.64513225043217e-43    155.489130434783        0.444675108988997
27      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006414      1.3930963837399e-42     168.294755877034        0.392360390284409
26      105     translational elongation
GO:0006413      4.5023842499722e-42     123.95905707196 0.567988374506954       28
152     translational initiation
GO:0006612      6.4663478484945e-40     113.261904761905        0.571725140128711
27      153     protein targeting to membrane
GO:0000956      1.17612228885946e-38    100.387323943662        0.631513390076811
27      169     nuclear-transcribed mRNA catabolic process
GO:0019080      4.84290716918424e-38    106.020571428571        0.564251608885198
26      151     viral genome expression
GO:0019083      4.84290716918424e-38    106.020571428571        0.564251608885198
26      151     viral transcription
GO:0006402      5.27938708898755e-38    94.3443708609272        0.665144280672618
27      178     mRNA catabolic process
GO:0043624      7.01178526608285e-38    104.33633295838 0.571725140128711       26
153     cellular protein complex disassembly
GO:0043241      1.72853211291102e-37    100.349025974026        0.590408968237492
26      158     protein complex disassembly
GO:0034623      2.5435747712546e-36     89.4000965250965        0.650197218185593
26      174     cellular macromolecular complex disassembly
GO:0072594      2.63709814775386e-36    80.3389830508475        0.762300186838281
27      204     establishment of protein localization to organelle
GO:0006401      3.03156197171403e-36    79.8820224719101        0.766036952460037
27      205     RNA catabolic process
GO:0032984      5.57634709354595e-36    86.4481792717087        0.668881046294374
26      179     macromolecular complex disassembly
GO:0019058      5.98952653037679e-33    64.2843205574913        0.863192858625701
26      231     viral infectious cycle
GO:0022415      1.45271594129644e-31    56.2023809523809        0.971559061656633
26      260     viral reproductive process
GO:0071845      1.54278392957137e-30    50.8878737541528        1.06124143657878
26      284     cellular component disassembly at cellular level
GO:0022411      2.24011454451842e-30    50.0967829880044        1.07618849906581
26      288     cellular component disassembly
GO:0033365      3.31416810940732e-26    31.280269058296 1.76749013909072        27
473     protein localization to organelle
GO:0006605      3.50782138071011e-26    31.2080536912752        1.77122690471248
27      474     protein targeting
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GO:0016032      2.92028648718522e-25    30.5270588235294        1.68528129541208
26      451     viral reproduction
GO:0042273      4.67891000109376e-10    209.766763848396        0.0448411874610754
5       12      ribosomal large subunit biogenesis
GO:0022613      9.0147554393954e-09     14.9915433403806        0.840772264895163
10      225     ribonucleoprotein complex biogenesis
GO:0071843      1.60445580432567e-08    14.061135371179 0.893086983599751       10
239     cellular component biogenesis at cellular level
GO:0042254      7.36950037898148e-08    17.5837187789084        0.556778077641686
8       149     ribosome biogenesis
GO:0006364      1.09399988477819e-07    21.9565694231191        0.388623624662653
7       104     rRNA processing
GO:0016072      1.61093682834633e-07    20.6688700681677        0.411044218393191
7       110     rRNA metabolic process
GO:0034660      9.72266698510121e-07    10.2326086956522        1.06497820220054
9       285     ncRNA metabolic process
GO:0034470      8.94038674369838e-06    10.9610847756587        0.747353124351256
7       200     ncRNA processing
Tissue: Artery_Tibial=>Thyroid  Type:   asymmetric
SourceGene:     LYZ(ENSG00000090382.2)
TargetGeneSet:  VWA1    RPL22   RPL5    RP11    KCNC4-AS1       CSDE1   NGF
SPRR1B  RPS27   C1orf43 RGS2    TOMM20  RPS7    CCDC104 OLA1    IHH     C3orf32
RPL15   RPL14   IMPDH2  RPL24   POLQ    GATA2   WDR19   SLC10A4 CCNI    ELMOD2  HHIP
RPS3A   BTF3    CTB     GNB2L1  RPL15P3 HLA-H   RPL10A  RP1     EEF1A1  ELFN1
CYP3A5  LRRC4   CDCA2   DUSP26  RPL7    EIF3E   EIF3H   RPS6    RPL35   SET
EEF1A1P5        RPL7A   WAC     IPO7    RASSF10 TAF6L   EHD1    SAC3D1  MMP3
AMIGO2  RPL14P1 LEMD3   LYZ     NAP1L1  SLC9A7P1        RPL6    POMP    TPT1
CCNB1IP1        C14orf166       SEC11A  RSL1D1  BFAR    RPS15A  MT1F    RTN4RL1
INCA1   RPL26   RPL23A  RPL17   CTD     ATP8B3  LYL1    RPL18A  C19orf60        LIPE
EXOC3L2 FBXO46  PLEKHA4 RPS11   RPL28   RPS5    AHCY    SNX21   SOX18   EIF3L
C22orf46        SYP     RPS4X   RPSAP9  PLXNB3  FAM3A
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      1.28219985360447e-32    70.5481481481481        0.610338384886859
24      105     translational elongation
GO:0006614      1.28219985360447e-32    70.5481481481481        0.610338384886859
24      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.65082798032538e-32    69.6829268292683        0.616151131409591
24      106     cotranslational protein targeting to membrane
GO:0045047      1.65082798032538e-32    69.6829268292683        0.616151131409591
24      106     protein targeting to ER
GO:0072599      1.65082798032538e-32    69.6829268292683        0.616151131409591
24      106     establishment of protein localization to endoplasmic reticulum
GO:0006415      2.23213933103101e-32    79.2856798457088        0.528959933568611
23      91      translational termination
GO:0006413      8.4233156010459e-32     50.6658456486043        0.883537471455263
26      152     translational initiation
GO:0070972      2.81039982626144e-31    60.736170212766 0.685904089682375       24
118     protein localization to endoplasmic reticulum
GO:0000184      3.5062605041112e-31     60.0926315789474        0.691716836205107
24      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006612      2.28515658252251e-28    44.1488372093023        0.889350217977995
24      153     protein targeting to membrane
GO:0000956      2.8176107971175e-27     39.2331034482759        0.982354162341706
24      169     nuclear-transcribed mRNA catabolic process
GO:0034623      5.85431298116393e-27    37.912  1.01141789495537        24      174
cellular macromolecular complex disassembly
GO:0019080      7.16972779958561e-27    41.9437756147541        0.877724724932531
23      151     viral genome expression
GO:0019083      7.16972779958561e-27    41.9437756147541        0.877724724932531
23      151     viral transcription
GO:0072594      9.2505363782843e-27     33.5858346747467        1.18580029063733
25      204     establishment of protein localization to organelle
GO:0043624      9.86168389136766e-27    41.2926860025221        0.889350217977995
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23      153     cellular protein complex disassembly
GO:0006402      1.03365059022287e-26    36.9168831168831        1.03466888104629
24      178     mRNA catabolic process
GO:0032984      1.18888940060951e-26    36.6761290322581        1.04048162756903
24      179     macromolecular complex disassembly
GO:0043241      2.1451797018786e-26     39.7493624772313        0.918413950591655
23      158     protein complex disassembly
GO:0006401      3.43348159778401e-25    31.3502762430939        1.19161303716006
24      205     RNA catabolic process
GO:0071845      4.10172742036373e-23    23.0809501995943        1.65082001245589
25      284     cellular component disassembly at cellular level
GO:0022411      5.81602459443904e-23    22.7234645872269        1.67407099854681
25      288     cellular component disassembly
GO:0019058      1.71592017692334e-22    25.6665353089533        1.34274444675109
23      231     viral infectious cycle
GO:0022415      2.63356083777877e-21    22.4797675866362        1.51131409591032
23      260     viral reproductive process
GO:0033365      7.49727073773741e-19    13.9597315436242        2.74942910525223
26      473     protein localization to organelle
GO:0006605      7.90080609728781e-19    13.9275708128079        2.75524185177496
26      474     protein targeting
GO:0016032      5.83811772398419e-16    12.279646085491 2.62154868175213        23
451     viral reproduction
GO:0042273      5.07494776283997e-07    89.74375        0.0697529582727839      4
12      ribosomal large subunit biogenesis
Tissue: Artery_Tibial=>Thyroid  Type:   asymmetric
SourceGene:     MLX(ENSG00000108788.6)
TargetGeneSet:  UBE2J2  RP4     NOL9    DNAJC11 RP11    DFFA    DNAJC16 ARHGEF19
ARHGEF19-AS1    CROCCP3 ATP13A2 RCC2    KDM1A   TCEB3   LDLRAP1 SEPN1   XKR8    EYA3
MED18   RCC1    PRDX3P2 GMEB1   SNRNP40 HDAC1   ZMYM1   NCDN    RNF220  MMACHC
TTC22   GADD45A FRRS1   CYB561D1        AMIGO1  HSD3BP5 ANKRD34A        RPRD2
GOLPH3L LYSMD1  SNX27   THEM4   PYGO2   FLAD1   RUSC1-AS1       UBQLN4  RRNAD1
USP21   METTL13 MRPS14  BAP1    INTS7   TMEM206 PARP1   PYCR2   COG2    C1orf131
ZNF238  ADSS    PGBD2   SMC6    PGAM1P6 C2orf44 DNMT3A  C2orf18 TMEM214 PREB
SLC5A6  EIF2B4  PPM1G   CCDC121 EHD3    FAM98A  GEMIN6  PCBP1-AS1       CCT7
CCDC142 AUP1    ART4    MRPL15  GGCX    C2orf68 MRPL35  RMND5A  ZNF2    C2orf29
POLR1B  FOXD4L1 AMMECR1L        ORC2    TTLL4   EIF4E2  ASB1    DTYMK   RPUSD3
CHCHD4  ACAA1   MYD88   GORASP1 ZNF445  PTH1R   KLHL18  CTD     NME6    SLC25A20
NPRL2   ARL4D   ABHD10  WDR52   ADPRH   SRPRB   MSL2    SLC25A36        GRK7
UBQLN4P1        ABCC5   ABCF3   ALG3    PSMD2   MUC4    LRCH3   ZNF141  MYL5
MRFAP1L1        YIPF7   CLOCK   COX18   BRIP1   GTF2H2C ARSB    SERINC5 ZCCHC9
WDR36   PHAX    CDKN2AIPNL      SFXN1   C5orf25 SSR1    MAK     PFDN6   DAXX
SYNGAP1 ZBTB9   TAF8    RPL7L1  DLK2    AARS2   TDRD6   MCM3    VTA1    RSPH3   IQCE
C7orf26 MIOS    CDK13   URGCP   PSPH    SBDSP1  BAZ1B   ZKSCAN5 ZKSCAN1 TAF6
CNPY4   SLC12A9 METTL2A TNPO3   SMO     NFE2L1  C7orf49 ZNF398  ZNF862  LONRF1
CHMP7   EXTL3   INTS9   TTI2    ARMC1   DERL1   LRRC6   ZNF623  SNAPC3  KLHL9   PLAA
FAM122A FXN     C9orf40 CEP78   FOXE1   RNF20   TRIM32  PSMD5   ZBTB43  TRUB2
TBC1D13 CCBL1   TOR1B   EXOSC2  BRD3    NACC2   C9orf69 QSOX2   SDCCAG3 NUDT5
ZNF485  ZFAND4  ERCC6   CSTF2T  MSS51   AP3M1   POLR3A  IDE     MYOF    ENTPD7  BTRC
TAF5    SMC3    FAM175B CTR9    CAPRIN1 TTC9C   ZBTB3   MARK2   PLCB3   GPR137
RPS6KA4 MEN1    CPT1A   UCP3    C11orf30        FAM76B  DLAT    ZW10    PAFAH1B2
DDX6    DPAGT1  RNF26   ZNF202  HYLS1   APPL2   VPS26B  RAD52   NCAPD2  KIAA1467
REP15   BCDIN3D MFSD5   SMUG1   PDE1B   ZC3H10  OBFC2B  TIMELESS        KIF5A
TMEM19  TMPO    TRPV4   TCHP    ANAPC7  VPS29   ATXN2   RNF34   ORAI1   C12orf65
SBNO1   SNRNP35 BRI3BP  GOLGA3  KRR1P1  PDS5B   PROSER1 KBTBD6  KBTBD7  NAA16
ITM2B   BORA    TTC5    MRPL52  ACIN1   SYNJ2BP PROX2   NEK9    POMT2   CPSF2
BTBD7   GOLGA8B ZFYVE19 LCMT2   TUBGCP4 DUOX1   AP4E1   RNF111  PARP16  DIS3L
PIAS1   CALML4  ANP32A  HEXA    MPI     ZSCAN2  ZNF774  NR2F2   ALDH1A3 GLYR1   USP7
ERCC4   C16orf88        UBFD1   MAZ     TAOK2   GDPD3   TBC1D10B        CNEP1R1
HEATR3  CIAPIN1 GOT2    E2F4    CTCF    TMEM170A        VN2R10P MLYCD   USP10
GALNS   CENPBD1 VPS53   ANKFY1  ZFP3    DHX33   SLC16A13        GPS2    WRAP53
KRBA2   USP32P2 C17orf51        SPAG5-AS1       KIAA0100        CRLF3   TEFM
PEX12   DHRS11  PIP4K2B MED1    LEPREL4 CNP     FAM134C PSME3   RUNDC1  ZNF652
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PPP1R9B RSAD1   ANKRD40 COX11   APPBP2  DCAF7   FTSJ3   PSMC5   POLG2   FAM104A
CD300A  QRICH2  RP13    ZNF397  WDR7    ZADH2   LMNB2   ZNF555  ZBTB7A  FEM1A
ZNF562  ZNF799  ZNF490  WDR83   SAMD1   TMEM221 GLT25D1 PIK3R2  LSM4    ZNF253
ZNF429  ANKRD27 NUDT19  ZNF792  LIN37   ZNF790  ZNF781  ZNF546  MIA     BLOC1S3
MYPOP   GRWD1   FUT2    BAX     ZNF613  ZNF480  ZNF808  ZNF677  U2AF2   ZNF835
ZNF264  ZNF543  ZNF547  ZNF17   ZNF549  ZNF814  ZNF329  ZSCAN22 ZNF132  FASTKD5 MKKS
CSRP2BP CRNKL1  NANP    CDK5RAP1        RBL1    FITM2   PI3     ZSWIM1  NCOA5
ELMO2   KRT18P4 ADNP    ZFP64   VAPB    RGS19   SON     PRDM15  UBE2G2  CECR5
ZNF74   KRT18P5 CRKL    UBE2L3  ZNF70   NF2     RNF215  PRR14L  TOMM22  TNRC6B
XPNPEP3 L3MBTL2 TCF20   PPP2R3B-AS1     HDHD1   TLR8    ZNF41   ZNF81   RPL7P57
FTSJ1   GPKOW   PPP1R3F FAM123B RBM41   AIFM1   NAA10   UBL4A
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
Tissue: Artery_Tibial=>Thyroid  Type:   asymmetric
SourceGene:     RP1-92O14.6(ENSG00000229431.1)
TargetGeneSet:  RUNX3   LCK     CYP4A22 GBP5    RP4     CD2     ANKRD20A12P     RP11
SLAMF6  CD84    CD48    LY9     CD247   XCL2    PTPN7   TRAF3IP3        IGKV1D-39
ZAP70   ITGA4   RUFY4   FBXO36  PDCD1   GPR15   PARP15  RHOH    CXCL9   CXCL10
DAPP1   IL7R    FYB     ITK     TAGAP   CCR6    CARD11  IKZF1   TRBV29-1
TRBC2   CDKN2B-AS1      TSPAN32 CD5     AMICA1  CD3E    CD3D    LAG3    CLEC7A
TESPA1  TRAC    PATL2   TPSB2   SEPT1   ITGAL   ACAP1   C17orf66        CCL4L1
FMNL1   TMC8    DENND1C DNASE2  MAP4K1  NKG7    SIRPG   UBASH3A CECR1   IGLV2-11
IL2RB   KLHDC7B WWC3-AS1        IL2RG   MTCP1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0042110      7.91799160308697e-19    27.0586868686869        1.14787903951284
19      319     T cell activation
GO:0046649      1.14899298458457e-17    21.1652542372881        1.55809286554564
20      433     lymphocyte activation
GO:0050863      9.87449168117062e-16    27.9316452374705        0.795239083800429
15      221     regulation of T cell activation
GO:0050870      2.39477060932062e-14    30.0443037974684        0.615320739049201
13      171     positive regulation of T cell activation
GO:0051249      3.86222033178807e-14    21.3760588947156        1.01833783129195
15      283     regulation of lymphocyte activation
GO:0002696      5.57899666146866e-14    23.8548425859168        0.838419486540724
14      233     positive regulation of leukocyte activation
GO:0050867      8.3966696993133e-14     23.1045645086167        0.863608054805896
14      240     positive regulation of cell activation
GO:0002694      2.43773151427523e-13    18.6711711711712        1.15507577330289
15      321     regulation of leukocyte activation
GO:0051251      4.6343104045604e-13     23.4273927392739        0.773648882430282
13      215     positive regulation of lymphocyte activation
GO:0050865      6.37990227168931e-13    17.391644693474 1.23423984499343        15
343     regulation of cell activation
GO:0002429      1.15672041073631e-12    31.3968412634946        0.478582797038267
11      133     immune response-activating cell surface receptor signaling pathway
GO:0050852      1.78391606113461e-12    38.2825040128411        0.356238322607432
10      99      T cell receptor signaling pathway
GO:0002768      2.7847198420019e-12     28.7779204107831        0.518164832883537
11      144     immune response-regulating cell surface receptor signaling pathway
GO:0030098      5.69787603438948e-12    22.1984375      0.734066846585011       12
204     lymphocyte differentiation
GO:0030217      6.71253741383032e-12    26.3740958788898        0.561345235623832
11      156     T cell differentiation
GO:0050851      1.61161905646764e-11    30.1011378002528        0.442599128088022
10      123     antigen receptor-mediated signaling pathway
GO:0050778      3.46996677047776e-10    13.340930674264 1.30980554978894        13
364     positive regulation of immune response
GO:0002521      5.45838406235542e-10    14.5955172413793        1.08670680229742
12      302     leukocyte differentiation
GO:0002757      5.59221983302669e-10    16.9778963414634        0.845616220330773
11      235     immune response-activating signal transduction
GO:0050900      7.30755948021455e-10    16.5279957582185        0.86720642170092
11      241     leukocyte migration
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GO:0002764      9.89526932126761e-10    16.0319028506741        0.892394989966092
11      248     immune response-regulating signaling pathway
GO:0030097      6.43672619411107e-09    10.3325925925926        1.66604387239637
13      463     hemopoiesis
GO:0002253      7.03563355743526e-09    13.1454098915989        1.07591170161235
11      299     activation of immune response
GO:0031294      8.45751436674455e-09    32.7833333333333        0.26987751712684
7       75      lymphocyte costimulation
GO:0031295      8.45751436674455e-09    32.7833333333333        0.269877517126842
7       75      T cell costimulation
GO:0048534      1.42906661055106e-08    9.62448132780083        1.78119161303716
13      495     hemopoietic or lymphoid organ development
GO:0045580      1.58926020043176e-08    29.709037037037 0.295066085392014       7
82      regulation of T cell differentiation
GO:0045619      5.94068377160562e-08    24.1905797101449        0.356238322607432
7       99      regulation of lymphocyte differentiation
GO:0033077      7.69733822378621e-08    34.0173913043478        0.219500380596499
6       61      T cell differentiation in thymus
GO:0045061      3.42675928321822e-07    92.2179487179487        0.0611722372154176
4       17      thymic T cell selection
GO:0045582      1.2475444866316e-06     31.8062943262411        0.190713445436302
5       53      positive regulation of T cell differentiation
GO:0045058      1.50173135517509e-06    59.9125 0.0863608054805896      4       24
T cell selection
GO:0045621      2.74531788601454e-06    26.7674505412467        0.223098747491523
5       62      positive regulation of lymphocyte differentiation
GO:0071350      3.63567199059503e-06    146.867346938776        0.0323853020552211
3       9       cellular response to interleukin-15
GO:0002252      8.39595002105175e-06    7.78471408303004        1.38896962147948
9       386     immune effector process
GO:0070672      9.4495803812895e-06     97.891156462585 0.0431804027402948      3
12      response to interleukin-15
Tissue: Artery_Tibial=>Thyroid  Type:   asymmetric
SourceGene:     RP11-398A8.3(ENSG00000241163.1)
TargetGeneSet:  RP1     RPL22   RPL11   RP4     GAPDHP32        RPS27   C1orf100
THPO    LRPPRC  PPM1B   FAM161A RPL32   RPL15   RP11    HGD     ABCC5   RPL35A
RPL34   LPCAT1  BTF3    NSA2    PCDHGB8P        RPS14   OR2B6   RPL10A  ZNF117
RPL30   POLR1E  C9orf153        RPL35   RPL27A  EIF3M   RPS25   PHB2    RPL18AP3
GPN3    MLEC    WDR90   NUDT21  NOL3    KLHDC4  DVL2    ADORA2B RPL17   RPL19
RPL27   MRPL10  UTP18   XAB2    ANO8    RPL18A  SNRPD2  GLTSCR2 RPL18   SLC6A16
RPL13A  RPS11   OTOR    U6      ZNFX1-AS1       PMEPA1  EIF3D   RPL3    EFCAB6
SSX2B   LAS1L
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      2.24254460945105e-33    130.245454545455        0.340045671579821
21      91      translational termination
GO:0006413      4.68572913134875e-32    82.0615153788447        0.567988374506954
23      152     translational initiation
GO:0006414      6.28665788110763e-32    108.431818181818        0.392360390284409
21      105     translational elongation
GO:0006614      6.28665788110763e-32    108.431818181818        0.392360390284409
21      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      7.82262904892689e-32    107.148663101604        0.396097155906166
21      106     cotranslational protein targeting to membrane
GO:0045047      7.82262904892689e-32    107.148663101604        0.396097155906166
21      106     protein targeting to ER
GO:0072599      7.82262904892689e-32    107.148663101604        0.396097155906166
21      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      9.11874317632008e-31    93.8144329896907        0.440938343367241
21      118     protein localization to endoplasmic reticulum
GO:0000184      1.10484427653315e-30    92.8506493506493        0.444675108988997
21      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      2.32300005459506e-28    69.8384615384615        0.564251608885198
21      151     viral genome expression
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GO:0019083      2.32300005459506e-28    69.8384615384615        0.564251608885198
21      151     viral transcription
GO:0006612      3.110465836935e-28      68.7706611570248        0.571725140128711
21      153     protein targeting to membrane
GO:0043624      3.110465836935e-28      68.7706611570248        0.571725140128711
21      153     cellular protein complex disassembly
GO:0043241      6.33905511835966e-28    66.2375580623756        0.590408968237492
21      158     protein complex disassembly
GO:0000956      2.79484968933089e-27    61.267199017199 0.631513390076811       21
169     nuclear-transcribed mRNA catabolic process
GO:0034623      5.30088093437068e-27    59.2442067736185        0.650197218185593
21      174     cellular macromolecular complex disassembly
GO:0006402      8.7213255440415e-27     57.7185871453387        0.665144280672618
21      178     mRNA catabolic process
GO:0032984      9.85870964498321e-27    57.349252013809 0.668881046294374       21
179     macromolecular complex disassembly
GO:0072594      1.69617848285117e-25    49.4277198211624        0.762300186838281
21      204     establishment of protein localization to organelle
GO:0006401      1.88559175218445e-25    49.1556324110672        0.766036952460037
21      205     RNA catabolic process
GO:0019058      2.47146800524597e-24    42.9909090909091        0.863192858625701
21      231     viral infectious cycle
GO:0022415      3.09241419212308e-23    37.6972232788132        0.971559061656633
21      260     viral reproductive process
GO:0071845      2.01202174463804e-22    34.1991012789492        1.06124143657878
21      284     cellular component disassembly at cellular level
GO:0022411      2.70405805785441e-22    33.6772216547497        1.07618849906581
21      288     cellular component disassembly
GO:0016032      3.04439881613852e-18    20.669978858351 1.68528129541208        21
451     viral reproduction
GO:0033365      8.05583481382574e-18    19.6329444891392        1.76749013909072
21      473     protein localization to organelle
GO:0006605      8.41035788686445e-18    19.5881998795906        1.77122690471248
21      474     protein targeting
GO:0022613      5.42881346003134e-10    16.9542490762878        0.840772264895163
11      225     ribonucleoprotein complex biogenesis
GO:0071843      1.02968832075048e-09    15.8974908200734        0.893086983599751
11      239     cellular component biogenesis at cellular level
GO:0042254      7.36950037898148e-08    17.5837187789084        0.556778077641686
8       149     ribosome biogenesis
GO:0006364      2.34516328586075e-06    18.2385204081633        0.388623624662653
6       104     rRNA processing
GO:0016072      3.2541389883178e-06     17.1790865384615        0.411044218393191
6       110     rRNA metabolic process
Tissue: Artery_Tibial=>Thyroid  Type:   asymmetric
SourceGene:     RP11-469M7.1(ENSG00000260006.1)
TargetGeneSet:  UBE2J2  RP4     TTC34   CEP104  DFFB    RP13    THAP3   ERRFI1  LZIC
RP11    DFFA    PLOD1   DNAJC16 ARHGEF19        ARHGEF19-AS1    CROCCP3 ATP13A2
HP1BP3  TCEB3   LDLRAP1 SH3BGRL3        XKR8    EYA3    MED18   RCC1    PRDX3P2
SNRNP40 TXLNA   FAM167B HDAC1   ZMYM1   NCDN    C1orf216        LSM10   ZMPSTE24
SLFNL1  RNF220  MMACHC  ATRX    STIL    C1orf123        TTC22   OMA1    MYSM1
ATG4C   ALG6    GADD45A HHLA3   SYDE2   CCBL2   FRRS1   PSMA5   ATXN7L2 CYB561D1
CEPT1   GDAP2   GAPDHP32        LIX1L   GNRHR2  BOLA1   TARS2   GOLPH3L ARNT
GABPB1  LYSMD1  SNX27   INTS3   DENND4B PYGO2   FLAD1   FAM189B UBQLN4  BGLAP   CCT3
C1orf182        ARHGEF11        USP21   HSD17B7 POGK    METTL13 PIGC    CACYBP
MRPS14  SMG7    TRMT1L  PTGS2   C1orf98 KLHL12  BTG2    TMEM81  TMCC2   CD46
INTS7   MARC1   TP53BP2 PARP1   LBR     COG2    C1orf131        TOMM20  MTR     ADSS
HSD17B7P1       PGBD2   SMC6    TTC32   UBXN2A  DNMT3A  RAB10   PREB    SLC5A6
CCDC121 SUPT7L  EHD3    SLC30A6 FAM98A  GEMIN6  ARHGEF33        PLEKHH2 PAPOLG  XPO1
FAM161A PCBP1-AS1       SPR     CCT7    AUP1    ART4    MRPL15  GGCX    C2orf68
MRPL35  RMND5A  PLGLB1  MRPS5   ZNF2    LMAN2L  TBC1D8  C2orf29 GPR45   POLR1B
FOXD4L1 STEAP3  STEAP3-AS1      TMEM37  LY75    BBS5    C2orf77 HSPD1   SATB2
CASP10  ICA1L   WDR12   KLF7-IT1        CREB1   IDH1    ATIC    RQCD1   BCS1L
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TTLL4 NHEJ1 COL4A3 EIF4E2 RNPEPL1 DTYMK TTLL3 CRELD1 CHCHD4 C3orf19
METTL6 GORASP1 ZNF619 ZNF620 C3orf23 CTD NME6 PLXNB1 NPRL2 HEMK1
DUSP7 PHF7 SCT FLNB-AS1 SHQ1 ARL4D ABHD10 WDR52 KIAA1407
TIMMDC1 GTF2E1 PTPLB SEC61A1 CDV3 SRPRB MSL2 SLC25A36 ZBTB38 GRK7
GK5 TRPC1 UBQLN4P1 SIAH2 MLF1 SERPINI2 WDR49 ACTL6A
DCUN1D1 PARL ABCC5 ABCF3 ALG3 POLR2H EPHB3 CRYGS TBCCD1 DNAJB11 RFC4
U2 CEP19 LRCH3 ZNF732 ZNF141 MYL5 DGKQ CTBP1 TMEM128 ZNF518B
NFXL1 CLOCK COX18 ANKRD17 CXCL2 CXCL11 FAM47E THAP9 CASP6 CCNA2
KIAA1109 ANKRD50 IL15 TIGD4 MFAP3L IRF2 EXOC3 LPCAT1 BRIP1
MARCH6 FAM105B C5orf51 SNX18 GPX8 SLC38A9 IPO11 PTCD2 ARSB FAM151B
ZCCHC9 FAM81B FAM174A PPIP5K2 WDR36 EPB41L4A-AS1 APC XBP1P1 PHAX
P4HA2-AS1 P4HA2 SHROOM1 C5orf65 IGIP CTB HARS2 DIAPH1 SH3RF2
HMGXB3 IRGM MED7 TSPAN17 TRIM52 RP1 PXDC1 C6orf228 HIST1H2AC
HIST1H2BD HIST1H1PS1 HIST1H3E HIST1H2BH HIST1H3J
OR2B6 SCAND3 TRIM27 PPP1R11 GNL1 DDR1 CSNK2B C6orf25 HSPA1L PFDN6
SYNGAP1 ZBTB9 NUDT3 PPIL1 TAF8 CNPY3 AARS2 BAG2 LINC00472
MB21D1 MTO1 UBE2J1 PREP C6orf203 TRMT11 PEX7 VIP SERAC1
MRPL18 SUN1 RNF216P1 C7orf26 MIOS C7orf46 CDK13 URGCP CAMK2B
VOPP1 PSPH ZNF117 SBDS SBDSP1 BAZ1B CLIP2 STEAP4 RBM48 PPP1R9A
ZKSCAN5 FAM200A ZKSCAN1 CNPY4 SLC12A9 PLOD3 CLDN15 C7orf53 CAV2 CADPS2 GCC1
IMPDH1 METTL2A TNPO3 SMO TRPV6 ZNF786 ZNF398 ZNF862 GIMAP4 CDK5
ABCF2 SMARCD3 CTA FDFT1 LONRF1 FAM160B2 CHMP7 PPP2R2A EXTL3
INTS9 HMBOX1 FUT10 TTI2 C8orf40 CYP7A1 YTHDF3 ARMC1 GDAP1 INTS8
GAPDHP62 GRHL2 ENY2 DERL1 WDR67 ZHX1 LRRC6 ZFAT C8orf73
ZNF623 NRBP2 ZNF252 CBWD1 RANBP6 SNAPC3 KLHL9 C9orf11 DNAJA1 VCP
HMGB3P24 DCAF10 FXN SMC5 C9orf40 CEP78 C9orf103 LINC00476
FOXE1 NANS ALG2 RNF20 NIPSNAP3B TRIM32 TBC1D13 CCBL1 DOLPP1
TOR1B EXOSC2 SURF4 C9orf69 SDCCAG3 FAM69B MAMDC4 C9orf142 SSNA1
TUBB4B NOXA1 KLF6 FBXO18 NUDT5 CDNF BMI1 LINC00202 ZNF485
ZFAND4 ERCC6 CSTF2T ADO PBLD DNA2 P4HA1 MSS51 CHCHD1 AP3M1
MINPP1 BTAF1 IDE MYOF FRAT1 LINC00263 BTRC TMEM180 SUFU TAF5
ZDHHC6 METTL10 FAM175B CTAGE7P STK32C CYP2E1 AP2A2 IFITM10 ZNF195 CHRNA10
UBQLNL TRIM34 TRIM5 RRP8 MRPL17 RIC3 ZNF143 TPH1 MPPED2 SLC35C1 ETFA
CELF1 B3GAT3 TTC9C ZBTB3 C11orf84 MARK2 STIP1 FKBP2 PLCB3
GPR137 RPS6KA4 MEN1 PPP2R5B GPHA2 SAC3D1 EFEMP2 RBM14 7SK SUV420H1
KRTAP5-9 FOLR3 CLPB MRPL48 UCP3 C11orf30 SLC36A4 FAM76B
MSANTD4 RDX C11orf93 TIMM8B ZW10 USP28 RNF214 SETP16 H2AFX
DPAGT1 C2CD2L CBL HSPA8 ZNF202 STT3A HYLS1 APPL2 VPS26B RAD52
FKBP4 NCAPD2 RPL13AP20 KIAA1467 REP15 PUS7L ENDOU BCDIN3D
TARBP2 SMUG1 SUOX ZC3H10 TIMELESS ZBTB39 TMEM194A TBC1D30
LEMD3 DYRK2 TMEM19 CSRP2 TMPO CKAP4 POLR3B FICD C12orf34
ANAPC7 VPS29 DYNLL1 POP5 MLEC RNF34 C12orf65 SBNO1 SNRNP35 UBC
BRI3BP SFSWAP PUS1 GOLGA3 RPL23AP67 ZMYM5 KRR1P1 LNX2 PDS5B
NHLRC3 KBTBD6 KBTBD7 NAA16 ITM2B DLEU1 RPS4XP16 DHRS12 SUGT1 BORA
LMO7 DNAJC3-AS1 DNAJC3 UGGT2 RAP2A PROZ PCID2 TTC5 PARP2 DAD1
MRPL52 ACIN1 SFTA3 MGAT2 DNAAF2 NEMF TXNDC16 GNPNAT1 HNRPCP SYNJ2BP
MAP3K9 RBM25 ZNF410 PROX2 NEK9 POMT2 AHSA1 SPTLC2 RPS6KA5 CPSF2
BTBD7 PAPOLA RPS20P33 GOLGA8B ZFYVE19 PPP1R14D RPAP1 ZFP106
TP53BP1 PATL2 B2M MYEF2 HDC AP4E1 PIGB RNF111 NARG2 CSNK1G1
PARP16 DIS3L SMAD6 FEM1B ANP32A HEXA CSK SCAMP2 GOLGA6L5
ZSCAN2 CHD2 NR2F2 LRRC28 ASB7 ALDH1A3 SOLH FBXL16 CCDC154 MRPS34
NTHL1 ZNF205 ATF7IP2 ERCC4 UBFD1 PLK1 MAZ TAOK2 TBX6 GDPD3
SULT1A3 TBC1D10B FBXL19-AS1 FBXL19 CNEP1R1 HEATR3 PAPD5 SALL1
CCL22 DOK4 EXOC3L1 CTCF DDX19B TMEM170A C16orf46 MLYCD
ZC3H18 CENPBD1 VPS53 RAP1GAP2 ZMYND15 RNF167 ZFP3 DERL2 PITPNM3
SLC16A13 WRAP53 KRBA2 COX10-AS1 ZSWIM7 ALKBH5 LLGL1 C17orf51
WSB1 C17orf108 SUPT6H ABHD15 BLMH CRLF3 RNF135 CCT6B ZNF830
PEX12 DHRS11 PIP4K2B LEPREL4 ACLY KAT2A FAM134C RUNDC1 UBTF C17orf69
ZNF652 DLX4 PPP1R9B RSAD1 C17orf67 TRIM25 RAD51C HEATR6 APPBP2
DCAF7 CEP95 HN1 GGA3 UNK TRIM65 QRICH2 ENGASE CBX2 CBX8
SIRT7 PYCR1 LRRC45 RNMT RIOK3 ZNF397 MOCOS CCDC11 ONECUT2 BCL2
ZADH2 MIER2 C19orf21 CIRBP MOB3A DOT1L LMNB2 ZNF555 TLE6
PIAS4 ZBTB7A DPP9 SAFB CAPS ELAVL1 ZNF558 ZNF562 PIN1 ICAM1

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ZGLP1   RAB3D   ZNF627  ZNF440  ZNF433  ZNF844  ZNF442  ZNF799  ZNF490  WDR83   LYL1
STX10   SAMD1   SIN3B   NR2F6   ANO8    TMEM221 GLT25D1 PIK3R2  JUND    ZNF253
ZNF91   ANKRD27 NUDT19  KCTD15  ZNF792  LIN37   CAPNS1  ZNF565  ZNF529  ZNF790
ZNF781  MED29   ZFP36   ZNF546  MAP3K10 SHKBP1  MIA     SMG9    ZNF283  ZNF284
GEMIN7  BLOC1S3 FBXO46  DMPK    RSPH6A  MYPOP   KPTN    CARD8   FUT2    PPP1R15A
BAX     SLC6A16 PTOV1   NAPSA   C19orf63        CTU1    ZNF615  ZNF808  ZNF816
ZNF347  ZNF761  U2AF2   ZNF835  ZNF264  ZNF543  ZNF547  ZNF749  ZNF549  ZNF586
ZNF814  ZNF329  ZSCAN22 ZNF132  ZCCHC3  FAM110A NOP56   FASTKD5 PCNA    MKKS    GZF1
ABHD12  NANP    COMMD7  DNMT3B  PXMP4   ZNF341  MMP24   NFS1    NDRG3   RBL1
IFT52   FITM2   ADA     MATN4   SDC4    ZSWIM3  ZSWIM1  NCOA5   ELMO2   KRT18P4
TMEM189 ADNP    ZFP64   VAPB    C20orf151       TCFL5   DPH3P1  RGS19   PCMTD2
RBM11   RNGTTP1 TCP10L  TMEM50B C2CD2   SUMO3   CECR5   ZNF74   KRT18P5 CRKL
UBE2L3  SDF2L1  ZNF280B ZNF70   ASPHD2  HPS4    GAS2L1  NF2     CCDC157 RNF215
PRR14L  POLR2F  TNRC6B  SGSM3   XPNPEP3 L3MBTL2 EFCAB6  RP6     NCAPH2  CPT1B   ACR
PPP2R3B-AS1     HDHD1   ARHGAP6 TCEANC  REPS2   SCML1   ZNF673  ZNF41   ZNF81
ZNF630  RBM3    KCND1   PPP1R3F WNK3    FAM123B FAM155B CXorf65 ACRC    DMRTC1
PABPC5  BEX4    PGRMC1  EEF1A1P30       ZBTB33  AIFM1   ZNF449  FHL1    IDS
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GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
Tissue: Artery_Tibial=>Thyroid  Type:   cluster
SourceGene:     RP11-469M7.1(ENSG00000260006.1)
TargetGeneSet:  UBE2J2  RP4     TTC34   CEP104  DFFB    RP13    THAP3   ERRFI1  LZIC
RP11    DFFA    PLOD1   DNAJC16 ARHGEF19        ARHGEF19-AS1    CROCCP3 ATP13A2
HP1BP3  TCEB3   LDLRAP1 SH3BGRL3        XKR8    EYA3    MED18   RCC1    PRDX3P2
SNRNP40 TXLNA   FAM167B HDAC1   ZMYM1   NCDN    C1orf216        LSM10   ZMPSTE24
SLFNL1  RNF220  MMACHC  ATRX    STIL    C1orf123        TTC22   OMA1    MYSM1
ATG4C   ALG6    GADD45A HHLA3   SYDE2   CCBL2   FRRS1   PSMA5   ATXN7L2 CYB561D1
CEPT1   GDAP2   GAPDHP32        LIX1L   GNRHR2  BOLA1   TARS2   GOLPH3L ARNT
GABPB1  LYSMD1  SNX27   INTS3   DENND4B PYGO2   FLAD1   FAM189B UBQLN4  BGLAP   CCT3
C1orf182        ARHGEF11        USP21   HSD17B7 POGK    METTL13 PIGC    CACYBP
MRPS14  SMG7    TRMT1L  PTGS2   C1orf98 KLHL12  BTG2    TMEM81  TMCC2   CD46
INTS7   MARC1   TP53BP2 PARP1   LBR     COG2    C1orf131        TOMM20  MTR     ADSS
HSD17B7P1       PGBD2   SMC6    TTC32   UBXN2A  DNMT3A  RAB10   PREB    SLC5A6
CCDC121 SUPT7L  EHD3    SLC30A6 FAM98A  GEMIN6  ARHGEF33        PLEKHH2 PAPOLG  XPO1
FAM161A PCBP1-AS1       SPR     CCT7    AUP1    ART4    MRPL15  GGCX    C2orf68
MRPL35  RMND5A  PLGLB1  MRPS5   ZNF2    LMAN2L  TBC1D8  C2orf29 GPR45   POLR1B
FOXD4L1 STEAP3  STEAP3-AS1      TMEM37  LY75    BBS5    C2orf77 HSPD1   SATB2
CASP10  ICA1L   WDR12   KLF7-IT1        CREB1   IDH1    ATIC    RQCD1   BCS1L
TTLL4   NHEJ1   COL4A3  EIF4E2  RNPEPL1 DTYMK   TTLL3   CRELD1  CHCHD4  C3orf19
METTL6  GORASP1 ZNF619  ZNF620  C3orf23 CTD     NME6    PLXNB1  NPRL2   HEMK1
DUSP7   PHF7    SCT     FLNB-AS1        SHQ1    ARL4D   ABHD10  WDR52   KIAA1407
TIMMDC1 GTF2E1  PTPLB   SEC61A1 CDV3    SRPRB   MSL2    SLC25A36        ZBTB38  GRK7
GK5     TRPC1   UBQLN4P1        SIAH2   MLF1    SERPINI2        WDR49   ACTL6A
DCUN1D1 PARL    ABCC5   ABCF3   ALG3    POLR2H  EPHB3   CRYGS   TBCCD1  DNAJB11 RFC4
U2      CEP19   LRCH3   ZNF732  ZNF141  MYL5    DGKQ    CTBP1   TMEM128 ZNF518B
NFXL1   CLOCK   COX18   ANKRD17 CXCL2   CXCL11  FAM47E  THAP9   CASP6   CCNA2
KIAA1109        ANKRD50 IL15    TIGD4   MFAP3L  IRF2    EXOC3   LPCAT1  BRIP1
MARCH6  FAM105B C5orf51 SNX18   GPX8    SLC38A9 IPO11   PTCD2   ARSB    FAM151B
ZCCHC9  FAM81B  FAM174A PPIP5K2 WDR36   EPB41L4A-AS1    APC     XBP1P1  PHAX
P4HA2-AS1       P4HA2   SHROOM1 C5orf65 IGIP    CTB     HARS2   DIAPH1  SH3RF2
HMGXB3  IRGM    MED7    TSPAN17 TRIM52  RP1     PXDC1   C6orf228        HIST1H2AC
HIST1H2BD       HIST1H1PS1      HIST1H3E        HIST1H2BH       HIST1H3J
OR2B6   SCAND3  TRIM27  PPP1R11 GNL1    DDR1    CSNK2B  C6orf25 HSPA1L  PFDN6
SYNGAP1 ZBTB9   NUDT3   PPIL1   TAF8    CNPY3   AARS2   BAG2    LINC00472
MB21D1  MTO1    UBE2J1  PREP    C6orf203        TRMT11  PEX7    VIP     SERAC1
MRPL18  SUN1    RNF216P1        C7orf26 MIOS    C7orf46 CDK13   URGCP   CAMK2B
VOPP1   PSPH    ZNF117  SBDS    SBDSP1  BAZ1B   CLIP2   STEAP4  RBM48   PPP1R9A
ZKSCAN5 FAM200A ZKSCAN1 CNPY4   SLC12A9 PLOD3   CLDN15  C7orf53 CAV2    CADPS2  GCC1
IMPDH1  METTL2A TNPO3   SMO     TRPV6   ZNF786  ZNF398  ZNF862  GIMAP4  CDK5
ABCF2   SMARCD3 CTA     FDFT1   LONRF1  FAM160B2        CHMP7   PPP2R2A EXTL3
INTS9   HMBOX1  FUT10   TTI2    C8orf40 CYP7A1  YTHDF3  ARMC1   GDAP1   INTS8
GAPDHP62        GRHL2   ENY2    DERL1   WDR67   ZHX1    LRRC6   ZFAT    C8orf73
ZNF623  NRBP2   ZNF252  CBWD1   RANBP6  SNAPC3  KLHL9   C9orf11 DNAJA1  VCP
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HMGB3P24        DCAF10  FXN     SMC5    C9orf40 CEP78   C9orf103        LINC00476
FOXE1   NANS    ALG2    RNF20   NIPSNAP3B       TRIM32  TBC1D13 CCBL1   DOLPP1
TOR1B   EXOSC2  SURF4   C9orf69 SDCCAG3 FAM69B  MAMDC4  C9orf142        SSNA1
TUBB4B  NOXA1   KLF6    FBXO18  NUDT5   CDNF    BMI1    LINC00202       ZNF485
ZFAND4  ERCC6   CSTF2T  ADO     PBLD    DNA2    P4HA1   MSS51   CHCHD1  AP3M1
MINPP1  BTAF1   IDE     MYOF    FRAT1   LINC00263       BTRC    TMEM180 SUFU    TAF5
ZDHHC6  METTL10 FAM175B CTAGE7P STK32C  CYP2E1  AP2A2   IFITM10 ZNF195  CHRNA10
UBQLNL  TRIM34  TRIM5   RRP8    MRPL17  RIC3    ZNF143  TPH1    MPPED2  SLC35C1 ETFA
CELF1   B3GAT3  TTC9C   ZBTB3   C11orf84        MARK2   STIP1   FKBP2   PLCB3
GPR137  RPS6KA4 MEN1    PPP2R5B GPHA2   SAC3D1  EFEMP2  RBM14   7SK     SUV420H1
KRTAP5-9        FOLR3   CLPB    MRPL48  UCP3    C11orf30        SLC36A4 FAM76B
MSANTD4 RDX     C11orf93        TIMM8B  ZW10    USP28   RNF214  SETP16  H2AFX
DPAGT1  C2CD2L  CBL     HSPA8   ZNF202  STT3A   HYLS1   APPL2   VPS26B  RAD52
FKBP4   NCAPD2  RPL13AP20       KIAA1467        REP15   PUS7L   ENDOU   BCDIN3D
TARBP2  SMUG1   SUOX    ZC3H10  TIMELESS        ZBTB39  TMEM194A        TBC1D30
LEMD3   DYRK2   TMEM19  CSRP2   TMPO    CKAP4   POLR3B  FICD    C12orf34
ANAPC7  VPS29   DYNLL1  POP5    MLEC    RNF34   C12orf65        SBNO1   SNRNP35 UBC
BRI3BP  SFSWAP  PUS1    GOLGA3  RPL23AP67       ZMYM5   KRR1P1  LNX2    PDS5B
NHLRC3  KBTBD6  KBTBD7  NAA16   ITM2B   DLEU1   RPS4XP16        DHRS12  SUGT1   BORA
LMO7    DNAJC3-AS1      DNAJC3  UGGT2   RAP2A   PROZ    PCID2   TTC5    PARP2   DAD1
MRPL52  ACIN1   SFTA3   MGAT2   DNAAF2  NEMF    TXNDC16 GNPNAT1 HNRPCP  SYNJ2BP
MAP3K9  RBM25   ZNF410  PROX2   NEK9    POMT2   AHSA1   SPTLC2  RPS6KA5 CPSF2
BTBD7   PAPOLA  RPS20P33        GOLGA8B ZFYVE19 PPP1R14D        RPAP1   ZFP106
TP53BP1 PATL2   B2M     MYEF2   HDC     AP4E1   PIGB    RNF111  NARG2   CSNK1G1
PARP16  DIS3L   SMAD6   FEM1B   ANP32A  HEXA    CSK     SCAMP2  GOLGA6L5
ZSCAN2  CHD2    NR2F2   LRRC28  ASB7    ALDH1A3 SOLH    FBXL16  CCDC154 MRPS34
NTHL1   ZNF205  ATF7IP2 ERCC4   UBFD1   PLK1    MAZ     TAOK2   TBX6    GDPD3
SULT1A3 TBC1D10B        FBXL19-AS1      FBXL19  CNEP1R1 HEATR3  PAPD5   SALL1
CCL22   DOK4    EXOC3L1 CTCF    DDX19B  TMEM170A        C16orf46        MLYCD
ZC3H18  CENPBD1 VPS53   RAP1GAP2        ZMYND15 RNF167  ZFP3    DERL2   PITPNM3
SLC16A13        WRAP53  KRBA2   COX10-AS1       ZSWIM7  ALKBH5  LLGL1   C17orf51
WSB1    C17orf108       SUPT6H  ABHD15  BLMH    CRLF3   RNF135  CCT6B   ZNF830
PEX12   DHRS11  PIP4K2B LEPREL4 ACLY    KAT2A   FAM134C RUNDC1  UBTF    C17orf69
ZNF652  DLX4    PPP1R9B RSAD1   C17orf67        TRIM25  RAD51C  HEATR6  APPBP2
DCAF7   CEP95   HN1     GGA3    UNK     TRIM65  QRICH2  ENGASE  CBX2    CBX8
SIRT7   PYCR1   LRRC45  RNMT    RIOK3   ZNF397  MOCOS   CCDC11  ONECUT2 BCL2
ZADH2   MIER2   C19orf21        CIRBP   MOB3A   DOT1L   LMNB2   ZNF555  TLE6
PIAS4   ZBTB7A  DPP9    SAFB    CAPS    ELAVL1  ZNF558  ZNF562  PIN1    ICAM1
ZGLP1   RAB3D   ZNF627  ZNF440  ZNF433  ZNF844  ZNF442  ZNF799  ZNF490  WDR83   LYL1
STX10   SAMD1   SIN3B   NR2F6   ANO8    TMEM221 GLT25D1 PIK3R2  JUND    ZNF253
ZNF91   ANKRD27 NUDT19  KCTD15  ZNF792  LIN37   CAPNS1  ZNF565  ZNF529  ZNF790
ZNF781  MED29   ZFP36   ZNF546  MAP3K10 SHKBP1  MIA     SMG9    ZNF283  ZNF284
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BAX     SLC6A16 PTOV1   NAPSA   C19orf63        CTU1    ZNF615  ZNF808  ZNF816
ZNF347  ZNF761  U2AF2   ZNF835  ZNF264  ZNF543  ZNF547  ZNF749  ZNF549  ZNF586
ZNF814  ZNF329  ZSCAN22 ZNF132  ZCCHC3  FAM110A NOP56   FASTKD5 PCNA    MKKS    GZF1
ABHD12  NANP    COMMD7  DNMT3B  PXMP4   ZNF341  MMP24   NFS1    NDRG3   RBL1
IFT52   FITM2   ADA     MATN4   SDC4    ZSWIM3  ZSWIM1  NCOA5   ELMO2   KRT18P4
TMEM189 ADNP    ZFP64   VAPB    C20orf151       TCFL5   DPH3P1  RGS19   PCMTD2
RBM11   RNGTTP1 TCP10L  TMEM50B C2CD2   SUMO3   CECR5   ZNF74   KRT18P5 CRKL
UBE2L3  SDF2L1  ZNF280B ZNF70   ASPHD2  HPS4    GAS2L1  NF2     CCDC157 RNF215
PRR14L  POLR2F  TNRC6B  SGSM3   XPNPEP3 L3MBTL2 EFCAB6  RP6     NCAPH2  CPT1B   ACR
PPP2R3B-AS1     HDHD1   ARHGAP6 TCEANC  REPS2   SCML1   ZNF673  ZNF41   ZNF81
ZNF630  RBM3    KCND1   PPP1R3F WNK3    FAM123B FAM155B CXorf65 ACRC    DMRTC1
PABPC5  BEX4    PGRMC1  EEF1A1P30       ZBTB33  AIFM1   ZNF449  FHL1    IDS
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GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
Tissue: Artery_Tibial=>Thyroid  Type:   asymmetric
SourceGene:     RP11-496I2.3(ENSG00000257898.1)
TargetGeneSet:  B3GALT6 RPL22   PLEKHG5 RP3     RPL11   RP4     PABPC4  YBX1    RPS8
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CCDC104 INPP4A  RPL31   FOXD4L1 STEAP3-AS1      RPL37A  RPL32   RPL15   CCRL1
EIF1B   RPL14   LARS2   SLC52A1 RPL10AP6        THOC7   RPL24   CNBP    RPL35A
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RPL34   RPS3A   TLR3    RPL37   ITGA2   BTF3    NSA2    EPB41L4A-AS1    CCNI2   SKP1
CTB     THG1L   GNB2L1  EXOC2   BTN3A3  RPL10A  RPL39P3 EEF1A1  RWDD1   MRPS12
ZDHHC4  VOPP1   PIK3CG  RPS20   SNHG6   RPL7    RPL30   EIF3E   EIF3H   PARP10  RPS6
VCP     SIT1    ANP32B  U4      RPL12   SET     ENDOG   RPL7A   SLC2A6  TUBB4B  CCNY
TSPAN15 RPS3AP5 RPL13AP5        TRIM5   RPL27A  RASSF10 C11orf58        CTD
INTS5   CLPB    RPS25   CDON    PFDN5   PPM1H   RPL14P1 NAP1L1  FAM71C  POLR3B  GPN3
RPL6    MLEC    BRI3BP  TPT1    RCBTB2  CCNB1IP1        RPL36A  RPL7AP6 BTBD7
RPS3AP6 CSK     SCAMP2  ANP32BP1        NTHL1   RPS15A  LYRM1   C16orf54
ADCY7   LPCAT2  GABARAP RPL26   RPL23A  RPL17   RPL19   EIF1    RPL27   ITGB3
LUC7L3  TRIM25  CYB561  LRRC45  PHLPP1  BCL2    MED16   TMIGD2  VAV1    RFX1    ANO8
UBA52   ARMC6   LRFN1   SNRPD2  RPS11   RPS5    AP5S1   SEC23B  SDC4    ZNFX1-AS1
ZFP64   POLR2CP RTN4R   RIMBP3  ZNF70   EIF3D   RPL3    TNRC6B  UXT     RPS23P8
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GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
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38      91      translational termination
GO:0006414      7.0171850235729e-56     102.789356984479        0.879177911563214
39      105     translational elongation
GO:0006413      8.52636321611516e-56    71.9246059750647        1.27271469102484
43      152     translational initiation
GO:0006614      7.02328282744798e-54    97.463405862255 0.879177911563214       38
105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.08863645954581e-53    96.0233876683203        0.887551034530482
38      106     cotranslational protein targeting to membrane
GO:0045047      1.08863645954581e-53    96.0233876683203        0.887551034530482
38      106     protein targeting to ER
GO:0072599      1.08863645954581e-53    96.0233876683203        0.887551034530482
38      106     establishment of protein localization to endoplasmic reticulum
GO:0000184      2.544223793924e-53      84.717987804878 0.996401633104975       39
119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0070972      1.44053772536786e-51    81.5512048192771        0.988028510137707
38      118     protein localization to endoplasmic reticulum
GO:0019080      7.05958218321539e-47    57.6016632903295        1.26434156805757
38      151     viral genome expression
GO:0019083      7.05958218321539e-47    57.6016632903295        1.26434156805757
38      151     viral transcription
GO:0006612      1.23819243971341e-46    56.5919329491881        1.28108781399211
38      153     protein targeting to membrane
GO:0043624      1.23819243971341e-46    56.5919329491881        1.28108781399211
38      153     cellular protein complex disassembly
GO:0000956      1.62965664813558e-46    51.9512195121951        1.41505778146841
39      169     nuclear-transcribed mRNA catabolic process
GO:0043241      4.86135258011712e-46    54.214859437751 1.32295342882845        38
158     protein complex disassembly
GO:0034623      5.73253131166412e-46    50.009485094851 1.45692339630475        39
174     cellular macromolecular complex disassembly
GO:0006402      1.52190575946733e-45    48.5566766099316        1.49041588817383
39      178     mRNA catabolic process
GO:0032984      1.93497356766425e-45    48.2064459930314        1.4987890111411 39
179     macromolecular complex disassembly
GO:0006401      1.46130671957922e-44    42.3943135054246        1.71649020829008
40      205     RNA catabolic process
GO:0072594      4.95839958975132e-43    40.830376940133 1.70811708532281       39
204     establishment of protein localization to organelle
GO:0019058      3.03134643812145e-39    33.5355515325551        1.93419140543907
38      231     viral infectious cycle
GO:0022415      1.12270140301278e-38    30.3637015781923        2.17701197148986
39      260     viral reproductive process
GO:0071845      1.42567564632147e-38    28.508399109492 2.37796692270431        40
284     cellular component disassembly at cellular level
GO:0022411      2.54419471907449e-38    28.0406212664277        2.41145941457339
40      288     cellular component disassembly
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41      474     protein targeting
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40      451     viral reproduction
GO:0033365      1.17391236470769e-29    15.8492287514612        3.9604871635181 40
473     protein localization to organelle
GO:0042273      2.69734245956887e-10    124.55652173913 0.100477475607224       6
12      ribosomal large subunit biogenesis
GO:0022613      6.02907803749116e-10    9.51482479784367        1.88395266763546
15      225     ribonucleoprotein complex biogenesis
GO:0071843      1.39171583155575e-09    8.91130390835579        2.00117638917722
15      239     cellular component biogenesis at cellular level
GO:0042254      4.12671955524885e-09    11.4053438692828        1.24759532212304
12      149     ribosome biogenesis
GO:0006364      1.56556302110038e-08    13.64385662258  0.870804788595945       10
104     rRNA processing
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10      110     rRNA metabolic process
GO:0034470      1.11109670401426e-07    8.2814756978333 1.67462459345374        12
200     ncRNA processing
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285     ncRNA metabolic process
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Tissue: Artery_Tibial=>Thyroid  Type:   asymmetric
SourceGene:     SERTAD2(ENSG00000179833.3)
TargetGeneSet:  UBE2J2  RP4     LZIC    DFFA    CLCN6   DNAJC16 ARHGEF19
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PHACTR4 PRDX3P2 TAF12   GMEB1   SNRNP40 TINAGL1 PEF1    TMEM39B TXLNA   HDAC1
ZMYM1   LSM10   INPP5B  ZMPSTE24        SLFNL1  RNF220  RP11    C1orf123
MYSM1   NFIA    ZNHIT6  CEPT1   GOLPH3L ARNT    GABPB1  LYSMD1  SNX27   CHTOP   SHE
PYGO2   FLAD1   UBQLN4  BGLAP   CCT3    ARHGEF11        USP21   POGK    METTL13
MRPS14  SMG7    BAP1    TRMT1L  CDC73   KLHL12  SOX13   TMEM81  CD46    FBXO28
PYCR2   C1orf131        MTR     OR2L3   PGBD2   SMC6    DNMT3A  C2orf18 PREB
SLC5A6  EIF2B4  PPM1G   SLC30A6 FAM98A  GEMIN6  PLEKHH2 ABCG5   MSH6    PAPOLG
PPP3R1  SNRPG   SPR     CCT7    CCDC142 AUP1    ART4    MRPL15  C2orf68 MRPL35
RMND5A  RPIA    MRPS5   ZNF2    ANKRD36C        LMAN2L  POLR1B  AMMECR1L
DNAJC10 ICA1L   WDR12   CREB1   RQCD1   TTLL4   COL4A3  EIF4E2  DTYMK   CHCHD4
C3orf19 ACAA1   GORASP1 ZNF620  NME6    C3orf62 DUSP7   SCT     FLNB-AS1        SHQ1
CLCP1   ABHD10  KIAA1407        ARHGAP31        POGLUT1 GTF2E1  PTPLB   ZNF148
SRPRB   MSL2    SLC25A36        UBQLN4P1        MYNN    ACTL6A  DCUN1D1 ABCF3   ALG3
POLR2H  CRYGS   MUC4    LRCH3   MRFAP1L1        UBE2K   DCAF4L1 CORIN   CLOCK
GRSF1   THAP9   COQ2    KIAA1109        IL15    LSM6    TIGD4   MFAP3L  IRF2
BRIP1   CTD     MARCH6  C5orf51 SNX18   IPO11   MRPS27  DMGDH   ZCCHC9  WDR36   PHAX
P4HA2-AS1       IGIP    HARS    G3BP1   GEMIN5  CTB     C6orf228        HIST1H2BM
TRIM27  LY6G6C  LSM2    AGPAT1  RING1   PFDN6   ARMC12  TAF8    RPL7L1  XPO5
TDRD6   MTO1    TSPYL4  GOPC    VIP     SUN1    C7orf26 MIOS    TRGJP1  CDK13
URGCP   PSPH    BAZ1B   RBM48   CCDC132 ZKSCAN5 ZKSCAN1 CNPY4   SLC12A9 CLDN15
C7orf53 METTL2A TNPO3   SMO     NFE2L1  PRSS37  OR9A3P  ZNF786  ZNF398  ABCF2
RPL23AP53       CTA     NEIL2   POLR3D  CHMP7   PPP2R2A INTS9   TM2D2   YTHDF3
ARMC1   TERF1   INTS8   GRHL2   DERL1   TG      ZNF623  ZNF252  SNAPC3  KLHL9
DCAF10  FXN     C9orf40 CEP78   BICD2   FOXE1   MURC    RNF20   NIPSNAP3B
C9orf84 PKN3    TBC1D13 TOR1B   EXOSC2  BRD3    C9orf69 SDCCAG3 TAF3    NUDT5
C10orf140       BMI1    ZNF485  ZFAND4  ERCC6   CSTF2T  ADO     MSS51   FUT11
AP3M1   TEP1    BTAF1   MYOF    BTRC    TAF5    SMC3    FAM175B AP2A2   CHRNA10 RRP8
ZNF143  RNF141  MPPED2  SLC35C1 CELF1   TTC9C   ZBTB3   MARK2   STIP1   PLCB3   MEN1
DPF2    MRPL21  KRTAP5-9        UCP3    PPME1   C11orf30        RSF1    FAM76B  RDX
C11orf93        ZW10    PAFAH1B2        DDX6    C2CD2L  ZNF202  HYLS1   VPS26B
RAD52   FKBP4   NCAPD2  KIAA1467        KIAA0528        REP15   BCDIN3D TARBP2
SMUG1   DNAJC14 DYRK2   TMPO    SART3   ANAPC7  ATXN2   POP5    RNF34   C12orf65
SNRNP35 PUS1    GOLGA3  MRPS31P2        PSPC1-OT1       LNX2    NHLRC3  KBTBD6
KBTBD7  NAA16   RPS4XP16        DHRS12  RAP2A   PCID2   TTC5    PARP2   MRPL52
RBM23   AJUBA   ACIN1   ZFHX2   FITM1   NEMF    MAP3K9  PROX2   NEK9    AHSA1
CPSF2   BTBD7   TJP1    GOLGA8B BUB1B   ZFYVE19 PPP1R14D        NDUFAF1 MYEF2   HDC
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AP4E1   PIGB    RNF111  NARG2   CSNK1G1 UBAP1L  DIS3L   SMAD6   FEM1B   ANP32A  HEXA
MPI     ZSCAN2  WDR73   NR2F2   ASB7    FBXL16  CCDC154 ZNF205  USP7    ERCC4
UBFD1   MAZ     TAOK2   GDPD3   SULT1A3 CD2BP2  TBC1D10B        FBXL19-AS1
FBXL19  PAPD5   CTCF    TMEM170A        C16orf46        MLYCD   USP10   ZC3H18
RNMTL1  SGSM2   RAP1GAP2        DHX33   DERL2   SLC16A13        ZSWIM7  PIGL
ALKBH5  C17orf51        SDF2    C17orf63        BLMH    CRLF3   UTP6    ZNF830
PEX12   DHRS11  PIP4K2B MED1    CNP     NAGLU   FAM134C PSME3   RUNDC1  UBTF
C17orf69        UBE2Z   ZNF652  PPP1R9B APPBP2  DCAF7   FTSJ3   SMARCD2 FAM104A HN1
UNK     QRICH2  CANT1   ENGASE  FSCN2   SIRT7   RP13    ZNF397  CCDC11  BCL2    DSEL
RTTN    ZADH2   MIER2   LMNB2   ZNF555  PIAS4   ZBTB7A  DPP9    SAFB    PCP2
ELAVL1  PIN1    ZGLP1   ZNF627  ZNF441  ZNF799  ZNF490  WDR83   FARSA   TRMT1
SAMD1   NR2F6   GLT25D1 SUGP1   ANKRD27 KCTD15  WTIP    KRTDAP  LIN37   ZNF790
ZNF571  ZNF781  ZNF546  MAP3K10 MIA     IRGQ    ZNF284  BLOC1S3 DMPK    MYPOP
STRN4   KPTN    KCNJ14  BAX     SIGLEC16        NAPSA   CTU1    ZNF615  ZNF808
ZNF347  ZNF677  ZNF761  U2AF2   ZNF264  ZNF543  ZNF547  ZNF749  ZNF549  ZNF586
ZNF587  ZNF814  ZNF417  ZNF329  ZSCAN22 ZNF132  FAM110A NOP56   NANP    COMMD7
DNMT3B  RBL1    FITM2   RP3     ZSWIM3  ZSWIM1  NCOA5   ELMO2   ARFGEF2 KRT18P4
TMEM189 ADNP    ZFP64   CSTF1   VAPB    TCFL5   DPH3P1  RBM11   TCP10L  C21orf59
CECR5   KRT18P5 CRKL    UBE2L3  ZNF70   HPS4    RNF215  PRR14L  ANKRD54 POLR2F
XPNPEP3 L3MBTL2 HDHD1   SCML1   ATP6AP2 ZNF673  ZNF41   GPKOW   PPP1R3F SHROOM4 PHF8
WNK3    FAM155B CXorf65 ACRC    DMRTC1  PABPC5  UTP14A  ZNF449  NAA10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0071843      2.48233480270064e-06    3.45626671218069        7.06200262957581
22      239     cellular component biogenesis at cellular level
GO:0022613      3.37420959179176e-06    3.50405679513185        6.64832883537471
21      225     ribonucleoprotein complex biogenesis
GO:0034660      4.16704383617833e-06    3.14035538062234        8.42121652480797
24      285     ncRNA metabolic process
GO:0006353      4.24157232674311e-06    5.84808800419068        2.3933983807349 12
81      DNA-dependent transcription, termination
GO:0006397      7.8812546341673e-06     2.68889039793562        11.7897031347312
29      399     mRNA processing
GO:0000377      1.01642442008761e-05    3.48358505564388        6.02781814407307
19      204     RNA splicing, via transesterification reactions with bulged
adenosine as nucleophile
GO:0000398      1.01642442008761e-05    3.48358505564388        6.02781814407307
19      204     nuclear mRNA splicing, via spliceosome
GO:0000375      1.43651180966434e-05    3.3906862745098 6.17555878485918        19
209     RNA splicing, via transesterification reactions
Tissue: Artery_Tibial=>Thyroid  Type:   asymmetric
SourceGene:     TTI1(ENSG00000101407.8)
TargetGeneSet:  DFFB    ERRFI1  LZIC    RP11    DFFA    PLOD1   DNAJC16 ARHGEF19
ARHGEF19-AS1    CROCCP3 HP1BP3  TCEB3   RP1     XKR8    EYA3    MED18   PHACTR4
TXLNA   SLFNL1  MMACHC  C1orf123        MYSM1   GADD45A RP4     SLC35A3 ATXN7L2
CYB561D1        GDAP2   PIAS3   GOLPH3L LYSMD1  SNX27   INTS3   GBAP1   FAM189B CLK2
UBQLN4  SEMA4A  VHLL    CCT3    C1orf182        USP21   POGK    VAMP4   SMG7
KLHL12  SOX13   TMEM81  SRGAP3  CD55    CD46    ATF3    PGBD2   ID2     TTC32
C2orf44 SLC5A6  CCDC121 UBASH3A EHD3    FAM98A  GEMIN6  ARHGEF33        SNORA67
PAPOLG  XPO1    DBIL5P2 PPP3R1  AUP1    MRPL35  RMND5A  RPIA    MRPS5   ZNF2
LMAN2L  C2orf29 RBP4    AMMECR1L        R3HDM1  C2orf77 ANKAR   OSGEPL1 SATB2
ICA1L   WDR12   SPAG16  BCS1L   DTYMK   CRELD1  C3orf19 RFTN1   GORASP1 ZNF619
ZDHHC3  NME6    DUSP7   ABHD6   SHQ1    ADPRH   CDV3    SLC25A36        TIPARP-AS1
PIK3CA  ABCC5   ABCF3   POLR2H  CRYGS   RFC4    TMEM128 DCAF4L1 YIPF7   REST
CENPC1  AREGB   THAP9   CCNA2   IL15    BRIP1   MARCH6  C5orf51 CTD     IPO11
ZNF366  ZCCHC9  FAM174A XBP1P1  P4HA2   SHROOM1 CTB     HARS    HARS2   PCDHGB8P
ARAP3   PCDH12  LSM11   CPEB4   TSPAN17 GNL1    PRR3    C6orf25 LSM2    NOTCH4
PFDN6   TAF8    GUSBP4  LINC00472       C6orf203        MIOS    CDK13   URGCP   PSPH
GS1     RHBDD2  RBM48   CCDC132 DLX5    ZKSCAN1 METTL2A TNPO3   CNOT4   ZNF398
ZNF862  GIMAP4  SLC35G5 HMBOX1  TTI2    C8orf40 ARMC1   INTS8   GAPDHP62
GRHL2   LRRC6   ZNF623  RANBP6  SNAPC3  KLHL9   FANCG   C9orf103        SECISBP2
FAM22G  ALG2    NR4A3   RNF20   TRIM32  LHX6    PRPS1P2 ZBTB43  SH2D3C  CCBL1
EXOSC2  AK8     C9orf69 QSOX2   SDCCAG3 INPP5E  NOXA1   FBXO18  CDNF    BMI1
LINC00202       ZNF485  ERCC6   CSTF2T  CHST3   MSS51   AP3M1   ENTPD7  C10orf2 BTRC
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NSMCE4A ZNF195  CHRNA10 UBQLNL  TRIM34  TRIM5   RRP8    ZNF143  SLC35C1 TTC9C
ZBTB3   STIP1   PLCB3   RPS6KA4 MEN1    PPP2R5B C11orf85        DPF2    RBM14
SUV420H1        UCP3    C11orf30        FAM76B  C11orf34        ZW10    DPAGT1
HSPA8   ZNF202  VPS26B  RAD52   FKBP4   KLRAP1  REP15   PUS7L   TUBA1C  BCDIN3D
ACVRL1  KRT81   SMUG1   OBFC2B  TIMELESS        DYRK2   IL26    ALDH2   DYNLL1
RNF34   GOLGA3  EFHA1   KBTBD6  KBTBD7  ITM2B   RPS4XP16        DHRS12  BORA
DNAJC3-AS1      RAP2A   PROZ    PCID2   TTC5    PARP2   ACIN1   KLHDC1  HNRPCP  EXD2
MAP3K9  NEK9    AHSA1   SPTLC2  ZC3H14  RPS6KA5 BTBD7   GOLGA8B THBS1   ZFYVE19
PPP1R14D        ZFP106  CSNK1G1 PARP16  ZSCAN2  ZNF774  FBXL16  LMF1    ERCC4
UBFD1   DCTN5   PLK1    MAZ     GDPD3   CNEP1R1 SALL1   DOK4    DDX19B  TMEM170A
ZC3H18  GALNS   SRR     ZMYND15 DHX33   DERL2   SLC35G6 C17orf51        WSB1
TMEM199 UTP6    CDK5R1  CCL2    CCT6B   DHRS11  PIP4K2B WIPF2   LEPREL4 FAM134C
HOXB-AS2        HOXB4   DLX4    PPP1R9B PCTP    TRIM25  HEATR6  FTSJ3   HN1
QRICH2  AFMID   CANT1   CBX2    RP13    HRH4    ZNF24   C18orf54        ONECUT2
ZADH2   ZNF555  MRPL54  TNFSF9  PEX11G  ZGLP1   RAB3D   ZNF788  ZNF799  ZNF490
WDR83   TRMT1   SAMD1   TMEM221 JUND    SUGP1   ZNF253  NUDT19  KCTD15  ZNF565
ZNF260  HKR1    ZFP36   MIA     SMG9    ZNF284  ZNF225  GEMIN7  BLOC1S3 MYPOP
CPT1C   NR1H2   NAPSA   CTU1    ZNF175  ZNF816  ZNF347  ZNF761  U2AF2   ZNF835
ZNF264  ZNF543  ZNF547  ZNF749  ZNF549  ZNF550  ZNF814  ZNF329  ZSCAN22 ZNF132
NOP56   CRNKL1  DNMT3B  ZNF341  EDEM2   NFS1    SCAND1  FITM2   ZSWIM3  ZSWIM1
NCOA5   KRT18P4 ADNP    ZFP64   FAM209B GTPBP5  ITSN1   HMGN1   PRDM15  DSTNP1
CECR5   KRT18P5 CRKL    UBE2L3  NF2     RNF215  PRR14L  NCAPH2  SHANK3  PPP2R3B-AS1
HDHD1   SCML1   CXorf36 ZNF673  ZNF41   NUS1P1  ZNF81   KCND1   SHROOM4 FAM123B
BHLHB9  ZNF449
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
Tissue: Thyroid=>Heart_Left_Ventricle   Type:   asymmetric
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SourceGene:     APOM(ENSG00000204444.6) s
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TargetGeneSet: HP1BP3 NUDC EYA3 RCC1 RP11 LEPROT CCBL2 RPAP2
ALG14 FAM46C APH1A GOLPH3L CCT3 USP21 HSD17B7 CENPL CACYBP TMEM81
INTS7 IRF2BP2 ZNF692 PQLC3 SLC5A6 HNRPLL XPO1 CCT4 C2orf42 CCT7 AUP1
LMAN2L LYG1 GPR17 ARL6IP6 DNAJC10 HSPD1 SATB2 SLC23A3 CRELD1 NUP210
NGLY1 STT3B TRANK1 ZNF619 CCK HEMK1 PPP4R2 CPOX TPRA1 MLF1 FXR1
SOX2 PPP1R2 TCTEX1D2 CEP19 ABCA11P HGFAC DCAF16 TBC1D19 PGM2
APBB2 GNPDA2 UBE2D3 TBCK PLK4 CTSO PPID SH3RF1 ANKRD37 C5orf55 CCT5
CTD GPBP1 KLHL35 FAM13B BRD8 WDR55 PCDHB16 ADRB2 SNRNP48 GNL1
CNPY3 RP1 HSP90AB1 AARS2 FBXO9 PM20D2 SESN1 MICAL1 RSPH4A TCP1
KLHL7-AS1 TRA2A STYXL1 SAP25 MOSPD3 NAPEPLD RBM28 C7orf29 GBX1
SLC39A14 GTF2E2 THAP1 PYCRL ZNF623 NRBP2 DNAJA1 RECK C9orf71
NCBP1 KIAA0368 ZBTB34 FPGS MAMDC4 WAC OR13A1 PBLD HNRNPH3
P4HA1 AP2A2 C11orf91 EML3 NXF1 STIP1 SLC25A45 EED
CHORDC1 SRSF8 PHLDB1 DPAGT1 HINFP HSPA8 RAD52 FKBP4 RP4 IFFO1
CDKN1B TM7SF3 DAZAP2 DNAJC14 PAN2 PTGES3 ARHGAP9 HSP90B1 SELPLG LINC00173
GCN1L1 CRYL1 HSPH1 LHFP RPS4XP16 SUGT1 GPR180 PCID2 ABHD4
RBM23 ACIN1 ZC2HC1C AHSA1 ZC3H14 PAPOLA VRK1 HSP90AA1 ATPBD4
TMEM87A PIGB ANKDD1A C15orf44 POLG DNASE1L2 TBC1D24 GDPD3
ZDHHC7 CDK10 MIR22HG C17orf108 UNC119 DHRS13 KAT2A NMT1 STXBP4
WIPI1 QRICH2 JMJD6 C17orf90 IMPACT ABCA7 CIRBP SAFB PNPLA6 RETN
ZNF788 ATP13A1 DPY19L3 MED29 DEDD2 KPTN ZNF580 TRIM28 PYGB TTI1
SNHG11 RNF114 DNAJC5 USP16 MORC3 TOP3B PRR14L TRIOBP RANGAP1 FAM118A
TBC1D22A GPR173 RP6

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0006457	5.05E-14	10.53814103	2.46626531	21	216	protein folding

GO:0006458 1.69E-06 14.34033372 0.582312643 7 51 'de novo' protein folding

GO:0051084 1.30E-05 13.43962264 0.525223168 6 46 'de novo' posttranslational protein folding

Tissue: Heart_Left_Ventricle=>Thyroid Type: asymmetric

SourceGene: ATP13A1(ENSG00000105726.11) ATPase type 13A1

TargetGeneSet: C1orf159 HP1BP3 TXLNA CTPS U2 CCT3 C1orf114
PREB SLC5A6 FAM98A CCT4 SPR CCT7 LMAN2L ARL6IP6 SSB STAT4 NEK4
KIAA1407 RP11 CCT5 RPP40 SNRNP48 HIST1H2BK APOM RP1 PEX6
HSP90AB1 TDRD6 MTO1 LCA5 CA3 TCEA1P1 DNAJA1 PTAR1 GTF3C5 DNA2
CTD IPO7 STIP1 C2CD3 EED CEP57 RNF214 FKBP4 RP4 GPR162 CCT2
AMDHD1 OR7E36P NEK9 AHSA1 HSP90AA1 EXOC3L4 FBXL19-AS1 CYB5D2
MED31 C17orf108 SDF2 MLLT6 KAT2A PHB ZNF441 CTA LARGE
HDHD1 FAM45B KDM5D

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0006457	2.28E-10	18.57632362	0.777247249	11	216	protein folding
GO:0051084	6.07E-07	37.25480021	0.165524877	5	46	'de novo' posttranslational protein folding
GO:0006458	1.03E-06	33.19380204	0.183516712	5	51	'de novo' protein folding

Tissue: Thyroid=>Heart_Left_Ventricle Type: asymmetric

SourceGene: CRIPT(ENSG00000119878.5) cysteine-rich PDZ-binding protein

TargetGeneSet: RP11 DFFB EPHA2 MFAP2 HSPG2 NUDC EYA3 RCC1
PTPRU C1orf212 ZNF691 GPBP1L1 SLC35D1 CYR61 KIAA1107 RPAP2
FRRS1 SASS6 NOTCH2 ECM1 GOLPH3L BNIPL LYSMD1 CREB3L4 PYGO2 FAM189B CCT3
CRABP2 CD1C CASQ1 USP21 B4GALT3 HSD17B7 RGS5 METTL13 FAM163A LAMC1
TMEM81 RBBP5 ACTA1 TFB2M PXDN NBAS RHOB C2orf44 EMILIN1 SLC5A6 ASB3

XPO1	C2orf42	SPR	CCDC142	AUP1	HTRA2	LOXL3	SEMA4F	ELMOD3	LINC00152	
MRPS5	LMAN2L	FBLN7	STEAP3	TNFAIP6	ITGA4	COL3A1	COL5A2	SATB2	IDH1	FN1
BCS1L	SLC23A3	FAM134A	COL6A3	LRRFIP1	CRELD1	TRANK1	ZNF619	IP6K1	TNNC1	
EPHA3	CPOX	ABI3BP	CBLB	CCDC80	CHCHD6	TPRA1	IL20RB	ARID4A	SSR3	
PPM1L	FXR1	EIF4A2	HRASLS	PPP1R2	ABCA11P	SPON2	WDR1	APBB2	11-Sep	
BMP2K	TIGD2	UNC5C	ADH1A	UBE2D3	TBCK	ARSJ	SEC24D	PDE5A	CTSO	PPID
SH3RF1	LPCAT1	CTD	SLC38A9	KLHL35	LHFPL2	ARSK	FAM13B	BRD8	CYSTM1	SOX9
TCERG1	MIR143HG		CSF1R	PDGFRB	SPARC	C5orf4	PDLIM7	ZNF184	GNL1	
COL11A2	RGL2	TEAD3	TOMM6	SRF	HSP90AB1		FBXO9	EYS	MTO1	
COL12A1	KIAA1009		PM20D2	SESN1	RSPH4A	SLC35F1	TRMT11	BMPR1APS1		
TCF21	FNDC1	TCP1	TTYH3	ZNF890P	ACTB	C7orf26	TRA2A	RP9P	7-Sep	VWC2
GRB10	PSPH	SEMA3C	KIAA1324L		COL1A2	ZKSCAN5	FAM200A	TAF6	GCC1	ARF5
CALU	TNPO3	ZYX	CHPF2	PPP2R2A	GTF2E2	PLAT	THAP1	SDC2	UHRF2	
TYRP1	DNAJB5	TPM2	GLIPR2	GNE	RG9MTD3	NOL8	OGN	ECM2	COL15A1	
KIAA0368		ZBTB34	FPGS	C9orf114		COL5A1	COBRA1	WAC	ITGB1	
ZNF37BP	CSGALNACT2		EGR2	FRAT1	FRAT2	MARVELD1		KAZALD1	TMEM180	TAF5
FAM160B1		VENTX	AP2A2	HTATIP2	SLC39A13		LRRC55	PRG2	SLC43A1	
STIP1	MEN1	CFL1	EFEMP2	EIF1AD	RELT	RAB6A	PICALM	SCN4B	IFT46	
PHLDB1	DPAGT1	HINFP	SRPR	RAD52	FKBP4	RP4	TSPAN9	NTN4	EMP1	
REP15	FAR2	C12orf35		LIMA1	ZC3H10	PAN2	AVIL	CTDSP2	MSRB3	
BBS10	CMKLR1	SIRT4	CCDC169	LHFP	EBPL	SUGT1	LINC00346		ADPRHL1	
ARHGEF40		LRFN5	RPL32P29		FRMD6	DACT1	MAX	ZFYVE1	ABCD4	
C14orf118		VRK1	PLD4	FAN1	ACTC1	ATPBD4	GPR176	BAHD1	ZFYVE19	
MFAP1	CTDSPL2	FBN1	TPM1	ANKDD1A	CILP	IGDCC4	NPTN	LOXL1	COMMD4	
WDR61	ADAMTSL3		POLG	MRPL28	RHOT2	PGPEP1	TBC1D24	VASN	MAZ	
BCL7C	HERPUD1	HSD11B2	TSNAXIP1		CENPN	CDK10	DEF8	RNMTL1	ZMYND15	PFN1
SPAG7	DERL2	EIF5A	CTC1	C17orf39		SMCR7	SDF2	ZNF830	FBXL20	
KAT2A	FAM134C	NMT1	SCRN2	COPZ2	COL1A1	MRC2	FTSJ3	GGA3	RECQL5	
SRP68	QRICH2	SPHK1	ARHGAP28		CXXC1	POLRMT	MOB3A	PNPLA6	ZNF558	KRI1
CNN1	ZNF788	PRKACA	C19orf44		DDA1	DPY19L3	ZNF585B	PSMC4	LTBP4	
TMEM91	DEDD2	ZNF233	VASP	KPTN	LIN7B	ZNF473	SHANK1	ZNF577	ZNF816	
CCDC106	ZNF667	ZNF211	ZNF671	ZNF329	SNRPB	DDRGK1	SLC23A2	CRNKL1	PYGB	
ZNF337	TTI1	KIAA1755		PKIG	SYS1	PCMTD2	LINC00478		C21orf119	
RCAN1	C21orf2	COL6A1	COL6A2	MMP11	TFIP11	DUSP18	MYH9	MFNG	TRIOBP	
GALR3	RANGAP1	TOB2	POLDIP3	GPM6B	DMD	GPR173	SPIN4	RP6	ARMCX4	
RAB9B	NRK	KIAA1210		SRPK3	NLGN4Y					

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term

GO:0030198	2.21E-10	6.896178093	3.431458031	20	161	extracellular matrix organization
GO:0043062	2.47E-10	6.847124413	3.452771435	20	162	extracellular structure organization

GO:0007411	1.27E-06	3.486063596	7.310497543	23	343	axon guidance
GO:0030199	4.95E-06	12.62701252	0.703342329	7	33	collagen fibril organization

GO:0030029	1.87E-05	2.844863297	9.207390492	24	432
actin filament-based process					

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Tissue: Thyroid=>Heart_Left_Ventricle   Type:   asymmetric

SourceGene:     CXCL17(ENSG00000189377.3)       chemokine (C-X-C motif) ligand 17
(no ESTs in heart or thyroid)

TargetGeneSet:  WRAP73  DFFB    HSPG2   ASAP3   PTPRU   COL16A1 GPBP1L1 NRD1
RPAP2   CTSO    BNIPL   EFNA4   USP21   DPT     TMEM81  C2orf44 ARHGEF33
SEMA4F  PROM2   FBLN7   LYPD1   DCAF17  FRZB    COL3A1  COL5A2  FN1     RBM6
ABI3BP  COL6A6  ARID4A  SPON2   11-Sep  ARSJ    PDE5A   RAB33B  ADAMTS12
KLHL35  LOX     PHF15   SPARC   RP11    ZFP62   DTNBP1  ZNF184  ZNRD1-AS1
MOCS1   TPBG    KIAA1009        CASP8AP2        FNDC1   VWC2    COL1A2  CALU    ZYX
MATN2   COL14A1 GLIS3-AS1       TYRP1   RG9MTD3 OGN     ASPN    ECM2    TNFSF8
COL5A1  ITGB1   ZNF37BP SPON1   SLC39A13        DPAGT1  HINFP   PUS3    CLEC4A  EMP1
C12orf35        LUM     SLC41A2 TMEM119 TMEM233 COL4A1  COL4A2  FRMD6   ABCD4
GPR176  FBN1    CILP    LOXL1   VASN    MMP2    TXNL4B  CDK10   ASGR1   MFAP4
FLOT2   MLLT6   STAT3   COL1A1  GGA3    WDR45L  NR2C2AP ZNF600  DDRGK1  PYGB
FAM83D  RP3     COL6A2  CTA     GPM6B   LAMP2

GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term

GO:0030198      5.75E-15        20.10539346     1.047263165     16      161
extracellular matrix organization
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GO:0043062	6.34E-15	19.9662803	1.053767905	16	162
extracellular structure organization					
GO:0030199	4.78E-13	63.23382353	0.214656425	9	33
collagen fibril organization					
GO:0071230	2.28E-09	41.17528736	0.227665905	7	35
cellular response to amino acid stimulus					
GO:0071229	7.37E-09	33.89486139	0.266694346	7	41
cellular response to acid					
GO:0071418	3.12E-08	26.78374766	0.325237008	7	50
cellular response to amine stimulus					

GO:0071417 cellular response to organic nitrogen	4.14E-08	25.58978289	0.338246488	7	52
GO:0043200 response to amino acid stimulus	2.01E-07	19.83610781	0.42280811	7	65
GO:0001101 response to acid	1.28E-06	14.72929561	0.552902913	7	85
GO:0014075 response to amine stimulus	4.69E-06	11.95246648	0.669988236	7	103
GO:0001957 intramembranous ossification	5.26E-06	157.7362637	0.039028441	3	6

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GO:0036072      5.26E-06        157.7362637     0.039028441     3       6
direct ossification




GO:0007411      1.37E-05        5.598599216     2.231125874     11      343     axon
guidance




GO:0043588      1.94E-05        17.47801661     0.331741748     5       51      skin
development




Tissue: Thyroid=>Heart_Left_Ventricle   Type:   asymmetric



SourceGene:     DNAJA3(ENSG00000103423.9)       "DnaJ (Hsp40) homolog, subfamily A,
member 3"



TargetGeneSet:  KLHL21  HAX1    MEF2D   MRPL24  TAGLN2  ADCY10  MYL3    FTH1P23
NAP1L5  RPS23   RNF44   FGFR4   SSR1    LEMD2   TOMM7   BMPER   MRPS24  CTA
NDUFB2  RP11    MMP16   NDUFB9  GRIN3A  PSMB7   USP20   PPP1R26 RSU1    NDUFB8
NDUFS3  C11orf10        COX8A   ADRBK1  PRKRIR  C11orf67        ZBTB44  FOXJ2   FAR2
RHOJ    SLIRP   NDUFB1  YY1     AP4E1   TEPP    PSMB6   PSMB3   SAFB2   C19orf79
OLFM2   COX6B1  POLR2I  FBL     ETFB    PROCR   ROMO1   RPS21   HSPA13  NDUFV3  GGA1
NDUFB11 HSD17B10        COX7B

GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
```

GO:0022904	2.98E-14	45.1804878	0.345443222	11	96	respiratory electron transport chain
GO:0022900	1.26E-12	31.13940115	0.482181164	11	134	electron transport chain
GO:0045333	2.39E-12	29.22137405	0.510968099	11	142	cellular respiration
GO:0006120	2.89E-09	62.47391304	0.129541208	6	36	"mitochondrial electron transport, NADH to ubiquinone"
GO:0015980	9.26E-09	12.78287739	1.104698637	11	307	energy derivation by oxidation of organic compounds
GO:0042773	1.55E-08	45.6776246	0.169123244	6	47	ATP synthesis coupled electron transport
GO:0042775	1.55E-08	45.6776246	0.169123244	6	47	mitochondrial ATP synthesis coupled electron transport
GO:0006119	5.66E-08	35.98745819	0.20870528	6	58	

oxidative phosphorylation

GO:0006091 2.74E-07 8.995847225 1.540101031 11 428
generation of precursor metabolites and energy

Tissue: Thyroid=>Heart_Left_Ventricle Type: asymmetric

SourceGene: ENOSF1(ENSG00000132199.11) enolase superfamily member 1

TargetGeneSet: KLHL17 CPSF3L TAS1R3 TNFRSF14 RP1 HP1BP3 NUDC RP11
GPBP1L1 RPAP2 PRPF38B CCT3 USP21 CACYBP TMEM183A ZC3H11A TMEM81
INTS7 MTR SMC6 SLC5A6 ASB3 CCT4 AFTPH C2orf42 SPR PCGF1 AUP1
MRPS5 ARL6IP6 DNAJC10 HSPD1 ILKAP CRELD1 GHRLOS CHCHD4 NGLY1 ABHD14A-ACY1
CBLB SLC9C1 TPRA1 FXR1 DCUN1D1 PGM2 NUDT10 PLK4 CTSO PPID CCT5
MEF2C BRD8 WDR55 PCDHB16 ZNF300P1 SNRNP48 GNL1 CNPY3 HSP90AB1
VIP TCP1 PARK2 NUPL2 RP9 PSPH STYXL1 MAGI2 FAM133B THAP1
C8orf44 PYCRL DNAJA1 GNE FAM95B1 GKAP1 NCBP1 FAM73B RP11-88G17 WAC
HNRNPH3 DNA2 ANXA7 KIAA0913 C10orf131 PPP2R2D HTATIP2 NXF1
STIP1 EIF1AD ANO1 CAPN5 CHORDC1 MED17 ZBTB44 RAD52 FKBP4 RP4
IFFO1 REP15 PTGES3 SIRT4 ZCCHC8 C12orf65 HSPH1 SUGT1 PCID2
ACIN1 DHRS1 TRIM9 ZC2HC1C AHSA1 SMEK1 PAPOLA HSP90AA1 EHD4
DTWD1 ANKDD1A DPP8 C15orf42 SPNS3 C17orf108 COASY HOXB-AS1
MRC2 QRICH2 JMJD6 CIRBP SAFB PEX11G SAMD1 ZNF91 DPY19L3 DEDD2 KPTN
TRPM4 TFPT SLC23A2 RRBP1 DDX27 RNF114 STMN3 MORC3 THAP7-AS1
TRIOBP RANGAP1 CYB5R3 ARSD GPR173 GDPD2

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GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term








GO:0006457      1.86E-10        10.44332791     1.733859248     15      216     
protein folding








GO:0006458      3.15E-06        17.32121212     0.409383434     6       51      'de
novo' protein folding









Tissue: Heart_Left_Ventricle=>Thyroid   Type:   asymmetric
SourceGene:     ENSG00000233038.1
TargetGeneSet:  FCRL5   LIN9    IGKJ5   IGKC    IGKJ3   IGKJ2   IGKV1-16
IGKV2-28        IGKV1-39        MST1    RP11    KCNMB2-IT1      TMPRSS11CP      IGJ
C7orf50 BMPER   PCLO    IL18    MEG3    IGHA2   IGHG2   IGHGP   IGHG1   IGHG3
IGHV3-43        SNORA10 TGIF1   IGLV3-21        IGLV2-8 IGLC3   ASMT    MAMLD1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006958      1.71372213274009e-09    145.353535353535        0.0553594906926856
5       50      complement activation, classical pathway
GO:0006956      5.63834339914804e-09    112.672413793103        0.0697529582727839
5       63      complement activation
GO:0002455      6.61742347366508e-09    108.901515151515        0.0719673379004913
5       65      humoral immune response mediated by circulating immunoglobulin
GO:0072376      2.16244266875052e-08    84.7579693034238        0.0907895647360044
5       82      protein activation cascade
GO:0002460      2.5644627071602e-08     48.8914285714286        0.200401356307522
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6       181     adaptive immune response based on somatic recombination of immune
receptors built from immunoglobulin superfamily domains
GO:0002250      4.38173798530615e-08    44.509375       0.219223583143035       6
198     adaptive immune response
GO:0016064      9.97147565448117e-08    61.4451114922813        0.122898069337762
5       111     immunoglobulin mediated immune response
GO:0019724      1.13997696105075e-07    59.7414512093411        0.126219638779323
5       114     B cell mediated immunity
GO:0006959      1.60147054710837e-07    55.6254856254856        0.135077157290153
5       122     humoral immune response
GO:0002449      7.64940235407775e-07    40.0476992143659        0.18490069891357
5       167     lymphocyte mediated immunity
GO:0002443      2.42520447463488e-06    31.3967343336275        0.233617050723133
5       211     leukocyte mediated immunity
GO:0002253      1.32836322946249e-05    21.8630179344465        0.33104975434226
5       299     activation of immune response
Tissue: Thyroid=>Heart_Left_Ventricle   Type:   asymmetric







SourceGene:     FAAH2(ENSG00000165591.6)        fatty acid amide hydrolase 2







TargetGeneSet:  PLA2G2A ASAP3   PDIK1L  PTPRU   GPBP1L1 YIPF1   GNG12   CYR61   RP11
BNIPL   CREB3L4 PYGO2   FAM189B USP21   HSD17B7 DPT     PRRX1   LAMC1   ZC3H11A
ITPKB-IT1       KLHL29  C2orf44 ARHGEF33        HTRA2   LOXL3   SEMA4F  PROM2
FBLN7   COL3A1  COL5A2  FN1     B3GNT7  CRELD1  C3orf45 TNNC1   VGLL3   EPHA3
ABI3BP  BZW1P2  COL6A6  ECT2    ST6GAL1 BCL6    SPON2   11-Sep  UNC5C   CXXC4   ARSJ
LPCAT1  SLC38A9 LHFPL2  LOX     GRAMD3  PHF15   H2AFJ   ZNF354B ID4     ZNRD1-AS1
TMEM63B TDRD6   EYS     KIAA1009        PM20D2  CASP8AP2        TCF21   FNDC1
WDR27   LFNG    VWC2    GS1     COL1A2  SLC12A9 ZYX     INTS9   PPP2CB  PLAT    GDF6
IGHEP2  TYRP1   IL11RA  RG9MTD3 OGN     OMD     ECM2    KIAA1958        COL5A1
ITGB1   NAMPTL  ZNF37BP DNAJC12 INSC    SLC39A13        MEN1    EFEMP2  PICALM
AMOTL1  KBTBD3  TAGLN   DPAGT1  PUS3    RAD52   EMP1    FAR2    C12orf35
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LIMA1 GLI1 GLIPR1 NUDT4 CMKLR1 TMEM119 DTX1 CCDC169 RPS4XP16
GPR180 ADPRHL1 ARHGEF40 LRFN5 FRMD6 ABCD4 GPR176 BAHD1 GLDN CTD
ANKDD1A LRRK1 VASN CDH11 HSD11B2 FTSJD1 TXNL4B CENPN CDK10 SERPINF2
NLGN2 MFAP4 RAB34 MLLT6 STAT3 PTRF C17orf53 COPZ2 COL1A1
RNF43 KCNJ2 ENGASE ACTG1 WDR45L ARHGAP28 ZADH2 POLR2E PNPLA6
ZNF558 OLFM2 COL5A3 TPM4 TSHZ3 ANKRD27 PSMC4 LYPD5 ZNF233 ZFP112
ZNF577 ZNF211 DDRGK1 SLC24A3 EMILIN3 PCMTD2 C21orf2 COL6A1 COL6A2 GPM6B
PPP1R3F SPIN4 PLS3 KIAA1210 PGRMC1 LAMP2 SRPK3 VAMP7

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0030199	1.51E-11	41.86523438	0.312850322	9	33	collagen fibril organization
GO:0030198	3.15E-11	11.93128228	1.526330358	15	161	extracellular matrix organization

GO:0043062	3.44E-11	11.8492807	1.535810671	15	162
extracellular structure organization					
GO:0031589	6.19E-08	7.835168117	1.915023182	13	202
cell-substrate adhesion					
GO:0010810	2.55E-07	11.7703125	0.891149401	9	94
regulation of cell-substrate adhesion					
GO:0070208	1.55E-06	71.71929825	0.094803128	4	10
protein heterotrimerization					

GO:0043588	8.25E-06	14.52315522	0.483495952	6	51	skin development
GO:0071230	1.84E-05	18.03535354	0.331810947	5	35	cellular response to amino acid stimulus

Tissue: Thyroid=>Heart_Left_Ventricle Type: asymmetric

SourceGene: HIST1H2BD(ENSG00000158373.7) "histone cluster 1, H2bd"

TargetGeneSet: KLHL17 MXRA8 TNFRSF14 RP13 RP11 ZBTB17 HP1BP3 RCC1
IPO13 GPBP1L1 LEPROT SLC35D1 RPAP2 CEPT1 RP4 APH1A GOLPH3L BNIPL
S100A9 DENND4B FAM189B CCT3 KIRREL USP21 B4GALT3 HSD17B7 CACYBP TMEM183A
ZC3H11A TMEM81 INTS7 CAPN2 ARF1 MTR ZNF672 ZNF692 SMC6 CCT4
AFTPH C2orf42 SPR PCGF1 LMAN2L DNAJC10 COL5A2 HSPD1 ICA1L IKZF2
SLC23A3 FBXO36 COL6A3 CRELD1 CHCHD4 PLCL2 NGLY1 ZNF619 RBM6 MANF
PPP4R2 CPOX MSL2 MYNN FXR1 EIF4A2 PPP1R2 APBB2 SRP72 TBCK GLRB
PPID SH3RF1 LPCAT1 CCT5 FAM105B GPBP1 P4HA2-AS1 P4HA2 WDR55
PCDHB16 ZNF300P1 PDLIM7 ZNF354A ZNF879 SNRNP48 ZNF184 SCAND3 GNL1
SLC39A7 RP1 TOMM6 CNPY3 HSP90AB1 TDRD6 BAI3 RARS2 PM20D2
C6orf203 VNN2 VIP SERAC1 FNDC1 PNLDC1 ZNF92 STYXL1 RBM48
SLC25A13 GIMAP4 SLC39A14 KIF13B GTF2E2 GINS4 THAP1 GSDMD
PYCRL ZNF623 NRBP2 DNAJA1 NOL6 RECK GKAP1 OGN NCBP1 COL15A1 COQ4
C9orf114 CCBL1 RP11-88G17 COL5A1 MAMDC4 NUDT5 WAC ITGB1 PBLD
DNA2 C10orf32 DCHS1 ZNF143 HTATIP2 C11orf46 STIP1 GPR137
SLC25A45 RBM14 RBM4B EED CHORDC1 MED17 SRSF8 DPAGT1 HSPA8
ZBTB44 RAD52 FKBP4 EMP1 REP15 C12orf35 LIMA1 DAZAP2 PAN2
PTGES3 ARHGAP9 MRPL42 HSP90B1 SELPLG C12orf65 HSPH1 RPS4XP16
SUGT1 COL4A2 PCID2 ACIN1 LRFN5 MLH3 ZC2HC1C AHSA1 SERPINA1
PAPOLA HSP90AA1 ZFYVE19 TRIM69 PIGB ANKDD1A IGDCC4 LOXL1 WDR61
DNASE1L2 TBC1D24 PRKCB FUS C16orf58 CENPN CDK10 RNF167
C17orf108 SDF2 RAB34 DHRS13 CCT6B ARHGAP23 KAT2A SCRN2
KCNJ2 HN1 QRICH2 JMJD6 HEXDC VPS4B ATP9B ABCA7 CIRBP GIPC3
C19orf59 WDR83 SAMD1 PRKACA DPY19L3 DEDD2 CD177 ZNF233 ZFP112 KPTN
PIH1D1 CTU1 FPR2 ZNF577 ZNF761 ZNF580 TRIM28 PTPRA DDRGK1 PYGB
IFT52 RP3 RNF114 STMN3 MORC3 THAP7-AS1 PRR14L MYH9 TRIOBP

RANGAP1 LMF2 ASMTL PPP1R3F GPR173 KIAA1210 HPRT1

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0006457	1.36E-09	6.942193676	3.019306622	18	216	protein folding

Tissue: Thyroid=>Heart_Left_Ventricle Type: asymmetric

SourceGene: MIA(ENSG00000261857.1) melanoma inhibitory activity

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TargetGeneSet:  FAM41C  KLHL17  UBE2J2  CPSF3L  RP11    TNFRSF14        HP1BP3  NUDC
EYA3    SLFNL1  RNF220  GPBP1L1 RP1     LEPROT  SLC35D1 FPGT-TNNI3K     TYW3
WDR63   CCBL2   RPAP2   CNN3    CEPT1   PTGFRN  GDAP2   RP4     APH1A   BNIPL
SNX27   FAM189B CLK2    PMF1    TMEM79  CCT3    USP21   HSD17B7 ADCY10  CACYBP
LAMC1   SMG7    SWT1    TMEM81  INTS7   JMJD4   TFB2M   ZNF692  SMC6    C2orf44
SLC5A6  LTBP1   CDC42EP3        EML4    CCDC88A XPO1    CCT4    AFTPH   C2orf42 SPR
PCGF1   ELMOD3  MRPS5   LMAN2L  RFX8    METAP1D HSPD1   ALS2CR12        BCS1L
SLC23A3 RBM44   ILKAP   CRELD1  C3orf19 NGLY1   SLC25A38        CPOX    KIAA1524
WDR52   SEMA5B  SIAH2   FXR1    PARL    POLR2H  MAGEF1  EIF4A2  BCL6    PPP1R2
CEP19   ABCA11P NOP14   DCAF16  PARM1   HELQ    UBE2D3  TBCK    SEC24D  CTSO    PPID
CPE     SH3RF1  DCTD    ENPP6   CCT5    CTD     PPWD1   BRD8    SOX9    PCDHB16
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PCDHGA2 NDST1   FNDC9   ADRA1B  ZNRD1-AS1       GNL1    VWA7    HLA-DRA HLA-DMB
HLA-DMA SLC39A7 SPDEF   HSP90AB1        SLC35B2 BAI3    COL12A1 SENP6   SNX3    RP3
RSPH4A  FUCA2   C6orf97 TCP1    PNLDC1  CDK13   PSPH    STYXL1  MAGI2   RBM48   TAF6
STAG3   CLDN15  TMEM168 ST7-AS1 DYNLL1  LZTS1   POLR3D  ADAM28  KIF13B  DCTN6
GTF2E2  TTI2    THAP1   RB1CC1  ZNF623  SCRIB   CYHR1   MTND4P14        DNAJA1  GNE
GKAP1   NOL8    NCBP1   COL15A1 NIPSNAP3B       DAB2IP  PRPS1P2 ZBTB34  FPGS
RP11-88G17      QSOX2   CDNF    ZNF37BP ERCC6   ANXA7   FGFBP3  C10orf131
FRAT2   C10orf62        C10orf2 C10orf32        TAF5    BAG3    C10orf125
AP2A2   PRKCDBP WT1-AS  PIGCP1  NXF1    STIP1   SLC25A45        CFL1    EFEMP2
EIF1AD  ZDHHC24 RBM14   RBM4B   ANO1-AS1        CAPN5   ANKRD42 EED     CHORDC1
MED17   TMPRSS5 PHLDB1  HINFP   ZNF202  SRPR    KCNJ5   RAD52   FKBP4   TAPBPL
C12orf71        REP15   PAN2    PTGES3  AVIL    CRADD   APPL2   PLBD2   SIRT4
HSPH1   FAM48A  LHFP    RPS4XP16        DHRS12  SUGT1   ACIN1   NEDD8   CTSG
RPL32P29        SLC38A6 SNAPC1  EIF2B2  POMT2   AHSA1   ZC3H14  PAPOLA  VRK1
HSP90AA1        ATPBD4  EHD4    TMEM87A PIGB    POLR2M  DPP8    NPTN    WDR61   PRC1
SOLH    TPSAB1  TBC1D24 PDPK1   CLDN9   NPIP    NPIPP1  ATXN2L  GDPD3   CTF1
HERPUD1 TSNAXIP1        SLC7A6OS        AARS    BANP    CDK10   DERL2   TRIM16
TRPV2   LGALS9  NUFIP2  ANKRD13B        CCT6B   TBC1D3  KAT2A   NAGLU   COASY   NMT1
CUEDC1  DDX42   HELZ    NT5C    RECQL5  QRICH2  JMJD6   LRRC45  CXXC1   ATP9B
APBA3   SAFB2   SAFB    PNPLA6  ZNF558  TRMT1   SAMD1   DEDD2   ZNF284  PPP1R37 KPTN
KCNJ14  IRF3    ZNF137P MYADM   ZNF580  ZNF667  SLC23A2 CRNKL1  ZNF337  MT1P3
EPB41L1 PLCG1   PKIG    PABPC1L DDX27   RNF114  C20orf11        C21orf2 C21orf67
THAP7-AS1       TFIP11  TPST2   PRR14L  TRIOBP  ST13    CYB5R3  ACR     ARSD
HDHD1   ZNF673  RP6     ACRC    RAB9B   SLC6A8
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GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0006457	1.63E-10	6.586630836	3.736765622	21	216	protein folding

GO:0006986	1.47E-05	5.492979221	2.231679469	11	129
response to unfolded protein					

Tissue: Thyroid=>Heart_Left_Ventricle   Type: asymmetric

SourceGene: NUDT3(ENSG00000112664.4)   nudix (nucleoside diphosphate linked moiety X)-type motif 3

TargetGeneSet: FAM41C KLHL17 C1orf159 CPSF3L TAS1R3 DVL1 TNFRSF14
RP13 KLHL21 RP11 NMNAT1 ZBTB17 RSG1 HP1BP3 CDC42 ZBTB40 FUCA1
UBXN11 PIGV NUDC EYA3 RCC1 CITED4 RNF220 GPBP1L1 RP1 LEPROT
SLC35D1 TYW3 CCBL2 KIAA1107 RPAP2 ALG14 RP4 FRRS1 C1orf194
CEPT1 APH1A GOLPH3L BNIPL PSMB4 SNX27 FAM189B SMG5 CCT3 USP21
B4GALT3 HSD17B7 METTL13 CACYBP CEP350 TRMT1L GS1 TMEM183A ZC3H11A
TMEM81 INTS7 TARBP1 IRF2BP2 MTR ZNF692 SMC6 C2orf44 SLC5A6 LTBP1
ARHGEF33 EML4 CCDC88A BCL11A XPO1 CCT4 AFTPH C2orf42 SPR
PCGF1 AUP1 HTRA2 GCFC2 ELMOD3 RNF181 RNF103 RMND5A MRPS5 LMAN2L RFX8
HS6ST1 ARL6IP6 DNAJC10 HIBCH HSPD1 SATB2 ALS2CR12 TRAK2 IKZF2
XRCC5 SLC23A3 RBM44 CRELD1 CHCHD4 C3orf19 CAPN7 PLCL2-AS1 NGLY1
ZNF619 ZNF852 KIAA1143 RBM6 MANF PPP4R2 ZNF717 CGGBP1 CPOX CBLB
KIAA1524 SLC9C1 WDR52 KLF15 TPRA1 PPM1L FXR1 ATP11B DCUN1D1 PARL
MAGEF1 TBCCD1 BCL6 PPP1R2 UBXN7 ABCA11P HGFAC DCAF16 CTD RASGEF1B
NUDT10 RG9MTD2 UBE2D3 SLC9B1 TBCK PLK4 GAB1 CTSO PPID ANKRD37
LPCAT1 FAM134B NIPBL C5orf51 TRIM23 KLHL35 BRD8 SOX9 WDR55 PCDHB16
TCERG1 ZNF300P1 RANBP17 CREBRF PDLIM7 ZNF354A SNRNP48 GNL1 DDX39B
HLA-DRA HLA-DMB HLA-DMA SLC39A7 SPDEF ARMC12 TOMM6 HSP90AB1 TDRD6 BAI3
MTO1 RARS2 PM20D2 UFL1 SESN1 RP3 RSPH4A TRMT11 HECA VIP
SERAC1 FNDC1 PNLDC1 WDR27 C7orf50 KLHL7-AS1 ADCYAP1R1 7-Sep
CDK13 LANCL2 PSPH STYXL1 MAGI2 CLDN12 RBM48 FAM200A STAG3 ZCWPW1
PRKAR2B ARF5 ZYX C7orf29 GBX1 UBE3C ZNF596 SLC39A14 CHMP7
ADAM28 KIF13B GTF2E2 TTI2 GINS4 THAP1 MSC ZBTB10 ENY2 C8orf76
PYCRL ZNF623 NRBP2 CYHR1 ZNF250 KDM4C TYRP1 TOPORS DNAJA1 GNE
RG9MTD3 GKAP1 NOL8 NCBP1 GRIN3A CDC26 ZBTB34 FPGS C9orf114
RP11-88G17 RXRA FAM166A EXD3 NOXA1 USP6NL WAC ITGB1 NELL1
ZNF37BP ERCC6 HNRNPH3 DNA2 P4HA1 ANXA7 KIAA0913 KAT6B C10orf131
FRAT2 C10orf32 TAF5 MXI1 FAM160B1 ZRANB1 C10orf125
PRKCDBP ZNF143 HTATIP2 DNAJC24 PIGCP1 ALKBH3 CELF1 FADS3 NXF1 MARK2
STIP1 TRPT1 GPR137 MEN1 SLC25A45 CFL1 EFEMP2 EIF1AD CD248
RBM14 RBM4B CAPN5 EED CHORDC1 MED17 IFT46 PHLDB1 DPAGT1 HINFP OAF
SRPR PRDM10 ZBTB44 RAD52 CACNA2D4 FKBP4 IFFO1 CDKN1B WBP11
REP15 FAR2 C12orf35 SAT2 LIMA1 DAZAP2 PAN2 PTGES3 AVIL
CTDSP2 BBS10 SELPLG ALKBH2 DTX1 SIRT4 C12orf65 ZNF605 CRYL1
PTPN2P2 HSPH1 RPS4XP16 DHRS12 SUGT1 UGGT2 PCID2 ACIN1 SEC23A
FBXO33 LRFN5 RPL32P29 MAPK1IP1L MAX ABCD4 ZC2HC1C C14orf118
AHSA1 PAPOLA VRK1 HERC2P3 FAN1 ZFYVE19 EHD4 HAUS2 PIGB POLR2M
ANKDD1A IGDCC4 LOXL1 COMMD4 WDR61 POLG BLM WASH4P RHOT2 TBC1D24 NPIP
NPIPP1 CLN3 MAZ FUS C16orf58 FTO HERPUD1 HSD11B2 TSNAXIP1

TMEM231 CENPN KLHDC4 BANP CDK10 RNMTL1 SGSM2 SPNS3 PFN1 DERL2
EIF5A COX10-AS1 MEIS3 C17orf39 MEIS3P2 C17orf108 SDF2
RAB34 RHOT1 ARHGAP23 KAT2A CCR10 NMT1 SCRN2 SP2 DDX42 NT5C
RECQL5 QRICH2 JMJD6 CHMP6 ARHGDIA LRRC45 ARHGAP28 CABYR HNRNPA1P7
ASXL3 ZNF397 RNF165 CXXC1 ZNF236 ABCA7 CIRBP SAFB2 SAFB PRR22
PNPLA6 ZNF558 COL5A3 ZGLP1 KEAP1 WDR83 SAMD1 PRKACA SLC27A1 ZNF91
DPY19L3 ZNF571 FAM98C MED29 EID2B DEDD2 ZNF284 ZNF233 ZFP112 TMEM160 KPTN
FUT2 TSKS ZNF577 ZNF615 ZNF808 ZNF580 ZNF667 NSFL1C SNRPB PTPRA
DDRGK1 SLC23A2 PYGB MT1P3 MMP24 TTI1 IFT52 C20orf111 PKIG SYS1
NCOA5 RNF114 C20orf166-AS1 PCMTD2 HSPA13 LINC00478 MORC3 C21orf2
SCARF2 THAP7-AS1 TFIP11 TPST2 PRR14L TRIOBP H1F0 RANGAP1 PPPDE2
ASMTL PPP1R3F MAGED1 GPR173 RP6 MAGEC2 ARMCX4 BEX4 KIAA1210
FAM127C VAMP7 TMSB4Y

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0035511	1.67E-05	Inf	0.076811293	3	3	oxidative DNA demethylation

```
Tissue: Thyroid=>Heart_Left_Ventricle   Type:   asymmetric



SourceGene:     PLD5(ENSG00000180287.11)        "phospholipase D family, member 5"



TargetGeneSet:  PODN    RP11    BNIPL   TKT     FMOD    NID1    RHOB    IL1R1
SCN7A   COL5A2  COL4A4  COL6A3  CLSTN2  PDGFRA  11-Sep  SPOCK1  C5orf62 SNX14
EPB41L2 SASH1   KIAA1324L       INTS9   RECK    SVEP1   OR2K2   SPON1   EMP1
PTPRQ   LIG4    AKAP5   FBLN5   MMP2    SF3B3   CRISPLD2        ASGR1   KCNJ2
SETBP1  DSEL    MN1     CHRDL1

GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
```

GO:0030198	8.73E-11	33.78552632	0.378797315	9	161
extracellular matrix organization

GO:0043062	9.23E-11	33.56235294	0.381150093	9	162
extracellular structure organization

Tissue: Thyroid=>Heart_Left_Ventricle	Type:	asymmetric

SourceGene:	PTPLB(ENSG00000206527.5)	"protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b"

TargetGeneSet:	FAM41C	TAS1R3	TNFRSF14	RP1	WRAP73	ZBTB17	FBXO42
HP1BP3	FUCA1	PNRC2	NUDC	EYA3	RCC1	RP11	GPBP1L1	LEPROT	TYW3
CCBL2	RP4	ZNF326	RPAP2	ALG14	PRPF38B	SNX27	JTB	CCT3	USP21

HSD17B7 CACYBP TMEM183A TMEM81 INTS7 MTR ZNF672 ZNF692 THADA
CCDC88A CCT4 AFTPH C2orf42 PCGF1 AUP1 ELMOD3 MRPS5 ANKRD36C
LMAN2L MTND3P10 WDSUB1 HSPD1 SLC23A3 CRELD1 CHCHD4 PLCL2-AS1
NGLY1 DHX30 MANF FRMD4B KIAA1524 WDR52 TPRA1 MYNN FXR1
EIF2B5 EIF4A2 ABCA11P NOP14 DCAF16 CHIC2 NUDT10 UBE2D3 TBCK PLK4
GUSBP5 PPID CCT5 SOX9 WDR55 PCDHB16 PCDHGA2 ZNF300P1 FNDC9
ZNF184 GNL1 SLC39A7 SPDEF HSP90AB1 SLC35B2 RP3 RSPH4A C6orf97 VIP
TCP1 PNLDC1 C6orf70 HOXA10 STYXL1 MAGI2 RBM48 FAM133B SLC25A13
TMEM168 GBX1 LZTS1 TTI2 GOLGA7 GINS4 THAP1 EBAG9 PYCRL ZNF623
CYHR1 UHRF2 KDM4C DNAJA1 NOL6 C9orf100 HMGB3P24 GKAP1
NCBP1 RAB14 FPGS RP11-88G17 EXD3 TAF3 WAC ZNF32-AS2 PBLD
HNRNPH3 C10orf131 FRAT2 TAF5 BAG3 BUB3 PPP2R2D C10orf125 CTD
SLC22A18AS PRG2 FADS3 NXF1 STIP1 SLC25A45 EIF1AD ZDHHC24
RBM14 EED CHORDC1 MED17 HINFP HSPA8 KCNJ5 FKBP4 ATF1 PAN2
PTGES3 ALKBH2 PLBD2 HSPH1 FANCB INTS6 DHRS12 SUGT1 PCID2 RPL32P29
MAX EIF2B2 POMT2 AHSA1 PAPOLA HSP90AA1 TUBGCP5 TMEM87A MFAP1 PIGB
ANKDD1A PRC1 DNASE1L2 TBC1D24 MGRN1 NPIP NPIPP1 PKD1P6 BANP
SGSM2 DERL2 CNTROB MEIS3 MEIS3P2 C17orf108 UTP6 CCT6B KRT19
KAT2A NAGLU QRICH2 JMJD6 IMPACT ASXL3 CIRBP SAFB YJEFN3 DEDD2
TRPM4 NOSIP TSKS TFPT ZNF580 TRIM28 RRBP1 POFUT1 DDX27 RNF114
C20orf11 STMN3 MORC3 C21orf67 TPST2 PRR14L TRIOBP RANGAP1
C22orf26 GTSE1 ARSD GPR173

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0006457	8.80E-11	8.367201426	2.555947685	18	216	protein folding

```
GO:0000226      1.90E-05        4.507318038     3.183101515     13      269
microtubule cytoskeleton organization
```

```
Tissue: Heart_Left_Ventricle=>Thyroid   Type:   asymmetric
SourceGene:     RP11-135J2.4(ENSG00000228063.1)
TargetGeneSet:  FCRL5   IGKJ5   IGKC    IGKJ2   IGKV1-17        IGKV3D-20       AGA
UBTD2   MRPS17  ANKRD20A19P     SLC39A2 RP11    IGHG1   IGHG3   IGHJ5   IGHJ3
IGHV3-73        SBK1    IGLV1-40        IGLV2-11        IGLV2-8 IGLL5   IGLC1
IGLC3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006958      5.73461135878179e-13    392.618181818182        0.0380596498512214
6       50      complement activation, classical pathway
GO:0006956      2.44254125353039e-12    302.8   0.0479551588125389      6       63
complement activation
GO:0002455      2.96754069301776e-12    292.494915254237        0.0494775448065878
6       65      humoral immune response mediated by circulating immunoglobulin
GO:0072376      1.25167763479958e-11    226.8   0.062417825756003       6       82
protein activation cascade
GO:0016064      8.02400420274271e-11    163.828571428571        0.0844924226697114
6       111     immunoglobulin mediated immune response
GO:0019724      9.44257001614251e-11    159.244444444444        0.0867760016607847
6       114     B cell mediated immunity
GO:0006959      1.42774536701093e-10    148.179310344828        0.0928655456369801
6       122     humoral immune response
GO:0002449      9.58785477132851e-10    106.427329192547        0.127119230503079
6       167     lymphocyte mediated immunity
GO:0002460      1.55867569635427e-09    97.8171428571429        0.137775932461421
6       181     adaptive immune response based on somatic recombination of immune
receptors built from immunoglobulin superfamily domains
GO:0002250      2.67678847039623e-09    89.05   0.150716213410837       6       198
adaptive immune response
GO:0002443      3.92363245231903e-09    83.3268292682927        0.160611722372154
6       211     leukocyte mediated immunity
GO:0002253      3.16044752134614e-08    57.9399317406143        0.227596706110304
6       299     activation of immune response
GO:0050778      1.01797558856702e-07    47.2022346368715        0.277074250916892
6       364     positive regulation of immune response
GO:0002252      1.44141824975688e-07    44.4    0.293820496851429       6       386
immune effector process
```

```
Tissue: Heart_Left_Ventricle=>Thyroid   Type:   asymmetric
SourceGene:     RP11-175D17.3(ENSG00000236643.1)
TargetGeneSet:  PLA2G2D CCDC163P        AMPD1   RP11    FCRL5   IGKJ5   IGKC
IGKJ4   IGKJ3   IGKJ2   IGKJ1   IGKV4-1 IGKV1-5 IGKV1-12        IGKV1-16
IGKV3-20        IGKV2-24        SP140   EOMES   CCR4    PARP15  IGJ     RP3
NCF1C   BLK     MS4A1   IGHA2   IGHG2   IGHGP   IGHA1   IGHG1   IGHG3   IGHD    IGHM
IGHJ5   IGHV3-7 IGHV3-33        IGHV3-48        IGHV4-59        SCARNA15        CD19
P2RX5   TBC1D27 CCL4    CD79A   IGLV1-51        IGLV1-47        IGLV1-44
IGLV1-40        IGLV3-25        IGLV2-23        IGLV3-21        IGLV2-14
IGLV2-11        IGLV2-8 IGLV3-1 IGLL5   IGLC1   IGLC2   IGLC3   IGLC7   WAS
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006958      3.1938931138853e-20     193.137973137973        0.110718981385371
11      50      complement activation, classical pathway
GO:0006956      5.17450829290118e-19    144.722527472527        0.139505916545568
11      63      complement activation
GO:0002455      7.50120043233589e-19    139.3430335097  0.143934675800983       11
65      humoral immune response mediated by circulating immunoglobulin
GO:0072376      1.14709519640839e-17    105.853789403085        0.181579129472009
11      82      protein activation cascade
GO:0016064      3.72901390844983e-16    75.0042857142857        0.245796138675524
11      111     immunoglobulin mediated immune response
GO:0019724      5.04997115378365e-16    72.8044382801664        0.252439277558646
11      114     B cell mediated immunity
GO:0002253      6.56781311201327e-16    38.5723196881092        0.66209950868452
14      299     activation of immune response
GO:0006959      1.08954706873963e-15    67.5195195195195        0.270154314580306
11      122     humoral immune response
GO:0050778      1.00974770116133e-14    31.2644444444444        0.806034184485503
14      364     positive regulation of immune response
GO:0002449      3.68503467947307e-14    47.8916361416361        0.36980139782714
11      167     lymphocyte mediated immunity
GO:0002460      9.00267805846482e-14    43.9044817927171        0.400802712615044
11      181     adaptive immune response based on somatic recombination of immune
receptors built from immunoglobulin superfamily domains
GO:0002250      2.42687592582153e-13    39.8655462184874        0.43844716628607
11      198     adaptive immune response
GO:0002443      4.8856649306588e-13     37.2402380952381        0.467234101446267
11      211     leukocyte mediated immunity
GO:0002252      1.5521457949534e-11     22.5320855614973        0.854750536295066
12      386     immune effector process
Tissue: Heart_Left_Ventricle=>Thyroid   Type:   cluster
SourceGene:     RP11-236B18.3(ENSG00000225525.1)
TargetGeneSet:  PLA2G2D FCRL5   CD84    CHIT1   IGKJ5   IGKC    IGKJ3   IGKJ2
IGKJ1   IGKV4-1 IGKV1-5 IGKV1-6 IGKV3-7 IGKV1-9 IGKV3-15        IGKV1-17
IGKV3-20        IGKV2-24        IGKV2-28        IGKV1-39        IGKV2D-28
IGKV3D-20       LAP3    ICOS    CCDC51  KLHL7   IGJ     RASSF6  CXCL13  GZMK    RP11
TSPAN33 KIAA0196        ZBTB43  TAF1D   POU2AF1 GS1     FLT3    TRAV12-1
IGHG1   IGHG3   IGHM    IGHV1-2 IGHV2-5 IGHV3-7 IGHV3-15        IGHV1-18
IGHV3-21        IGHV3-22        IGHV3-23        IGHV1-24        IGHV3-30
IGHV1-46        IGHV3-48        IGHV5-51        IGHV3-53        IGHV4-55
IGHV4-59        IGHV4-61        IGHV2-70        KREMEN2 CCL4L1  MFSD11  ANGPTL4
FFAR2   CD37    IGLV1-51        IGLV7-46        IGLV1-44        IGLV1-40
IGLV2-23        IGLV3-19        IGLV2-18        IGLV2-11        IGLV3-10
IGLV3-9 IGLV2-8 IGLV3-1 IGLL5   IGLC1   IGLC2   IGLC3   IGLC5   IGLC6   IGLC7
APOBEC3C
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006959      4.5849197390771e-24     98.1612349914237        0.320808248564113
16      122     humoral immune response
GO:0006958      9.45629359658127e-24    202.041081081081        0.131478790395128
13      50      complement activation, classical pathway
GO:0006956      2.73173090141433e-22    149.3752        0.165663275897862       13
63      complement activation
GO:0002455      4.27126034024078e-22    143.61  0.170922427513667       13      65
```

```
humoral immune response mediated by circulating immunoglobulin
GO:0072376      1.128945768015e-20      108.099710144928        0.215625216248011
13      82      protein activation cascade
GO:0016064      7.25210199108449e-19    75.9571428571429        0.291882914677185
13      111     immunoglobulin mediated immune response
GO:0019724      1.04135872730982e-18    73.6855445544554        0.299771642100893
13      114     B cell mediated immunity
GO:0002460      1.04693841228951e-17    49.7614770459082        0.475953221230365
14      181     adaptive immune response based on somatic recombination of immune
receptors built from immunoglobulin superfamily domains
GO:0002250      3.74836676948325e-17    45.1100543478261        0.520656009964708
14      198     adaptive immune response
GO:0002449      1.72341146454477e-16    48.1472727272727        0.439139159919729
13      167     lymphocyte mediated immunity
GO:0002443      3.71519761846452e-15    37.3323232323232        0.554840495467442
13      211     leukocyte mediated immunity
GO:0002253      1.20494452304226e-14    28.9169590643275        0.786243166562868
14      299     activation of immune response
GO:0050778      1.80555239275062e-13    23.4383333333333        0.957165594076534
14      364     positive regulation of immune response
GO:0002252      4.02349071322156e-13    22.0176971326165        1.01501626185039
14      386     immune effector process
Tissue: Heart_Left_Ventricle=>Thyroid   Type:   asymmetric
SourceGene:     RP11-764K9.1(ENSG00000225411.1)
TargetGeneSet:  RP4     GBP4    GBP6    AMY2A   SLAMF1  RPL31   IL1A    RPL32
RPL14   RPL24   RPL35A  TET2    AGA     BTF3    CTD     NPM1    LTB     RPL10A
MRPS12  AHR     TRGV4   TRBV19  RPS20   GRIP1   RPL7    HSD17B3 RP13    FAM13C  RP11
SLC6A13 RPL14P1 IRAK3   PGAM1P5 KDM2B   TM9SF2  TRAV3   RPL7AP6 NUMB    U6
RPS3AP6 RSL1D1  RPL17   ICAM4   RFX1    IL4I1   CXADR   RBX1    ALG12
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      6.41128520091338e-13    60.5093808630394        0.220399972320255
9       91      translational termination
GO:0006414      2.40275164761738e-12    51.6346153846154        0.254307660369525
9       105     translational elongation
GO:0006614      2.40275164761738e-12    51.6346153846154        0.254307660369525
9       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      2.62141405736306e-12    51.0987311657415        0.25672963808733
9       106     cotranslational protein targeting to membrane
GO:0045047      2.62141405736306e-12    51.0987311657415        0.25672963808733
9       106     protein targeting to ER
GO:0072599      2.62141405736306e-12    51.0987311657415        0.25672963808733
9       106     establishment of protein localization to endoplasmic reticulum
GO:0043241      2.66016827471332e-12    38.5621621621622        0.382672479413189
10      158     protein complex disassembly
GO:0070972      6.99900852258675e-12    45.4350741002117        0.28579337070099
9       118     protein localization to endoplasmic reticulum
GO:0000184      7.55932440136553e-12    45.0188811188811        0.288215348418795
9       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0032984      9.2783898894966e-12     33.7207100591716        0.433534011487094
10      179     macromolecular complex disassembly
GO:0019080      6.54295004255737e-11    34.7957746478873        0.365718635388554
9       151     viral genome expression
GO:0019083      6.54295004255737e-11    34.7957746478873        0.365718635388554
9       151     viral transcription
GO:0006413      6.94340123210026e-11    34.5500268961807        0.368140613106359
9       152     translational initiation
GO:0006612      7.36533111351605e-11    34.3076923076923        0.370562590824164
9       153     protein targeting to membrane
GO:0043624      7.36533111351605e-11    34.3076923076923        0.370562590824164
9       153     cellular protein complex disassembly
GO:0000956      1.79734922251437e-10    30.8423076923077        0.409314234309044
9       169     nuclear-transcribed mRNA catabolic process
GO:0034623      2.33236914653626e-10    29.8972027972028        0.421424122898069
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9       174     cellular macromolecular complex disassembly
GO:0006402      2.85681397983336e-10    29.1813837050523        0.431112033769289
9       178     mRNA catabolic process
GO:0072594      9.59066382228669e-10    25.2443786982249        0.494083454432219
9       204     establishment of protein localization to organelle
GO:0022411      1.00003837357733e-09    20.3424460431655        0.697529582727839
10      288     cellular component disassembly
GO:0006401      1.00146514526641e-09    25.1138147566719        0.496505432150024
9       205     RNA catabolic process
GO:0019058      2.86870699769166e-09    22.1320166320166        0.559476852812954
9       231     viral infectious cycle
GO:0022415      8.07273389821069e-09    19.5349371743794        0.629714206629299
9       260     viral reproductive process
GO:0071845      1.73863495664393e-08    17.7998601398601        0.687841671856619
9       284     cellular component disassembly at cellular level
GO:0016032      7.23299505154884e-08    12.6757369614512        1.09231195073005
10      451     viral reproduction
GO:0033365      1.3215335997197e-06     10.4084880636605        1.14559546052176
9       473     protein localization to organelle
GO:0006605      1.3448823802972e-06     10.3853598014888        1.14801743823957
9       474     protein targeting
GO:0042273      2.82087160676787e-06    150.072916666667        0.02906373261366
3       12      ribosomal large subunit biogenesis
Tissue: Heart_Left_Ventricle=>Thyroid   Type:   asymmetric



SourceGene:     TCFL5(ENSG00000101190.8)        transcription factor-like 5 (basic
helix-loop-helix)



TargetGeneSet:  RP11    ZMPSTE24        UQCRH   URB2    HEATR1  SLC52A1 ALG3
NOP14   TMEM33  TIGD4   WDR36   SRFBP1  GEMIN5  BYSL    RN5S223 SP4     ABCF2   TTI2
NUDCD1  ZC3H3   CYHR1   NCBP1   NGB     PDZD7   TARBP2  IRF9    SETD1A  ARMC5   NIP7
ZC3H18  CANT1   PTBP1   RAVER1  UPF1    ZNF793  ZNF571  ZNF576  GRWD1   PRMT1
ZNF417  TRIM28  TOMM34  URB1    GART

GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term



GO:0022613      4.64E-11        28.72194135     0.513805273     10      225
ribonucleoprotein complex biogenesis



GO:0071843      8.41E-11        26.93943421     0.545775379     10      239
cellular component biogenesis at cellular level



GO:0042254      9.56E-07        22.18337218     0.34025327      6       149
ribosome biogenesis
```

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GO:0022618      2.27E-06        28.42857143     0.216940004     5       95
ribonucleoprotein complex assembly



GO:0071826      2.92E-06        26.92293233     0.228357899     5       100
ribonucleoprotein complex subunit organization



Tissue: Thyroid=>Heart_Left_Ventricle   Type:   asymmetric



SourceGene:     USP35(ENSG00000118369.8)        ubiquitin specific peptidase 35



TargetGeneSet:  MXRA8   CTNNBIP1        RP11    CMPK1   PODN    NEGR1   GSTM5
BNIPL   KIRREL  TKT     RGS5    DPT     LAMC1   CFH     FMOD    AKT3    ZNF692
GRHL1   RHOB    KLHL29  C2orf56 EFEMP1  SPRED2  ANTXR1  IL1R1   CYBRD1  COL5A2
SLC23A3 SCARNA6 COL6A3  ITPR1   FBLN2   HEMK1   C3orf78 VGLL3   EPHA3   ABI3BP
CCDC80  CLSTN2  IGSF10  SPON2   EVC     AFAP1   APBB2   GABRB1  ATP10D  PDGFRA
11-Sep  PTPN13  PKD2    U6      UNC5C   GLRB    SH3RF1  SPOCK1  PDGFRB  C5orf62 EBF1
GNL1    TNFRSF21        RP3     PM20D2  MAN1A1  EPB41L2 HBS1L   SASH1   FNDC1
COL28A1 IGFBP3  EGFR    EBF2    BNIP3L  INTS9   KIF13B  CTD     GDF6    OGN     OMD
ASPN    ECM2    SVEP1   SLC27A4 COL5A1  VIM     KIAA1462        DNAJC12 MARVELD1
SPON1   GPR137  SLCO2B1 DPAGT1  KCNA5   EMP1    RERG    EPS8    DCN     ANAPC7
HMGB1   LHFP    ITGBL1  ADPRHL1 MMP14   LRFN5   MAP3K9  FBLN5   FBN1    ALDH1A2
PTPN9   TPSAB1  ZNF423  FTO     MMP2    CDH11   SF3B3   FTSJD1  CHD3    COX10-AS1
TLCD1   NUFIP2  CCT6B   KCNJ2   SETBP1  DSEL    COL5A3  CARM1   NFIX    LTBP4
ZFP112  PTPRA   EPB41L1 APCDD1L ICOSLG  C21orf2 COL6A2  MN1     GALR3   FBLN1   CTA
OFD1    CHRDL1  GPC3    ZNF275

GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
```

GO:0030198	3.46E-13	14.90706076	1.348072798	16	161
extracellular matrix organization					
GO:0043062	3.82E-13	14.80391389	1.356445921	16	162
extracellular structure organization					
GO:0031589	1.01E-06	7.402617801	1.691370839	11	202
cell-substrate adhesion					
GO:0030199	7.45E-06	22.01662562	0.276313058	5	33
collagen fibril organization					

GO:0061438	1.12E-05	121.4152542	0.050238738	3	6
renal system vasculature morphogenesis					
GO:0061439	1.12E-05	121.4152542	0.050238738	3	6
kidney vasculature morphogenesis					
GO:0022617	1.16E-05	19.88181313	0.301432427	5	36
extracellular matrix disassembly					

Tissue: Muscle_Skeletal=>Thyroid Type: asymmetric

SourceGene: C11orf54(ENSG00000182919.9) ester hydrolase C11orf54

TargetGeneSet: RUNX3 CD2 FAM46C FCRL5 LY9 PTPN7 LAX1 MAL CD8B
IGKJ5 IGKC IGKJ4 IGKJ1 IGKV4-1 IGKV5-2 IGKV1-6 IGKV1-9 IGKV3-11
IGKV6-21 IGKV1D-13 IGKV3D-11 CD96 TIGIT RHOH IGJ RP11
GZMA CTD FAM26F TRGV5 U3 FAM27E1 FAM22A SNORD14A POLA2
C11orf54 POU2AF1 REXO2 CD3E CD3D PRKAG1 LCP1 TRAV12-2
HAUS4 PLD4 IGHG3 IGHJ6 IGHJ5 IGHV6-1 IGHV1-2 IGHV2-5 IGHV3-15
IGHV1-18 IGHV3-21 IGHV3-23 IGHV3-30 IGHV3-33
IGHV4-34 IGHV4-39 IGHV1-46 IGHV3-48 IGHV3-49
IGHV5-51 IGHV3-53 IGHV4-59 IGHV4-61 IGHV2-70
1-Sep GPR114 IKZF3 TMEM106A VMAC ZNF83 FER1L4 IGLV4-69
IGLV1-51 IGLV9-49 IGLV1-44 IGLV7-43 IGLV3-25
IGLV3-19 IGLV2-11 IGLV3-1 IGLC2 IGLC3 IGLC6 RAC2 CBX7 RP4
PIM2 IL2RG

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0006958	1.07E-14	98.56783537	0.141858695	9	50	"complement activation, classical pathway"
GO:0006956	9.85E-14	74.77083333	0.178741956	9	63	complement activation
GO:0002455	1.33E-13	72.09040179	0.184416303	9	65	humoral immune response mediated by circulating immunoglobulin

GO:0016064	4.35E-13	45.70105398	0.314926303	10	111	
immunoglobulin mediated immune response						
GO:0019724	5.70E-13	44.37344913	0.323437824	10	114	B
cell mediated immunity						
GO:0002449	8.25E-13	33.50299145	0.473808041	11	167	
lymphocyte mediated immunity						
GO:0006959	1.14E-12	41.18087558	0.346135216	10	122	
humoral immune response						
GO:0072376	1.17E-12	55.23672945	0.23264826	9	82	
protein activation cascade						
GO:0002460	2.00E-12	30.71372549	0.513528476	11	181	
adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains						

GO:0002250	5.34E-12	27.88823529	0.561760432	11	198		adaptive immune response
GO:0002443	1.07E-11	26.05166667	0.598643692	11	211		leukocyte mediated immunity
GO:0002252	2.58E-11	17.47232861	1.095149125	13	386		immune effector process
GO:0002253	4.51E-10	17.97939815	0.848314996	11	299		activation of immune response
GO:0050778	3.58E-09	14.60122757	1.032731299	11	364		positive regulation of immune response
GO:0042110	2.09E-07	12.79233871	0.905058473	9	319	T	cell activation

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GO:0046649      2.56E-07        10.66651415     1.228496298     10      433
lymphocyte activation







Tissue: Muscle_Skeletal=>Thyroid        Type:   cluster
SourceGene:     C11orf54(ENSG00000182919.9)
TargetGeneSet:  RUNX3   CD2     FAM46C  FCRL5   LY9     PTPN7   LAX1    MAL     CD8B
IGKJ5   IGKC    IGKJ4   IGKJ1   IGKV4-1 IGKV5-2 IGKV1-6 IGKV1-9 IGKV3-11
IGKV6-21        IGKV1D-13       IGKV3D-11       CD96    TIGIT   RHOH    IGJ     RP11
GZMA    CTD     FAM26F  TRGV5   U3      FAM27E1 FAM22A  SNORD14A        POLA2
C11orf54        POU2AF1 REXO2   CD3E    CD3D    PRKAG1  LCP1    TRAV12-2
HAUS4   PLD4    IGHG3   IGHJ6   IGHJ5   IGHV6-1 IGHV1-2 IGHV2-5 IGHV3-15
IGHV1-18        IGHV3-21        IGHV3-23        IGHV3-30        IGHV3-33
IGHV4-34        IGHV4-39        IGHV1-46        IGHV3-48        IGHV3-49
IGHV5-51        IGHV3-53        IGHV4-59        IGHV4-61        IGHV2-70
SEPT1   GPR114  IKZF3   TMEM106A        VMAC    ZNF83   FER1L4  IGLV4-69
IGLV1-51        IGLV9-49        IGLV1-44        IGLV7-43        IGLV3-25
IGLV3-19        IGLV2-11        IGLV3-1 IGLC2   IGLC3   IGLC6   RAC2    CBX7    RP4
PIM2    IL2RG
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006958      1.07045074677632e-14    98.5678353658537        0.141858694900007
9       50      complement activation, classical pathway
GO:0006956      9.852512107991e-14      74.7708333333333        0.178741955574009
9       63      complement activation
GO:0002455      1.32541446159318e-13    72.0904017857143        0.184416303370009
9       65      humoral immune response mediated by circulating immunoglobulin
GO:0016064      4.34557281079881e-13    45.7010539763654        0.314926302678015
10      111     immunoglobulin mediated immune response
GO:0019724      5.70453571225452e-13    44.3734491315136        0.323437824372016
10      114     B cell mediated immunity
GO:0002449      8.25067236558966e-13    33.5029914529915        0.473808040966023
11      167     lymphocyte mediated immunity
GO:0006959      1.13719065670266e-12    41.1808755760369        0.346135215556017
10      122     humoral immune response
GO:0072376      1.17441085855504e-12    55.2367294520548        0.232648259636011
9       82      protein activation cascade
GO:0002460      1.99948012484219e-12    30.7137254901961        0.513528475538025
11      181     adaptive immune response based on somatic recombination of immune
receptors built from immunoglobulin superfamily domains
GO:0002250      5.33749431796508e-12    27.8882352941176        0.561760431804027
11      198     adaptive immune response
GO:0002443      1.06649145406103e-11    26.0516666666667        0.598643692478029
11      211     leukocyte mediated immunity
GO:0002252      2.57978683847137e-11    17.4723286097281        1.09514912462805
13      386     immune effector process
GO:0002253      4.50582818573953e-10    17.9793981481481        0.848314995502041
11      299     activation of immune response
GO:0050778      3.57602950676341e-09    14.6012275731822        1.03273129887205
11      364     positive regulation of immune response
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GO:0042110      2.09246316077927e-07    12.7923387096774        0.905058473462044
9       319     T cell activation
GO:0046649      2.56462609546679e-07    10.6665141462671        1.22849629783406
10      433     lymphocyte activation
Tissue: Muscle_Skeletal=>Thyroid        Type:   cluster
SourceGene:     ENSG00000182648.7
TargetGeneSet:  RP4     PLOD1   GBP5    CD2     RAB13   CD84    SLAMF1  CD48
SLAMF7  LY9     PTPN7   LAX1    RASSF3  FAIM3   TRAF3IP3        CHRM3-AS2       RP11
RBKS    MAL     IGKJ5   IGKC    IGKJ4   IGKJ2   IGKJ1   IGKV4-1 IGKV1-5 IGKV1-9
IGKV3-11        IGKV1-16        IGKV1-17        IGKV3-20        IGKV1-27
IGKV2-30        IGKV1-33        IGKV1-39        IGKV1D-27       PAX8    ARL6IP6
ITGA4   RUFY4   SP140   PDCD1   ATG7    PPARG   DNAH1   FAM86DP CD96    SIDT1
ACTG1P1 HLTF-AS1        MCF2L2  RHOH    IGJ     CXCL10  EXOSC9  GZMK    GZMA
ATG12   OR2I1P  RP1     TAGAP   TRGV9   NCF1    STAG3L1 HNRNPA1P8       TRBV29-1
CSPP1   FAM92A1 ZHX1    PAICSP1 CDNF    P4HA1   ANXA7   FAM22A  CWF19L1 MS4A1   CD5
NUMA1   CD3E    CD3D    CD3G    LAG3    OLR1    REP15   H1FNT   KRR1P1  TRAC
BCL2L2  HNRPCP  DDX24   EXOC3L4 PLD4    IGHG2   IGHG1   IGHG3   IGHJ6   IGHJ5
IGHV1-2 IGHV3-7 IGHV3-9 IGHV3-11        IGHV3-15        IGHV1-18        IGHV3-23
IGHV4-31        IGHV3-33        IGHV4-34        IGHV4-39        IGHV3-49
IGHV5-51        IGHV4-59        IGHV3-66        IGHV1-69        IL16    TCEB2
TNFRSF17        SEPT1   ITGAL   NLRC5   KIF1C   CCL5    ACACA   RAB37   CD7
THOC1   GZMM    CCDC94  CYP4F8  MAP4K1  MED29   SELV    CD79A   ESF1    FER1L4  MX1
UBASH3A PDXK    C21orf67        IGLV10-54       IGLV1-47        IGLV1-40
IGLV2-23        IGLV3-21        IGLV3-19        IGLV2-14        IGLV2-8 IGLV3-1
IGLC2   SSTR3   DDX17   SPIN2B  IL2RG   BEX2    MTCP1   SASH3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0002449      1.66142026815146e-13    17.9731781376518        1.07473531243513
15      167     lymphocyte mediated immunity
GO:0002443      3.41187240157216e-13    15.0921078921079        1.35789910732821
16      211     leukocyte mediated immunity
GO:0046649      3.12441095274885e-12    9.25072141696242        2.7865891633797 20
433     lymphocyte activation
GO:0002252      3.88485481421508e-12    9.78823919287134        2.48411874610754
19      386     immune effector process
GO:0050778      1.42827202853624e-11    9.7193063583815 2.34253684866099        18
364     positive regulation of immune response
GO:0006958      2.57203013223223e-11    37.4137630662021        0.321777039651235
9       50      complement activation, classical pathway
GO:0006956      2.26936872040733e-10    28.3809523809524        0.405439069960556
9       63      complement activation
GO:0002455      3.03310069282267e-10    27.3635204081633        0.418310151546606
9       65      humoral immune response mediated by circulating immunoglobulin
GO:0006959      3.34336945914543e-10    17.2178642056691        0.785135976749014
11      122     humoral immune response
GO:0042110      1.7145708730557e-09     8.89043522267206        2.05293751297488
15      319     T cell activation
GO:0002460      1.78298176662382e-09    12.4383081306158        1.16483288353747
12      181     adaptive immune response based on somatic recombination of immune
receptors built from immunoglobulin superfamily domains
GO:0016064      2.24733764799014e-09    17.0070380532029        0.714345028025742
10      111     immunoglobulin mediated immune response
GO:0072376      2.54310053819614e-09    20.9662426614481        0.527714345028026
9       82      protein activation cascade
GO:0019724      2.92119921605593e-09    16.5129749768304        0.733651650404816
10      114     B cell mediated immunity
GO:0002250      4.9501471041309e-09     11.2879330943847        1.27423707701889
12      198     adaptive immune response
GO:0002253      6.65456799691893e-09    8.75069953364424        1.92422669711439
14      299     activation of immune response
GO:0050863      1.6946632877093e-07     9.03763066202091        1.42225451525846
11      221     regulation of T cell activation
GO:0051249      2.5589078126252e-07     7.70097034303676        1.82125804442599
12      283     regulation of lymphocyte activation
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GO:0002694      9.78514014293024e-07    6.73570658036677        2.06580859456093
12      321     regulation of leukocyte activation
GO:0050865      1.95808857459254e-06    6.27816940807877        2.20739049200747
12      343     regulation of cell activation
GO:0050870      1.41352685719421e-05    8.19631901840491        1.10047747560722
8       171     positive regulation of T cell activation
GO:0002696      1.87270457946094e-05    6.76052295918367        1.49948100477476
9       233     positive regulation of leukocyte activation
Tissue: Muscle_Skeletal=>Thyroid        Type:   asymmetric
SourceGene:     ENSG00000244256.1
TargetGeneSet:  RP11    C1orf159        RP4     CEP104  LZIC    DFFA    PLOD1
DNAJC16 HP1BP3  LDLRAP1 EYA3    PHACTR4 RCC1    PEF1    TXLNA   TMEM234 NCDN
FOXO6   PPCS    CCDC24  DNAJC6  RBMXL1  CYB561D1        GOLPH3L SNX27   INTS3
SLC39A1 TDRD10  MSTO1   UBQLN4  CCT3    POGK    MYBPH   ZNF238  ID2     C2orf48
PDIA6   SLC5A6  PPM1G   ARHGEF33        CCT4    PCBP1-AS1       SPR     MOB1A   DQX1
AUP1    SEMA4F  C2orf68 MRPS5   LMAN2L  NOSTRIN KRT18P19        HSPD1   ALS2CR12
FZD5    ASB1    HDLBP   DTYMK   TTLL3   CRELD1  SLC6A1-AS1      NME6    WDR6
FAM116A SLC25A36        CPA3    SLC33A1 SSR3    LRCH3   TMEM128 UGDH-AS1
DCAF4L1 ANKRD17 CDKL2   CTSO    DNAJC21 FBXO4   KIF2A   PAPD4   PCDHGA1 TCOF1
TMED9   SSR1    HCG17   DAXX    SYNGAP1 NUDT3   FANCE   BRPF3   NFYA    RP1
AARS2   BAG2    SYNCRIP PEX7    KIAA0895        URGCP   HSPB1   CYP3A43 TNPO3
CNOT4   HIPK2   XKR6    NEIL2   POLR3D  CHMP7   CTD     C8orf40 STMN2   GAPDHP62
GRHL2   LRRC6   ZNF623  PLAA    VCP     ATP8B5P MCART1  FAM22G  NANS    ALG2
PRPS1P2 CCBL1   TOR1B   PRRC2B  SURF4   MAMDC4  C9orf169        TUBB4B  NOXA1
KRT8P37 CDNF    SUV39H2 C10orf114       ZDHHC16 CYP2E1  RP13    UBQLNL  SLC35C1
CELF1   PATL1   GANAB   MARK2   STIP1   FKBP2   GPR137  SYVN1   RBM14   7SK
C2CD3   CHORDC1 ATM     RNF214  DPAGT1  RNF26   HSPA8   STT3A   RAD52   CBX3P4
FKBP4   TEAD4   NCAPD2  PEX5    RPL13AP20       KIAA1467        REP15   PUS7L
H1FNT   TUBA1C  RAB5B   RNF41   OS9     TSPAN31 TBC1D30 TSPAN8  ALDH2   C12orf65
GOLGA3  ITM2B   DNAJC3-AS1      DNAJC3  PCID2   OR11H7  MRPL52  AJUBA   ACIN1
NEDD8   FANCM   GNPNAT1 HNRPCP  MAP3K9  AHSA1   ZC3H14  HSP90AA1        GOLGA8B
ZFYVE19 PPP1R14D        ZFP106  TP53BP1 PPIP5K1 PPIB    MAN2C1  DNAJA4  SELS    HN1L
SULT1A3 TBC1D10B        FBXL19-AS1      SALL1   CMTM4   C16orf46        ZC3H18
RNF167  KCTD11  FLOT2   CCT6B   WIPF2   UBE2Z   ZNF652  SRP68   QRICH2  CANT1
ENGASE  CSNK1D  TMEM241 ZNF397  MBD1    AP3D1   ZNF555  ELAVL1  ZGLP1   ZNF441  JAK3
PGPEP1  MIA     SMG9    ZNF284  BLOC1S3 KPTN    PRMT1   ZNF347  ZNF761  ZNF329  MCM8
HM13    TOMM34  STK4    ADNP    C20orf11        PDXK    UBE2G2  KRT18P5 UBE2L3
SDF2L1  ZNF70   MORC2   PRR14L  CTA     RANGAP1 RP6     ZBED4   ALG12   CRELD2
CXorf58 FAM123B KIAA2022        MAGT1   TIMM8A  MID2    LONRF3  ZNF449  FHL1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006457      4.70322619491241e-14    9.20170244263509        3.06414780984015
23      216     protein folding
GO:0006986      2.21067554751856e-06    6.78874716058012        1.82997716421009
11      129     response to unfolded protein
GO:0035966      3.71122598459935e-06    6.40540206185567        1.92927825064009
11      136     response to topologically incorrect protein
Tissue: Muscle_Skeletal=>Thyroid        Type:   cluster
SourceGene:     ENSG00000244256.1
TargetGeneSet:  RP11    C1orf159        RP4     CEP104  LZIC    DFFA    PLOD1
DNAJC16 HP1BP3  LDLRAP1 EYA3    PHACTR4 RCC1    PEF1    TXLNA   TMEM234 NCDN
FOXO6   PPCS    CCDC24  DNAJC6  RBMXL1  CYB561D1        GOLPH3L SNX27   INTS3
SLC39A1 TDRD10  MSTO1   UBQLN4  CCT3    POGK    MYBPH   ZNF238  ID2     C2orf48
PDIA6   SLC5A6  PPM1G   ARHGEF33        CCT4    PCBP1-AS1       SPR     MOB1A   DQX1
AUP1    SEMA4F  C2orf68 MRPS5   LMAN2L  NOSTRIN KRT18P19        HSPD1   ALS2CR12
FZD5    ASB1    HDLBP   DTYMK   TTLL3   CRELD1  SLC6A1-AS1      NME6    WDR6
FAM116A SLC25A36        CPA3    SLC33A1 SSR3    LRCH3   TMEM128 UGDH-AS1
DCAF4L1 ANKRD17 CDKL2   CTSO    DNAJC21 FBXO4   KIF2A   PAPD4   PCDHGA1 TCOF1
TMED9   SSR1    HCG17   DAXX    SYNGAP1 NUDT3   FANCE   BRPF3   NFYA    RP1
AARS2   BAG2    SYNCRIP PEX7    KIAA0895        URGCP   HSPB1   CYP3A43 TNPO3
CNOT4   HIPK2   XKR6    NEIL2   POLR3D  CHMP7   CTD     C8orf40 STMN2   GAPDHP62
GRHL2   LRRC6   ZNF623  PLAA    VCP     ATP8B5P MCART1  FAM22G  NANS    ALG2
PRPS1P2 CCBL1   TOR1B   PRRC2B  SURF4   MAMDC4  C9orf169        TUBB4B  NOXA1
KRT8P37 CDNF    SUV39H2 C10orf114       ZDHHC16 CYP2E1  RP13    UBQLNL  SLC35C1
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CELF1   PATL1   GANAB   MARK2   STIP1   FKBP2   GPR137  SYVN1   RBM14   7SK
C2CD3   CHORDC1 ATM     RNF214  DPAGT1  RNF26   HSPA8   STT3A   RAD52   CBX3P4
FKBP4   TEAD4   NCAPD2  PEX5    RPL13AP20       KIAA1467        REP15   PUS7L
H1FNT   TUBA1C  RAB5B   RNF41   OS9     TSPAN31 TBC1D30 TSPAN8  ALDH2   C12orf65
GOLGA3  ITM2B   DNAJC3-AS1      DNAJC3  PCID2   OR11H7  MRPL52  AJUBA   ACIN1
NEDD8   FANCM   GNPNAT1 HNRPCP  MAP3K9  AHSA1   ZC3H14  HSP90AA1        GOLGA8B
ZFYVE19 PPP1R14D        ZFP106  TP53BP1 PPIP5K1 PPIB    MAN2C1  DNAJA4  SELS    HN1L
SULT1A3 TBC1D10B        FBXL19-AS1      SALL1   CMTM4   C16orf46        ZC3H18
RNF167  KCTD11  FLOT2   CCT6B   WIPF2   UBE2Z   ZNF652  SRP68   QRICH2  CANT1
ENGASE  CSNK1D  TMEM241 ZNF397  MBD1    AP3D1   ZNF555  ELAVL1  ZGLP1   ZNF441  JAK3
PGPEP1  MIA     SMG9    ZNF284  BLOC1S3 KPTN    PRMT1   ZNF347  ZNF761  ZNF329  MCM8
HM13    TOMM34  STK4    ADNP    C20orf11        PDXK    UBE2G2  KRT18P5 UBE2L3
SDF2L1  ZNF70   MORC2   PRR14L  CTA     RANGAP1 RP6     ZBED4   ALG12   CRELD2
CXorf58 FAM123B KIAA2022        MAGT1   TIMM8A  MID2    LONRF3  ZNF449  FHL1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006457      4.70322619491241e-14    9.20170244263509        3.06414780984015
23      216     protein folding
GO:0006986      2.21067554751856e-06    6.78874716058012        1.82997716421009
11      129     response to unfolded protein
GO:0035966      3.71122598459935e-06    6.40540206185567        1.92927825064009
11      136     response to topologically incorrect protein
Tissue: Muscle_Skeletal=>Thyroid        Type:   asymmetric
SourceGene:     GAPVD1(ENSG00000165219.14)
TargetGeneSet:  MTND1P23        NUDC    WASF2   EYA3    MED18   PHACTR4 GNG5    ETV3
TROVE2  ZNF281  RP11    ADAM18  C2orf18 MOB1A   PRKAR2A IP6K1   KIAA2018
RNF168  ZNF141  RFC1    SETD7   MTMR12  PHAX    CTB     MTND5P11        RBM22
PPP1R18 BTBD9   MTRNR2L9        ARID1B  FOXK1   PURB    MEPCE   CBLL1   GCC1
NEIL2   HR      CTD     KAT6A   C9orf102        NIPSNAP3A       ZBTB43  GTF3C4
NCLP1   NRBF2   POLR3A  TSSC4   MTRNR2L8        SPTY2D1 ATG13   HEXIM1  OSBP
MARK2   RSF1    DDX6    RNF26   ERC1    ZBTB39  GCN1L1  SBNO1   RNF6    N4BP2L2-IT1
RBM23   SOCS6   DLST    GOLGA8IP        TJP1    EMP2    FTO-IT1 NFATC3  VPS4A
ATXN1L  METTL16 NCOR1   SMCR8   MED1    WIPF2   PSME3   ZNF652  RPS2P48 MAP3K3
CANT1   MYL12B  NFIC    FEM1A   ZNF557  ZNF121  ZNF562  ZNF791  DNAJB1  ZNF429
ZFP82   ARHGAP35        KCNJ14  ZNF480  ZNF264  ZNF543  ZNF749  ZNF329  FASTKD5
CRNKL1  PLAGL2  PHF20   ZSWIM1  ZNFX1   TSHZ2   C20orf11        PRR14L  SMCR7L
RRP7A   PPARA   CERK    USP9X   GNL3L
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
Tissue: Muscle_Skeletal=>Thyroid        Type:   cluster
SourceGene:     KLF4(ENSG00000136826.9)
TargetGeneSet:  RP4     CTNNBIP1        PLOD1   HP1BP3  TCEB3   LYPLA2  EYA3
TXLNA   MRPS15  ZMPSTE24        CTPS    LEPRE1  CCDC24  EIF2B3  CYP4A11 OMA1
SRSF11  BCL10   FNBP1L  RP11    CYB561D1        AMPD2   MAN1A2  SEC22B  NOTCH2NL
GOLPH3L CERS2   INTS3   DENND4B CREB3L4 FLAD1   SLC50A1 MSTO1   UBQLN4  CCT3
C1orf182        USP21   HSD17B7 POGK    RNASEL  ZC3H11A TMEM81  CDK18   ELK4
C1orf96 SIPA1L2 OR11L1  NOL10   PDIA6   TTC32   RAB10   SLC5A6  XPO1    CCT4
PPP3R1  PCBP1-AS1       PCYOX1  PCGF1   AUP1    MRPS5   RALB    HNRNPA3 HSPD1
C2orf69 WDR12   PARD3B  METTL21A        RPE     RQCD1   TTLL4   ABCB6   ATG4B
CRELD1  CHCHD4  SEMA3F  SLC38A3 IFRD2   HEMK1   RAD54L2 DUSP7   POC1A   PHF7    ARF4
TFG     TMEM39A COPG1   NUDT16  UBA5    ACTG1P1 SLC25A36        SLC33A1 SSR3
MFSD1   MCCC1   ALG3    TNIP2   GRPEL1  UGDH-AS1        DCAF4L1 TEC     SEC31A
THAP9   TMSB4XP8        EIF4E   C4orf32 SEC24D  PPP1R14BP3      SLC10A7 STOX2   SDHA
MTRR    CTD     MARCH6  FAM105A IPO11   PIK3R1  ANKRA2  ZCCHC9  TMEM167A
EPB41L4A-AS1    XBP1P1  CSNK1G3 CHSY3   SMAD5   CTB     ARAP3   PCDH12  ADRB2
FAM114A2        MFAP3   TMED9   B4GALT7 ZFP62   TRIM52  SSR1    C6orf228
ZSCAN12P1       TRIM27  TUBB    C6orf25 VARS    NUDT3   PPIL1   BYSL    GPR110
BEND6   LINC00472       PGM3    LATS1   MRPL18  MICALL2 TSPAN13 C7orf46 STK31   CYCS
RALA    PURB    SNORA5A IGFBP3  LANCL2  PSPH    C7orf53 AASS    CEP41   LUC7L2
OR2A7   ABCB8   SMARCD3 PINX1   NEIL2   FAM160B2        POLR3D  R3HCC1  PPP2R2A
GTF2E2  PPAPDC1B        AP3M2   C8orf46 RNF19A  GAPDHP62        GRHL2   BAALC
NUDCD1  ATAD2   LRRC6   BOP1    KLHL9   DNAJA1  VCP     MCART1  C9orf41 RFK     OMD
C9orf156        NANS    ALG2    FSD1L   HDHD3   RBM18   ZBTB26  PRPS1P2 CCBL1
METTL11A        SURF4   INPP5E  SLC6A2  FBXO18  CELF2   SUV39H2 PBLD    AP3M1
CYP2C9  ZDHHC16 OCRL    TACC2   TRIM68  UBQLNL  MRPL17  NLRP14  COPB1   CAPRIN1
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SLC35C1 B3GAT3  C11orf84        STIP1   FKBP2   GPR137  PPP2R5B SYVN1   RBM14
PITPNM1 NUMA1   CLPB    CHCHD8  KCNE3   CHORDC1 PAFAH1B2        HMBS    DPAGT1
TBCEL   HSPA8   MSANTD2 STT3A   HYLS1   RAD52   FKBP4   TEAD4   HIN1L   NOP2
CLEC1A  KIAA1467        REP15   PPHLN1  PUS7L   H1FNT   TUBA1C  FMNL3   TARBP2  NPFF
RAB5B   CNPY2   PAN2    METTL1  METTL21B        TBC1D30 TSPAN8  DCN     NR2C1
IKBIP   MTERFD3 C12orf34        ANAPC7  ATXN2   ALDH2   DYNLL1  PUS1    GOLGA3  U6
GTF3A   FANCB   RFC3    KBTBD6  DHRS12  SUGT1   DNAJC3-AS1      DNAJC3  RAP2A
SLC15A1 TMTC4   CARKD   PROZ    PCID2   FAM70B  DAD1    MRPL52  PRMT5-AS1
PRMT5   PSME2   NEDD8   EAPP    GNPNAT1 CDKN3   SOCS6   AHSA1   C14orf142
HSP90AA1        ZFYVE19 TP53BP1 FBN1    GABPB1  NEDD4   NARG2   RORA    PARP16
SKOR1   IL16    PRC1    SELS    TMEM8A  SOLH    HN1L    IGFALS  TRAF7   ATF7IP2
USP31   UBFD1   TBX6    PHKG2   ZNF267  ABCC11  SALL1   BBS2    GPR56   C16orf57
E2F4    NUTF2   FTLP14  CYB5B   CHST4   BCAR1   C16orf46        AFG3L1P GAS8
CYB5D2  RPAIN   COX10-AS1       SLC47A2 MAP2K3  KSR1    PIPOX   UTP6    SLFN11
MMP28   CCL16   LEPREL4 LSM12   ATXN7L3 SLC25A39        PNPO    CDK5RAP3        DDX5
HN1     QRICH2  AFMID   CBX8    SIRT7   PYCR1   CSNK1D  C17orf62        NARF    FN3K
TBCD    TMEM241 RPRD1A  MBD1    ZADH2   ZNF555  TLE2    NCLN    ELAVL1  ZNF562  PPAN
ZGLP1   ELOF1   ZNF440  DNASE2  TRMT1   JAK3    MPV17L2 LSM4    YJEFN3  KCTD15
FXYD1   ZNF146  ZNF260  MIA     SMG9    BLOC1S3 VASP    MYPOP   NOVA2   PTGIR
DHX34   PRMT1   PTOV1   CTU1    ZNF761  ISOC2   ZNF550  ZNF814  FKBP1A  FOXA2   GZF1
ENTPD6  NANP    HM13    ZNF341  EDEM2   RPN2    EMILIN3 YWHAB   TOMM34  KRT18P4
DPH3P1  TMEM50B UBE2L3  SDF2L1  ZNF70   UPB1    GAL3ST1 SGSM3   RP6     ALG12
CRELD2  TRABD   TUBGCP6 HDHD1   RAI2    MAOB    ZNF673  ZNF81   ZNF630  WDR13
RRAGB   MAGT1   PGK1    ARMCX4  ARMCX2  NKRF    PHF6    MOSPD1  FAM50A
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006487      4.10627332612179e-09    8.30734614929144        2.19002145180264
15      92      protein N-linked glycosylation
GO:0018279      1.31551960315768e-07    7.44790560953703        2.07099854681337
13      87      protein N-linked glycosylation via asparagine
GO:0018196      1.51082844816065e-07    7.34807653575025        2.09480312781122
13      88      peptidyl-asparagine modification
GO:0006457      2.30035398870351e-07    4.38114134542706        5.14178949553664
20      216     protein folding
GO:0006986      2.37363259406325e-06    5.16173913043478        3.07079094872327
14      129     response to unfolded protein
GO:0035966      4.4510566391263e-06     4.86313959264779        3.23742301570826
14      136     response to topologically incorrect protein
GO:0070085      1.16383774428643e-05    3.43610169491525        6.07016815445298
19      255     glycosylation
Tissue: Muscle_Skeletal=>Thyroid        Type:   asymmetric
SourceGene:     LMOD3(ENSG00000163380.11)
TargetGeneSet:  MEGF6   ANGPTL7 FAM46B  COL16A1 CYP4B1  NEXN    RP11    OLFML3  NGF
FCGR1A  S100A10 HAPLN2  ATP1A2  ANGPTL1 GLT25D2 DISC1   RP4     LYST    NID1    RHOB
ITSN2   VIT     EHBP1   FIGN    PDE11A  SESTD1  ZNF385B PID1    EFHD1   CXCR7
PGAM1P4 CIDEC   PPARG   VIPR1   CLEC3B  TNNC1   ALDH1L1 MBNL1   MME     MME-AS1
ADIPOQ  ADIPOQ-AS1      KLB     CORIN   SEPT11  USP53   SH3D19  NPY1R   PDLIM3
SLC12A7 PIK3R1  GPR98   LVRN    LOX     SNCAIP  SPOCK1  ADRB2   RP1     MYO1G   EGFR
CTB     AZGP1   NYAP1   CAV1    WNT2    LEP     LCP1    OSR2    MAMDC2  OMD
HDHD3   GSN     ARHGAP21        SFRP5   ADD3    EBF3    INPP5A  TNNT3   H19
PDE3B   CAPRIN1 CD44    IL18BP  POU2F3  IGFBP6  TSPAN8  DCN     MLXIP   RXFP2
DCLK1   CAB39L  RN7SKP7 PRKD1   ZFYVE21 TPM1    PML     MFGE8   ANPEP   NDRG4
MMP28   PNMT    CD300LG C17orf62        CABLES1 CYB5A   COL5A3  CACNA1A JAK3
FOXA2   CST3    EXOSC3P1        MTND1P10        RP3     PMM1    WNT7B   MIR221
FAAH2   ITM2A   TBX22   DRP2    ZBTB33  AFF2    MAMLD1  PDZD4
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0044057      1.48109479301536e-06    5.44316502634734        2.97218185592693
14      417     regulation of system process
GO:0008217      3.37093466593401e-06    10.0691729323308        0.905196872188776
8       127     regulation of blood pressure
Tissue: Muscle_Skeletal=>Thyroid        Type:   cluster
SourceGene:     MTND1P23(ENSG00000225972.1)
TargetGeneSet:  WASH7P  MTND1P23        MTND2P28        AURKAIP1        RP13    LZIC
DFFA    SNORA59A        DNAJC16 RP11    PAQR7   RP1     WASF2   EYA3    PHACTR4
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SNRNP40 MFI2    NSUN4   SELRC1  NFIA    NSRP1P1 RP4     U6      RBMXL1  TAF13
MRPL53P1        BCAS2   BCL9    LCE2B   GATAD2B JTB     MIR555  ETV3    KIRREL-IT1
HMGN1P4 TROVE2  KRT8P29 FAM108A4P       ZC3H11B FTH1P2  HMGN2P19        AKT3-IT1
C2orf18 PPP1CB  WDR43   AAK1    C2orf68 EIF5B   MZT2B   H3F3AP4 KRT18P29
CYP20A1 RQCD1   CLN5    CAPN10  ARPC4   RPL29   PSMC1P1 KIAA2018        ZBTB20
POU5F1P6        ATP5G1P3        GMPS    RNF168  SENP5   PSAPL1  HSP90AB2P
RELL1   RAC1P2  ANKRD17 EIF4E   CTD     NUP155  EMB     SREK1IP1        CENPK
ANKRA2  PHAX    C5orf15 CTB     MTND5P11        KDM3B   ZMAT2   RBM27   RANP1
C6orf47 AGPAT1  RXRB    TAF8    RPL7L1  CDC5L   RP3     MTRNR2L9        FKBP1C
PHACTR2 ARID1B  WTAP    BRAT1   FOXK1   AP5Z1   POLR2J4 RPL35P5 RPS3AP26
ZKSCAN5 RPL19P12        CBLL1   RN5S245 ZNF212  LSM12P1 FAM150A JPH1    KIAA1429
ST13P6  PTK2    LRRC19  FAM22G  ZNF462  SKA2L   DPM2    PRRC2B  FRMD4A  DCLRE1C
YWHAZP3 PRINS   POLR3A  RPS3AP5 NHP2P1  EIF2S2P3        FBXL15  PRDX3   OR52E8
TMEM9B  MTRNR2L8        MRVI1-AS1       ATG13   ARHGAP1 C11orf31        HNRNPUL2
MARK2   BAD     SF1     RPL37P2 ACER3   RSF1    FAM76B  CWF19L2 SDHD    PAFAH1B2
DDX6    ERC1    KIAA0528        ARID2   SMARCD1 CERS5   SLC11A2 CBX5    MRS2P2
LRRIQ1  BRAP    PARP4-AS1       RBM22P2 MFAP1P1 N4BP2L2-IT1     TDRD3   ARGLU1
RNASE4  ACIN1   PRPF39  GNPNAT1 DLST    ZFYVE21 RPS26P49        GOLGA8IP        TJP1
HMGN2P5 MGA     VPS39   HMGN2P46        FAM96A  MTFMT   IDH3A   IQGAP1  CRTC3
CHTF18  EMP2    PKD1P1  DCTN5   C16orf53        SULT1A3 CD2BP2  UBE2MP1 DNAJA2
FTO-IT1 NOL3    NFATC3  CIRH1A  VPS4A   YWHAE   METTL16 RNASEK  VAMP2   NCOR1
TP53I13 TAF15   C17orf96        FBXL20  MED1    WIPF2   IGFBP4  FAM134C PSME3
KANSL1  KPNB1   ZNF652  KAT7    RPS2P48 SCARNA20        MED13   GH1     SLC38A10
ANAPC11 MYL12B  MPPE1   SERPINB7        ZNF407  C19orf24        NFIC    CRB3
ZNF562  FBXL12  ZNF791  BRD4    ZNF429  ZNF568  NOVA2   ZNF480  ZNF813  ZNF543
ZNF544  ZSCAN22 CRNKL1  SCAND1  TSHZ2   RPL12P4 RAB22A  NDUFV3  FAM108A5P       CTA
TTC28   SF3A1   MYH9    TOMM22  RPS19BP1        TRABD   ARSA    PRDX4   USP9X   RP6
OTUD5   GNL3L   TLE1P1  RPSAP14 HK2P1   MTND4P24        MMGT1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006397      5.91291960082991e-07    4.53119739342927        4.50051899522524
18      399     mRNA processing
GO:0008380      3.81086233695306e-06    4.60029835029835        3.64327728184901
15      323     RNA splicing
Tissue: Muscle_Skeletal=>Thyroid        Type:   cluster
SourceGene:     NNAT(ENSG00000053438.7)
TargetGeneSet:  UBE2J2  RP11    DFFA    DNAJC16 RSG1    RCC2    LDLRAP1 YTHDF2
SNRNP40 TXLNA   NCDN    AKIRIN1 KIF2C   LDLRAD1 PGM1    CCBL2   KCND3   SEC22B
GOLPH3L PYGO2   MIR555  UBQLN4  CCT3    CDC73   KRT8P29 ACBD3   ZNF678  URB2
ZNF238  DNMT3A  DPYSL5  SLC5A6  PPM1G   ARHGEF33        MSH6    FBXO11  REL
PCBP1-AS1       PCBP1   MOB1A   SH2D6   MRPS5   TBC1D8  MAP4K4  MFSD9   TMEM182
POLR1B  MYO7B   SMPD4   GORASP2 HSPD1   C2orf69 CREB1   METTL21A        FZD5
TTLL4   NHEJ1   HMGB1P3 PRRT3-AS1       LARS2   TMEM89  WDR6    ZBTB11  ZBTB20
TMEM39A COPG1   H1FX-AS1        MED12L  SLC33A1 GMPS    MCCC1   ZNF141  TMEM128
TADA2B  EXOC7   ANKRD17 EIF4E   COL25A1 SEC24D  IRF2    SLC12A7 FAM105B SNX18   CCNO
KIF2A   PAPD4   EPB41L4A-AS1    DTWD2   SRFBP1  SEC24A  CTB     ADRB2   CAMK2A
FAM114A2        MFAP3   FBXW11  TMED9   ZSCAN12P1       TRIM27  HCG18   SNORD48
SRPK1   BRPF3   BYSL    PGM3    UBE2J1  TSPYL4  LATS1   RSPH3   FAM120B HUS1
BAZ1B   ZKSCAN1 SH2B2   METTL2A MTPN    EPHA1   ZNF786  NEIL2   LCP1    POLR3D  CTD
CHMP7   EXTL3   LSM12P1 WHSC1L1 KAT6A   LRRC6   EIF2C2  EEF1D   NRBP2   BOP1
DNAJA1  ATP8B5P DCAF10  FAM22G  NANS    ALG2    MRPL50  TTLL11  NEK6    OLFML2A
METTL11A        SURF4   TUBB4B  OPTN    AP3M1   ALDH18A1        CC2D2B  RRP12
ENTPD7  ZDHHC6  NHLRC2  MRPL17  SPTY2D1 LIN7C   CAPRIN1 TRIM44  ZBTB3   C11orf84
MARK2   STIP1   GPR137  GPHA2   SYVN1   RBM14   CLPB    PRSS23  CHORDC1 DDX6
HSPA8   FKBP4   RP4     GNB3    ASUN    PUS7L   DDX23   TIMELESS        TMEM194A
METTL1  SLC16A7 TBC1D30 HELB    C12orf34        ATXN2   C12orf65        SBNO1
GOLGA3  LNX2    COG3    TPTE2P3 DNAJC3  TTC5    RBM23   ARHGAP5 HMGB1P14
SYNJ2BP MAP3K9  ZC3H14  BTBD7   CYP46A1 WDR25   HSP90AA1        TRAF3   NIPA2   MGA
TP53BP1 PIGB    PARP16  IDH3A   C15orf38        SOLH    CLDN9   MTRNR2L4
EARS2   DCTN5   TAOK2   SRCAP   DNAJA2  BCAR1   C16orf46        ZC3H18  VPS53
PELP1   SHISA6  ALKBH5  C17orf108       MMP28   CNTNAP1 PSME3   UBTF    UBE2Z
PPP1R9B DCAF7   CANT1   CSNK1D  FOXK2   RP13    GNAL    ZNF397  TPGS2   MBD1
AP3D1   ZNF555  SEMA6B  TNFSF14 ZNF121  ZNF562  ZNF441  BRD4    JAK3    PIK3R2
MPV17L2 ARMC6   GATAD2A ZNF91   MAP3K10 SMG9    DHX34   PRMT1   ZNF347  PEG3
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ZNF587  ZNF417  SEC23B  FOXA2   ZNF341  NCOA5   ADNP    C20orf201       FAM207CP
URB1    C21orf59        OLIG1   RPS5P2  PRDM15  UBE2G2  KRT18P5 HIC2    ZNF70   XBP1
PRR14L  GGA1    TCF20   RP6     TMSB4X  ZNF81   SMC1A   MAGEH1  KIAA2022        MID2
ZBTB33  CUL4B   XIAP    HCFC1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
Tissue: Muscle_Skeletal=>Thyroid        Type:   asymmetric
SourceGene:     NR1I3(ENSG00000143257.7)
TargetGeneSet:  SEPT2P1 KCNA3   FAM46C  SLAMF7  PTPRC   IGKV1OR2-118    EOMES
TRAT1   CD96    GZMA    GPSM3   RP1     TAGAP   CARD11  ARL4A   TRGC1   TRGV4
PLEKHA2 CHRNA6  RP11    APBB1IP PRF1    CD59    CD3E    CD3D    SPIC    LCP1
TRAV2   IGHV6-1 IGHV3-49        IGHV4OR15-8     RASGRP1 ITGAL   TNK1    CCL5
TMIGD2  MYO1F   ADAM33  IL2RB   CENPM   PIM2    IL2RG   MTCP1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0046649      3.64642720047823e-07    12.3767688679245        0.988789703134731
9       433     lymphocyte activation
GO:0042102      3.66187242958608e-07    42.0286885245902        0.150716213410837
5       66      positive regulation of T cell proliferation
GO:0042110      4.43334223453641e-07    14.5152411575563        0.728461698152377
8       319     T cell activation
GO:0002252      1.86362804014922e-06    11.8857142857143        0.881461490554287
8       386     immune effector process
GO:0050870      2.13674031793135e-06    19.1959595959596        0.390492007473531
6       171     positive regulation of T cell activation
GO:0050671      2.38586772474431e-06    28.1142072213501        0.219223583143035
5       96      positive regulation of lymphocyte proliferation
GO:0032946      2.51146686554061e-06    27.8066770186335        0.221507162134108
5       97      positive regulation of mononuclear cell proliferation
GO:0050852      2.77825602583929e-06    27.2112462006079        0.226074320116255
5       99      T cell receptor signaling pathway
GO:0051249      2.8322941466464e-06     13.7951505016722        0.646252854473739
7       283     regulation of lymphocyte activation
GO:0070665      2.91975102891644e-06    26.9229323308271        0.228357899107328
5       100     positive regulation of leukocyte proliferation
GO:0042129      3.06685408569195e-06    26.640625       0.230641478098401       5
101     regulation of T cell proliferation
GO:0002694      6.49763083231527e-06    12.093091621754 0.733028856134524       7
321     regulation of leukocyte activation
GO:0042098      6.59049025861439e-06    22.6058786346397        0.269462320946647
5       118     T cell proliferation
GO:0045061      7.21868328547381e-06    102.885714285714        0.0388208428482458
3       17      thymic T cell selection
GO:0051251      8.00881384652893e-06    15.1079213184476        0.490969483080756
6       215     positive regulation of lymphocyte activation
GO:0050851      8.07333000487323e-06    21.6404358353511        0.280880215902014
5       123     antigen receptor-mediated signaling pathway
GO:0050863      9.37404367992686e-06    14.6801033591731        0.504670957027195
6       221     regulation of T cell activation
GO:0050865      1.00205734608208e-05    11.2836538461538        0.783267593938136
7       343     regulation of cell activation
GO:0002429      1.1816084699071e-05     19.9358258928571        0.303716005812747
5       133     immune response-activating cell surface receptor signaling pathway
GO:0002696      1.26720978076269e-05    13.8923152227117        0.532073904920075
6       233     positive regulation of leukocyte activation
GO:0050778      1.47416451699015e-05    10.60407239819  0.831222752750675       7
364     positive regulation of immune response
GO:0050867      1.49935907178376e-05    13.4700854700855        0.548058957857588
6       240     positive regulation of cell activation
GO:0038110      1.51494826074357e-05    930.129032258065        0.00685073697321985
2       3       interleukin-2-mediated signaling pathway
GO:0002768      1.73717388402897e-05    18.3440390544707        0.328835374714553
5       144     immune response-regulating cell surface receptor signaling pathway
GO:0050670      1.73717388402897e-05    18.3440390544707        0.328835374714553
5       144     regulation of lymphocyte proliferation
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GO:0032944      1.7963050440714e-05     18.2117346938776        0.331118953705626
5       145     regulation of mononuclear cell proliferation
Tissue: Muscle_Skeletal=>Thyroid        Type:   cluster
SourceGene:     RP11-55L3.2(ENSG00000213493.3)
TargetGeneSet:  DNAJC11 UBIAD1  RP1     PAQR7   EYA3    PHACTR4 SNRNP40 HDAC1
PRPF38A TARS2   METTL13 DHX9    PPM1G   POLR1B  CLN5    TEX264  WDR82   COPG1
KDM5A   PSMD2   BOD1L   FIP1L1  KIT     GARS    SLCO4C1 AP3S1   IK      HAVCR2  RP3
TMEM151B        POLR2J4 SUMF2   COPS6   CASP2   ADRA1D  ELP3    TEX10   RNF20
FKBP15  ATP6V1G1        EXOSC2  POLR3A  NAT10   RP11    NUP160  GANAB   TMEM179B
VPS11   NCKAP1L SUOX    OBFC2B  CENPC1P1        SART3   SUPT16H YLPM1   MGA     MPI
HIRIP3  RNF40   CTCF    TMCO7   SF3B3   DHX38   RP13    RPA1    TSR1    RNF167  TP53
PFAS    ERAL1   AP2B1   CDK12   PSME3   GPATCH8 EFTUD2  BCAS3   DCAF7   EIF4A3  MAU2
IDH3B   DDX27   PRPF6   LINC00515       ITGB2   L3MBTL2 XRCC6   SLC35A2 SMC1A
GNL3L   RBM41
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0008380      9.38632128306859e-08    8.61430102587659        1.67635457753789
12      323     RNA splicing
GO:0000377      9.40777010348585e-08    11.2466296590008        1.05875025949761
10      204     RNA splicing, via transesterification reactions with bulged
adenosine as nucleophile
GO:0000398      9.40777010348585e-08    11.2466296590008        1.05875025949761
10      204     nuclear mRNA splicing, via spliceosome
GO:0000375      1.18048959291484e-07    10.9601855431001        1.08470002075981
10      209     RNA splicing, via transesterification reactions
GO:0006397      1.19572460637369e-07    7.59944843723884        2.07079094872327
13      399     mRNA processing
Tissue: Muscle_Skeletal=>Thyroid        Type:   asymmetric
SourceGene:     RP11-629O1.2(ENSG00000261220.1)
TargetGeneSet:  NOC2L   UBE2J2  DNAJC16 TCEB3   LYPLA2  TXLNA   MARCKSL1
S100PBP SF3A3   CTPS    EIF2B3  RP11    CDC7    ATXN7L2 AMPD2   KCND3   SLC39A1
FLAD1   UBQLN4  CCT3    HAPLN2  PFKFB2  NOL10   ITSN2   DNMT3A  SLC5A6  MRPS5
SEMA4C  MAP4K4  MTND5P28        IWS1    GORASP2 HSPD1   TTLL4   HMGB1P3 EFHD1   DPH3
SLC25A38        ZDHHC3  CDCP1   SEMA3F  IFRD2   ARF4    PXK     COPG1   H1FX-AS1
MED12L  GMPS    MCCC1   SLC12A7 ARSB    GPR98   FSTL4   ADRB2   MAK     TRIM27
RANP1   PPP1R18 DAXX    ITPR3   BRPF3   BYSL    GPR110  SYTL3   HEATR2  CCZ1
IGFBP3  PRKAG2  PINX1   GATA4   POLR3D  INTS9   KLF10   NUDCD1  DERL1   EEF1D   PLAA
DNAJA1  DCAF12  CCL19   DCAF10  FXN     NCBP1   CDK5RAP2        OLFML2A NUP188
METTL11A        SURF4   GRIN1   NGB     NUDT5   RRP12   ENTPD7  TMEM123 SPTY2D1
CAPRIN1 CHST1   PATL1   CCDC86  C11orf84        MARK2   STIP1   IL18BP  CLPB
P2RY6   DDX10   ARCN1   HSPA8   FKBP4   RP4     NOP2    DDX23   METTL1  UTP20
ATXN2   DHX37   PUS1    GOLGA3  RGCC    ATP11A  RBM23   EIF2B2  AHSA1   ZC3H14  CTD
DUOXA1  DUOX1   SLTM    PARP16  IDH3A   SOLH    CARHSP1 UBFD1   DCTN5   CD2BP2  MT1F
CIRH1A  BCAR1   COX4NB  ZC3H18  TSR1    CYB5D2  C17orf51        C17orf108       UTP6
CDK12   LEPREL4 CNTNAP1 PSME3   UBE2Z   PPP1R9B FAM20A  HN1     MRPL38  PTPN2
ZNF397  MBD1    PTBP1   TNFSF14 ANGPTL4 ZNF121  ZNF441  EMR2    ANKLE1  JAK3
CCDC124 MPV17L2 MAP3K10 ETHE1   BCL3    PRMT1   ZNF587  PAK7    TOMM34  RPL12P9
EXOSC3P1        RUNX1   PRDM15  UBE2L3  HPS4    MORC2   GGA1    TCF20   ZNF81
TSC22D3 RP13    TMSB4Y
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022613      8.33411188747106e-08    6.92553975776725        2.31990865684036
14      225     ribonucleoprotein complex biogenesis
GO:0071843      1.7581208002344e-07     6.4881646090535 2.46425852882153        14
239     cellular component biogenesis at cellular level
GO:0022618      6.03014277432934e-06    9.27040026086248        0.979516988443706
8       95      ribonucleoprotein complex assembly
GO:0071826      8.84007004973229e-06    8.76349059512797        1.03107051415127
8       100     ribonucleoprotein complex subunit organization
Tissue: Muscle_Skeletal=>Thyroid        Type:   asymmetric
SourceGene:     RP11-734I18.1(ENSG00000251129.1)
TargetGeneSet:  SDHC    IFT172  CCDC104 RPL15   RPL29   MLF1    RP11    CC2D2A
LAMTOR3 MTND5P11        CTB     GNB2L1  EIF3E   EIF3H   ZNF618  RPL12   EEF1A1P5
COX15   MRPL16  SLC48A1 RPL6    ASB16   RPL12P4 IFNGR2  EIF3L   RPL3    RPS4X
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
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GO:0006413      8.94682028637923e-13    64.2182817182817        0.241920974327036
9       152     translational initiation
GO:0000184      4.72339942275701e-10    55.921875       0.189398657532351       7
119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006415      4.88666401663353e-09    59.5557093425606        0.144834267524739
6       91      translational termination
GO:0000956      5.53154659155372e-09    38.5270061728395        0.268977925403086
7       169     nuclear-transcribed mRNA catabolic process
GO:0006402      7.93522129315348e-09    36.4762426900585        0.283302193619819
7       178     mRNA catabolic process
GO:0006414      1.16321782613037e-08    51.0837789661319        0.167116462528545
6       105     translational elongation
GO:0006614      1.16321782613037e-08    51.0837789661319        0.167116462528545
6       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.23176224574141e-08    50.5694117647059        0.168708047885959
6       106     cotranslational protein targeting to membrane
GO:0045047      1.23176224574141e-08    50.5694117647059        0.168708047885959
6       106     protein targeting to ER
GO:0072599      1.23176224574141e-08    50.5694117647059        0.168708047885959
6       106     establishment of protein localization to endoplasmic reticulum
GO:0006401      2.11025172744099e-08    31.4425505050505        0.326274998270016
7       205     RNA catabolic process
GO:0070972      2.35052545672698e-08    45.1134453781513        0.187807072174936
6       118     protein localization to endoplasmic reticulum
GO:0019080      1.02708662569541e-07    34.7659229208925        0.240329388969621
6       151     viral genome expression
GO:0019083      1.02708662569541e-07    34.7659229208925        0.240329388969621
6       151     viral transcription
GO:0006612      1.11068333584869e-07    34.2881152460984        0.243512559684451
6       153     protein targeting to membrane
GO:0043624      1.11068333584869e-07    34.2881152460984        0.243512559684451
6       153     cellular protein complex disassembly
GO:0043241      1.34449694415459e-07    33.1486068111455        0.251470486471524
6       158     protein complex disassembly
GO:0034623      2.38085620590658e-07    29.9579831932773        0.27693585219016
6       174     cellular macromolecular complex disassembly
GO:0032984      2.81460650567542e-07    29.081944916695 0.284893778977233       6
179     macromolecular complex disassembly
GO:0072594      6.07562117312445e-07    25.3654188948307        0.324683412912601
6       204     establishment of protein localization to organelle
GO:0019058      1.25703115685503e-06    22.2792156862745        0.367656217562798
6       231     viral infectious cycle
GO:0022415      2.49964104162857e-06    19.6952292728115        0.413812192927825
6       260     viral reproductive process
GO:0071845      4.16356426373618e-06    17.9644519678375        0.452010241505778
6       284     cellular component disassembly at cellular level
GO:0022411      4.5129496406714e-06     17.7046307884856        0.458376582935437
6       288     cellular component disassembly
Tissue: Muscle_Skeletal=>Thyroid        Type:   asymmetric
SourceGene:     SMAD7(ENSG00000101665.3)
TargetGeneSet:  RP11    SEMA4A  TTC24   FCRL5   FCRL2   KIF21B  STAMBP  IGKJ5   IGKC
IGKJ2   IGKJ1   IGKV3-11        IGKV1-12        IGKV3-15        SP140   OR2A5
CNTNAP2 SYT12   CRTAM   ARHGAP9 GS1     TRDC    IGHA2   IGHG2   IGHG1   GPR114
IFT20   FAM209A IGLV3-10        IGLV2-8 IGLC2   IGLC3   MIAT
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006958      3.34410537044235e-09    122.974358974359        0.0622794270292713
5       50      complement activation, classical pathway
GO:0006956      1.09859748955005e-08    95.3249336870027        0.0784720780568819
5       63      complement activation
GO:0002455      1.28906736371292e-08    92.1346153846154        0.0809632551380527
5       65      humoral immune response mediated by circulating immunoglobulin
GO:0002449      3.60247991194033e-08    44.3229813664596        0.208013286277766
6       167     lymphocyte mediated immunity
```

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GO:0072376      4.20414596204078e-08    71.7082917082917        0.102138260328005
5       82      protein activation cascade
GO:0002460      5.8222716843612e-08     40.7371428571429        0.225451525845962
6       181     adaptive immune response based on somatic recombination of immune
receptors built from immunoglobulin superfamily domains
GO:0002250      9.92797013957539e-08    37.0859375      0.246626531035914       6
198     adaptive immune response
GO:0002443      1.44733874159179e-07    34.7024390243902        0.262819182063525
6       211     leukocyte mediated immunity
GO:0016064      1.93212855523158e-07    51.9847605224964        0.138260328004982
5       111     immunoglobulin mediated immune response
GO:0019724      2.20811624721492e-07    50.5434015525759        0.141997093626739
5       114     B cell mediated immunity
GO:0002252      2.2681262098458e-07     23.5975053969777        0.480797176665975
7       386     immune effector process
GO:0006959      3.09915170958394e-07    47.0611439842209        0.151961801951422
5       122     humoral immune response
GO:0050778      3.52128674649164e-06    19.6578212290503        0.453394228773095
6       364     positive regulation of immune response
Tissue: Muscle_Skeletal=>Thyroid        Type:   asymmetric
SourceGene:     TBCAP3(ENSG00000249055.1)
TargetGeneSet:  ACAP3   ARHGEF10L       RPL11   LRRC8B  SLC35A3 MAN1A2  OTUD7B  LMNA
RGS4    KCNT2   TSSC1   RP11    CCDC88A NR4A2   NPPC    ARF4    PPIAP16 MAGI1-IT1
TFG     ATP6V1A PFN2    DEFB131 TAPT1   MOB1B   SEC31A  SEC24D  STOX2   C5orf27
STARD4  PHF15   CAMLG   RPS14   CNOT8   THG1L   CPEB4   ELOVL2  RP3     CCND3
KLHDC3  UFL1    FOXO3   C7orf50 SLC29A4 ZCWPW1  TMEM168 MKRN1   ZYX     FAM82B
DGAT1   CTD     GOLGA2  RPL7A   IL15RA  STOX1   PTPRE   PRMT3   DRAP1   NDUFS8  RPS3
CALCOCO1        RPL41   ARL1    TCP11L2 VSIG10  RNU4-2  CHFR    SCFD1   RPL32P29
SIPA1L1 TGFB3   FOXN3   TELO2   ECI1    CLUAP1  RPS15A  C16orf58        GPR56
BCAR1   C16orf7 TP53I13 RPL17   PLEKHH3 SUPT4H1 BTBD17  FAM100B C17orf70
ARHGDIA ATP8B1  FBN3    ILVBL   COPE    RPS11   ISOC2   NECAB3  UCKL1   LINC00158
ARVCF   APOL2   TRABD   CCDC22  MAGED2  FOXO4   RP4     FAM199X
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      2.4029949032464e-08     20.2579730687456        0.478582797038267
8       91      translational termination
GO:0006414      7.43372609414547e-08    17.3171619163129        0.552210919659539
8       105     translational elongation
GO:0006614      7.43372609414547e-08    17.3171619163129        0.552210919659539
8       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      8.00688636884317e-08    17.1392557022809        0.557470071275344
8       106     cotranslational protein targeting to membrane
GO:0045047      8.00688636884317e-08    17.1392557022809        0.557470071275344
8       106     protein targeting to ER
GO:0072599      8.00688636884317e-08    17.1392557022809        0.557470071275344
8       106     establishment of protein localization to endoplasmic reticulum
GO:0019080      9.17468376821776e-08    13.4640529745638        0.794131893986575
9       151     viral genome expression
GO:0019083      9.17468376821776e-08    13.4640529745638        0.794131893986575
9       151     viral transcription
GO:0070972      1.84678499912722e-07    15.2566844919786        0.620579890665006
8       118     protein localization to endoplasmic reticulum
GO:0000184      1.97159417954415e-07    15.1181770005299        0.625839042280811
8       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0000956      2.40668033314045e-07    11.9342350746269        0.888796623071068
9       169     nuclear-transcribed mRNA catabolic process
GO:0006402      3.73811607986339e-07    11.2915305131149        0.936128987613314
9       178     mRNA catabolic process
GO:0006401      1.22282571351335e-06    9.71756015839171        1.07812608124005
9       205     RNA catabolic process
GO:0006413      1.28258848919235e-06    11.6266339869281        0.799391045602381
8       152     translational initiation
GO:0006612      1.3476829986127e-06     11.5456389452333        0.804650197218186
8       153     protein targeting to membrane
```

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GO:0043624      1.3476829986127e-06     11.5456389452333        0.804650197218186
8       153     cellular protein complex disassembly
GO:0043241      1.71710525455108e-06    11.156862745098 0.830945955297211       8
158     protein complex disassembly
GO:0019058      3.27711101709493e-06    8.56373537716821        1.21486402325099
9       231     viral infectious cycle
GO:0034623      3.53234654863319e-06    10.070163004961 0.915092381150093       8
174     cellular macromolecular complex disassembly
GO:0032984      4.35900428544295e-06    9.77227382180943        0.941388139229119
8       179     macromolecular complex disassembly
GO:0022415      8.56194963266732e-06    7.55877980614854        1.36737942010933
9       260     viral reproductive process
GO:0072594      1.13913791253346e-05    8.51080432172869        1.07286692962425
8       204     establishment of protein localization to organelle
GO:0071845      1.73410816782255e-05    6.88738127544098        1.49359905888866
9       284     cellular component disassembly at cellular level
GO:0022411      1.93742077695957e-05    6.78671160327395        1.51463566535188
9       288     cellular component disassembly
Tissue: Muscle_Skeletal=>Thyroid        Type:   cluster
SourceGene:     TBCAP3(ENSG00000249055.1)
TargetGeneSet:  ACAP3   ARHGEF10L       RPL11   LRRC8B  SLC35A3 MAN1A2  OTUD7B  LMNA
RGS4    KCNT2   TSSC1   RP11    CCDC88A NR4A2   NPPC    ARF4    PPIAP16 MAGI1-IT1
TFG     ATP6V1A PFN2    DEFB131 TAPT1   MOB1B   SEC31A  SEC24D  STOX2   C5orf27
STARD4  PHF15   CAMLG   RPS14   CNOT8   THG1L   CPEB4   ELOVL2  RP3     CCND3
KLHDC3  UFL1    FOXO3   C7orf50 SLC29A4 ZCWPW1  TMEM168 MKRN1   ZYX     FAM82B
DGAT1   CTD     GOLGA2  RPL7A   IL15RA  STOX1   PTPRE   PRMT3   DRAP1   NDUFS8  RPS3
CALCOCO1        RPL41   ARL1    TCP11L2 VSIG10  RNU4-2  CHFR    SCFD1   RPL32P29
SIPA1L1 TGFB3   FOXN3   TELO2   ECI1    CLUAP1  RPS15A  C16orf58        GPR56
BCAR1   C16orf7 TP53I13 RPL17   PLEKHH3 SUPT4H1 BTBD17  FAM100B C17orf70
ARHGDIA ATP8B1  FBN3    ILVBL   COPE    RPS11   ISOC2   NECAB3  UCKL1   LINC00158
ARVCF   APOL2   TRABD   CCDC22  MAGED2  FOXO4   RP4     FAM199X
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      2.4029949032464e-08     20.2579730687456        0.478582797038267
8       91      translational termination
GO:0006414      7.43372609414547e-08    17.3171619163129        0.552210919659539
8       105     translational elongation
GO:0006614      7.43372609414547e-08    17.3171619163129        0.552210919659539
8       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      8.00688636884317e-08    17.1392557022809        0.557470071275344
8       106     cotranslational protein targeting to membrane
GO:0045047      8.00688636884317e-08    17.1392557022809        0.557470071275344
8       106     protein targeting to ER
GO:0072599      8.00688636884317e-08    17.1392557022809        0.557470071275344
8       106     establishment of protein localization to endoplasmic reticulum
GO:0019080      9.17468376821776e-08    13.4640529745638        0.794131893986575
9       151     viral genome expression
GO:0019083      9.17468376821776e-08    13.4640529745638        0.794131893986575
9       151     viral transcription
GO:0070972      1.84678499912722e-07    15.2566844919786        0.620579890665006
8       118     protein localization to endoplasmic reticulum
GO:0000184      1.97159417954415e-07    15.1181770005299        0.625839042280811
8       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0000956      2.40668033314045e-07    11.9342350746269        0.888796623071068
9       169     nuclear-transcribed mRNA catabolic process
GO:0006402      3.73811607986339e-07    11.2915305131149        0.936128987613314
9       178     mRNA catabolic process
GO:0006401      1.22282571351335e-06    9.71756015839171        1.07812608124005
9       205     RNA catabolic process
GO:0006413      1.28258848919235e-06    11.6266339869281        0.799391045602381
8       152     translational initiation
GO:0006612      1.3476829986127e-06     11.5456389452333        0.804650197218186
8       153     protein targeting to membrane
GO:0043624      1.3476829986127e-06     11.5456389452333        0.804650197218186
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8       153     cellular protein complex disassembly
GO:0043241      1.71710525455108e-06    11.156862745098 0.830945955297211       8
158     protein complex disassembly
GO:0019058      3.27711101709493e-06    8.56373537716821        1.21486402325099
9       231     viral infectious cycle
GO:0034623      3.53234654863319e-06    10.070163004961 0.915092381150093       8
174     cellular macromolecular complex disassembly
GO:0032984      4.35900428544295e-06    9.77227382180943        0.941388139229119
8       179     macromolecular complex disassembly
GO:0022415      8.56194963266732e-06    7.55877980614854        1.36737942010933
9       260     viral reproductive process
GO:0072594      1.13913791253346e-05    8.51080432172869        1.07286692962425
8       204     establishment of protein localization to organelle
GO:0071845      1.73410816782255e-05    6.88738127544098        1.49359905888866
9       284     cellular component disassembly at cellular level
GO:0022411      1.93742077695957e-05    6.78671160327395        1.51463566535188
9       288     cellular component disassembly
Tissue: Muscle_Skeletal=>Thyroid        Type:   asymmetric
SourceGene:     U2(ENSG00000222389.1)
TargetGeneSet:  MAN1C1  RPS7    MFF     JAGN1   BMP2K   RP11    CTD     PLEKHG4B
ATP6V0E1        CPEB4   RPL10A  RPS3AP26        RPL35   RPL7A   P2RX3   RPL6    CHKB
RPS15A  FSCN2   TP53INP2
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      4.01611449165716e-10    101.294117647059        0.100754273060688
6       91      translational termination
GO:0006414      9.61586459350121e-10    86.8848484848485        0.11625493045464
6       105     translational elongation
GO:0006614      9.61586459350121e-10    86.8848484848485        0.11625493045464
6       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.01867392935224e-09    86.01   0.117362120268494       6       106
cotranslational protein targeting to membrane
GO:0045047      1.01867392935224e-09    86.01   0.117362120268494       6       106
protein targeting to ER
GO:0072599      1.01867392935224e-09    86.01   0.117362120268494       6       106
establishment of protein localization to endoplasmic reticulum
GO:0072594      1.03536178759999e-09    56.2131979695431        0.225866722026157
7       204     establishment of protein localization to organelle
GO:0070972      1.95364559544598e-09    76.7303571428571        0.130648398034738
6       118     protein localization to endoplasmic reticulum
GO:0000184      2.05615156802194e-09    76.046017699115 0.131755587848592       6
119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      8.65497447098544e-09    59.1310344827586        0.167185661891911
6       151     viral genome expression
GO:0019083      8.65497447098544e-09    59.1310344827586        0.167185661891911
6       151     viral transcription
GO:0006413      9.00527408901662e-09    58.7219178082192        0.168292851705764
6       152     translational initiation
GO:0006612      9.36723534542493e-09    58.3183673469388        0.169400041519618
6       153     protein targeting to membrane
GO:0043624      9.36723534542493e-09    58.3183673469388        0.169400041519618
6       153     cellular protein complex disassembly
GO:0043241      1.13628486543256e-08    56.3802631578947        0.174935990588887
6       158     protein complex disassembly
GO:0000956      1.70119170987948e-08    52.5349693251534        0.187115078541277
6       169     nuclear-transcribed mRNA catabolic process
GO:0034623      2.0256353412196e-08     50.9535714285714        0.192651027610546
6       174     cellular macromolecular complex disassembly
GO:0006402      2.32062780153623e-08    49.7546511627907        0.197079786865961
6       178     mRNA catabolic process
GO:0032984      2.39967536614885e-08    49.4635838150289        0.198186976679815
6       179     macromolecular complex disassembly
GO:0006401      5.38891409876322e-08    42.9226130653266        0.226973911840011
6       205     RNA catabolic process
```

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GO:0019058      1.09526014563922e-07    37.8933333333333        0.255760847000208
6       231     viral infectious cycle
GO:0022415      2.20453366736355e-07    33.4984251968504        0.287869351601965
6       260     viral reproductive process
GO:0033365      3.40946410365617e-07    23.3149737720553        0.523700781952806
7       473     protein localization to organelle
GO:0006605      3.45863552375854e-07    23.2633832976445        0.52480797176666
7       474     protein targeting
GO:0071845      3.70908453898079e-07    30.5546762589928        0.314441907134454
6       284     cellular component disassembly at cellular level
GO:0022411      4.02707066625748e-07    30.1127659574468        0.318870666389869
6       288     cellular component disassembly
GO:0016032      5.48524295696051e-06    18.8629213483146        0.499342606048024
6       451     viral reproduction
Tissue: Nerve_Tibial=>Thyroid   Type:   asymmetric
SourceGene:     AK3(ENSG00000147853.10)
TargetGeneSet:  RPL22   RP3     CNKSR1  JTB     RPS27   FAM78B  NDUFB1P2
RPL14   RPL29   METTL15P1       RP11    RPS3A   STK32A  PCYOX1L PRELID1 DEK
EEF1A1  CASD1   RPS3AP26        PCOLCE  RPL7    EEF1A1P5        RPL7A   RPS3AP5
RPL27A  CTD     COPS7A  TFCP2   NACA    RPL18AP3        SPG20OS LINC00571       FHP1
POLE2   CES3    LGALS9  RPL19   VPS25   EPX     TCAM1   LRRC37A3        RPS15   DHPS
GLTSCR2 RPS5    MAFB    RP4     PISD    RPL3    RPS4X   SPRY3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      9.52400953644563e-22    104.945054945055        0.254307660369525
14      105     translational elongation
GO:0006415      1.3235913401609e-20     108.621212121212        0.220399972320255
13      91      translational termination
GO:0006614      9.4483628916079e-20     92.001976284585 0.254307660369525       13
105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.07537836841364e-19    91.0063538611926        0.25672963808733
13      106     cotranslational protein targeting to membrane
GO:0045047      1.07537836841364e-19    91.0063538611926        0.25672963808733
13      106     protein targeting to ER
GO:0072599      1.07537836841364e-19    91.0063538611926        0.25672963808733
13      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      4.62144617185643e-19    80.5380952380952        0.28579337070099
13      118     protein localization to endoplasmic reticulum
GO:0000184      5.18084198822889e-19    79.7727272727273        0.288215348418795
13      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      1.2693059713826e-17     61.1376811594203        0.365718635388554
13      151     viral genome expression
GO:0019083      1.2693059713826e-17     61.1376811594203        0.365718635388554
13      151     viral transcription
GO:0006413      1.38603847599456e-17    60.6935905820798        0.368140613106359
13      152     translational initiation
GO:0006612      1.51258162845701e-17    60.2558441558442        0.370562590824164
13      153     protein targeting to membrane
GO:0043624      1.51258162845701e-17    60.2558441558442        0.370562590824164
13      153     cellular protein complex disassembly
GO:0043241      2.32048493093861e-17    58.1576802507837        0.382672479413189
13      158     protein complex disassembly
GO:0000956      5.66828256766503e-17    54.0151515151515        0.409314234309044
13      169     nuclear-transcribed mRNA catabolic process
GO:0019058      8.25737690205258e-17    43.6221198156682        0.559476852812954
14      231     viral infectious cycle
GO:0034623      8.33715556476071e-17    52.3193111236589        0.421424122898069
13      174     cellular macromolecular complex disassembly
GO:0006402      1.12576743050793e-16    51.0366391184573        0.431112033769289
13      178     mRNA catabolic process
GO:0032984      1.21219596404493e-16    50.7256297918949        0.433534011487094
13      179     macromolecular complex disassembly
GO:0022415      4.34881362463966e-16    38.4010840108401        0.629714206629299
14      260     viral reproductive process
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GO:0072594      6.76709447762259e-16    44.0088053307949        0.494083454432219
13      204     establishment of protein localization to organelle
GO:0006401      7.21494711640007e-16    43.7765151515151        0.496505432150024
13      205     RNA catabolic process
GO:0071845      4.97717584360643e-14    30.8428379738343        0.687841671856619
13      284     cellular component disassembly at cellular level
GO:0022411      5.95874574839357e-14    30.3856198347107        0.697529582727839
13      288     cellular component disassembly
GO:0016032      8.67784210839148e-13    21.3257055682685        1.09231195073005
14      451     viral reproduction
GO:0033365      3.21483071021847e-11    17.9276679841897        1.14559546052176
13      473     protein localization to organelle
GO:0006605      3.30068489648991e-11    17.887497535003 1.14801743823957        13
474     protein targeting
Tissue: Nerve_Tibial=>Thyroid   Type:   asymmetric
SourceGene:     ATP6V0CP1(ENSG00000230201.4)
TargetGeneSet:  IGSF21  AKR7A2  C1QA    C1QC    C1QB    MACF1   CD53    FCER1G
FCGR3A  CCL15   TMEM177 TTC30B  TRANK1  GOLGA4  SLC9A9  FAM53A  AASDH   ODAM    RP11
HERC5   CFI     MARCH1  CCDC111 TLR3    FAM105A PCDHGA1 CTB     AIF1    HLA-DRB6
RP1     CCNC    FAM26F  SNX10   TBXAS1  ZNF282  NUB1    CTD     DOK2    MS4A6A
MS4A7   PTPRCAP C3AR1   KIF21A  SELPLG  CLIP1   TDRD3   BATF    SAMD15  GALC
EFCAB11 MPI     TTC23   CORO1A  MLYCD   CAMTA2  DHX58   VPS25   MKS1    SMURF2
C19orf35        GNA15   EBI3    CD209   DOCK6   HCST    SIGLEC16        CD33
SIGLEC8 PCNA    HCK     PXMP4   ASIP    CSTF1   CASS4   PWP2    ITGB2   C22orf28
ATF4    ARSA    GTPBP6  CYBB    VSIG4   BTK     MAGEA5
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0002253      1.08199749417542e-06    8.55642566624173        1.38627084630821
10      299     activation of immune response
GO:0002252      1.4377197720213e-06     7.33804761904762        1.78963393536779
11      386     immune effector process
GO:0002460      1.8017739586064e-06     11.1382384637994        0.839180679537748
8       181     adaptive immune response based on somatic recombination of immune
receptors built from immunoglobulin superfamily domains
GO:0002250      3.52042987973701e-06    10.1295272078501        0.917998754411459
8       198     adaptive immune response
GO:0050778      6.28010223781468e-06    6.95311725641788        1.68763407376652
10      364     positive regulation of immune response
GO:0006956      1.0510244848342e-05     19.9193548387097        0.292090512767283
5       63      complement activation
GO:0019724      1.42428302192121e-05    13.0018214936248        0.528544737388416
6       114     B cell mediated immunity
GO:0050900      1.48767819098159e-05    8.23510584127446        1.11736212026849
8       241     leukocyte migration
Tissue: Thyroid=>Nerve_Tibial   Type:   asymmetric
SourceGene:     CCT8L1P(ENSG00000020219.8)
TargetGeneSet:  C1QC    C1QB    CD52    DHDDS   RPS6KA1 ERMAP   CPT2    IFI44   CD84
ARHGAP30        PTPRC   TMEM81  PTRHD1  DNAJC27 QPCT    CCDC88A FBXO41  LOXL3   PROC
COL3A1  CLK1    CASP8   EBP     STAB1   PDHB    ACPP    P2RY13  FAM131A DAPP1
CCNA2   APC     CSF1R   RP11    LY86    GPSM3   DEFA6   AKIRIN2 FAM54A  COL1A2
PIK3CG  IRF5    TAS2R5  DOK2    ADAM28  PPP2R2A LYN     KIAA0196        FAM49B
FAM83H  C9orf40 SYK     SUSD3   PTGS1   FAM78A  PRKCQ   CDC123  APBB1IP WDFY4
HELLS   BLNK    NDUFS3  MRPL16  MS4A6A  FEN1    FERMT3  SF1     SLCO2B1 IL10RA
SORL1   NDUFA9  LPAR5   CD4     PTPN6   PLBD1   LRMP    MED21   LARP4   BIN2
NCKAP1L HVCN1   ERP29   DTX1    LCP1    ARL11   CKAP2   RNASE1  MAX     BCL11B  CTD
PLCB2   VPS18   PARP16  CORO1A  ITGAM   IRF8    ZNF469  CYBA    SNORA67 NDEL1
AKAP10  ADAP2   C17orf75        DDX52   MRPS23  DSC2    VAV1    EMR1    STXBP2
MYO1F   GMIP    ZNF506  TYROBP  ZNF567  RASGRP4 KCNN4   CD33    LAIR1   ZNF548
ERGIC3  ZNF295  ITGB2   CECR6   PITPNB  CYTH4   JOSD1   CBX7    RP1     KLHDC7B TLR7
PHEX    CYBB    GPR34   WAS     BTK     ARHGAP4
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0046649      7.58581529715495e-09    6.29006024096386        3.41581897446543
18      433     lymphocyte activation
GO:0042110      3.01210299330702e-08    6.99411881977671        2.51650404816276
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15	319	T cell activation
GO:0002275	6.55562844714552e-08	23.9841840402588	0.362881461490554
7	46	myeloid cell activation involved in immune response
GO:0002253	9.50110401902084e-08	6.90273684210526	2.3587294996886 14
299	activation of immune response
GO:0070527	2.97791658404737e-07	46.9298820445609	0.149885821050446
5	19	platelet aggregation
GO:0002757	3.30392783566779e-07	7.44605644948562	1.85385094457131
12	235	immune response-activating signal transduction
GO:0007596	3.5152353649221e-07	5.0485886362175 3.92858625700644	17
498	blood coagulation
GO:0050900	4.32944640858016e-07	7.24788081171333	1.90118330911356
12	241	leukocyte migration
GO:0050851	5.3431215864553e-07	10.693984962406 0.970313473116047	9
123	antigen receptor-mediated signaling pathway
GO:0002764	5.87667026407685e-07	7.02941176470588	1.95640440107951
12	248	immune response-regulating signaling pathway
GO:0002521	7.33830439665032e-07	6.25660351502278	2.38239568195973
13	302	leukocyte differentiation
GO:0050778	1.03071600127173e-06	5.5948	2.8714967822296 14	364
positive regulation of immune response
GO:0002429	1.0347493362279e-06	9.82465437788018	1.04920074735312
9	133	immune response-activating cell surface receptor signaling pathway
GO:0002283	1.1616190191301e-06	74.4415584415584	0.0867760016607847
4	11	neutrophil activation involved in immune response
GO:0045730	1.61200452732009e-06	31.2712975098296	0.2051069130164 5
26	respiratory burst
GO:0002768	2.01128258708995e-06	9.01714285714286	1.13597674901391
9	144	immune response-regulating cell surface receptor signaling pathway
GO:0050853	2.85580633788103e-06	27.3566513761468	0.228773095287523
5	29	B cell receptor signaling pathway
GO:0050867	3.01409784877097e-06	6.5793869504388 1.89329458168985	11
240	positive regulation of cell activation
GO:0050865	3.02778961756455e-06	5.46327632763276	2.70583350633174
13	343	regulation of cell activation
GO:0030097	3.48796668194308e-06	4.6973079004329 3.65248079717667	15
463	hemopoiesis
GO:0030155	4.46380198729616e-06	6.29963033675915	1.97218185592693
11	250	regulation of cell adhesion
GO:0002263	5.67745663290834e-06	9.33355209187859	0.970313473116047
8	123	cell activation involved in immune response
GO:0002366	5.67745663290834e-06	9.33355209187859	0.970313473116047
8	123	leukocyte activation involved in immune response
GO:0033628	7.51772815983642e-06	21.8761467889908	0.27610545982977
5	35	regulation of cell adhesion mediated by integrin
GO:0051251	7.62662529661527e-06	6.62851782363977	1.69607639609716
10	215	positive regulation of lymphocyte activation
GO:0048534	7.82275545149041e-06	4.37405303030303	3.90492007473531
15	495	hemopoietic or lymphoid organ development
GO:0050870	8.24329624974661e-06	7.5	1.34897238945402	9	171
positive regulation of T cell activation
GO:0002694	8.55643832069019e-06	5.34094802969732	2.53228150301017
12	321	regulation of leukocyte activation
GO:0050863	9.71160843328381e-06	6.4372949325556 1.7434087606394 10	221
regulation of T cell activation
GO:0002252	1.08749423599764e-05	4.81862341730152	3.04504878555117
13	386	immune effector process
GO:0034109	1.14067743349607e-05	19.883236030025 0.299771642100893	5
38	homotypic cell-cell adhesion
GO:0043299	1.14067743349607e-05	19.883236030025 0.299771642100893	5
38	leukocyte degranulation
GO:0042119	1.29942252501971e-05	34.72	0.149885821050446	4	19
neutrophil activation
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GO:0051249      1.44271115055245e-05    5.52238006853227        2.23250986090928
11      283     regulation of lymphocyte activation
GO:0002696      1.53947515461982e-05    6.0857192135219 1.83807348972389        10
233     positive regulation of leukocyte activation
GO:0007229      1.55215477456752e-05    12.7912186379928        0.536433464812124
6       68      integrin-mediated signaling pathway
GO:0090330      1.63543084703709e-05    96.8445945945946        0.0552210919659539
3       7       regulation of platelet aggregation
Tissue: Nerve_Tibial=>Thyroid   Type:   asymmetric
SourceGene:     CTD-3074O7.7(ENSG00000254596.1)
TargetGeneSet:  CSDE1   INTS3   TOMM20  PDIA6   DTYMK   EIF1B   RP11    CNBP
UGDH-AS1        PAPSS1  LARP7   NUDT6   AMACR   APBB3   SH3RF2  NPM1    WTAP
PLEKHA8 CROT    TECPR1  LUC7L2  RP4     TRPV6   SGK3    EIF3H   ERP44   TUBB4B  TET1
EIF3M   PDHX    FKBP2   C11orf85        STT3A   PUS7L   PRR13   HSP90B1 NUS1P2
EIF4A1P7        ENTPD5  MOAP1   CKMT1A  PDIA3   PPIB    TMC3    EIF1    CLTC
RAB12   TMEM241 TLE6    FKBP8   RPN2    C20orf151       SDF2L1  CCDC134 ALG12
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006457      5.63442705220163e-10    20.8914386584289        0.64272368694208
10      216     protein folding
GO:0006487      7.45249247180947e-06    21.6591046581972        0.27375268147533
5       92      protein N-linked glycosylation
Tissue: Thyroid=>Nerve_Tibial   Type:   asymmetric
SourceGene:     CYP1B1(ENSG00000138061.7)
TargetGeneSet:  PHF13   RPS6KA1 ZC3H12A LYST-IT1        FOSL2   RP11    LOXL3
UNC50   BAZ2B   EBP     TRAM1L1 POC5    CD74    SLC36A2 RBM24   HLA-DRA HLA-DMA
HLA-DOA HLA-DPA1        HLA-DPB1        PPARD   VEGFA   GS1     ABHD11  ABHD11-AS2
CLDN12  IRF5    SYK     NR4A3   ARL5B   APBB1IP SWAP70  CAPN5   PTPN6   FAR2
CDK17   ARL11   DOCK9   RPGRIP1 CTD     PRSS27  CDRT4   TMEM101 RNFT1   PRR22
FAM125A GMIP    ZNF85   PVR     BRSK1   ZIK1    SNTA1   MAFB    CECR6   FBXW4P1
JOSD1   GPR34   PNMA6A  RENBP
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0002504      8.99884222033228e-11    122.599431818182        0.0761192997024427
6       22      antigen processing and presentation of peptide or polysaccharide
antigen via MHC class II
GO:0060333      9.20173883057114e-09    32.3976098191214        0.273337485295135
7       79      interferon-gamma-mediated signaling pathway
GO:0071346      3.12439656035624e-08    26.7837476610532        0.325237007819528
7       94      cellular response to interferon-gamma
GO:0034341      9.91663303037464e-08    22.3790250447227        0.384056466680507
7       111     response to interferon-gamma
GO:0050867      1.1458642519952e-07     13.4653151726322        0.830392360390284
9       240     positive regulation of cell activation
GO:0050870      1.14730045992857e-07    16.638036809816 0.591654556778078       8
171     positive regulation of T cell activation
GO:0031294      2.11424996885467e-07    28.3241106719368        0.259497612621964
6       75      lymphocyte costimulation
GO:0031295      2.11424996885467e-07    28.3241106719368        0.259497612621964
6       75      T cell costimulation
GO:0051251      6.61372722724634e-07    13.0609615827007        0.743893156182963
8       215     positive regulation of lymphocyte activation
GO:0019886      7.73840549732255e-07    306.340425531915        0.0207598090097571
3       6       antigen processing and presentation of exogenous peptide antigen via
MHC class II
GO:0050863      8.1445014274641e-07     12.6876816454281        0.76465296519272
8       221     regulation of T cell activation
GO:0002696      1.21311071480848e-06    12.0008465608466        0.806172583212234
8       233     positive regulation of leukocyte activation
GO:0002495      2.15619759798687e-06    183.778723404255        0.0276797453463428
3       8       antigen processing and presentation of peptide antigen via MHC class
II
GO:0050865      2.28697402150652e-06    9.24514385862422        1.18676908172445
9       343     regulation of cell activation
GO:0050778      3.72036959373266e-06    8.68526279628994        1.2594284132586 9
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364     positive regulation of immune response
GO:0050851      3.93543317118726e-06    16.6480186480186        0.425576084700021
6       123     antigen receptor-mediated signaling pathway
GO:0051249      5.15417293342853e-06    9.78424242424243        0.979170991626877
8       283     regulation of lymphocyte activation
GO:0002429      6.18604377546172e-06    15.3264137437366        0.460175766382949
6       133     immune response-activating cell surface receptor signaling pathway
GO:0002768      9.76847894324836e-06    14.0938735177866        0.498235416234171
6       144     immune response-regulating cell surface receptor signaling pathway
GO:0042110      1.23690374992472e-05    8.62961261675088        1.10372984568542
8       319     T cell activation
GO:0002694      1.29427009876945e-05    8.57325422181652        1.11064978202201
8       321     regulation of leukocyte activation
GO:0019882      1.33066251569055e-05    13.3141344956413        0.525915161580513
6       152     antigen processing and presentation
GO:0046649      1.50768866598216e-05    7.23613667740451        1.4981662168708 9
433     lymphocyte activation
GO:0002757      1.51476330399005e-05    10.1194410444716        0.81309251954882
7       235     immune response-activating signal transduction
Tissue: Nerve_Tibial=>Thyroid   Type:   asymmetric
SourceGene:     ENSG00000206651.1
TargetGeneSet:  CLSTN1  C1QA    C1QC    C1QB    CMPK1   CD53    CTSS    CD84
FCGR2A  FCGR2B  7SK     ARL4C   BTD     CCR5    RP11    CD200R1 CD86    UBA5
P2RY13  TM4SF19-AS1     CSF1R   HAVCR2  DOCK2   HOXA10  ERV3-1  NCF1C   TFEC
TRBV30  PIGO    TRIM14  SMC2    ALOX5   PSAP    CTSD    FOLR2   IL10RA  CD3E    M6PR
NCKAP1L LCP1    SUCLA2  RNASE6  NOMO2   SPN     CORO1A  SMCR8   VAV1    ACP5    CD37
LAIR1   CRLS1   PLTP    MX1     ITGB2   RAC2    CYBB    WAS
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0042110      1.05061286416583e-06    10.228064516129 1.08165524877171        9
319     T cell activation
GO:0045060      5.93078768896842e-06    117.342391304348        0.0372984568541969
3       11      negative thymic T cell selection
GO:0043383      7.8888501007261e-06     104.297101449275        0.0406892256591239
3       12      negative T cell selection
GO:0046649      1.26953278577271e-05    7.41757075471698        1.46820289253339
9       433     lymphocyte activation
Tissue: Thyroid=>Nerve_Tibial   Type:   asymmetric
SourceGene:     HIST1H2BI(ENSG00000168242.3)
TargetGeneSet:  RPL11   IL22RA1 PUM1    RP11    RPS27   CAMSAP2 UBC     MBNL1
RANBP3L RPL37   CTB     RPL10A  HEY2    RPL30   ASTN2   LCN2    RPS24   ACTR1A
KRTAP5-9        RPS25   COMMD6  U6      RPL7AP6 KDM6B   RPL26   RPL17   ZNF14
C19orf18        FOXRED2 SMC1A   CHIC1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      1.78325549682361e-16    118.065843621399        0.157428551657325
10      91      translational termination
GO:0006414      7.89882819762901e-16    100.568421052632        0.181648328835375
10      105     translational elongation
GO:0006614      7.89882819762901e-16    100.568421052632        0.181648328835375
10      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      8.7133434798242e-16     99.5138888888889        0.183378312919521
10      106     cotranslational protein targeting to membrane
GO:0045047      8.7133434798242e-16     99.5138888888889        0.183378312919521
10      106     protein targeting to ER
GO:0072599      8.7133434798242e-16     99.5138888888889        0.183378312919521
10      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      2.63560516523313e-15    88.3827160493827        0.204138121929278
10      118     protein localization to endoplasmic reticulum
GO:0000184      2.87467034349544e-15    87.565749235474 0.205868106013425       10
119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      3.28262315323143e-14    67.5413711583924        0.26122759670611
10      151     viral genome expression
GO:0019083      3.28262315323143e-14    67.5413711583924        0.26122759670611
10      151     viral transcription
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GO:0006413      3.51044963663819e-14    67.0610328638498        0.262957580790257
10      152     translational initiation
GO:0006612      3.75236081255074e-14    66.5874125874126        0.264687564874403
10      153     protein targeting to membrane
GO:0043624      3.75236081255074e-14    66.5874125874126        0.264687564874403
10      153     cellular protein complex disassembly
GO:0043241      5.20125158025491e-14    64.3153153153153        0.273337485295135
10      158     protein complex disassembly
GO:0000956      1.02855993134244e-13    59.8197064989518        0.292367310220746
10      169     nuclear-transcribed mRNA catabolic process
GO:0034623      1.38113512859077e-13    57.9756097560976        0.301017230641478
10      174     cellular macromolecular complex disassembly
GO:0006402      1.73742476558946e-13    56.5793650793651        0.307937166978064
10      178     mRNA catabolic process
GO:0032984      1.83847693355907e-13    56.2406311637081        0.30966715106221
10      179     macromolecular complex disassembly
GO:0072594      6.85030496520499e-13    48.9072164948454        0.352916753165871
10      204     establishment of protein localization to organelle
GO:0006401      7.19472842217583e-13    48.6529914529915        0.354646737250017
10      205     RNA catabolic process
GO:0019058      2.37606065091673e-12    42.8506787330317        0.399626323437824
10      231     viral infectious cycle
GO:0022415      7.71088005492001e-12    37.8026666666667        0.449795861878071
10      260     viral reproductive process
GO:0071845      1.849551847592e-11      34.4330900243309        0.491315479897585
10      284     cellular component disassembly at cellular level
GO:0022411      2.12382569663949e-11    33.9280575539568        0.498235416234171
10      288     cellular component disassembly
GO:0016032      1.70492184763235e-09    21.1413454270597        0.780222821950038
10      451     viral reproduction
GO:0033365      2.69983390067445e-09    20.1051115910727        0.818282471801259
10      473     protein localization to organelle
GO:0006605      2.75534740067316e-09    20.0603448275862        0.820012455885406
10      474     protein targeting
GO:0022613      1.84274587978072e-06    20.4859408795962        0.389246418932946
6       225     ribonucleoprotein complex biogenesis
GO:0071843      2.61556716958861e-06    19.2360515021459        0.413466196110996
6       239     cellular component biogenesis at cellular level
Tissue: Nerve_Tibial=>Thyroid   Type:   asymmetric
SourceGene:     IQCK(ENSG00000174628.12)
TargetGeneSet:  KDM1A   RPL11   PRPF38A SETDB1  WNT9A   RPL31   RPL32   GRK7
RPL35A  RPL34   EXOSC9  RPL37   RPS23   ZSCAN12 RPS18   RPS10   MEA1    RP11
PDCD2   AQP1    CTD     RPL30   ANKRD20A3       NDST2   FAM175B SAAL1   WDR74
TRMT112 FAU     RPS3    PA2G4   ZSCAN29 UBE2I   POLR2C  TRIM16  RPL17   RPL27
RPL38   RPL36   POLR2I  ZNF606  FKBP1A-SDCBP2   RPS21   ERVH48-1        TSPEAR
C22orf23        GPKOW
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      1.06484340271148e-27    137.225225225225        0.258182824718013
17      91      translational termination
GO:0019080      1.44397720200429e-27    93.4166666666667        0.428413258598021
19      151     viral genome expression
GO:0019083      1.44397720200429e-27    93.4166666666667        0.428413258598021
19      151     viral transcription
GO:0006414      1.4857246303972e-26     115.28125       0.297903259290015       17
105     translational elongation
GO:0006614      1.4857246303972e-26     115.28125       0.297903259290015       17
105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.76672101846751e-26    113.977996254682        0.300740433188015
17      106     cotranslational protein targeting to membrane
GO:0045047      1.76672101846751e-26    113.977996254682        0.300740433188015
17      106     protein targeting to ER
GO:0072599      1.76672101846751e-26    113.977996254682        0.300740433188015
17      106     establishment of protein localization to endoplasmic reticulum
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GO:0070972      1.24071833493747e-25    100.351897689769        0.334786519964016
17      118     protein localization to endoplasmic reticulum
GO:0000184      1.44521759105512e-25    99.3611111111111        0.337623693862016
17      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0000956      1.06403217343371e-24    73.9021019291679        0.479482388762023
18      169     nuclear-transcribed mRNA catabolic process
GO:0006402      2.80491330611982e-24    69.7010869565217        0.505016953844025
18      178     mRNA catabolic process
GO:0019058      6.30270425777528e-24    57.8391938250429        0.655387170438032
19      231     viral infectious cycle
GO:0006413      1.15304133202581e-23    74.8996913580247        0.431250432496021
17      152     translational initiation
GO:0006612      1.29511764163764e-23    74.34375        0.434087606394021       17
153     protein targeting to membrane
GO:0043624      1.29511764163764e-23    74.34375        0.434087606394021       17
153     cellular protein complex disassembly
GO:0043241      2.2879148116028e-23     71.682328605201 0.448273475884022       17
158     protein complex disassembly
GO:0006401      3.85853626245071e-23    59.5242966751918        0.581620649090028
18      205     RNA catabolic process
GO:0022415      6.23240340013473e-23    50.7753677857412        0.737665213480036
19      260     viral reproductive process
GO:0034623      1.25149674302523e-22    64.3049363057325        0.493668258252024
17      174     cellular macromolecular complex disassembly
GO:0032984      2.05714880735212e-22    62.298353909465 0.507854127742025       17
179     macromolecular complex disassembly
GO:0072594      2.01448505144395e-21    53.875  0.578783475192028       17      204
establishment of protein localization to organelle
GO:0016032      2.2914474365241e-21     34.1372093023256        1.27956542799806
21      451     viral reproduction
GO:0071845      5.98474503630991e-19    37.520443196005 0.805757387032039       17
284     cellular component disassembly at cellular level
GO:0022411      7.59513456674918e-19    36.9561808118081        0.81710608262404
17      288     cellular component disassembly
GO:0033365      3.14167204277754e-15    21.6756213450292        1.34198325375407
17      473     protein localization to organelle
GO:0006605      3.25327734533402e-15    21.6266411378556        1.34482042765207
17      474     protein targeting
GO:0022613      2.89559201436361e-06    13.4031300593632        0.638364127050031
7       225     ribonucleoprotein complex biogenesis
GO:0042254      3.62671779673266e-06    17.1032967032967        0.422738910802021
6       149     ribosome biogenesis
GO:0071843      4.31571459631471e-06    12.5818965517241        0.678084561622033
7       239     cellular component biogenesis at cellular level
GO:0006364      1.06890887301401e-05    20.0771604938272        0.295066085392014
5       104     rRNA processing
GO:0016072      1.40496412678571e-05    18.9219576719577        0.312089128780015
5       110     rRNA metabolic process
Tissue: Nerve_Tibial=>Thyroid   Type:   asymmetric
SourceGene:     KLF15(ENSG00000163884.3)
TargetGeneSet:  TNFRSF25        HP1BP3  TXLNA   GPBP1L1 TAL1    RP1     GDAP2
UBQLN4  CCT3    PTPRVP  URB2    SLC5A6  CCT4    PCBP1-AS1       AUP1    ART4
MRPS5   RBM43   HSPD1   HMGB1P3 CGGBP1  PVRL3-AS1       POGLUT1 KIAA0226
TNIP2   TMEM128 ARHGAP24        TRIM2   CCT5    DNAJC21 RP11    C6orf228
ZNF193  NUDT3   BRPF3   RPL7L1  LRRC73  STX1A   PINX1   POLR3D  CHMP7   TMEM68
CYHR1   DNAJA1  C9orf80 C9orf114        METTL11A        FAM69B  FBXO18  HNRNPF
P4HA1   TRIM68  UBQLNL  GVINP1  SLC35C1 C11orf84        STIP1   GPR137  C11orf30
EED     ATM     HSPA8   SLC6A12 FKBP4   RP4     C12orf33        REP15   CCT2
C12orf65        RAN     HSPH1   PCID2   TEP1    SOCS6   AHSA1   ZC3H14  HSP90AA1
HERC2P2 ZFYVE19 PPP1R14D        TP53BP1 CSK     C16orf57        NIP7    TMEM170A
MIR423  CTD     ZNF441  ZNF702P ZNF761  ZNF71   ZNF329  SNHG11  TOP1    TOMM34  CTA
RANGAP1 ZNF630
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
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GO:0006457      5.40303927786045e-10    14.1335992023928        1.06124143657878
12      216     protein folding
GO:0006458      1.71557085096681e-07    29.4051282051282        0.250570894747768
6       51      'de novo' protein folding
GO:0051084      2.90875758793648e-06    26.4948263118995        0.226005120752889
5       46      'de novo' posttranslational protein folding
Tissue: Thyroid=>Nerve_Tibial   Type:   asymmetric
SourceGene:     MAGI2(ENSG00000187391.12)
TargetGeneSet:  C1orf159        ZBTB8OS PPCS    ATP5F1  RP11    CFLAR   CAMP
PARP3   UBA3    ATP6V1A NDUFB5  NDUFC1  GUSBP5  PDCD6   UBLCP1  RP1     MRPS18B
SENP6   LSM5    MPLKIP  DUS4L   POT1    LACTB2  U1      C9orf133        NDUFB6
SURF1   C10orf125       MRPL23  IMMP1L  CSTF3   CUL5    C11orf1 ATP5L   CACNA2D4
IFFO1   MAP3K12 ERH     NDUFB1  COX5A   COMMD4  RHOT2   NDUFB10 LCMT1   TXNDC17 SNF8
SKA2    SPHK1   SNRPD1  UQCR11  C19orf70        LIG1    RN5S493 SLC2A11 RBM3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      8.04425735051335e-12    43.5730223123732        0.285654971974258
9       96      respiratory electron transport chain
GO:0045333      8.86289230077006e-12    32.77318640955  0.422531312711923       10
142     cellular respiration
GO:0022900      1.66916152454155e-10    30.2463529411765        0.398726731714068
9       134     electron transport chain
GO:0015980      1.66753391637132e-08    14.3975104581165        0.913500795792679
10      307     energy derivation by oxidation of organic compounds
GO:0006119      1.74184387725757e-08    44.7692307692308        0.172583212234447
6       58      oxidative phosphorylation
GO:0006120      6.45991136676516e-08    61.0229202037351        0.107120614490347
5       36      mitochondrial electron transport, NADH to ubiquinone
GO:0042773      2.56578666390117e-07    45.0062656641604        0.139851913362397
5       47      ATP synthesis coupled electron transport
GO:0042775      2.56578666390117e-07    45.0062656641604        0.139851913362397
5       47      mitochondrial ATP synthesis coupled electron transport
GO:0006091      3.7358954967509e-07     10.1420907641003        1.27354508338523
10      428     generation of precursor metabolites and energy
Tissue: Thyroid=>Nerve_Tibial   Type:   asymmetric
SourceGene:     RP11-1007G5.2(ENSG00000254588.1)
TargetGeneSet:  IL22RA1 KPNA7   RP11    ILF3    IMPDH2  ANKRD37 CTD     RPL37
RPL10A  RPL39P3 EEF1A1  MRPS12  FBXO43  RPS24   VWA5A   RPS29   RPL7AP6 RPS3AP6
ALKBH5  HILS1   RPS19   SNRPD2  RPL28   C19orf18        C21orf7 EEF1B2P3
RPS4Y1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      1.364216758407e-13      131.381443298969        0.123520863608055
8       105     translational elongation
GO:0006415      5.73667225715822e-12    119.583333333333        0.107051415126981
7       91      translational termination
GO:0006614      1.59949056608047e-11    102.4   0.123520863608055       7       105
SRP-dependent cotranslational protein targeting to membrane
GO:0006613      1.71154309927941e-11    101.358585858586        0.124697252785274
7       106     cotranslational protein targeting to membrane
GO:0045047      1.71154309927941e-11    101.358585858586        0.124697252785274
7       106     protein targeting to ER
GO:0072599      1.71154309927941e-11    101.358585858586        0.124697252785274
7       106     establishment of protein localization to endoplasmic reticulum
GO:0070972      3.67578705037832e-11    90.3252252252252        0.138813922911909
7       118     protein localization to endoplasmic reticulum
GO:0000184      3.90314413768745e-11    89.5125 0.139990312089129       7       119
nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      2.10735439400921e-10    69.4652777777778        0.177634765760155
7       151     viral genome expression
GO:0019083      2.10735439400921e-10    69.4652777777778        0.177634765760155
7       151     viral transcription
GO:0006413      2.20774045242664e-10    68.9813793103448        0.178811154937375
7       152     translational initiation
GO:0006612      2.31217887521436e-10    68.5041095890411        0.179987544114594
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7       153     protein targeting to membrane
GO:0043624      2.31217887521436e-10    68.5041095890411        0.179987544114594
7       153     cellular protein complex disassembly
GO:0043241      2.89998430384273e-10    66.212582781457 0.185869490000692       7
158     protein complex disassembly
GO:0000956      4.65526458386655e-10    61.6691358024691        0.198809770950107
7       169     nuclear-transcribed mRNA catabolic process
GO:0034623      5.71276192231528e-10    59.8017964071856        0.204691716836205
7       174     cellular macromolecular complex disassembly
GO:0006402      6.70019047479182e-10    58.3865497076023        0.209397273545083
7       178     mRNA catabolic process
GO:0032984      6.9686108506441e-10     58.043023255814 0.210573662722303       7
179     macromolecular complex disassembly
GO:0072594      1.73913476203622e-09    50.5883248730964        0.239983392152792
7       204     establishment of protein localization to organelle
GO:0006401      1.79951730198254e-09    50.3292929292929        0.241159781330012
7       205     RNA catabolic process
GO:0019058      4.13384965419902e-09    44.40625        0.271745899937721       7
231     viral infectious cycle
GO:0022415      9.38945783179033e-09    39.2359683794466        0.305861186077088
7       260     viral reproductive process
GO:0071845      1.72847995398527e-08    35.7758122743682        0.334094526330358
7       284     cellular component disassembly at cellular level
GO:0022411      1.90356726981663e-08    35.2565836298932        0.338800083039236
7       288     cellular component disassembly
GO:0033365      2.32883793308273e-08    26.7029868578256        0.556432080824856
8       473     protein localization to organelle
GO:0006605      2.3674714037337e-08     26.6437768240343        0.557608470002076
8       474     protein targeting
GO:0016032      4.0825539604407e-07     22.0563063063063        0.530551518926026
7       451     viral reproduction
Tissue: Thyroid=>Nerve_Tibial   Type:   asymmetric
SourceGene:     RP11-417O11.6(ENSG00000226458.1)
TargetGeneSet:  NADK    HP1BP3  RPL11   PPP1R8  XKR8    7SK     PPCS    UQCRH
BEND5   RP11    GTF2B   WARS2   S100A6  ACBD6   DHX9    SLC5A6  MRPL33  MORN2
PPM1B   PSME4   NONOP2  TMEM17  NFU1    DCTN1   CCDC115 U6      SETD5   UBE2E1
CCDC72  RPL24   FNDC3B  KCNMB3  RPL39L  SENP5   LETM1   NAA11   MRPS18C NDUFC1
HADHAP1 FRG1    RPL37   EEF1A1P19       CTD     UQCRQ   TMEM14C TMEM14B GABBR1  APOM
C6orf48 COX6A1P2        C6orf226        RPL39P3 LINC00222       MRPS12  SUMO4
PHF14   TOMM7   YAE1D1  MRPS24  GS1     MKLN1   C8orf40 C8orf59 RPL30   COX6C
POLR2K  C9orf46 MTAP    GBA2    FAM27D1 SEC61B  ATP5C1  CDNF    RPS24   C10orf116
AGAP11  IFIT2   IFIT3   ENTPD1  RPLP2   PRKCDBP RPL27A  LMO2    ALKBH3  CELF1
C11orf10        MTA2    FAU     NADSYN1 ATP5L   RPS25   C12orf57        KLRG1   FGD4
PFDN5   ALKBH2  C12orf51        RPS2P5  DOCK9   EAPP    RPS29   CGRRF1  LGALS3  ERH
RPL7AP6 NEK9    NDUFB1  RPL3P4  HERC2P3 RSL24D1 RPLP1   NDUFB10 DNASE1L2
ERVK13-1        SRRM2   TNFRSF17        USP31   NUDT21  C17orf67        STARD6
RAB27B  PIP5K1C RPL36   INSR    PIN1    ZNF208  COX6B1  RPS19   ETHE1   SNRPD2
ZNF845  PTPRA   LINC00493       RP3     IFT52   PFDN4   ATP5J   N6AMT1  KCNE1
PLA2G6  EEF1B2P3        PHF8    NDUFA1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006614      2.85187993110751e-14    23.8361204013378        0.770188914261989
14      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      3.2662520390078e-14     23.5753780718336        0.77752404677877
14      106     cotranslational protein targeting to membrane
GO:0045047      3.2662520390078e-14     23.5753780718336        0.77752404677877
14      106     protein targeting to ER
GO:0072599      3.2662520390078e-14     23.5753780718336        0.77752404677877
14      106     establishment of protein localization to endoplasmic reticulum
GO:0006415      9.97513105924338e-14    25.5681003584229        0.667497059027057
13      91      translational termination
GO:0070972      1.50034564504427e-13    20.8375836120401        0.86554563698014
14      118     protein localization to endoplasmic reticulum
GO:0006414      6.67721192852802e-13    21.65603085554  0.770188914261989       13
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105     translational elongation
GO:0000184      3.43323659244544e-12    18.7773382024751        0.872880769496921
13      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      4.65830556068635e-12    15.781656616947 1.10760501003391        14
151     viral genome expression
GO:0019083      4.65830556068635e-12    15.781656616947 1.10760501003391        14
151     viral transcription
GO:0006612      5.58034789813552e-12    15.552392868314 1.12227527506747        14
153     protein targeting to membrane
GO:0072594      2.20564378957146e-11    12.3460666317809        1.49636703342329
15      204     establishment of protein localization to organelle
GO:0006413      7.89217215308798e-11    14.2862226347954        1.11494014255069
13      152     translational initiation
GO:0043624      8.57319919396345e-11    14.1831797235023        1.12227527506747
13      153     cellular protein complex disassembly
GO:0022904      1.02303691109126e-10    19.425386996904 0.704172721610961       11
96      respiratory electron transport chain
GO:0043241      1.28533505959621e-10    13.689284390063 1.15895093765137        13
158     protein complex disassembly
GO:0006401      2.87805973677657e-10    11.2768040063738        1.50370216594007
14      205     RNA catabolic process
GO:0000956      2.98479905878361e-10    12.7141577060932        1.23963739533596
13      169     nuclear-transcribed mRNA catabolic process
GO:0034623      4.29033958791117e-10    12.3149669404929        1.27631305791987
13      174     cellular macromolecular complex disassembly
GO:0006402      5.68761026823276e-10    12.0130335614207        1.30565358798699
13      178     mRNA catabolic process
GO:0032984      6.09615116983799e-10    11.9398238113745        1.31298872050377
13      179     macromolecular complex disassembly
GO:0022415      6.73842771840518e-10    9.48643193541153        1.90713445436302
15      260     viral reproductive process
GO:0019058      1.38006469738166e-09    9.90743338008415        1.69441561137638
14      231     viral infectious cycle
GO:0022900      3.78745454984021e-09    13.3882755669662        0.982907757248633
11      134     electron transport chain
GO:0045333      6.99654227157378e-09    12.5635998392929        1.04158881738288
11      142     cellular respiration
GO:0016032      2.83744530199301e-08    6.12248226583131        3.30814476506816
17      451     viral reproduction
GO:0071845      1.54326233186212e-07    7.25953259532595        2.08317763476576
13      284     cellular component disassembly at cellular level
GO:0022411      1.81385744427727e-07    7.15190615835777        2.11251816483288
13      288     cellular component disassembly
GO:0033365      1.78833529976849e-06    4.99796055472911        3.46951768043734
15      473     protein localization to organelle
GO:0006605      1.83567570389682e-06    4.98671263377146        3.47685281295412
15      474     protein targeting
GO:0015980      2.52252795364082e-06    6.0800576992427 2.25188568265172        12
307     energy derivation by oxidation of organic compounds
GO:0006119      4.01204607330287e-06    16.4919230769231        0.425437685973289
6       58      oxidative phosphorylation
Tissue: Thyroid=>Nerve_Tibial   Type:   asymmetric
SourceGene:     RP11-757C15.3(ENSG00000254593.1)
TargetGeneSet:  CAPZB   KHDRBS1 PSMB2   SLFNL1  RP1     C1orf123        CCDC76
GDAP2   RP4     S100A6  PFN1P1  MORF4L1P1       PTRHD1  DDX50P1 PAPOLG  NFU1
UBE2E3  ING5    TOP2B   IQCF1   PSMD6   ST3GAL6-AS1     TTC14   MAGEF1  RAC1P2
RAPGEF2 RP11    TRIM27  KCTD20  COX6A1P2        C6orf226        YWHAZP4 NDUFA4
MALSU1  NPC1L1  PILRB   PSMC2   POLR3D  TOX     C8orf59 COX6C   MTAP    SKA2L
ATP5C1  IFIT3   IFIT1   TAF5    BNIP3   C11orf10        NADSYN1 SNORA25 SNORA32
TAF1D   ATP5L   OAF     DAZAP2  IRAK3   CKAP2   RHOJ    NEK9    NDUFB1  SRP14
PLA2G4B SENP8   NDUFB10 ZNF263  SMYD4   PSMB6   ZFP161  EPG5    ATP5A1  ZNF812
COX6B1  EID2    ZNF28   ZSCAN22 ROMO1   MRPL39  N6AMT1  KCNE1   CHAF1B  HMGB1P10
LGALS1  TCEAL8  NDUFA1
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GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      2.60977985895883e-10    27.9154196486662        0.411874610753581
9       96      respiratory electron transport chain
GO:0022900      5.17620117142398e-09    19.3775094339623        0.57490831084354
9       134     electron transport chain
GO:0045333      8.62946122562942e-09    18.2017307419492        0.609231195073005
9       142     cellular respiration
GO:0006119      4.74561742215685e-06    23.7272426348891        0.248840910663622
5       58      oxidative phosphorylation
GO:0015980      5.91764803658849e-06    8.02956819045207        1.31714068230572
9       307     energy derivation by oxidation of organic compounds
GO:0006120      1.6323489044894e-05     30.9418103448276        0.154452979032593
4       36      mitochondrial electron transport, NADH to ubiquinone
GO:0006200      1.69040885833644e-05    17.9436090225564        0.321777039651235
5       75      ATP catabolic process
Tissue: Thyroid=>Nerve_Tibial   Type:   asymmetric
SourceGene:     SEPSECS(ENSG00000109618.7)
TargetGeneSet:  CTNNBIP1        HP1BP3  ZDHHC18 PSMB2   EIF2C3  INPP5B  RP3     RP4
UQCRH   MOB3C   CPT2    LRRC40  PIGK    IFI44   ATP5F1  GDAP2   MRPS21  S100A6
S100A4  INTS3   CRABP2  B4GALT3 PIGC    RP11    ACBD6   DENND1B TIMM17A PTPN14
KIAA1383        LYST-IT1        FH      CPSF3   DDX1    TTC32   PUM2    FOSL2
DDX50P1 ATL2    ASS1P2  ETAA1   NFU1    CAPG    CNNM3   AMMECR1L        UBE2E3
KCTD18  CFLAR   IMPDH1P10       CASP8   LANCL1  SLC23A3 AGAP1-IT1       SETD5
ZNF385D EBP     CSRNP1  QARS    RHOA    RBM5    SPCS1   PDHB    PSMD6   ADAMTS9-AS2
UBA3    ARL6IP5 ATG3    ATP6V1A ZBTB20  KALRN   ARID4A  KPNA4   FAM131A MAGEF1
SENP5   RELL1   ANKRD17 DNAJB14 PPA2    ANXA5   NUDT6   INTU    OTUD4   NDUFS6  CTD
TXNDC15 SOX9    NDFIP1  PRRC2A  APOM    HNRNPC  DEFA6   FANCE   C6orf226
GTPBP2  MAD2L1BP        VEGFA   GCM1    HACE1   LINC00222       ZNF259P1
FAM54A  NUDT1   YAE1D1  URGCP   HUS1    GS1     ZKSCAN1 GPC2    PSMC2   ST7-AS1
NDUFA5  OPN1SW  GSTK1   CASP2   POLR3D  TNFRSF10A       LOXL2   RNF122  KAT6A
C8orf40 HOOK3   LACTB2  RPS20P21        C8orf59 DECR1   COX6C   NDUFB9  KIAA0196
RP13    HSF1    CD274   LINC00032       HRCT1   C9orf40 LINC00475       STXBP1
ZDHHC12 C9orf169        ATP5C1  CDC123  C10orf102       MARVELD1        PPRC1
DMBT1   NUP98   SMPD1   COMMD9  ALKBH3  NDUFS3  MRPL16  FEN1    C11orf84        RCE1
SNORA32 SNORA8  SNORA18 ATP5L   TBCEL   HIN1L   NDUFA9  PTPN6   SCAF11  H1FNT
FMNL3   ITGA5   ATXN2   RFC5    MPHOSPH8        SACS    RFC3    TUBGCP3 PARP2
LGALS3  CHMP4BP1        MAX     NEK9    ANGEL1  NDUFB1  TMEM85  TMEM62  NARG2   PKM2
LOXL1   COX5A   IMP3    SCAPER  PSMA4   NPRL3   NDUFB10 HCFC1R1 CTA     DCUN1D3
USP31   C16orf54        PYCARD  LPCAT2  NAE1    RANBP10 ZNF821  C16orf46
MIR4720 ZNF469  CYBA    NDEL1   C17orf75        SMARCE1 HEXIM1  HILS1   RNF43   SKA2
DNAH17  USP36   C17orf90        MYADML2 MYL12B  ZFP161  ATP5A1  DYM     ELAC1
TICAM1  C19orf70        HSD11B1L        MAN2B1  NDUFB7  ZNF506  UQCRFS1 COX6B1
WDR62   EID2    KCNN4   ZNF404  PVR     CACNG8  ZIK1    ZSCAN22 ZNF446  PCNA
RALGAPA2        CBFA2T2 MYH7B   ERGIC3  ROMO1   SNHG11  IFT52   GDAP1L1 KRT18P4
SLCO4A1 RPL10P1 MORC3   MRPL40  CRYBB1  MAFF    JOSD1   PRDX3P1 SERHL   CA5BP1
ATP6AP2 ZNF630  PHF8    RP6     CXorf65 CSTF2   TCEAL8  MID2    C1GALT1C1       SSR4
ARHGAP4 VAMP7
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0045333      5.95369350768205e-15    12.9407454895137        1.95543560999239
20      142     cellular respiration
GO:0022904      1.39047326264504e-14    16.7576158019196        1.32198463774133
17      96      respiratory electron transport chain
GO:0022900      3.3191026465857e-13     12.118879786626 1.84527022351394        18
134     electron transport chain
GO:0015980      2.52703603108403e-10    6.09126771731589        4.2275967061103 22
307     energy derivation by oxidation of organic compounds
GO:0006091      5.22707937323311e-09    4.70087694483734        5.89384817659678
24      428     generation of precursor metabolites and energy
GO:0006119      5.74537505179864e-09    15.6569664902998        0.798699051968722
10      58      oxidative phosphorylation
GO:0042773      1.28826821569728e-08    17.7182825484765        0.647221645560861
9       47      ATP synthesis coupled electron transport
GO:0042775      1.28826821569728e-08    17.7182825484765        0.647221645560861
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9       47      mitochondrial ATP synthesis coupled electron transport
GO:0006120      2.44259415397913e-08    21.2774869109948        0.495744239153  8
36      mitochondrial electron transport, NADH to ubiquinone
Tissue: Nerve_Tibial=>Thyroid   Type:   asymmetric
SourceGene:     TRMT2A(ENSG00000099899.9)
TargetGeneSet:  PARK7   MYOM3   ZNF642  TDPX2   AKR1A1  MKNK1   PSRC1   VPS45
TARS2   PSMD4   CHTOP   RUSC1-AS1       CCT3    CCL15   DARS2   NEK7    ATF3
C1orf131        FH      C2orf43 SLC4A1AP        PCBP1-AS1       CCDC142 C2orf68
TMEM177 PSMD14  PMS1    WDR12   ATIC    BCS1L   TTLL4   SLC16A14        PSMD1
DTYMK   MLH1    RUVBL1  ASTE1   CEP63   EIF2B5  ALG3    SLC10A7 MARCH1  BRIP1
NDUFS6  SKP2    GTF2H2C PTCD2   HARS2   RP11    SLC36A1 TTC1    RPL26L1 PRR7
ACOT13  ZKSCAN3 ZNRD1-AS1       VPS52   MNF1    ABCC10  AARS2   MCM3    RP13    PREP
RTN4IP1 ANKRD61 COPS6   SLC12A9 CTA     KLHDC10 CDK5    COPS5   NUDT2   EXOSC3
FAM108B1        FKBP15  PSMB7   TRUB2   SLC2A6  ASAH2B  DNAJC12 SIRT1   SLC25A16
MRPS16  EXOSC1  ENTPD7  COX15   PDE3B   TRMT112 HMBS    APPL2   NDUFA9  COPS7A  USP5
PRKAG1  ATF7    STAT2   NUP37   ANAPC5  BRD7P5  PSMB5   PSMA3   ANGEL1  ZNF280D MPI
KIAA1024        DET1    TCEB2   ZNF174  ARL6IP1 CDC37P1 EXOC3L1 TUBB3   WRAP53
USP32P3 TMEM199 ALDOC   TEFM    PSMB3   ATP5G1  SNF8    INTS2   C17orf80        FDXR
ANAPC11 SMCHD1  ZNF397  HAUS1   PALM    YIF1B   EID2B   ZNF780A EXOSC5  ZNF225
ZNF135  TRIB3   C20orf203       ZNF341  RBL1    APP     MIS18A-AS1      ZNF70
ZMAT5   ATF4    ZNF81   NAA10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0051443      6.97727338314707e-10    19.42674291939  0.635526953152031       10
82      positive regulation of ubiquitin-protein ligase activity
GO:0031145      7.88209797771786e-10    19.1592801504163        0.643277281849007
10      83      anaphase-promoting complex-dependent proteasomal ubiquitin-dependent
protein catabolic process
GO:0051351      1.12547124189759e-09    18.3991228070175        0.666528267939935
10      86      positive regulation of ligase activity
GO:0051436      2.140548360725e-09      21.5147304988283        0.519272022697391
9       67      negative regulation of ubiquitin-protein ligase activity involved in
mitotic cell cycle
GO:0031397      2.2049634277003e-09     17.0456719273075        0.713030240121791
10      92      negative regulation of protein ubiquitination
GO:0051438      3.36151528468684e-09    16.2482900136799        0.744031554909695
10      96      regulation of ubiquitin-protein ligase activity
GO:0051352      4.12598286118423e-09    19.8002773925104        0.558023666182271
9       72      negative regulation of ligase activity
GO:0051437      4.12598286118423e-09    19.8002773925104        0.558023666182271
9       72      positive regulation of ubiquitin-protein ligase activity involved in
mitotic cell cycle
GO:0051444      4.12598286118423e-09    19.8002773925104        0.558023666182271
9       72      negative regulation of ubiquitin-protein ligase activity
GO:0051340      5.02731708972011e-09    15.5217864923747        0.775032869697599
10      100     regulation of ligase activity
GO:0051439      8.5054595135404e-09     18.0709159983115        0.604525638364127
9       78      regulation of ubiquitin-protein ligase activity involved in mitotic
cell cycle
GO:0000209      4.64095777366706e-08    10.3022442244224        1.24780292021313
11      161     protein polyubiquitination
GO:0031398      5.10327031114352e-08    11.917211328976 0.98429174451595        10
127     positive regulation of protein ubiquitination
GO:0031396      7.19090893205085e-08    9.83805259506842        1.30205522109197
11      168     regulation of protein ubiquitination
GO:0043161      7.59228779160501e-08    8.61441624365482        1.61981869766798
12      209     proteasomal ubiquitin-dependent protein catabolic process
GO:0010498      1.08915664639264e-07    8.31470588235294        1.67407099854681
12      216     proteasomal protein catabolic process
GO:0042770      1.2873709888606e-07     10.7156862745098        1.08504601757664
10      140     signal transduction in response to DNA damage
GO:0000216      1.67078785870657e-07    15.4582881906826        0.612275967061103
8       79      M/G1 transition of mitotic cell cycle
GO:0006521      2.67078153697813e-07    19.052  0.441768735727631       7       57
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regulation of cellular amino acid metabolic process
GO:0010565      3.14558599833867e-07    9.66435185185185        1.1935506193343 10
154     regulation of cellular ketone metabolic process
GO:0007346      6.2001778638116e-07     6.36144200626959        2.34834959518372
13      303     regulation of mitotic cell cycle
GO:0006977      7.42913194607956e-07    16.135593220339 0.511521694000415       7
66      DNA damage response, signal transduction by p53 class mediator resulting in
cell cycle arrest
GO:0072413      7.42913194607956e-07    16.135593220339 0.511521694000415       7
66      signal transduction involved in mitotic cell cycle checkpoint
GO:0072431      7.42913194607956e-07    16.135593220339 0.511521694000415       7
66      signal transduction involved in mitotic cell cycle G1/S transition DNA
damage checkpoint
GO:0072474      7.42913194607956e-07    16.135593220339 0.511521694000415       7
66      signal transduction involved in mitotic cell cycle G1/S checkpoint
GO:0072401      8.24323360175333e-07    15.8655555555556        0.519272022697391
7       67      signal transduction involved in DNA integrity checkpoint
GO:0072404      8.24323360175333e-07    15.8655555555556        0.519272022697391
7       67      signal transduction involved in G1/S transition checkpoint
GO:0072422      8.24323360175333e-07    15.8655555555556        0.519272022697391
7       67      signal transduction involved in DNA damage checkpoint
GO:0072395      9.13088353527624e-07    15.6043715846995        0.527022351394367
7       68      signal transduction involved in cell cycle checkpoint
GO:0071156      9.40758134296031e-07    6.70809523809524        2.04608677600166
12      264     regulation of cell cycle arrest
GO:0000084      9.48851097160211e-07    9.936   1.03854404539478        9       134
S phase of mitotic cell cycle
GO:0007093      1.29061935829855e-06    9.5504854368932 1.07729568887966        9
139     mitotic cell cycle checkpoint
GO:0033238      1.35260516890109e-06    14.64   0.558023666182271       7       72
regulation of cellular amine metabolic process
GO:0031571      1.48657480361926e-06    14.4171717171717        0.565773994879247
7       73      mitotic cell cycle G1/S transition DNA damage checkpoint
GO:0051320      1.63603628759187e-06    9.26278800173888        1.10829700366757
9       143     S phase
GO:0002479      1.78801043514461e-06    13.9911764705882        0.581274652273199
7       75      antigen processing and presentation of exogenous peptide antigen via
MHC class I, TAP-dependent
GO:0048002      1.87208952342203e-06    10.9530769230769        0.837035499273407
8       108     antigen processing and presentation of peptide antigen
GO:0042590      2.54570325230481e-06    13.2101851851852        0.612275967061103
7       79      antigen processing and presentation of exogenous peptide antigen via
MHC class I
GO:0000075      2.74253804769764e-06    6.65157944365865        1.87557954466819
11      242     cell cycle checkpoint
GO:0071158      2.7721241533322e-06     13.0283105022831        0.620026295758079
7       80      positive regulation of cell cycle arrest
GO:0031575      3.27562767974461e-06    12.6791111111111        0.635526953152031
7       82      mitotic cell cycle G1/S transition checkpoint
GO:0030330      3.42337532673402e-06    10.0423429781228        0.906788457546191
8       117     DNA damage response, signal transduction by p53 class mediator
GO:0002478      3.55465313198523e-06    12.5114035087719        0.643277281849007
7       83      antigen processing and presentation of exogenous peptide antigen
GO:0031400      3.56660021202779e-06    5.85458333333333        2.3250986090928 12
300     negative regulation of protein modification process
GO:0019884      4.17240953611961e-06    12.1888888888889        0.658777939242959
7       85      antigen processing and presentation of exogenous antigen
GO:0000959      4.36971911079224e-06    48.2424242424242        0.11625493045464
4       15      mitochondrial RNA metabolic process
GO:0070127      4.48128249109726e-06    197.298165137615        0.0387516434848799
3       5       tRNA aminoacylation for mitochondrial protein translation
GO:0071779      4.51332815998386e-06    12.0337552742616        0.666528267939935
7       86      G1/S transition checkpoint
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GO:0072331      4.97523235956747e-06    9.51438127090301        0.953290429728046
8       123     signal transduction by p53 class mediator
GO:0007050      5.50619454687212e-06    5.15772897514471        2.85987128918414
13      369     cell cycle arrest
GO:0032269      7.14397009421443e-06    5.02731423827314        2.92962424745692
13      378     negative regulation of cellular protein metabolic process
GO:0051329      7.35017499124349e-06    5.01321962797373        2.9373745761539 13
379     interphase of mitotic cell cycle
GO:0000077      7.50237979458588e-06    8.9640605296343 1.00754273060688        8
130     DNA damage checkpoint
GO:0051325      9.19849866292754e-06    4.90317614649165        2.99937720572971
13      387     interphase
GO:0031570      1.04609790727953e-05    8.54026442307692        1.05404470278873
8       136     DNA integrity checkpoint
GO:0002474      1.15129659673872e-05    10.3239130434783        0.767282541000623
7       99      antigen processing and presentation of peptide antigen via MHC class
I
GO:2000045      1.15129659673872e-05    10.3239130434783        0.767282541000623
7       99      regulation of G1/S transition of mitotic cell cycle
GO:0034660      1.30103427658037e-05    5.59062658090627        2.20884367863816
11      285     ncRNA metabolic process
GO:0000082      1.40440791450296e-05    6.99127859141023        1.44156113763753
9       186     G1/S transition of mitotic cell cycle
GO:0010564      1.88225320034168e-05    4.56419557167687        3.20863608054806
13      414     regulation of cell cycle process
Tissue: Nerve_Tibial=>Thyroid   Type:   asymmetric
SourceGene:     VNN2(ENSG00000112303.9)
TargetGeneSet:  C1QC    C1QB    RP1     CHI3L2  SLAMF8  FCER1G  FCGR2A  FCGR3A
FCGR2B  GALNT14 POLQ    P2RY13  PDE6B   CFI     NDNF    CD180   LY86    LST1    AIF1
HLA-DRA HLA-DOA SNX10   TFEC    TBXAS1  SPI1    MS4A6A  MS4A7   CTSC    RAD51AP1
C3AR1   RP11    SLC26A10        BATF    SAMD15  CD209   KANK2   ASF1B   TYROBP
CYP2S1  CXCL17  SIGLEC10        CTD     SIGLEC5 LAIR1   MIR1302-5       RGS19
ITGB2   GPR34   BTK
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0002460      5.66274072390625e-07    17.3561476837339        0.501003390768805
7       181     adaptive immune response based on somatic recombination of immune
receptors built from immunoglobulin superfamily domains
GO:0002250      1.03635928815936e-06    15.7924797715374        0.548058957857588
7       198     adaptive immune response
GO:0002253      1.32280493150263e-06    12.1305841924399        0.82762438585565
8       299     activation of immune response
GO:0050778      5.70180234759249e-06    9.87008426966292        1.00754273060688
8       364     positive regulation of immune response
GO:0002449      6.03478962875416e-06    15.6192911947388        0.462251747283925
6       167     lymphocyte mediated immunity
GO:0019724      1.47667513385958e-05    18.7444298820446        0.315549096948308
5       114     B cell mediated immunity
Tissue: Nerve_Tibial=>Thyroid   Type:   asymmetric
SourceGene:     ZNF214(ENSG00000149050.5)
TargetGeneSet:  NECAP2  RP4     HP1BP3  CEP85   HDAC1   SLFNL1  HHLA3   HSD3BP5
INTS3   RP11    TDRD10  RUSC1-AS1       UBQLN4  CCT3    NEK7    KLHL12  RN5S78
PDIA6   C2orf43 SLC5A6  CAD     TRMT61B THADA   MSH2    PCBP1-AS1       CCT7
HTRA2   SEMA4F  C2orf68 POLR1B  TMEM177 ATIC    BCS1L   TTLL4   DTYMK   TRANK1
LARS2   USP4    CBX5P1  CCDC14  PLXNA1  ATP2C1  ABCC5   ALG3    TBCCD1  LRCH3
ZNF141  TBC1D19 UGDH-AS1        TBCK    CPE     LPCAT1  CCT5    PAPD4   ZCCHC9
PCDHGC4 CTB     RPL26L1 RPP40   ZSCAN23 C6orf25 AARS2   MCM3    MTO1    C6orf162
RP3     MRPL18  COL28A1 MIOS    C7orf42 SGCE    ZKSCAN1 SLC12A9 PLOD3   SMO
TAS2R5  POLR3D  CHMP7   TTI2    C8orf40 LRRC6   JRK     ZNF623  EXOSC4  SNAPC3
FAM205A VCP     C9orf103        BICD2   TRIM32  TRAF1   TUBB4B  ZNF239  ERCC6
AP3M1   EXOSC1  MORN4   ENTPD7  CYP2E1  POLR2L  RP13    TCP11L1 TTC9C   STIP1
GPR137  RBM14   RBM4B   C2CD3   POLD3   ALG8    EED     ATM     DPAGT1  TMEM218
RAD52   DCP1B   FKBP4   NCAPD2  KIAA1467        REP15   PAN2    STAT2   TIMELESS
NUP37   ALDH2   DYNLL1  RAN     ST6GALNAC4P1    ZMYM2   ITM2B   PCID2   TTC5    DAD1
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PSMB5   AHSA1   ZFYVE19 RPAP1   TP53BP1 UBFD1   ZNF48   RPGRIP1L        ZNF319
C16orf57        C16orf70        TMEM170A        SDR42E1 GALNS   CTNS    KRBA2
C17orf51        SDF2    NUFIP2  CRLF3   TEFM    PIP4K2B TMEM101 GNG8    HEATR6
POLG2   HN1     ZNF397  ZADH2   MAST3   ZNF790  YIF1B   SMG9    FUT2    ZNF841
ZNF808  ZNF137P ZNF17   ZNF132  VN1R108P        ZNF341  NFATC2  APP     SON
TOP3B   IGLV1-50        ZNF70   ZBED4   ALG12   GEMIN8  ZNF81   RPS7P14 TTC3P1
PNMA6C
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
Tissue: Skin_Sun_Exposed_Lower_leg=>Thyroid     Type:   asymmetric
SourceGene:     ANKRD13B(ENSG00000198720.7)
TargetGeneSet:  YTHDF2  KCND3   MAN1A2  GJA5    RP11    MNDA    DARC    FCER1G
FCGR3A  CR1     PLEK    STT3B   MYD88   CCRL1   PROS1   PLCXD2-AS1      TLR1
MOCS2   PCDHGA6 F13A1   LY86    LST1    AIF1    CFB     DDO     GPR146  MSR1    LY96
GBGT1   FCN1    NCOA4   SPI1    CLNS1A  CASP4   IQSEC3  ATP5G2  LCP1    U6
MRPL46  PABPN1L GAS8    CD68    VPS25   ABCA7   GNA15   TNFSF14 C3      C19orf38
LRRC25  TYROBP  SIGLEC7 LAIR1   HCK     SPATA25 RUNX1   ITGB2   PKDREJ  TLR8    CYBB
INE1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006954      5.5734770359018e-10     11.4728618421053        1.66244550550135
14      462     inflammatory response
GO:0002252      7.12235579674237e-10    12.5344057193923        1.38896962147948
13      386     immune effector process
GO:0050778      4.5365958326799e-09     11.971875       1.30980554978894        12
364     positive regulation of immune response
GO:0002253      7.03563355743526e-09    13.1454098915989        1.07591170161235
11      299     activation of immune response
GO:0031347      1.495622186636e-07      9.5866724738676 1.4501418586949 11      403
regulation of defense response
GO:0030449      3.42675928321822e-07    92.2179487179487        0.0611722372154176
4       17      regulation of complement activation
GO:2000257      3.42675928321822e-07    92.2179487179487        0.0611722372154176
4       17      regulation of protein activation cascade
GO:0006909      6.08708689018233e-07    23.3461956521739        0.309459552972113
6       86      phagocytosis
GO:0071219      8.51283009204456e-07    21.9652173913043        0.327451387447236
6       91      cellular response to molecule of bacterial origin
GO:0031349      8.72426768161208e-07    12.5269196822595        0.770050515535257
8       214     positive regulation of defense response
GO:0002673      1.02676702691067e-06    33.1938020351526        0.183516711646253
5       51      regulation of acute inflammatory response
GO:0071216      1.66876279571164e-06    19.4334239130435        0.367033423292506
6       102     cellular response to biotic stimulus
GO:0050727      2.8628699268569e-06     13.1768518518519        0.629714206629299
7       175     regulation of inflammatory response
GO:0001774      3.63567199059503e-06    146.867346938776        0.0323853020552211
3       9       microglial cell activation
GO:0002920      3.81175880456876e-06    46.0673076923077        0.107951006850737
4       30      regulation of humoral immune response
GO:0007229      4.35105782734731e-06    24.2080378250591        0.24468894886167
5       68      integrin-mediated signaling pathway
GO:0032101      4.56601747025234e-06    8.42606783501033        1.28821534841879
9       358     regulation of response to external stimulus
GO:0006959      4.7428214144455e-06     16.0603448275862        0.439000761192997
6       122     humoral immune response
GO:0070613      5.64636154537336e-06    41.2931034482759        0.118746107535811
4       33      regulation of protein processing
GO:0002281      7.10524156150625e-06    110.135204081633        0.0395820358452702
3       11      macrophage activation involved in immune response
GO:0031663      8.06349374928719e-06    37.4140625      0.129541208220884       4
36      lipopolysaccharide-mediated signaling pathway
GO:0042116      1.00509720627651e-05    35.2083333333333        0.136737942010934
4       38      macrophage activation
GO:0045088      1.10908638510616e-05    10.6129273504274        0.773648882430282
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7       215     regulation of innate immune response
GO:0071222      1.38442755006828e-05    18.8048332019963        0.309459552972113
5       86      cellular response to lipopolysaccharide
GO:0006957      1.55554109967332e-05    80.0816326530612        0.0503771365303439
3       14      complement activation, alternative pathway
GO:0002757      1.9736253071039e-05     9.66832358674464        0.845616220330773
7       235     immune response-activating signal transduction
GO:0045089      2.01351993913003e-05    12.3075151166139        0.564943602518857
6       157     positive regulation of innate immune response
GO:0002275      2.1752826216248e-05     28.4861111111111        0.16552487717113
4       46      myeloid cell activation involved in immune response
GO:0002764      2.78970365820371e-05    9.13840479483633        0.892394989966092
7       248     immune response-regulating signaling pathway
GO:0002526      3.64588615020768e-05    15.2117021276596        0.377828523977579
5       105     acute inflammatory response
GO:0001794      3.80124591832027e-05    575.92  0.0107951006850737      2       3
type IIa hypersensitivity
GO:0001796      3.80124591832027e-05    575.92  0.0107951006850737      2       3
regulation of type IIa hypersensitivity
GO:0001798      3.80124591832027e-05    575.92  0.0107951006850737      2       3
positive regulation of type IIa hypersensitivity
GO:0002445      3.80124591832027e-05    575.92  0.0107951006850737      2       3
type II hypersensitivity
GO:0002888      3.80124591832027e-05    575.92  0.0107951006850737      2       3
positive regulation of myeloid leukocyte mediated immunity
GO:0002892      3.80124591832027e-05    575.92  0.0107951006850737      2       3
regulation of type II hypersensitivity
GO:0002894      3.80124591832027e-05    575.92  0.0107951006850737      2       3
positive regulation of type II hypersensitivity
GO:0002274      3.9922535995047e-05     14.9113475177305        0.385025257767629
5       107     myeloid leukocyte activation
GO:0016064      4.76115698302669e-05    14.3446407065436        0.399418725347727
5       111     immunoglobulin mediated immune response
GO:0019724      5.4094204510524e-05     13.9469061097013        0.4102138260328 5
114     B cell mediated immunity
GO:0006968      6.26313193173497e-05    21.34375        0.215902013701474       4
60      cellular defense response
GO:0006956      7.59000707383041e-05    20.2542372881356        0.226697114386548
4       63      complement activation
GO:0002263      7.77010228724405e-05    12.8750450775334        0.442599128088022
5       123     cell activation involved in immune response
GO:0002366      7.77010228724405e-05    12.8750450775334        0.442599128088022
5       123     leukocyte activation involved in immune response
GO:0002697      8.03121432507186e-05    9.5010033444816 0.723271745899938       6
201     regulation of immune effector process
GO:0002758      9.3860821222551e-05     12.3473447500432        0.460590962563144
5       128     innate immune response-activating signal transduction
GO:0002218      0.000101002938279896    12.148085106383 0.467787696353194       5
130     activation of innate immune response
GO:0032640      0.000108416217172059    18.3769230769231        0.248287315756695
4       69      tumor necrosis factor production
GO:0032680      0.000108416217172059    18.3769230769231        0.248287315756695
4       69      regulation of tumor necrosis factor production
GO:0002282      0.000126124456521837    191.946666666667        0.0179918344751228
2       5       microglial cell activation involved in immune response
GO:0002237      0.000131959095993139    8.64587566030069        0.791640716905404
6       220     response to molecule of bacterial origin
GO:0071706      0.000135058853366826    17.3067632850242        0.262680783336793
4       73      tumor necrosis factor superfamily cytokine production
GO:0002885      0.000188750548594402    143.95  0.0215902013701474      2       6
positive regulation of hypersensitivity
GO:0002889      0.000202487136379226    30.3377902885292        0.115147740640786
3       32      regulation of immunoglobulin mediated immune response
```

GO:0009617	0.000209391343195116	6.53054726368159	1.2306414780984	7	342	response to bacterium
GO:0072376	0.000211917767969644	15.3002136752137	0.295066085392014	4	82	protein activation cascade
GO:0050900	0.000216623847505622	7.86160962072155	0.86720642170092	6	241	leukocyte migration
GO:0006897	0.000220888078517393	6.47120315581854	1.24143657878348	7	345	endocytosis
GO:0002576	0.000222058612382156	15.1054852320675	0.298664452287039	4	83	platelet degranulation
GO:0002712	0.000222171213862611	29.3244897959184	0.118746107535811	3	33	regulation of B cell mediated immunity
GO:0002866	0.000263641729934762	115.152	0.025188568265172	2	7	positive regulation of acute inflammatory response to antigenic stimulus
GO:0002449	0.00032529170250609	9.34922511163646	0.600927271469103	5	167	lymphocyte mediated immunity
GO:0006887	0.000332520106185679	7.23478260869565	0.939173759601412	6	261	exocytosis
GO:0050764	0.000339187854369615	25.1265306122449	0.136737942010934	3	38	regulation of phagocytosis
GO:0002524	0.000350712320370144	95.9533333333333	0.0287869351601965	2	8	hypersensitivity
GO:0002883	0.000350712320370144	95.9533333333333	0.0287869351601965	2	8	regulation of hypersensitivity
GO:0032490	0.000350712320370144	95.9533333333333	0.0287869351601965	2	8	detection of molecule of bacterial origin
GO:0002460	0.00047064011604471	8.59707446808511	0.651304407999446	5	181	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains
GO:0002863	0.0005610511925052	71.955	0.0359836689502457	2	10	positive regulation of inflammatory response to antigenic stimulus
GO:0002864	0.0005610511925052	71.955	0.0359836689502457	2	10	regulation of acute inflammatory response to antigenic stimulus
GO:0016485	0.000564831236692845	11.6805555555556	0.381426890872604	4	106	protein processing
GO:0002224	0.000672007986874714	11.1308411214953	0.399418725347727	4	111	toll-like receptor signaling pathway
GO:0030595	0.000672007986874714	11.1308411214953	0.399418725347727	4	111	leukocyte chemotaxis
GO:0002283	0.000684150292714912	63.9555555555556	0.0395820358452702	2	11	neutrophil activation involved in immune response
GO:0002438	0.000684150292714912	63.9555555555556	0.0395820358452702	2	11	acute inflammatory response to antigenic stimulus
GO:0002250	0.000707554587946299	7.83044868261493	0.712476645214864	5	198	adaptive immune response
GO:0051604	0.000818774151314756	10.5353982300885	0.421008926717874	4	117	protein maturation
GO:0045351	0.000819090435181635	57.556	0.0431804027402948	2	12	type I interferon biosynthetic process
GO:0071260	0.000857603344496901	17.930029154519	0.187115078541277	3	52	cellular response to mechanical stimulus
GO:0032496	0.000883257672061884	7.43947175348496	0.74846031416511	5	208	response to lipopolysaccharide
GO:0002443	0.000941813331973893	7.32958066515183	0.759255414850183	5	211	leukocyte mediated immunity
GO:0002714	0.000965788107013885	52.32	0.0467787696353194	2	13	positive regulation of B cell mediated immunity
GO:0002891	0.000965788107013885	52.32	0.0467787696353194	2	13	positive regulation of immunoglobulin mediated immune response
GO:0002221	0.00101707625361233	9.91597222222222	0.446197494983046	4	124	pattern recognition receptor signaling pathway
GO:0030168	0.00106755609284447	7.11912886391008	0.780845616220331	5	217	platelet activation

GO:0042108	0.00123937544339854	15.6811224489796	0.212303646806449	3	59	positive regulation of cytokine biosynthetic process
GO:0006911	0.00129412412379021	44.2646153846154	0.0539755034253685	2	15	phagocytosis, engulfment
GO:0050865	0.00138844014391652	5.44265256095988	1.23423984499343	6	343	regulation of cell activation
GO:0060326	0.00143200011832707	9.00694444444444	0.489377897723341	4	136	cell chemotaxis
GO:0030193	0.00149870439702866	14.6316326530612	0.226697114386548	3	63	regulation of blood coagulation
GO:0032675	0.00149870439702866	14.6316326530612	0.226697114386548	3	63	regulation of interleukin-6 production
GO:1900046	0.00149870439702866	14.6316326530612	0.226697114386548	3	63	regulation of hemostasis
GO:0042742	0.00163539136201152	8.67518248175183	0.507369732198464	4	141	defense response to bacterium
GO:0032635	0.00164018012153783	14.1576695194207	0.233893848176597	3	65	interleukin-6 production
GO:0050867	0.00166773326873936	6.41195110909914	0.863608054805896	5	240	positive regulation of cell activation
GO:0010324	0.00166849875966769	38.3573333333333	0.0611722372154176	2	17	membrane invagination
GO:0001817	0.00175072619479345	5.19004803547235	1.29181371531382	6	359	regulation of cytokine production
GO:0050818	0.00186763486545887	13.5014128728414	0.24468894886167	3	68	regulation of coagulation
GO:0002861	0.00187274628793963	35.9575	0.0647706041104422	2	18	regulation of inflammatory response to antigenic stimulus
GO:0051017	0.00194759934947191	13.2959183673469	0.248287315756695	3	69	actin filament bundle assembly
GO:0042119	0.00208825918356867	33.84	0.0683689710054668	2	19	neutrophil activation
GO:0002706	0.00228871577238622	12.5326530612245	0.262680783336793	3	73	regulation of lymphocyte mediated immunity
GO:0042994	0.00231495688787468	31.9577777777778	0.0719673379004913	2	20	cytoplasmic sequestering of transcription factor
GO:0031529	0.00255275925672425	30.2736842105263	0.0755657047955159	2	21	ruffle organization
GO:0045766	0.00276435842778494	11.6930612244898	0.280672617811916	3	78	positive regulation of angiogenesis
GO:0010543	0.00280158655868265	28.758	0.0791640716905404	2	22	regulation of platelet activation
GO:0001816	0.00282647226772585	4.69766402145971	1.4213549235347	6	395	cytokine production
GO:0061041	0.00286623451783342	11.5383995703545	0.284270984706941	3	79	regulation of wound healing
GO:0002822	0.00297040038127584	11.3877551020408	0.287869351601965	3	80	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains
GO:0002886	0.00306135947317336	27.3866666666667	0.082762438585565	2	23	regulation of myeloid leukocyte mediated immunity
GO:0002675	0.00333199908864514	26.14	0.0863608054805896	2	24	positive regulation of acute inflammatory response
GO:0051220	0.00333199908864514	26.14	0.0863608054805896	2	24	cytoplasmic sequestering of protein
GO:0046651	0.00336308482564778	7.05902777777778	0.618919105944225	4	172	lymphocyte proliferation
GO:0032943	0.00350517443624208	6.975	0.626115839734274	4	174	mononuclear cell proliferation
GO:0002819	0.0037650599096333	10.4336734693878	0.313057919867137	3	87	regulation of adaptive immune response
GO:0009595	0.00390556481050803	23.9583333333333	0.0935575392706387	2	26	detection of biotic stimulus

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GO:0045730      0.00390556481050803     23.9583333333333        0.0935575392706387
2       26      respiratory burst
GO:0070661      0.00411449750560518     6.65777153558052        0.654902774894471
4       182     leukocyte proliferation
GO:0042035      0.00427199267749964     9.95663265306122        0.327451387447236
3       91      regulation of cytokine biosynthetic process
GO:0002703      0.00440487920668883     9.84407246044485        0.33104975434226
3       92      regulation of leukocyte mediated immunity
GO:0043647      0.00452166054318574     22.1123076923077        0.100754273060688
2       28      inositol phosphate metabolic process
GO:0050766      0.00484546417881378     21.2918518518519        0.104352639955712
2       29      positive regulation of phagocytosis
GO:0070098      0.00517966953394122     20.53   0.107951006850737       2       30
chemokine-mediated signaling pathway
GO:0007015      0.0052514727330191      6.19895287958115        0.70168154452979
4       195     actin filament organization
GO:0000387      0.00552420050949671     19.8206896551724        0.111549373745762
2       31      spliceosomal snRNP assembly
GO:0032755      0.00552420050949671     19.8206896551724        0.111549373745762
2       31      positive regulation of interleukin-6 production
GO:0042089      0.00555871085164821     9.0271407532085 0.359836689502457       3
100     cytokine biosynthetic process
GO:0043900      0.00571447498593333     8.93440233236152        0.363435056397481
3       101     regulation of multi-organism process
GO:0002694      0.00579991613209956     4.74111230810665        1.15507577330289
5       321     regulation of leukocyte activation
GO:0060627      0.0058408906082348 5    6.00761421319797        0.723271745899938
4       201     regulation of vesicle-mediated transport
GO:0042107      0.00587284324787367     8.84353741496599        0.367033423292506
3       102     cytokine metabolic process
GO:0002437      0.00587898140103788     19.1586666666667        0.115147740640786
2       32      inflammatory response to antigenic stimulus
GO:0032760      0.00587898140103788     19.1586666666667        0.115147740640786
2       32      positive regulation of tumor necrosis factor production
GO:0042992      0.00587898140103788     19.1586666666667        0.115147740640786
2       32      negative regulation of transcription factor import into nucleus
GO:0008154      0.00705528491353845     8.25548710050058        0.392221991557678
3       109     actin polymerization or depolymerization
GO:0007249      0.00726627631974132     5.63055555555556        0.770050515535257
4       214     I-kappaB kinase/NF-kappaB cascade
GO:0050830      0.00739910375149829     16.9    0.129541208220884       2       36
defense response to Gram-positive bacterium
GO:0043299      0.0082187248167956      15.9588888888889        0.136737942010934
2       38      leukocyte degranulation
GO:0007596      0.00864094515181872     3.68690349946978        1.79198671372223
6       498     blood coagulation
GO:0048661      0.00864316817551764     15.5264864864865        0.140336308905958
2       39      positive regulation of smooth muscle cell proliferation
GO:0009612      0.00876971944583186     7.60461401952085        0.424607293612899
3       118     response to mechanical stimulus
GO:0030100      0.00876971944583186     7.60461401952085        0.424607293612899
3       118     regulation of endocytosis
GO:0071496      0.0094543803305764      5.20264317180617        0.831222752750675
4       231     cellular response to external stimulus
GO:0002696      0.00973707704665        5.15647743813683        0.838419486540724
4       233     positive regulation of leukocyte activation
GO:0010951      0.00981881947496151     7.28520408163265        0.442599128088022
3       123     negative regulation of endopeptidase activity
GO:0002824      0.00997415936298272     14.359  0.151131409591032       2       42
positive regulation of adaptive immune response based on somatic recombination of
immune receptors built from immunoglobulin superfamily domains
Tissue: Skin_Sun_Exposed_Lower_leg=>Thyroid     Type:   asymmetric
SourceGene:     C2orf68(ENSG00000168887.6)
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TargetGeneSet:  MRPL20  RBMXL1  HAX1    ADAR    ISG20L2 ATF6    RP11    DHX9
MIR4426 QARS    HNRNPU  RNASEH1 DDX1    POTEE   XRCC5   TRIP12  CIDECP  FANCD2
CTNNB1  SPCS1   POLR2B  NUP155  SKIV2L2 ANKRA2  CTD     AP3S1   DDX46   IK
LARP1   C6orf47 FTSJD2  UNC5CL  RPL24P4 LYRM2   RPL23P8 POLR2J3 ASH2L   JPH1
ST13P6  SMU1    SMC3    NUP160  STX5    DLAT    PRKAG1  BAZ2A   CHST11  RPS11P5
ATP11A  TOX4    DCAF11  DLST    HMGN2P5 ARHGAP11B       AQR     HMGN2P46
IDH3A   C15orf38        SV2B    FUS     UBE2MP1 CIRH1A  SF3B3   TSR1    TP53
VAMP2   TMEM199 CTB     PIGS    FAM134C PSME3   DHX8    KPNB1   ARMC7   MRPS7
CEP76   PIK3C3  CTIF    ZNF407  C19orf38        EMR2    UBE2M   RPS10L  RP4
DDX27   TPTE    SON     APOL6   TOMM22  ADSL    PPPDE2  TCF20   USP9X   RP6
SLC35A2 NONO    EIF4A1P2
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006397      8.48042610623201e-11    10.4408802685565        1.98795931077434
16      399     mRNA processing
GO:0008380      5.45111296043078e-10    10.9909608302645        1.60930039443637
14      323     RNA splicing
GO:0000377      6.31346020257997e-08    11.7933155969405        1.01640024911771
10      204     RNA splicing, via transesterification reactions with bulged
adenosine as nucleophile
GO:0000398      6.31346020257997e-08    11.7933155969405        1.01640024911771
10      204     nuclear mRNA splicing, via spliceosome
GO:0000375      7.92964531613603e-08    11.4929486140379        1.04131201992942
10      209     RNA splicing, via transesterification reactions
GO:0070934      0.000242444194982661    136.914285714286        0.0249117708117085
2       5       CRD-mediated mRNA stabilization
GO:0016556      0.000505853434055779    82.1371428571429        0.0348764791363919
2       7       mRNA modification
GO:0006734      0.00067229672626930l    68.4428571428571        0.0398588332987337
2       8       NADH metabolic process
GO:0009060      0.0011843179228636б     15.9866220735786        0.209258874818352
3       42      aerobic respiration
GO:0006084      0.00208065862872541     12.9809782608696        0.254100062279427
3       51      acetyl-CoA metabolic process
GO:0006281      0.00291638866751573     4.01067921440262        1.90824164417687
7       383     DNA repair
GO:0006103      0.00396282855922372     24.1378151260504        0.0946647290844924
2       19      2-oxoglutarate metabolic process
GO:0031023      0.00415249566492265     10.0399719495091        0.323853020552211
3       65      microtubule organizing center organization
GO:0022613      0.00525545134936841     4.80291723202171        1.12102968652688
5       225     ribonucleoprotein complex biogenesis
GO:0006091      0.00535079247908876     3.57047323223095        2.13244758148225
7       428     generation of precursor metabolites and energy
GO:0071843      0.006755172069383       4.51109835438194        1.19078264479967
5       239     cellular component biogenesis at cellular level
GO:0019674      0.00681960983346149     17.8335403726708        0.124558854058543
2       25      NAD metabolic process
GO:0043489      0.00681960983346149     17.8335403726708        0.124558854058543
2       25      RNA stabilization
GO:0048255      0.00681960983346149     17.8335403726708        0.124558854058543
2       25      mRNA stabilization
GO:0006099      0.00736424552645795     17.0892857142857        0.129541208220884
2       26      tricarboxylic acid cycle
GO:0009267      0.00792740317942642     7.87011557512383        0.40855304131202
3       82      cellular response to starvation
GO:0046356      0.00792791798315694     16.4045714285714        0.134523562383226
2       27      acetyl-CoA catabolic process
GO:0006370      0.00973118536622807     14.6438775510204        0.149470624870251
2       30      7-methylguanosine mRNA capping
Tissue: Skin_Sun_Exposed_Lower_leg=>Thyroid     Type:   cluster
SourceGene:     C2orf68(ENSG00000168887.6)
TargetGeneSet:  MRPL20  RBMXL1  HAX1    ADAR    ISG20L2 ATF6    RP11    DHX9
MIR4426 QARS    HNRNPU  RNASEH1 DDX1    POTEE   XRCC5   TRIP12  CIDECP  FANCD2
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CTNNB1  SPCS1   POLR2B  NUP155  SKIV2L2 ANKRA2  CTD     AP3S1   DDX46   IK
LARP1   C6orf47 FTSJD2  UNC5CL  RPL24P4 LYRM2   RPL23P8 POLR2J3 ASH2L   JPH1
ST13P6  SMU1    SMC3    NUP160  STX5    DLAT    PRKAG1  BAZ2A   CHST11  RPS11P5
ATP11A  TOX4    DCAF11  DLST    HMGN2P5 ARHGAP11B       AQR     HMGN2P46
IDH3A   C15orf38        SV2B    FUS     UBE2MP1 CIRH1A  SF3B3   TSR1    TP53
VAMP2   TMEM199 CTB     PIGS    FAM134C PSME3   DHX8    KPNB1   ARMC7   MRPS7
CEP76   PIK3C3  CTIF    ZNF407  C19orf38        EMR2    UBE2M   RPS10L  RP4
DDX27   TPTE    SON     APOL6   TOMM22  ADSL    PPPDE2  TCF20   USP9X   RP6
SLC35A2 NONO    EIF4A1P2
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006397      8.48042610623201e-11    10.4408802685565        1.98795931077434
16      399     mRNA processing
GO:0008380      5.45111296043078e-10    10.9909608302645        1.60930039443637
14      323     RNA splicing
GO:0000377      6.31346020257997e-08    11.7933155969405        1.01640024911771
10      204     RNA splicing, via transesterification reactions with bulged
adenosine as nucleophile
GO:0000398      6.31346020257997e-08    11.7933155969405        1.01640024911771
10      204     nuclear mRNA splicing, via spliceosome
GO:0000375      7.92964531613603e-08    11.4929486140379        1.04131201992942
10      209     RNA splicing, via transesterification reactions
GO:0070934      0.000242444194982661    136.914285714286        0.0249117708117085
2       5       CRD-mediated mRNA stabilization
GO:0016556      0.000505853434055779    82.1371428571429        0.0348764791363919
2       7       mRNA modification
GO:0006734      0.000672296726269301    68.4428571428571        0.0398588332987337
2       8       NADH metabolic process
GO:0009060      0.00118431792286366     15.9866220735786        0.209258874818352
3       42      aerobic respiration
GO:0006084      0.00208065862872541     12.9809782608696        0.254100062279427
3       51      acetyl-CoA metabolic process
GO:0006281      0.00291638866751573     4.01067921440262        1.90824164417687
7       383     DNA repair
GO:0006103      0.00396282855922372     24.1378151260504        0.0946647290844924
2       19      2-oxoglutarate metabolic process
GO:0031023      0.00415249566492265     10.0399719495091        0.323853020552211
3       65      microtubule organizing center organization
GO:0022613      0.00525545134936841     4.80291723202171        1.12102968652688
5       225     ribonucleoprotein complex biogenesis
GO:0006091      0.00535079247908876     3.57047323223095        2.13244758148225
7       428     generation of precursor metabolites and energy
GO:0071843      0.006755172069383       4.51109835438194        1.19078264479967
5       239     cellular component biogenesis at cellular level
GO:0019674      0.00681960983346149     17.8335403726708        0.124558854058543
2       25      NAD metabolic process
GO:0043489      0.00681960983346149     17.8335403726708        0.124558854058543
2       25      RNA stabilization
GO:0048255      0.00681960983346149     17.8335403726708        0.124558854058543
2       25      mRNA stabilization
GO:0006099      0.00736424552645795     17.0892857142857        0.129541208220884
2       26      tricarboxylic acid cycle
GO:0009267      0.00792740317942642     7.87011557512383        0.40855304131202
3       82      cellular response to starvation
GO:0046356      0.00792791798315694     16.4045714285714        0.134523562383226
2       27      acetyl-CoA catabolic process
GO:0006370      0.00973118536622807     14.6438775510204        0.149470624870251
2       30      7-methylguanosine mRNA capping
Tissue: Skin_Sun_Exposed_Lower_leg=>Thyroid     Type:   asymmetric
SourceGene:     CBX8(ENSG00000141570.6)
TargetGeneSet:  RP11    ACTA1   RAB10   CHAC2   XIRP2   MYL1    SUMF1   RFC1
PPP1R3A FAM90A11P       MYPN    ANKRD2  SLN     MYF6    MYBPC1  C12orf73
ACA64   MYH2    TCAP    PPP1R27 CKM     TNNT1   KRTAP11-1       PVALB   FAM45B
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
```

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GO:0030049      6.82931318946151e-12    201.384615384615        0.0512767282541001
6       39      muscle filament sliding
GO:0033275      6.82931318946151e-12    201.384615384615        0.0512767282541001
6       39      actin-myosin filament sliding
GO:0070252      1.09550346103916e-11    184.564102564103        0.0552210919659539
6       42      actin-mediated cell contraction
GO:0030048      9.28670025034424e-11    125.216255442671        0.0775724863331257
6       59      actin filament-based movement
GO:0006936      3.21718692437347e-10    44.7099567099567        0.314234309044357
8       239     muscle contraction
GO:0003012      7.52608626815069e-10    39.9548978153629        0.349733582451041
8       266     muscle system process
GO:0030029      3.38449798682131e-08    24.0274442538593        0.567988374506954
8       432     actin filament-based process
GO:0003009      1.84255948873129e-06    168.9375        0.0249809701750744      3
19      skeletal muscle contraction
GO:0006941      2.44499268606635e-06    53.9380281690141        0.0986090927963463
4       75      striated muscle contraction
GO:0050879      4.91524401869724e-06    117.464673913043        0.0341844855027334
3       26      multicellular organismal movement
GO:0050881      4.91524401869724e-06    117.464673913043        0.0341844855027334
3       26      musculoskeletal movement
GO:0003010      9.81137925112146e-06    848.823529411765        0.00525915161580513
2       4       voluntary skeletal muscle contraction
GO:0014721      9.81137925112146e-06    848.823529411765        0.00525915161580513
2       4       twitch skeletal muscle contraction
GO:0061061      9.83140057717353e-06    16.066806642489 0.537748252716075       6
409     muscle structure development
GO:0030239      1.1237674975672e-05     87.1028225806452        0.0447027887343436
3       34      myofibril assembly
GO:0030240      1.63394737183147e-05    565.843137254902        0.00657393951975642
2       5       skeletal muscle thin filament assembly
GO:0014866      2.44899890051702e-05    424.352941176471        0.0078887274237077
2       6       skeletal myofibril assembly
GO:0031032      2.64057118044168e-05    64.2410714285714        0.0591654556778078
3       45      actomyosin structure organization
GO:0007517      3.58101005777371e-05    16.9391179290508        0.398380734897239
5       303     muscle organ development
GO:0042692      0.000251743550383548    15.7688888888889        0.320808248564113
4       244     muscle cell differentiation
GO:0055002      0.000350809358083889    25.8317307692308        0.140682305722787
3       107     striated muscle cell development
GO:0045214      0.000372442933368624    84.7764705882353        0.0289253338869282
2       22      sarcomere organization
GO:0010927      0.000527800161591498    22.3625 0.161718912186008       3       123
cellular component assembly involved in morphogenesis
GO:0055001      0.000606537671670912    21.2886904761905        0.169607639609716
3       129     muscle cell development
GO:0051146      0.0013265864772265      16.1137048192771        0.222199155767767
3       169     striated muscle cell differentiation
GO:0060048      0.00143215215855968     41.2941176470588        0.0565358798699052
2       43      cardiac muscle contraction
GO:0030036      0.00145388941752792     9.72952380952381        0.511452494637049
4       389     actin cytoskeleton organization
GO:0060415      0.00193222176422744     35.2549019607843        0.0657393951975642
2       50      muscle tissue morphogenesis
GO:0001756      0.00216845350920103     33.1741637831603        0.069683758909418
2       53      somitogenesis
GO:0048644      0.00241769650587859     31.3246187363834        0.0736281226212719
2       56      muscle organ morphogenesis
GO:0061053      0.00295483586424565     28.1803921568627        0.0815168500449796
2       62      somite development
GO:0030241      0.00393945224456549     400.833333333333        0.00394436371185385
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1       3       skeletal muscle myosin thick filament assembly
GO:0031034      0.00393945224456549     400.833333333333        0.00394436371185385
1       3       myosin filament assembly
GO:0042396      0.00393945224456549     400.833333333333        0.00394436371185385
1       3       phosphagen biosynthetic process
GO:0048769      0.00393945224456549     400.833333333333        0.00394436371185385
1       3       sarcomerogenesis
GO:0071688      0.00393945224456549     400.833333333333        0.00394436371185385
1       3       striated muscle myosin thick filament assembly
GO:0014706      0.00460462018587363     10.2603764478764        0.344474430835236
3       262     striated muscle tissue development
GO:0035282      0.00463406501533718     22.2229102167183        0.1025534565082 2
78      segmentation
GO:0048747      0.00475071458473899     21.9327731092437        0.103868244412151
2       79      muscle fiber development
GO:0060537      0.00516431657442708     9.83472222222222        0.3589370977787 3
273     muscle tissue development
GO:0031033      0.00524933253300364     267.203703703704        0.00525915161580513
1       4       myosin filament organization
GO:0001778      0.00655758079782431     200.388888888889        0.00657393951975642
1       5       plasma membrane repair
GO:0000244      0.00786419895958823     160.3   0.0078887274237077      1       6
assembly of spliceosomal tri-snRNP
GO:0043353      0.00786419895958823     160.3   0.0078887274237077      1       6
enucleate erythrocyte differentiation
GO:0048739      0.00916918893672691     133.574074074074        0.00920351532765899
1       7       cardiac muscle fiber development
GO:0003015      0.00999174999097359     14.7760577915377        0.152515396858349
2       116     heart process
GO:0060047      0.00999174999097359     14.7760577915377        0.152515396858349
2       116     heart contraction
Tissue: Skin_Sun_Exposed_Lower_leg=>Thyroid     Type:   cluster
SourceGene:     CORO7(ENSG00000262246.1)
TargetGeneSet:  RP11    MFI2    TMSB4XP1        DPH2    KCND3   RBBP5   RRP15
HEATR1  DDIT3   POLR1B  DDX18   HNRNPKP2        USP37   GIGYF2  BRPF1   MYNN
OCIAD1-AS1      ZNF131  RIOK1   PAK1IP1 RPL7L1  CDC5L   CCNC    ZNF680  BAZ1B
TRIM4   TGS1    TG      FXN     EXOSC2  NGB     BMS1    SPTY2D1 NAT10   RPS3
PA2G4   RPL41   UTP20   SART3   NUFIP1  SUPT16H RSL1D1  SRCAP   ZNF778  NEURL4  DHX8
NOL11   C17orf101       HMG20B  ZNF121  SYCE2   ZNF576  ZNF749  ZSCAN22 CSRP2BP AHCY
TFIP11  RP4     GAPDHP1 ATP6AP2 TAF1    UTP14A  RAP2C
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0071843      8.31956408197553e-10    16.2771512113617        0.876548335755311
11      239     cellular component biogenesis at cellular level
GO:0022613      7.44588986654496e-09    15.3412655489454        0.825202408137845
10      225     ribonucleoprotein complex biogenesis
GO:0042254      1.11473650659671e-06    15.2774035517453        0.546467372500173
7       149     ribosome biogenesis
GO:0006364      3.82252748338727e-05    15.0452441077441        0.381426890872604
5       104     rRNA processing
GO:0016072      5.00360401007735e-05    14.1795634920635        0.403432288422946
5       110     rRNA metabolic process
GO:0016570      0.000369369644579804    7.08035043804756        0.9572347934399 6
261     histone modification
GO:0022618      0.000401071785835457    12.8342677730433        0.34841879454709
4       95      ribonucleoprotein complex assembly
GO:0016569      0.000416853690713839    6.9146490584495 0.979240190990243       6
267     covalent chromatin modification
GO:0071826      0.000487377959773485    12.1615646258503        0.366756625839042
4       100     ribonucleoprotein complex subunit organization
GO:0034660      0.000588487198610036    6.4603065660032 1.04525638364127        6
285     ncRNA metabolic process
GO:0016573      0.000651857061619797    11.2197802197802        0.396097155906166
4       108     histone acetylation
```

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GO:0018393      0.000698443637537373    11.0065460146323        0.403432288422946
4       110     internal peptidyl-lysine acetylation
GO:0018394      0.000772680266855757    10.7013667852462        0.414434987198118
4       113     peptidyl-lysine acetylation
GO:0016568      0.000798470522773041    5.16578725200507        1.53671026226559
7       419     chromatin modification
GO:0034470      0.000808439723585181    7.58707264957265        0.733513251678085
5       200     ncRNA processing
GO:0006475      0.000825168423407011    10.5070785070785        0.421770119714899
4       115     internal protein amino acid acetylation
GO:0000377      0.00088366756234403     7.43247487437186        0.748183516711646
5       204     RNA splicing, via transesterification reactions with bulged
adenosine as nucleophile
GO:0000398      0.00088366756234403     7.43247487437186        0.748183516711646
5       204     nuclear mRNA splicing, via spliceosome
GO:0000375      0.000984912130114098    7.24775326797386        0.766521348003598
5       209     RNA splicing, via transesterification reactions
GO:0006473      0.00122944119370842     9.39697169190257        0.469448481073974
4       128     protein acetylation
GO:0006337      0.001532475065685       40.2913165266106        0.0586810601342468
2       16      nucleosome disassembly
GO:0031498      0.001532475065685       40.2913165266106        0.0586810601342468
2       16      chromatin disassembly
GO:0032986      0.001532475065685       40.2913165266106        0.0586810601342468
2       16      protein-DNA complex disassembly
GO:0018205      0.00175565072825971     8.49754208252644        0.51712684243305
4       141     peptidyl-lysine modification
GO:0043543      0.00189624101207078     8.31370262390671        0.528129541208221
4       144     protein acylation
GO:0034623      0.00375623821690118     6.83217286914766        0.638156528959934
4       174     cellular macromolecular complex disassembly
GO:0032984      0.00415486758017016     6.63463556851312        0.656494360251886
4       179     macromolecular complex disassembly
GO:0000387      0.00573319951906942     19.4306964164976        0.113694554010103
2       31      spliceosomal snRNP assembly
GO:0008380      0.00645433658226166     4.61215932914046        1.18462390146011
5       323     RNA splicing
GO:0006354      0.00725196574203883     8.16742857142857        0.396097155906166
3       108     DNA-dependent transcription, elongation
Tissue: Skin_Sun_Exposed_Lower_leg=>Thyroid     Type:   asymmetric
SourceGene:     DYNLL1(ENSG00000088986.6)
TargetGeneSet:  RP4     SELL    TNNI1   XIRP2   GFRA3   RP1     MOG     LMOD2   NRAP
CSRP3   ANGPTL5 MYBPC1  MYL2    MYH7    CTD     MMP2    MYH1    TCAP    CKM
PVALB   RPSAP8  FAM127C
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0030049      6.63055833692767e-10    176.470588235294        0.0458791779115632
5       39      muscle filament sliding
GO:0033275      6.63055833692767e-10    176.470588235294        0.0458791779115632
5       39      actin-myosin filament sliding
GO:0070252      9.77614220520049e-10    162.128378378378        0.0494083454432219
5       42      actin-mediated cell contraction
GO:0030048      5.68604279134456e-09    110.956790123457        0.0694069614559546
5       59      actin filament-based movement
GO:0048738      1.6766067820844e-07     54.2575757575758        0.135284755380251
5       115     cardiac muscle tissue development
GO:0055008      1.89547834193003e-07    108.015009380863        0.0529375129748806
4       45      cardiac muscle tissue morphogenesis
GO:0006936      2.04235339756834e-07    33.244635193133 0.281157013355477       6
239     muscle contraction
GO:0060415      2.91927812134081e-07    96.2408026755853        0.0588194588609785
4       50      muscle tissue morphogenesis
GO:0003012      3.83791962639148e-07    29.7356643356643        0.312919521140405
6       266     muscle system process
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GO:0048644      4.63566068315803e-07    85.1005917159763        0.0658777939242959
4       56      muscle organ morphogenesis
GO:0006941      1.51316902074374e-06    62.2448537378115        0.0882291882914677
4       75      striated muscle contraction
GO:0007507      1.66962570045951e-06    22.8863636363636        0.402325098609093
6       342     heart development
GO:0030029      6.44751475380701e-06    17.9359795134443        0.508200124558854
6       432     actin filament-based process
GO:0055010      7.21868328547381e-06    102.885714285714        0.0388208428482458
3       33      ventricular cardiac muscle tissue morphogenesis
GO:0003015      8.65413335701117e-06    39.3461538461538        0.13646114455747
4       116     heart process
GO:0060047      8.65413335701117e-06    39.3461538461538        0.13646114455747
4       116     heart contraction
GO:0003229      9.4261519298055e-06     93.512987012987 0.0423500103799045      3
36      ventricular cardiac muscle tissue development
GO:0014706      9.76150598372339e-06    22.9847600518807        0.308213964431527
5       262     striated muscle tissue development
GO:0060537      1.1916725202437e-05     22.0242537313433        0.321154245380943
5       273     muscle tissue development
GO:0007517      1.97254232303307e-05    19.7651006711409        0.35644592069753
5       303     muscle organ development
GO:0003007      2.85819821851923e-05    28.7199597787833        0.184693100823472
4       157     heart morphogenesis
GO:0003208      3.05467779594253e-05    61.6457142857143        0.0623486263926372
3       53      cardiac ventricle morphogenesis
GO:0009582      6.75297557433346e-05    46.6493506493507        0.0811708532281503
3       69      detection of abiotic stimulus
GO:0007603      7.11967467526906e-05    213.703703703704        0.0129402809494153
2       11      phototransduction, visible light
GO:0061061      8.27676600816249e-05    14.4698844884488        0.481143173482804
5       409     muscle structure development
GO:0003231      9.01483592865506e-05    42.1555772994129        0.0894055774686873
3       76      cardiac ventricle development
GO:0007512      0.000100830265848504    174.824242424242        0.0152930593038544
2       13      adult heart development
GO:0003206      0.00010901190307642     39.4395604395604        0.0952875233547851
3       81      cardiac chamber morphogenesis
GO:0055003      0.000117553927184637    160.244444444444        0.016469448481074
2       14      cardiac myofibril assembly
GO:0009581      0.000130283379331782    37.0507745266781        0.101169469240883
3       86      detection of external stimulus
GO:0003205      0.000164358884169156    34.152380952381 0.10940419348142        3
93      cardiac chamber development
GO:0003009      0.000220135062408993    113.074509803922        0.0223513943671718
2       19      skeletal muscle contraction
GO:0009584      0.00024442533295198     106.785185185185        0.0235277835443914
2       20      detection of visible light
GO:0008015      0.000363425273176549    14.5459223051196        0.35644592069753
4       303     blood circulation
GO:0003013      0.000368003727025375    14.4964102564103        0.357622309874749
4       304     circulatory system process
GO:0050879      0.000416364046374626    80.0555555555556        0.0305861186077088
2       26      multicellular organismal movement
GO:0050881      0.000416364046374626    80.0555555555556        0.0305861186077088
2       26      musculoskeletal movement
GO:0055006      0.000555747467346677    68.6    0.0352916753165871      2       30
cardiac cell development
GO:0055013      0.000555747467346677    68.6    0.0352916753165871      2       30
cardiac muscle cell development
GO:0071482      0.000632803923949525    64.0177777777778        0.0376444536710262
2       32      cellular response to light stimulus
GO:0007602      0.000673164262056883    61.9483870967742        0.0388208428482458
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2       33      phototransduction
GO:0030239      0.000714742559025276    60.0083333333333        0.0399972320254654
2       34      myofibril assembly
GO:0006942      0.000893183771772659    53.3259259259259        0.0447027887343436
2       38      regulation of striated muscle contraction
GO:0009583      0.000989645204184707    50.5122807017544        0.0470555670887828
2       40      detection of light stimulus
GO:0048729      0.00107264463754218     10.7953846153846        0.475261227596706
4       404     tissue morphogenesis
GO:0044057      0.00120661265491822     10.4458930899609        0.490554286900561
4       417     regulation of system process
GO:0051606      0.00124909903274545     16.6873536299766        0.21880838696284
3       186     detection of stimulus
GO:0031032      0.00125175363671356     44.6232558139535        0.0529375129748806
2       45      actomyosin structure organization
GO:0055007      0.00193242469401933     35.5061728395062        0.0658777939242959
2       56      cardiac muscle cell differentiation
GO:0071478      0.00207135493513362     34.2333333333333        0.068230572278735
2       58      cellular response to radiation
GO:0016056      0.00352526115515339     451     0.00352916753165871     1       3
rhodopsin mediated signaling pathway
GO:0030241      0.00352526115515339     451     0.00352916753165871     1       3
skeletal muscle myosin thick filament assembly
GO:0031034      0.00352526115515339     451     0.00352916753165871     1       3
myosin filament assembly
GO:0034124      0.00352526115515339     451     0.00352916753165871     1       3
regulation of MyD88-dependent toll-like receptor signaling pathway
GO:0035845      0.00352526115515339     451     0.00352916753165871     1       3
photoreceptor cell outer segment organization
GO:0042396      0.00352526115515339     451     0.00352916753165871     1       3
phosphagen biosynthetic process
GO:0048769      0.00352526115515339     451     0.00352916753165871     1       3
sarcomerogenesis
GO:0071688      0.00352526115515339     451     0.00352916753165871     1       3
striated muscle myosin thick filament assembly
GO:0035051      0.00352717337339985     25.8738738738739        0.0894055774686873
2       76      cardiac cell differentiation
GO:0003010      0.00469774665905387     300.645833333333        0.00470555670887828
1       4       voluntary skeletal muscle contraction
GO:0014721      0.00469774665905387     300.645833333333        0.00470555670887828
1       4       twitch skeletal muscle contraction
GO:0031033      0.00469774665905387     300.645833333333        0.00470555670887828
1       4       myosin filament organization
GO:0006937      0.00480315999875744     21.9877394636015        0.104698636772542
2       89      regulation of muscle contraction
GO:0060041      0.0053427716163775 5    20.7855072463768        0.11058058265864
2       94      retina development in camera-type eye
GO:0008016      0.00556610375852272     20.3404255319149        0.112933361013079
2       96      regulation of heart contraction
GO:0001955      0.00586893363952024     225.46875       0.00588194588609785     1
5       blood vessel maturation
GO:0030240      0.00586893363952024     225.46875       0.00588194588609785     1
5       skeletal muscle thin filament assembly
GO:0090257      0.00674614320171622     18.3717948717949        0.124697252785274
2       106     regulation of muscle system process
GO:0055002      0.00686990117416381     18.1955555555556        0.125873641962494
2       107     striated muscle cell development
GO:0001957      0.00703882344487339     180.3625        0.00705833506331742     1
6       intramembranous ossification
GO:0009586      0.00703882344487339     180.3625        0.00705833506331742     1
6       rhodopsin mediated phototransduction
GO:0014866      0.00703882344487339     180.3625        0.00705833506331742     1
6       skeletal myofibril assembly
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GO:0036072      0.00703882344487339     180.3625        0.00705833506331742     1
6       direct ossification
GO:0043353      0.00703882344487339     180.3625        0.00705833506331742     1
6       enucleate erythrocyte differentiation
GO:0046548      0.00703882344487339     180.3625        0.00705833506331742     1
6       retinal rod cell development
GO:0000302      0.00750419816453199     17.3624242424242        0.131755587848592
2       112     response to reactive oxygen species
GO:0048739      0.00820741742212772     150.291666666667        0.00823472424053699
1       7       cardiac muscle fiber development
GO:0010927      0.00898948094198444     15.7719008264463        0.144695868798007
2       123     cellular component assembly involved in morphogenesis
GO:0042670      0.00937471691699199     128.8125        0.00941111341775656     1
8       retinal cone cell differentiation
GO:0046549      0.00937471691699199     128.8125        0.00941111341775656     1
8       retinal cone cell development
GO:0055001      0.00985084345743121     15.0204724409449        0.151754203861324
2       129     muscle cell development
GO:0030036      0.00994051330598178     7.79866765358993        0.457615389938413
3       389     actin cytoskeleton organization
Tissue: Skin_Sun_Exposed_Lower_leg=>Thyroid     Type:   asymmetric
SourceGene:     ENSG00000237411.1
TargetGeneSet:  RP4     NSRP1P1 TNNI1   ACTA1   LBH     XIRP2   TLK1    RP11
SH3PXD2B        GCNT6   TRDN    NRAP    RNU2-2  MYBPC1  MYH7    CTD     COX16   MYH2
MYH1    CKM     TNNT1   PRMT2   PVALB
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0030049      6.82931318946151e-12    201.384615384615        0.0512767282541001
6       39      muscle filament sliding
GO:0033275      6.82931318946151e-12    201.384615384615        0.0512767282541001
6       39      actin-myosin filament sliding
GO:0070252      1.09550346103916e-11    184.564102564103        0.0552210919659539
6       42      actin-mediated cell contraction
GO:0030048      9.28670025034424e-11    125.216255442671        0.0775724863331257
6       59      actin filament-based movement
GO:0006936      3.21718692437347e-10    44.7099567099567        0.314234309044357
8       239     muscle contraction
GO:0003012      7.52608626815069e-10    39.9548978153629        0.349733582451041
8       266     muscle system process
GO:0030029      7.50211871241557e-07    19.2252941176471        0.567988374506954
7       432     actin filament-based process
GO:0003010      9.81137925112146e-06    848.823529411765        0.00525915161580513
2       4       voluntary skeletal muscle contraction
GO:0014721      9.81137925112146e-06    848.823529411765        0.00525915161580513
2       4       twitch skeletal muscle contraction
GO:0006941      0.00012256166736417     37.3958333333333        0.0986090927963463
3       75      striated muscle contraction
GO:0003009      0.000276353744574814    99.757785467128 0.0249809701750744      2
19      skeletal muscle contraction
GO:0050879      0.0005223593393242      70.6274509803922        0.0341844855027334
2       26      multicellular organismal movement
GO:0050881      0.0005223593393242      70.6274509803922        0.0341844855027334
2       26      musculoskeletal movement
GO:0055010      0.000843990329769391    54.6527514231499        0.0433880008303924
2       33      ventricular cardiac muscle tissue morphogenesis
GO:0007507      0.000901575672369832    11.1195266272189        0.449657463151339
4       342     heart development
GO:0003229      0.0010046965926752      49.8200692041522        0.0473323645422462
2       36      ventricular cardiac muscle tissue development
GO:0055008      0.0015676762295726 7    39.3679890560876        0.0591654556778078
2       45      cardiac muscle tissue morphogenesis
GO:0060415      0.00193222176422744     35.2549019607843        0.0657393951975642
2       50      muscle tissue morphogenesis
GO:0003208      0.0021684535092010 3    33.1741637831603        0.069683758909418
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2       53      cardiac ventricle morphogenesis
GO:0048644      0.00241769650587859     31.3246187363834        0.0736281226212719
2       56      muscle organ morphogenesis
GO:0016056      0.00393945224456549     400.833333333333        0.00394436371185385
1       3       rhodopsin mediated signaling pathway
GO:0042396      0.00393945224456549     400.833333333333        0.00394436371185385
1       3       phosphagen biosynthetic process
GO:0003231      0.00440484670302872     22.8267090620032        0.0999238807002976
2       76      cardiac ventricle development
GO:0014706      0.00460462018587363     10.2603764478764        0.344474430835236
3       262     striated muscle tissue development
GO:0003206      0.00498807761938354     21.3745346239762        0.106497820220054
2       81      cardiac chamber morphogenesis
GO:0060537      0.00516431657442708     9.83472222222222        0.3589370977787 3
273     muscle tissue development
GO:0001672      0.00524933253300364     267.203703703704        0.00525915161580513
1       4       regulation of chromatin assembly or disassembly
GO:0006937      0.00599122113800982     19.3982420554429        0.117016123451664
2       89      regulation of muscle contraction
GO:0003205      0.00652463296512004     18.5404007756949        0.122275275067469
2       93      cardiac chamber development
GO:0001778      0.00655758079782431     200.388888888889        0.00657393951975642
1       5       plasma membrane repair
GO:0030240      0.00655758079782431     200.388888888889        0.00657393951975642
1       5       skeletal muscle thin filament assembly
GO:0060315      0.00655758079782431     200.388888888889        0.00657393951975642
1       5       negative regulation of ryanodine-sensitive calcium-release channel
activity
GO:0071800      0.00655758079782431     200.388888888889        0.00657393951975642
1       5       podosome assembly
GO:0007517      0.00689463365614857     8.8325  0.398380734897239       3       303
muscle organ development
GO:0000244      0.00786419895958823     160.3   0.0078887274237077      1       6
assembly of spliceosomal tri-snRNP
GO:0009586      0.00786419895958823     160.3   0.0078887274237077      1       6
rhodopsin mediated phototransduction
GO:0014866      0.00786419895958823     160.3   0.0078887274237077      1       6
skeletal myofibril assembly
GO:0043353      0.00786419895958823     160.3   0.0078887274237077      1       6
enucleate erythrocyte differentiation
GO:0090257      0.00840177241788033     16.2081447963801        0.139367517818836
2       106     regulation of muscle system process
GO:1901020      0.00916918893672691     133.574074074074        0.00920351532765899
1       7       negative regulation of calcium ion transmembrane transporter
activity
GO:0000302      0.00934076689784703     15.3176470588235        0.147256245242544
2       112     response to reactive oxygen species
GO:0048738      0.00982714459386267     14.9078604893285        0.151200608954398
2       115     cardiac muscle tissue development
Tissue: Skin_Sun_Exposed_Lower_leg=>Thyroid     Type:   asymmetric
SourceGene:     MADD(ENSG00000110514.13)
TargetGeneSet:  TNFRSF14        RPL11   RP4     RPL5    RP11    RPL32   PLCL2-AS1
RPL37   EEF1A1P19       BTF3    RP1     RPL10A  SAMD3   TOMM7   EIF4BP6 RPL30
BBIP1   FAU     RPS25   KRT4    ATP5G2  RPL41   RPL14P1 NAP1L1  RPL7AP6 UBE2I
TP53I13 TBC1D3  RPL17   CASC3   STAT5B  CCDC102B        POLR2I  ISOC2   ZNF8
RPS21   EIF3D
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0000184      1.50047049188817e-18    100.345794392523        0.230572278735036
12      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006415      6.50644801972714e-18    116.009558823529        0.176319977856204
11      91      translational termination
GO:0019080      2.865849493093e-17      77.0719424460432        0.292574908310844
12      151     viral genome expression
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GO:0019083	2.865849493093e-17	77.0719424460432	0.292574908310844	12	151	viral transcription
GO:0006413	3.10828516241801e-17	76.5160714285714	0.294512490485088	12	152	translational initiation
GO:0006414	3.37370061889609e-17	98.6351689612015	0.20344612829562	11	105	translational elongation
GO:0006614	3.37370061889609e-17	98.6351689612015	0.20344612829562	11	105	SRP-dependent cotranslational protein targeting to membrane
GO:0006613	3.76025564035194e-17	97.590092879257	0.205383710469864	11	106	cotranslational protein targeting to membrane
GO:0045047	3.76025564035194e-17	97.590092879257	0.205383710469864	11	106	protein targeting to ER
GO:0072599	3.76025564035194e-17	97.590092879257	0.205383710469864	11	106	establishment of protein localization to endoplasmic reticulum
GO:0000956	1.14116022391456e-16	68.1496815286624	0.327451387447236	12	169	nuclear-transcribed mRNA catabolic process
GO:0070972	1.27749015390823e-16	86.5728422210006	0.228634696560792	11	118	protein localization to endoplasmic reticulum
GO:0006402	2.15121092431852e-16	64.414156626506	0.344889627015431	12	178	mRNA catabolic process
GO:0072594	1.12958423475647e-15	55.58984375	0.395266763545775	12	204	establishment of protein localization to organelle
GO:0006401	1.19857635529966e-15	55.2979274611399	0.397204345720019	12	205	RNA catabolic process
GO:0006612	2.39677087220734e-15	65.0749792874896	0.296450072659332	11	153	protein targeting to membrane
GO:0043624	2.39677087220734e-15	65.0749792874896	0.296450072659332	11	153	cellular protein complex disassembly
GO:0043241	3.436052031534e-15	62.8395358143257	0.306137983530551	11	158	protein complex disassembly
GO:0019058	5.0767250836969e-15	48.6438356164384	0.447581482250363	12	231	viral infectious cycle
GO:0034623	1.0088421326474e-14	56.6077228437387	0.337139298318455	11	174	cellular macromolecular complex disassembly
GO:0032984	1.38290377756684e-14	54.9037114845938	0.346827209189675	11	179	macromolecular complex disassembly
GO:0022415	2.10447537193709e-14	42.8679435483871	0.503771365303439	12	260	viral reproductive process
GO:0071845	2.22343453693889e-12	33.5380305968541	0.550273337485295	11	284	cellular component disassembly at cellular level
GO:0022411	2.58900225122003e-12	33.0443830961988	0.558023666182271	11	288	cellular component disassembly
GO:0016032	1.42814313194492e-11	23.8906605922551	0.873849560584043	12	451	viral reproduction
GO:0033365	2.48859198781389e-11	22.7147505422993	0.916476368417411	12	473	protein localization to organelle
GO:0006605	2.55054753927791e-11	22.663961038961	0.918413950591655	12	474	protein targeting
GO:0022613	3.76983542061772e-06	17.6886674968867	0.435955989204899	6	225	ribonucleoprotein complex biogenesis
GO:0071843	5.33749530884311e-06	16.6094420600858	0.463082139644315	6	239	cellular component biogenesis at cellular level
GO:0042254	0.000183306887678686	16.4114942528736	0.288699743962356	4	149	ribosome biogenesis
GO:0007603	0.00019698305497146	123.196581196581	0.021313403916684	2	11	phototransduction, visible light
GO:0042273	0.000236096351242935	110.869230769231	0.023250986090928	2	12	ribosomal large subunit biogenesis
GO:0042274	0.00054339147293453	69.2644230769231	0.0348764791363919	2	18	ribosomal small subunit biogenesis
GO:0009584	0.000673184465959876	61.5598290598291	0.0387516434848799	2	20	detection of visible light
GO:0022618	0.000800324303079238	18.6926086956522	0.18407030655318			

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3       95      ribonucleoprotein complex assembly
GO:0071826      0.000928927504268237    17.7228865979381        0.1937582174244 3
100     ribonucleoprotein complex subunit organization
GO:0006364      0.00104074135129846     17.0162376237624        0.201508546121376
3       104     rRNA processing
GO:0016072      0.00122389145234099     16.0553271028037        0.21313403916684
3       110     rRNA metabolic process
GO:0071482      0.0017322920285817 4    36.9051282051282        0.0620026295758079
2       32      cellular response to light stimulus
GO:0007602      0.0018418472247155 7    35.712158808933 0.0639402117500519      2
33      phototransduction
GO:0009583      0.0026982209398674      29.1194331983806        0.0775032869697599
2       40      detection of light stimulus
GO:0071478      0.00559649222465406     19.7348901098901        0.112379766106152
2       58      cellular response to radiation
GO:0016056      0.00580189185011537     267.055555555556        0.00581274652273199
1       3       rhodopsin mediated signaling pathway
GO:0031125      0.00580189185011537     267.055555555556        0.00581274652273199
1       3       rRNA 3'-end processing
GO:0035845      0.00580189185011537     267.055555555556        0.00581274652273199
1       3       photoreceptor cell outer segment organization
GO:0046544      0.00580189185011537     267.055555555556        0.00581274652273199
1       3       development of secondary male sexual characteristics
GO:0034470      0.0066306653922795 3    8.66558375634518        0.387516434848799
3       200     ncRNA processing
GO:0000255      0.00772863236978594     178.024691358025        0.00775032869697599
1       4       allantoin metabolic process
GO:0000447      0.00772863236978594     178.024691358025        0.00775032869697599
1       4       endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA
and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
GO:0000469      0.00772863236978594     178.024691358025        0.00775032869697599
1       4       cleavage involved in rRNA processing
GO:0000478      0.00772863236978594     178.024691358025        0.00775032869697599
1       4       endonucleolytic cleavage involved in rRNA processing
GO:0000479      0.00772863236978594     178.024691358025        0.00775032869697599
1       4       endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA,
5.8S rRNA, LSU-rRNA)
GO:0006549      0.00772863236978594     178.024691358025        0.00775032869697599
1       4       isoleucine metabolic process
GO:0046449      0.00772863236978594     178.024691358025        0.00775032869697599
1       4       creatinine metabolic process
GO:0046642      0.00772863236978594     178.024691358025        0.00775032869697599
1       4       negative regulation of alpha-beta T cell proliferation
GO:0070669      0.00772863236978594     178.024691358025        0.00775032869697599
1       4       response to interleukin-2
GO:0009582      0.00783920174745108     16.4822043628014        0.133693170022836
2       69      detection of abiotic stimulus
GO:0008298      0.00965177200387202     133.509259259259        0.00968791087121998
1       5       intracellular mRNA localization
GO:0072338      0.00965177200387202     133.509259259259        0.00968791087121998
1       5       cellular lactam metabolic process
Tissue: Skin_Sun_Exposed_Lower_leg=>Thyroid     Type:   asymmetric
SourceGene:     PTDSS2(ENSG00000174915.7)
TargetGeneSet:  TNNI1   C1orf186        RP11    ACTA1   FAHD2A  MYL1    ANXA5
ERCC4   OR1F12P LY6G6E  STX7    SLC26A4 LZTS2   TNNI2   AGBL2   FADS3   MYBPC1
STK24-AS1       DDX18P1 SLC25A29        SLC24A1 CTD     MYLPF   MYH2    DBF4B
C19orf24        CKM     TNNT1   BPIFA2  SALL4
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0030049      4.45877744890921e-14    242.290865384615        0.0539755034253685
7       39      muscle filament sliding
GO:0033275      4.45877744890921e-14    242.290865384615        0.0539755034253685
7       39      actin-myosin filament sliding
GO:0070252      7.80225094085748e-14    221.476923076923        0.0581274652273199
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7       42      actin-mediated cell contraction
GO:0030048      9.73465781956882e-13    148.894970414201        0.0816552487717113
7       59      actin filament-based movement
GO:0006936      2.00080286424127e-08    32.9552387267904        0.330772956888797
7       239     muscle contraction
GO:0003012      4.18005688822706e-08    29.4636174636175        0.368140613106359
7       266     muscle system process
GO:0030029      1.12458856263389e-06    17.7451583710407        0.597882499481005
7       432     actin filament-based process
GO:0006941      3.04424438900589e-06    50.5633802816901        0.103799045048786
4       75      striated muscle contraction
GO:0003009      0.0003068190587918      94.2091503267974        0.0262957580790257
2       19      skeletal muscle contraction
GO:0050879      0.000579757517178671    66.6990740740741        0.0359836689502457
2       26      multicellular organismal movement
GO:0050881      0.000579757517178671    66.6990740740741        0.0359836689502457
2       26      musculoskeletal movement
GO:0007517      0.00070401627756025     11.8160535117057        0.419348141997094
4       303     muscle organ development
GO:0061061      0.00213735663531172     8.65802469135802        0.56605079233271
4       409     muscle structure development
GO:0006295      0.00414650474202016     379.710526315789        0.00415196180195142
1       3       nucleotide-excision repair, DNA incision, 3'-to lesion
GO:0006296      0.00414650474202016     379.710526315789        0.00415196180195142
1       3       nucleotide-excision repair, DNA incision, 5'-to lesion
GO:0010834      0.00414650474202016     379.710526315789        0.00415196180195142
1       3       telomere maintenance via telomere shortening
GO:0042396      0.00414650474202016     379.710526315789        0.00415196180195142
1       3       phosphagen biosynthetic process
GO:0003231      0.0048767138278522      21.5570570570571        0.105183032316103
2       76      cardiac ventricle development
GO:0014706      0.0053453877992392      9.65614353849648        0.362604664037091
3       262     striated muscle tissue development
GO:0000710      0.00552503948074912     253.122807017544        0.00553594906926856
1       4       meiotic mismatch repair
GO:0003010      0.00552503948074912     253.122807017544        0.00553594906926856
1       4       voluntary skeletal muscle contraction
GO:0009642      0.00552503948074912     253.122807017544        0.00553594906926856
1       4       response to light intensity
GO:0014721      0.00552503948074912     253.122807017544        0.00553594906926856
1       4       twitch skeletal muscle contraction
GO:0015705      0.00552503948074912     253.122807017544        0.00553594906926856
1       4       iodide transport
GO:0060537      0.00599176048850142     9.25555555555556        0.377828523977579
3       273     muscle tissue development
GO:0006937      0.0066303979558913      18.3192848020434        0.123174866791226
2       89      regulation of muscle contraction
GO:0001778      0.00690176123684949     189.828947368421        0.0069199363365857
1       5       plasma membrane repair
GO:0030240      0.00690176123684949     189.828947368421        0.0069199363365857
1       5       skeletal muscle thin filament assembly
GO:0003205      0.00721940175550811     17.5091575091575        0.128710815860494
2       93      cardiac chamber development
GO:0000244      0.00827667226933348     151.852631578947        0.00830392360390284
1       6       assembly of spliceosomal tri-snRNP
GO:0014866      0.00827667226933348     151.852631578947        0.00830392360390284
1       6       skeletal myofibril assembly
GO:0090257      0.00929093127083658     15.3066239316239        0.146702650335617
2       106     regulation of muscle system process
GO:0000712      0.00964977483455431     126.535087719298        0.00968791087121998
1       7       resolution of meiotic recombination intermediates
GO:0033683      0.00964977483455431     126.535087719298        0.00968791087121998
1       7       nucleotide-excision repair, DNA incision
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GO:0051307      0.00964977483455431     126.535087719298        0.00968791087121998
1       7       meiotic chromosome separation
Tissue: Skin_Sun_Exposed_Lower_leg=>Thyroid     Type:   asymmetric
SourceGene:     RP11-1084E5.1(ENSG00000253796.1)
TargetGeneSet:  TNFRSF18        PLA2G2D GBP4    HSD3BP3 FCRL5   FCRL3   FCRLA   CD84
SLAMF7  LAX1    GPR113  IGKJ4   IGKJ2   IGKJ1   IGKV1-5 IGKV1-12        IGKV3-15
IGKV6-21        IGKV2-30        CXCR2P1 TIGIT   PARP15  IGJ     HAVCR1  LTB     RP11
ZC3H12D TAGAP   TRGC1   TRGV7   BLK     PTK2B   PNOC    PAX5    MS4A1   POU2AF1
CRTAM   CLECL1  BIN2    GS1     FLT3    CYSLTR2 TRAV1-2 TRAV27  IGHG2   IGHM
IGHJ5   IGHJ3   IGHV6-1 IGHV2-5 IGHV3-11        IGHV4-31        IGHV3-33
IGHV3-66        IGHV1-69        IGHV3-74        ARRDC4  TNFRSF17        ITGAL
GPR114  SNORD68 P2RX5   TBC1D27 TNFRSF13B       RAB37   CD79A   NLRP7   GTSF1L  ZBP1
RSPH1   IGLV6-57        IGLV1-51        IGLV9-49        IGLV1-36        IGLV3-25
IGLV2-23        IGLV2-8 IGLL5   IGLC1   IL2RB   MTCP1   RP4     CSAG1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006959      1.30915259897009e-06    20.5359195402299        0.354577537886651
6       122     humoral immune response
GO:0046649      3.31811191594273e-06    8.9954974271012 1.25845962217148        9
433     lymphocyte activation
GO:0042113      4.88940263576622e-06    16.1700680272109        0.444675108988997
6       153     B cell activation
GO:0002449      8.09150784582112e-06    14.7494824016563        0.485364334648121
6       167     lymphocyte mediated immunity
GO:0002252      1.2838448008193e-05     8.73389355742297        1.12186007888727
8       386     immune effector process
GO:0002443      3.05321979791158e-05    11.5479674796748        0.613244758148225
6       211     leukocyte mediated immunity
GO:0042267      7.10970809712616e-05    44.2584615384615        0.0813784513182479
3       28      natural killer cell mediated cytotoxicity
GO:0050778      7.66078716559701e-05    7.87226890756302        1.05791986713722
7       364     positive regulation of immune response
GO:0002228      7.914037128239e-05      42.5532544378698        0.0842848245796139
3       29      natural killer cell mediated immunity
GO:0051250      0.00010048412649917     18.8539473684211        0.244135353954744
4       84      negative regulation of lymphocyte activation
GO:0033209      0.000152468956192974    33.5104895104895        0.104629437409176
3       36      tumor necrosis factor-mediated signaling pathway
GO:0051249      0.000155125843090672    8.50300842358604        0.822503632966577
6       283     regulation of lymphocyte activation
GO:0002695      0.00017558057522173     16.2037351443124        0.281918206352502
4       97      negative regulation of leukocyte activation
GO:0050866      0.000238202804191413    14.911933298593 0.305169192443429       4
105     negative regulation of cell activation
GO:0002694      0.000306434352846846    7.45714285714286        0.932945816898485
6       321     regulation of leukocyte activation
GO:0001909      0.000338648297043203    25.1136363636364        0.136599543284202
3       47      leukocyte mediated cytotoxicity
GO:0006958      0.00040687161867526     23.505728314239 0.1453186630683 3       50
complement activation, classical pathway
GO:0050865      0.000436394388543592    6.95944609297725        0.996886028648536
6       343     regulation of cell activation
GO:0006956      0.000803009247930836    18.3961538461538        0.18310151546058
3       63      complement activation
GO:0045954      0.000845353877431116    55.3692307692308        0.0435955989204899
2       15      positive regulation of natural killer cell mediated cytotoxicity
GO:0002455      0.000879712823769607    17.8002481389578        0.18891426198879
3       65      humoral immune response mediated by circulating immunoglobulin
GO:0002717      0.000964339849869892    51.4107142857143        0.0465019721818559
2       16      positive regulation of natural killer cell mediated immunity
GO:0030183      0.00100324756452195     16.9751479289941        0.197633381772888
3       68      B cell differentiation
GO:0001906      0.00104673776673337     16.7167832167832        0.200539755034254
3       69      cell killing
```

GO:0002683	0.00116752255233183	9.61740890688259	0.465019721818559	4	160	negative regulation of immune system process
GO:0071356	0.00133281622931245	15.3173076923077	0.21797799460245	3	75	cellular response to tumor necrosis factor
GO:0042269	0.00136661034477667	42.3294117647059	0.0552210919659539	2	19	regulation of natural killer cell mediated cytotoxicity
GO:0002715	0.00151566211163264	39.975	0.0581274652273199	2	20	regulation of natural killer cell mediated immunity
GO:0046651	0.00152453015269653	8.92293233082707	0.499896200954951	4	172	lymphocyte proliferation
GO:0032943	0.00159065866290391	8.81671826625387	0.505708947477683	4	174	mononuclear cell proliferation
GO:0002253	0.00166625680359298	6.48786541643685	0.869005605148433	5	299	activation of immune response
GO:0072376	0.00172353849898644	13.9532619279455	0.238322607432012	3	82	protein activation cascade
GO:0070661	0.00187524961800535	8.41573033707865	0.528959933568611	4	182	leukocyte proliferation
GO:0043552	0.00200710821962668	34.2571428571429	0.0668465850114179	2	23	positive regulation of phosphatidylinositol 3-kinase activity
GO:0001912	0.00218554691840735	32.6977272727273	0.0697529582727839	2	24	positive regulation of leukocyte mediated cytotoxicity
GO:0043551	0.00218554691840735	32.6977272727273	0.0697529582727839	2	24	regulation of phosphatidylinositol 3-kinase activity
GO:0050850	0.00218554691840735	32.6977272727273	0.0697529582727839	2	24	positive regulation of calcium-mediated signaling
GO:0090218	0.00218554691840735	32.6977272727273	0.0697529582727839	2	24	positive regulation of lipid kinase activity
GO:0007218	0.00224985752505742	12.6631299734748	0.26157359352294	3	90	neuropeptide signaling pathway
GO:0050869	0.00256410862520172	29.96875	0.0755657047955159	2	26	negative regulation of B cell activation
GO:0034612	0.00262425819952185	11.9707357859532	0.27610545982977	3	95	response to tumor necrosis factor
GO:0019221	0.00295183107394798	5.65999034749035	0.991073282125804	5	341	cytokine-mediated signaling pathway
GO:0031343	0.00318554101184146	26.6333333333333	0.0842848245796139	2	29	positive regulation of cell killing
GO:0043550	0.00318554101184146	26.6333333333333	0.0842848245796139	2	29	regulation of lipid kinase activity
GO:0050853	0.00318554101184146	26.6333333333333	0.0842848245796139	2	29	B cell receptor signaling pathway
GO:0001910	0.00340681136275634	25.6803571428571	0.0871911978409799	2	30	regulation of leukocyte mediated cytotoxicity
GO:0016064	0.00407240445033978	10.1858974358974	0.322607432011626	3	111	immunoglobulin mediated immune response
GO:0050848	0.00411243099306514	23.1903225806452	0.0959103176250778	2	33	regulation of calcium-mediated signaling
GO:0019724	0.00438827834974687	9.90852390852391	0.331326551795723	3	114	B cell mediated immunity
GO:0032655	0.00461728111549336	21.7818181818182	0.10172306414781	2	35	regulation of interleukin-12 production
GO:0031341	0.00487991712486397	21.1397058823529	0.104629437409176	2	36	regulation of cell killing
GO:0032615	0.00514930741245981	20.5342857142857	0.107535810670542	2	37	interleukin-12 production
GO:0071345	0.00650112841672883	4.66083078152044	1.19451941042142	5	411	cellular response to cytokine stimulus
GO:0002705	0.00722085666126351	17.1035714285714	0.127880423500104	2	44	positive regulation of leukocyte mediated immunity
GO:0002708	0.00722085666126351	17.1035714285714	0.127880423500104	2	44	positive regulation of lymphocyte mediated immunity
GO:0010522	0.00722085666126351	17.1035714285714	0.127880423500104			

```
2       44      regulation of calcium ion transport into cytosol
GO:0051924      0.00837453187443606     7.78396072013093        0.418517749636703
3       144     regulation of calcium ion transport
GO:0002291      0.00869440324222703     175.69512195122 0.00871911978409799     1
3       T cell activation via T cell receptor contact with antigen bound to MHC
molecule on antigen presenting cell
GO:0016056      0.00869440324222703     175.69512195122 0.00871911978409799     1
3       rhodopsin mediated signaling pathway
GO:0031585      0.00869440324222703     175.69512195122 0.00871911978409799     1
3       regulation of inositol 1,4,5-trisphosphate-sensitive calcium-release channel
activity
GO:0031987      0.00869440324222703     175.69512195122 0.00871911978409799     1
3       locomotion involved in locomotory behavior
GO:0038110      0.00869440324222703     175.69512195122 0.00871911978409799     1
3       interleukin-2-mediated signaling pathway
GO:0051643      0.00869440324222703     175.69512195122 0.00871911978409799     1
3       endoplasmic reticulum localization
GO:0001776      0.00889458699134167     15.2787234042553        0.142412289806934
2       49      leukocyte homeostasis
GO:0046427      0.0096081169746031      14.6530612244898        0.148225036329666
2       51      positive regulation of JAK-STAT cascade
Tissue: Skin_Sun_Exposed_Lower_leg=>Thyroid     Type:   cluster
SourceGene:     RP11-1084E5.1(ENSG00000253796.1)
TargetGeneSet:  TNFRSF18        PLA2G2D GBP4    HSD3BP3 FCRL5   FCRL3   FCRLA   CD84
SLAMF7  LAX1    GPR113  IGKJ4   IGKJ2   IGKJ1   IGKV1-5 IGKV1-12        IGKV3-15
IGKV6-21        IGKV2-30        CXCR2P1 TIGIT   PARP15  IGJ     HAVCR1  LTB     RP11
ZC3H12D TAGAP   TRGC1   TRGV7   BLK     PTK2B   PNOC    PAX5    MS4A1   POU2AF1
CRTAM   CLECL1  BIN2    GS1     FLT3    CYSLTR2 TRAV1-2 TRAV27  IGHG2   IGHM
IGHJ5   IGHJ3   IGHV6-1 IGHV2-5 IGHV3-11        IGHV4-31        IGHV3-33
IGHV3-66        IGHV1-69        IGHV3-74        ARRDC4  TNFRSF17        ITGAL
GPR114  SNORD68 P2RX5   TBC1D27 TNFRSF13B       RAB37   CD79A   NLRP7   GTSF1L  ZBP1
RSPH1   IGLV6-57        IGLV1-51        IGLV9-49        IGLV1-36        IGLV3-25
IGLV2-23        IGLV2-8 IGLL5   IGLC1   IL2RB   MTCP1   RP4     CSAG1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006959      1.30915259897009e-06    20.5359195402299        0.354577537886651
6       122     humoral immune response
GO:0046649      3.31811191594273e-06    8.9954974271012 1.25845962217148        9
433     lymphocyte activation
GO:0042113      4.88940263576622e-06    16.1700680272109        0.444675108988997
6       153     B cell activation
GO:0002449      8.09150784582112e-06    14.7494824016563        0.485364334648121
6       167     lymphocyte mediated immunity
GO:0002252      1.2838448008193e-05     8.73389355742297        1.12186007888727
8       386     immune effector process
GO:0002443      3.05321979791158e-05    11.5479674796748        0.613244758148225
6       211     leukocyte mediated immunity
GO:0042267      7.10970809712616e-05    44.2584615384615        0.0813784513182479
3       28      natural killer cell mediated cytotoxicity
GO:0050778      7.66078716559701e-05    7.87226890756302        1.05791986713722
7       364     positive regulation of immune response
GO:0002228      7.914037128239e-05      42.5532544378698        0.0842848245796139
3       29      natural killer cell mediated immunity
GO:0051250      0.00010048412649917     18.8539473684211        0.244135353954744
4       84      negative regulation of lymphocyte activation
GO:0033209      0.000152468956192974    33.5104895104895        0.104629437409176
3       36      tumor necrosis factor-mediated signaling pathway
GO:0051249      0.000155125843090672    8.50300842358604        0.822503632966577
6       283     regulation of lymphocyte activation
GO:0002695      0.00017558057522173     16.2037351443124        0.281918206352502
4       97      negative regulation of leukocyte activation
GO:0050866      0.000238202804191413    14.911933298593 0.305169192443429       4
105     negative regulation of cell activation
GO:0002694      0.000306434352846846    7.45714285714286        0.932945816898485
```

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6       321     regulation of leukocyte activation
GO:0001909      0.000338648297043203    25.1136363636364        0.136599543284202
3       47      leukocyte mediated cytotoxicity
GO:0006958      0.00040687161867526     23.505728314239 0.1453186630683 3       50
complement activation, classical pathway
GO:0050865      0.000436394388543592    6.95944609297725        0.996886028648536
6       343     regulation of cell activation
GO:0006956      0.000803009247930836    18.3961538461538        0.183101515466058
3       63      complement activation
GO:0045954      0.000845353877431116    55.3692307692308        0.0435955989204899
2       15      positive regulation of natural killer cell mediated cytotoxicity
GO:0002455      0.000879712823769607    17.8002481389578        0.18891426198879
3       65      humoral immune response mediated by circulating immunoglobulin
GO:0002717      0.000964339849869892    51.4107142857143        0.0465019721818559
2       16      positive regulation of natural killer cell mediated immunity
GO:0030183      0.00100324756452195     16.9751479289941        0.197633381772888
3       68      B cell differentiation
GO:0001906      0.00104673776673337     16.7167832167832        0.200539755034254
3       69      cell killing
GO:0002683      0.00116752255233183     9.61740890688259        0.465019721818559
4       160     negative regulation of immune system process
GO:0071356      0.00133281622931245     15.3173076923077        0.21797799460245
3       75      cellular response to tumor necrosis factor
GO:0042269      0.00136661034477667     42.3294117647059        0.0552210919659539
2       19      regulation of natural killer cell mediated cytotoxicity
GO:0002715      0.00151566211163264     39.975  0.0581274652273199      2       20
regulation of natural killer cell mediated immunity
GO:0046651      0.00152453015269653     8.92293233082707        0.499896200954951
4       172     lymphocyte proliferation
GO:0032943      0.00159065866290391     8.81671826625387        0.505708947477683
4       174     mononuclear cell proliferation
GO:0002253      0.00166625680359298     6.48786541643685        0.869005605148433
5       299     activation of immune response
GO:0072376      0.00172353849898644     13.9532619279455        0.238322607432012
3       82      protein activation cascade
GO:0070661      0.00187524961800535     8.41573033707865        0.528959933568611
4       182     leukocyte proliferation
GO:0043552      0.00200710821962668     34.2571428571429        0.0668465850114179
2       23      positive regulation of phosphatidylinositol 3-kinase activity
GO:0001912      0.00218554691840735     32.6977272727273        0.0697529582727839
2       24      positive regulation of leukocyte mediated cytotoxicity
GO:0043551      0.00218554691840735     32.6977272727273        0.0697529582727839
2       24      regulation of phosphatidylinositol 3-kinase activity
GO:0050850      0.00218554691840735     32.6977272727273        0.0697529582727839
2       24      positive regulation of calcium-mediated signaling
GO:0090218      0.00218554691840735     32.6977272727273        0.0697529582727839
2       24      positive regulation of lipid kinase activity
GO:0007218      0.00224985752505742     12.6631299734748        0.26157359352294
3       90      neuropeptide signaling pathway
GO:0050869      0.00256410862520172     29.96875        0.0755657047955159      2
26      negative regulation of B cell activation
GO:0034612      0.00262425819952185     11.9707357859532        0.27610545982977
3       95      response to tumor necrosis factor
GO:0019221      0.00295183107394798     5.65999034749035        0.991073282125804
5       341     cytokine-mediated signaling pathway
GO:0031343      0.00318554101184146     26.6333333333333        0.0842848245796139
2       29      positive regulation of cell killing
GO:0043550      0.00318554101184146     26.6333333333333        0.0842848245796139
2       29      regulation of lipid kinase activity
GO:0050853      0.00318554101184146     26.6333333333333        0.0842848245796139
2       29      B cell receptor signaling pathway
GO:0001910      0.00340681136275634     25.6803571428571        0.0871911978409799
2       30      regulation of leukocyte mediated cytotoxicity
```

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GO:0016064      0.00407240445033978     10.1858974358974        0.322607432011626
3       111     immunoglobulin mediated immune response
GO:0050848      0.00411243099306514     23.1903225806452        0.0959103176250778
2       33      regulation of calcium-mediated signaling
GO:0019724      0.00438827834974687     9.90852390852391        0.331326551795723
3       114     B cell mediated immunity
GO:0032655      0.00461728111549336     21.7818181818182        0.10172306414781
2       35      regulation of interleukin-12 production
GO:0031341      0.00487991712486397     21.1397058823529        0.104629437409176
2       36      regulation of cell killing
GO:0032615      0.00514930741245981     20.5342857142857        0.107535810670542
2       37      interleukin-12 production
GO:0071345      0.00650112841672883     4.66083078152044        1.19451941042142
5       411     cellular response to cytokine stimulus
GO:0002705      0.00722085666126351     17.1035714285714        0.127880423500104
2       44      positive regulation of leukocyte mediated immunity
GO:0002708      0.00722085666126351     17.1035714285714        0.127880423500104
2       44      positive regulation of lymphocyte mediated immunity
GO:0010522      0.00722085666126351     17.1035714285714        0.127880423500104
2       44      regulation of calcium ion transport into cytosol
GO:0051924      0.00837453187443606     7.78396072013093        0.418517749636703
3       144     regulation of calcium ion transport
GO:0002291      0.00869440324222703     175.69512195122 0.00871911978409799     1
3       T cell activation via T cell receptor contact with antigen bound to MHC
molecule on antigen presenting cell
GO:0016056      0.00869440324222703     175.69512195122 0.00871911978409799     1
3       rhodopsin mediated signaling pathway
GO:0031585      0.00869440324222703     175.69512195122 0.00871911978409799     1
3       regulation of inositol 1,4,5-trisphosphate-sensitive calcium-release channel
activity
GO:0031987      0.00869440324222703     175.69512195122 0.00871911978409799     1
3       locomotion involved in locomotory behavior
GO:0038110      0.00869440324222703     175.69512195122 0.00871911978409799     1
3       interleukin-2-mediated signaling pathway
GO:0051643      0.00869440324222703     175.69512195122 0.00871911978409799     1
3       endoplasmic reticulum localization
GO:0001776      0.00889458699134167     15.2787234042553        0.142412289806934
2       49      leukocyte homeostasis
GO:0046427      0.00960811169746031     14.6530612244898        0.148225036329666
2       51      positive regulation of JAK-STAT cascade
Tissue: Skin_Sun_Exposed_Lower_leg=>Thyroid     Type:   asymmetric
SourceGene:     RP11-293B20.1(ENSG00000260518.1)
TargetGeneSet:  CD53    FCGR2A  FCGR3A  RP11    CD86    PDE6B   RHOH    MOCS2   GZMA
DOCK2   LY86    GPSM3   RP1     DOK2    FAM203A TNFSF8  MRRF    AMPD3   CD3E    CD3D
BIN2    NCKAP1L SELPLG  LCP1    TRAV21  SLC7A7  CORO1A  CFDP1   CCL4L2  IKZF3   TNS4
SKAP1   ICAM2   CBX4    VAV1    CD37    LAIR1   C20orf196       TH1L    ITGB2
APOBEC3F        FAM127A
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0042110      2.68668050517739e-09    18.2614886731392        0.772610891979794
10      319     T cell activation
GO:0046649      3.35977389149501e-09    15.1988546603476        1.04871635180956
11      433     lymphocyte activation
GO:0030098      2.33314803451438e-08    21.4965986394558        0.494083454432219
8       204     lymphocyte differentiation
GO:0030217      7.78853087415086e-08    23.9379194630872        0.377828523977579
7       156     T cell differentiation
GO:0002521      4.77767431944924e-07    14.2323003275384        0.731437270777109
8       302     leukocyte differentiation
GO:0046631      1.47696702907015e-06    31.0367965367965        0.19860217286001
5       82      alpha-beta T cell activation
GO:0050870      3.07066414450078e-06    17.869592476489 0.414158189744654       6
171     positive regulation of T cell activation
GO:0051249      4.31125997728482e-06    12.8079710144928        0.685419694138814
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7       283     regulation of lymphocyte activation
GO:0045061      8.64692470749186e-06    96.4419642857143        0.0411736212026849
3       17      thymic T cell selection
GO:0002694      9.84499468954118e-06    11.2277070063694        0.777454847415404
7       321     regulation of leukocyte activation
GO:0051251      1.14494044477565e-05    14.0640158389705        0.520725209328074
6       215     positive regulation of lymphocyte activation
GO:0030097      1.1480459922469e-05     9.09141229141229        1.12137568334371
8       463     hemopoiesis
GO:0050863      1.33916112296405e-05    13.665757818765 0.535257075634904       6
221     regulation of T cell activation
GO:0050865      1.51423074279706e-05    10.4761904761905        0.830738357207114
7       343     regulation of cell activation
GO:0002696      1.80774351286182e-05    12.9324016405894        0.564320808248564
6       233     positive regulation of leukocyte activation
GO:0048534      1.86345632831662e-05    8.4745608031029 1.19887897031347        8
495     hemopoietic or lymphoid organ development
GO:0050867      2.13714392741034e-05    12.5393457117595        0.581274652273199
6       240     positive regulation of cell activation
GO:0050900      2.18791773820163e-05    12.4851063829787        0.583696629991004
6       241     leukocyte migration
GO:0045058      2.54398158559894e-05    64.2633928571429        0.0581274652273199
3       24      T cell selection
GO:0031294      3.10160964812008e-05    26.0699681962744        0.181648328835375
4       75      lymphocyte costimulation
GO:0031295      3.10160964812008e-05    26.0699681962744        0.181648328835375
4       75      T cell costimulation
GO:0046651      5.47850058892634e-05    14.2205588822355        0.416580167462459
5       172     lymphocyte proliferation
GO:0032943      5.78834884852929e-05    14.0502958579882        0.421424122898069
5       174     mononuclear cell proliferation
GO:0070661      7.16565160147345e-05    13.4077212806026        0.440799944640509
5       182     leukocyte proliferation
GO:0043374      0.000118766137090523    174.678787878788        0.016953844024635
2       7       CD8-positive, alpha-beta T cell differentiation
GO:0046635      0.000150299917042784    33.69375        0.104145041865615       3
43      positive regulation of alpha-beta T cell activation
GO:0045059      0.000158113906383722    145.555555555556        0.01937582174244
2       8       positive thymic T cell selection
GO:0042098      0.000181896641323896    16.1878890775325        0.28579337070099
4       118     T cell proliferation
GO:0036037      0.000202980038708031    124.753246753247        0.021797799460245
2       9       CD8-positive, alpha-beta T cell activation
GO:0050851      0.00021335795684026     15.5023041474654        0.297903259290015
4       123     antigen receptor-mediated signaling pathway
GO:0002757      0.000237560414639501    10.2797101449275        0.569164763684174
5       235     immune response-activating signal transduction
GO:0002429      0.000287787005463801    14.2905726431608        0.322123036468065
4       133     immune response-activating cell surface receptor signaling pathway
GO:0002764      0.000304705132251831    9.72085048010974        0.600650474015639
5       248     immune response-regulating signaling pathway
GO:0007603      0.000309165754825163    97.016835016835 0.026641754895855       2
11      phototransduction, visible light
GO:0043368      0.000309165754825163    97.016835016835 0.026641754895855       2
11      positive T cell selection
GO:0045060      0.000309165754825163    97.016835016835 0.026641754895855       2
11      negative thymic T cell selection
GO:0046634      0.000313218738697508    25.8966346153846        0.133208774479275
3       55      regulation of alpha-beta T cell activation
GO:0043383      0.000370434731468843    87.3090909090909        0.02906373261366
2       12      negative T cell selection
GO:0002768      0.000389446373958234    13.1576036866359        0.348764791363919
4       144     immune response-regulating cell surface receptor signaling pathway
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GO:0050670	0.000389446373958234	13.1576036866359	0.348764791363919	4	144	regulation of lymphocyte proliferation
GO:0032944	0.000399808628339826	13.0633722260352	0.351186769081724	4	145	regulation of mononuclear cell proliferation
GO:0033077	0.000425431799924838	23.207974137931	0.147740640786105	3	61	T cell differentiation in thymus
GO:0045086	0.000437120856360053	79.366391184573	0.031485710331465	2	13	positive regulation of interleukin-2 biosynthetic process
GO:0070663	0.000454602824247297	12.6115775519222	0.363296657670749	4	150	regulation of leukocyte proliferation
GO:0046632	0.000512923439393237	21.7046370967742	0.157428551657325	3	65	alpha-beta T cell differentiation
GO:0042102	0.000536458947008329	21.358630952381	0.15985052937513	3	66	positive regulation of T cell proliferation
GO:0002253	0.000715435393470298	8.00566893424036	0.724171337623694	5	299	activation of immune response
GO:0043372	0.000757536233832414	58.1858585858586	0.0411736212026849	2	17	positive regulation of CD4-positive, alpha-beta T cell differentiation
GO:0045577	0.000757536233832414	58.1858585858586	0.0411736212026849	2	17	regulation of B cell differentiation
GO:0045076	0.000949598362949957	51.3333333333333	0.0460175766382949	2	19	regulation of interleukin-2 biosynthetic process
GO:2000516	0.000949598362949957	51.3333333333333	0.0460175766382949	2	19	positive regulation of CD4-positive, alpha-beta T cell activation
GO:0009584	0.00105350659720668	48.4781144781145	0.0484395543560999	2	20	detection of visible light
GO:0007596	0.00112639128863686	5.85534062237174	1.20614490346689	6	498	blood coagulation
GO:0006909	0.00116068996689376	16.1893825301205	0.20829008373123	3	86	phagocytosis
GO:0042094	0.00116263356851686	45.9234449760766	0.0508615320739049	2	21	interleukin-2 biosynthetic process
GO:0046633	0.00116263356851686	45.9234449760766	0.0508615320739049	2	21	alpha-beta T cell proliferation
GO:0002697	0.00135700176970707	9.31324709349926	0.486817521278804	4	201	regulation of immune effector process
GO:0032673	0.00139644608680904	41.5440115440115	0.0557054875095149	2	23	regulation of interleukin-4 production
GO:0043029	0.00139644608680904	41.5440115440115	0.0557054875095149	2	23	T cell homeostasis
GO:0050671	0.00159389247516337	14.4385080645161	0.23250986090928	3	96	positive regulation of lymphocyte proliferation
GO:0032946	0.00164204411823343	14.2839095744681	0.234931838627085	3	97	positive regulation of mononuclear cell proliferation
GO:0009167	0.00165084146432016	37.9262187088274	0.0605494429451249	2	25	purine ribonucleoside monophosphate metabolic process
GO:0050778	0.00171932957720419	6.52599814298979	0.881599889281019	5	364	positive regulation of immune response
GO:0008360	0.00174106597559996	13.984375	0.239775794062695	3	99	regulation of cell shape
GO:0045619	0.00174106597559996	13.984375	0.239775794062695	3	99	regulation of lymphocyte differentiation
GO:0050852	0.00174106597559996	13.984375	0.239775794062695	3	99	T cell receptor signaling pathway
GO:0009126	0.00178569731497192	36.3434343434343	0.0629714206629299	2	26	purine nucleoside monophosphate metabolic process
GO:0070665	0.00179194860229972	13.8392396907216	0.2421977717805	3	100	positive regulation of leukocyte proliferation
GO:0042129	0.00184375387589325	13.6970663265306	0.244619749498305	3	101	regulation of T cell proliferation
GO:0032633	0.00192562655023593	34.8872727272727	0.0653933983807349	2	27	interleukin-4 production

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GO:0043370      0.00192562655023593     34.8872727272727        0.0653933983807349
2       27      regulation of CD4-positive, alpha-beta T cell differentiation
GO:2000514      0.00222060948894769     32.2985409652076        0.0702373538163449
2       29      regulation of CD4-positive, alpha-beta T cell activation
GO:0002252      0.00222277992826332     6.13954505686789        0.934883399072729
5       386     immune effector process
GO:0046638      0.00237561555054854     31.1428571428571        0.0726593315341499
2       30      positive regulation of alpha-beta T cell differentiation
GO:0030595      0.00241385960743403     12.4201388888889        0.268839526676355
3       111     leukocyte chemotaxis
GO:0051607      0.00253953689296051     12.1926136363636        0.273683482111965
3       113     defense response to virus
GO:0030838      0.00270053835413189     29.0626262626263        0.0775032869697599
2       32      positive regulation of actin filament polymerization
GO:0007602      0.00287040793370604     28.1231671554252        0.0799252646875649
2       33      phototransduction
GO:0007159      0.00359872757580016     24.9021645021645        0.0896131755587849
2       37      leukocyte cell-cell adhesion
GO:0009161      0.0039918667573981      23.5528255528256        0.0944571309943949
2       39      ribonucleoside monophosphate metabolic process
GO:0032663      0.0039918667573981      23.5528255528256        0.0944571309943949
2       39      regulation of interleukin-2 production
GO:0002260      0.00419560037852698     22.9314194577352        0.0968791087121998
2       40      lymphocyte homeostasis
GO:0009583      0.00419560037852698     22.9314194577352        0.0968791087121998
2       40      detection of light stimulus
GO:0046637      0.00419560037852698     22.9314194577352        0.0968791087121998
2       40      regulation of alpha-beta T cell differentiation
GO:0060326      0.00428179556092064     10.0679041353383        0.329388969621479
3       136     cell chemotaxis
GO:0043367      0.00440407944310129     22.3418803418803        0.0993010864300048
2       41      CD4-positive, alpha-beta T cell differentiation
GO:0035710      0.004835182637369       21.2490761271249        0.104145041865615
2       43      CD4-positive, alpha-beta T cell activation
GO:0030593      0.00505776132746409     20.7417027417027        0.10656701958342
2       44      neutrophil chemotaxis
GO:0032623      0.00505776132746409     20.7417027417027        0.10656701958342
2       44      interleukin-2 production
GO:0032273      0.00528499458136162     20.2579281183932        0.108988997301225
2       45      positive regulation of protein polymerization
GO:0002286      0.00551685987126941     19.7961432506887        0.11141097501903
2       46      T cell activation involved in immune response
GO:0009123      0.00551685987126941     19.7961432506887        0.11141097501903
2       46      nucleoside monophosphate metabolic process
GO:0042113      0.00594279085236457     8.91625 0.370562590824164       3       153
B cell activation
GO:0001776      0.00624002382385215     18.528691166989 0.118676908172445       2
49      leukocyte homeostasis
GO:0030888      0.00649019350462653     18.1414141414141        0.12109888589025
2       50      regulation of B cell proliferation
GO:0001766      0.00724884985550822     211.970588235294        0.00726593315341499
1       3       membrane raft polarization
GO:0002669      0.00724884985550822     211.970588235294        0.00726593315341499
1       3       positive regulation of T cell anergy
GO:0002913      0.00724884985550822     211.970588235294        0.00726593315341499
1       3       positive regulation of lymphocyte anergy
GO:0006922      0.00724884985550822     211.970588235294        0.00726593315341499
1       3       cleavage of lamin
GO:0009158      0.00724884985550822     211.970588235294        0.00726593315341499
1       3       ribonucleoside monophosphate catabolic process
GO:0009169      0.00724884985550822     211.970588235294        0.00726593315341499
1       3       purine ribonucleoside monophosphate catabolic process
GO:0031580      0.00724884985550822     211.970588235294        0.00726593315341499
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1       3       membrane raft distribution
GO:0032071      0.00724884985550822     211.970588235294        0.00726593315341499
1       3       regulation of endodeoxyribonuclease activity
GO:0032641      0.00724884985550822     211.970588235294        0.00726593315341499
1       3       lymphotoxin A production
GO:0032790      0.00724884985550822     211.970588235294        0.00726593315341499
1       3       ribosome disassembly
GO:0035507      0.00724884985550822     211.970588235294        0.00726593315341499
1       3       regulation of myosin-light-chain-phosphatase activity
GO:0035845      0.00724884985550822     211.970588235294        0.00726593315341499
1       3       photoreceptor cell outer segment organization
GO:0042109      0.00724884985550822     211.970588235294        0.00726593315341499
1       3       lymphotoxin A biosynthetic process
GO:0045404      0.00724884985550822     211.970588235294        0.00726593315341499
1       3       positive regulation of interleukin-4 biosynthetic process
GO:0060099      0.00724884985550822     211.970588235294        0.00726593315341499
1       3       regulation of phagocytosis, engulfment
GO:0060100      0.00724884985550822     211.970588235294        0.00726593315341499
1       3       positive regulation of phagocytosis, engulfment
GO:0045582      0.0072677375634005      17.0707070707071        0.128364819043665
2       53      positive regulation of T cell differentiation
GO:0042100      0.00836672552680524     15.8247933884298        0.138052729914885
2       57      B cell proliferation
GO:0050688      0.00836672552680524     15.8247933884298        0.138052729914885
2       57      regulation of defense response to virus
GO:0042108      0.00894251186372708     15.2674109516215        0.142896685350495
2       59      positive regulation of cytokine biosynthetic process
GO:0001771      0.00965377027737002     141.303921568627        0.00968791087121998
1       4       immunological synapse formation
GO:0002249      0.00965377027737002     141.303921568627        0.00968791087121998
1       4       lymphocyte anergy
GO:0002667      0.00965377027737002     141.303921568627        0.00968791087121998
1       4       regulation of T cell anergy
GO:0002870      0.00965377027737002     141.303921568627        0.00968791087121998
1       4       T cell anergy
GO:0002911      0.00965377027737002     141.303921568627        0.00968791087121998
1       4       regulation of lymphocyte anergy
GO:0006923      0.00965377027737002     141.303921568627        0.00968791087121998
1       4       cleavage of cytoskeletal proteins involved in apoptosis
GO:0009128      0.00965377027737002     141.303921568627        0.00968791087121998
1       4       purine nucleoside monophosphate catabolic process
GO:0032070      0.00965377027737002     141.303921568627        0.00968791087121998
1       4       regulation of deoxyribonuclease activity
GO:0032264      0.00965377027737002     141.303921568627        0.00968791087121998
1       4       IMP salvage
GO:0042097      0.00965377027737002     141.303921568627        0.00968791087121998
1       4       interleukin-4 biosynthetic process
GO:0045402      0.00965377027737002     141.303921568627        0.00968791087121998
1       4       regulation of interleukin-4 biosynthetic process
GO:0051665      0.00965377027737002     141.303921568627        0.00968791087121998
1       4       membrane raft localization
GO:2001185      0.00965377027737002     141.303921568627        0.00968791087121998
1       4       regulation of CD8-positive, alpha-beta T cell activation
GO:0045621      0.00983857231101985     14.5010101010101        0.15016261850391
2       62      positive regulation of lymphocyte differentiation
Tissue: Skin_Sun_Exposed_Lower_leg=>Thyroid     Type:   cluster
SourceGene:     RP11-320N21.1(ENSG00000245080.3)
TargetGeneSet:  NOC2L   KIAA0090        PSMB2   CYB5RL  MRPL37  CCDC76  AMY2A
SEC22B  PIAS3   RUSC1-AS1       METTL13 HEATR1  RNASEH1 CCT7    C2orf55 TMEM177 RP11
ATG7    XYLB    U4      RUVBL1  PSMD2   LMLN    CRMP1   CNGA1   CCT5    NHP2
ZSCAN23 ZNRD1-AS1       ATAT1   AARS2   BEND6   PLEKHA8 IGFBP1  COPS6   FAM115B GS1
EXOSC4  TUB     RPS6KA4 DLAT    DCPS    COPS7A  TAS2R20 PFKM    NUP37   PSMB5
RPAP1   PKM2    CCDC113 DPH1    PSMB6   TP53    PFAS    ZNF29P  ERAL1   PSMD11  LIG3
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PSMB3   TUBG1   PHB     C19orf55        PSMD8   GRWD1   RUVBL2  CBR1    PISD
XRCC6   ATXN10  POLA1   APEX2   PGK1    G6PD
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006977      1.69180334633732e-10    40.3546798029557        0.260328004982354
8       66      DNA damage response, signal transduction by p53 class mediator 
resulting in cell cycle arrest
GO:0072413      1.69180334633732e-10    40.3546798029557        0.260328004982354
8       66      signal transduction involved in mitotic cell cycle checkpoint
GO:0072431      1.69180334633732e-10    40.3546798029557        0.260328004982354
8       66      signal transduction involved in mitotic cell cycle G1/S transition 
DNA damage checkpoint
GO:0072474      1.69180334633732e-10    40.3546798029557        0.260328004982354
8       66      signal transduction involved in mitotic cell cycle G1/S checkpoint
GO:0072401      1.91539867176746e-10    39.6679349705984        0.264272368694208
8       67      signal transduction involved in DNA integrity checkpoint
GO:0072404      1.91539867176746e-10    39.6679349705984        0.264272368694208
8       67      signal transduction involved in G1/S transition checkpoint
GO:0072422      1.91539867176746e-10    39.6679349705984        0.264272368694208
8       67      signal transduction involved in DNA damage checkpoint
GO:0072395      2.16422956295763e-10    39.0040816326531        0.268216732406062
8       68      signal transduction involved in cell cycle checkpoint
GO:0031571      3.87650819970675e-10    35.9912087912088        0.287938550965331
8       73      mitotic cell cycle G1/S transition DNA damage checkpoint
GO:0000216      7.38828971619158e-10    32.9359011210118        0.311604733236454
8       79      M/G1 transition of mitotic cell cycle
GO:0071158      8.18441281880951e-10    32.4761904761905        0.315549096948308
8       80      positive regulation of cell cycle arrest
GO:0031575      1.00023942202098e-09    31.5940430226144        0.323437824372016
8       82      mitotic cell cycle G1/S transition checkpoint
GO:0071779      1.47116870827763e-09    29.9654631083203        0.339215279219431
8       86      G1/S transition checkpoint
GO:0006521      2.30334928262346e-09    40.1632 0.22482873157567        7       57
regulation of cellular amino acid metabolic process
GO:2000045      4.56365470640182e-09    25.6613590491142        0.390492007473531
8       99      regulation of G1/S transition of mitotic cell cycle
GO:0051436      7.34990694493526e-09    33.446  0.264272368694208       7       67
negative regulation of ubiquitin-protein ligase activity involved in mitotic cell 
cycle
GO:0033238      1.22625579913569e-08    30.8624615384615        0.283994187253477
7       72      regulation of cellular amine metabolic process
GO:0051352      1.22625579913569e-08    30.8624615384615        0.283994187253477
7       72      negative regulation of ligase activity
GO:0051437      1.22625579913569e-08    30.8624615384615        0.283994187253477
7       72      positive regulation of ubiquitin-protein ligase activity involved in 
mitotic cell cycle
GO:0051444      1.22625579913569e-08    30.8624615384615        0.283994187253477
7       72      negative regulation of ubiquitin-protein ligase activity
GO:0002479      1.63724525491548e-08    29.4947058823529        0.295827278389039
7       75      antigen processing and presentation of exogenous peptide antigen via 
MHC class I, TAP-dependent
GO:0030330      1.7213929464672e-08     21.3967421831118        0.461490554286901
8       117     DNA damage response, signal transduction by p53 class mediator
GO:0051439      2.1594916278439e-08     28.2425352112676        0.3076603695246 7
78      regulation of ubiquitin-protein ligase activity involved in mitotic cell 
cycle
GO:0042590      2.36225914332687e-08    27.8483333333333        0.311604733236454
7       79      antigen processing and presentation of exogenous peptide antigen via 
MHC class I
GO:0072331      2.55290897424942e-08    20.2718722271517        0.485156736558024
8       123     signal transduction by p53 class mediator
GO:0051443      3.07004488772205e-08    26.7288 0.323437824372016       7       82
positive regulation of ubiquitin-protein ligase activity
GO:0002478      3.34264755705798e-08    26.3752631578947        0.32738218808387
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7       83      antigen processing and presentation of exogenous peptide antigen
GO:0031145      3.34264755705798e-08    26.3752631578947        0.32738218808387
7       83      anaphase-promoting complex-dependent proteasomal ubiquitin-dependent
protein catabolic process
GO:0000077      3.94165223336479e-08    19.0993643358983        0.512767282541001
8       130     DNA damage checkpoint
GO:0019884      3.94971858815973e-08    25.6953846153846        0.335270915507577
7       85      antigen processing and presentation of exogenous antigen
GO:0000082      4.22080493396771e-08    15.0603813559322        0.733651650404816
9       186     G1/S transition of mitotic cell cycle
GO:0051351      4.28665798083472e-08    25.3683544303797        0.339215279219431
7       86      positive regulation of ligase activity
GO:0000084      4.99586841258498e-08    18.4878522837706        0.528544737388416
8       134     S phase of mitotic cell cycle
GO:0031570      5.60840019695119e-08    18.1964285714286        0.536433464812124
8       136     DNA integrity checkpoint
GO:0007093      6.64817448853105e-08    17.7759775665992        0.548266555947685
8       139     mitotic cell cycle checkpoint
GO:0031397      6.86285717730111e-08    23.5677647058824        0.362881461490554
7       92      negative regulation of protein ubiquitination
GO:0042770      7.02976646102498e-08    17.6400742115028        0.552210919659539
8       140     signal transduction in response to DNA damage
GO:0051320      8.28985944607622e-08    17.2444444444444        0.564044010795101
8       143     S phase
GO:0051438      9.22454663005284e-08    22.5022471910112        0.37865891633797
7       96      regulation of ubiquitin-protein ligase activity
GO:2000602      1.02690770372898e-07    16.7435031566583        0.579821465642516
8       147     regulation of interphase of mitotic cell cycle
GO:0002474      1.14169414322057e-07    21.7639130434783        0.390492007473531
7       99      antigen processing and presentation of peptide antigen via MHC class
I
GO:0051340      1.2239056893103e-07     21.5283870967742        0.394436371185385
7       100     regulation of ligase activity
GO:0090068      1.26419058489461e-07    16.2705865563008        0.595598920489931
8       151     positive regulation of cell cycle process
GO:0010565      1.47176005622437e-07    15.9329046687168        0.607432011625493
8       154     regulation of cellular ketone metabolic process
GO:0048002      2.0807229048262e-07     19.8120792079208        0.425991280880216
7       108     antigen processing and presentation of peptide antigen
GO:0051329      2.18365624736862e-07    9.11424858223062        1.49491384679261
11      379     interphase of mitotic cell cycle
GO:0051325      2.69142243053328e-07    8.91524051803885        1.52646875648744
11      387     interphase
GO:0031396      2.87416013552962e-07    14.5244897959184        0.662653103591447
8       168     regulation of protein ubiquitination
GO:0031398      6.29410745103251e-07    16.653  0.500934191405439       7       127
positive regulation of protein ubiquitination
GO:0006520      8.97584506929342e-07    7.8407838334354 1.72368694208013        11
437     cellular amino acid metabolic process
GO:0046365      1.79097767566084e-06    19.1256684491979        0.370770188914262
6       94      monosaccharide catabolic process
GO:0019882      2.11068667280847e-06    13.7576551724138        0.599543284201785
7       152     antigen processing and presentation
GO:0031400      2.38366102018076e-06    9.08698453608247        1.18330911355616
9       300     negative regulation of protein modification process
GO:0016052      2.73240688138478e-06    13.2054304635762        0.623209466472908
7       158     carbohydrate catabolic process
GO:0000209      3.09651986475303e-06    12.9454545454545        0.63504255760847
7       161     protein polyubiquitination
GO:0000075      4.48521167920036e-06    9.87964416535845        0.954536018268632
8       242     cell cycle checkpoint
GO:0044106      7.21446604962585e-06    11.3097727272727        0.721818559269255
7       183     cellular amine metabolic process
```

GO:0071156	8.49875948306201e-06	9.01658163265306	1.04131201992942	8	264	regulation of cell cycle arrest
GO:0016032	9.19777860880485e-06	6.73179910261977	1.77890803404609	10	451	viral reproduction
GO:0006007	1.11607128859528e-05	19.6758241758242	0.295827278389039	5	75	glucose catabolic process
GO:0009308	1.37475198092014e-05	10.1941538461538	0.796761469794478	7	202	amine metabolic process
GO:0032269	1.54541541720387e-05	7.1265243902439	1.49096948308076	9	378	negative regulation of cellular protein metabolic process
GO:0043161	1.71432678751984e-05	9.8360396039604	0.82437201577455	7	209	proteasomal ubiquitin-dependent protein catabolic process
GO:0010498	2.12055317973677e-05	9.50191387559809	0.851982561760432	7	216	proteasomal protein catabolic process
GO:0007346	2.30488984137643e-05	7.80297474922172	1.19514220469172	8	303	regulation of mitotic cell cycle
GO:0019320	2.71701511188135e-05	16.1866515837104	0.354992734066847	5	90	hexose catabolic process
GO:0051248	3.54646841588079e-05	6.37910583941606	1.65663275897862	9	420	negative regulation of protein metabolic process
GO:0007050	9.27819170873055e-05	6.3465430493527	1.45547020967407	8	369	cell cycle arrest
GO:0006096	0.000102335888881641	18.6545217957059	0.244550550134939	4	62	glycolysis
GO:0034644	0.000159123490207166	33.2638888888889	0.106497820220054	3	27	cellular response to UV
GO:0006310	0.000167194038994796	8.22428281657491	0.824372015777455	6	209	DNA recombination
GO:0010564	0.000204841947669952	5.625012566603	1.63296657670749	8	414	regulation of cell cycle process
GO:0071482	0.000266082225714309	27.5191570881226	0.126219638779323	3	32	cellular response to light stimulus
GO:0032392	0.000291873188185559	26.6	0.130164002491177	3	33	DNA geometric change
GO:0045786	0.000295410128982287	5.31468531468532	1.72368694208013	8	437	negative regulation of cell cycle
GO:0006273	0.000421539838176437	87.2	0.0315549096948308	2	8	lagging strand elongation
GO:0005996	0.000486257574063144	6.68320340184266	1.00581274652273	6	255	monosaccharide metabolic process
GO:0000338	0.000540606632178134	74.7376623376623	0.0354992734066847	2	9	protein deneddylation
GO:0010388	0.000540606632178134	74.7376623376623	0.0354992734066847	2	9	cullin deneddylation
GO:0006511	0.000543259288114523	5.50470588235294	1.4357483911148	7	364	ubiquitin-dependent protein catabolic process
GO:0016570	0.000549774824252818	6.52318339100346	1.02947892879386	6	261	histone modification
GO:0019941	0.000608344237296959	5.39615384615385	1.46335893709778	7	371	modification-dependent protein catabolic process
GO:0016569	0.000619583299297766	6.37052062204192	1.05314511106498	6	267	covalent chromatin modification
GO:0043632	0.000638074129706616	5.35089918256131	1.47519202823334	7	374	modification-dependent macromolecule catabolic process
GO:0006266	0.000674046648170741	65.3909090909091	0.0394436371185385	2	10	DNA ligation
GO:0030163	0.000676079825851976	4.66228051795667	1.95246003736766	8	495	protein catabolic process
GO:0006281	0.000734270793197293	5.21946808510638	1.51069130164002	7	383	DNA repair
GO:0051603	0.000804563710224911	5.13528795811518	1.53435748391115	7	389	proteolysis involved in cellular protein catabolic process
GO:0016573	0.000859442933124756	10.3701015965167	0.425991280880216			

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4       108     histone acetylation
GO:0044419      0.000867131900157234    5.06713178294574        1.55407930247042
7       394     interspecies interaction between organisms
GO:0018393      0.000920464419094877    10.1730153079388        0.433880008303924
4       110     internal peptidyl-lysine acetylation
GO:0031056      0.00094253406036512     17.3285024154589        0.193273821880839
3       49      regulation of histone modification
GO:0044257      0.000975204959013457    4.96167088607595        1.58563421216525
7       402     cellular protein catabolic process
GO:0006303      0.000983602004949684    52.3054545454545        0.0473323645422462
2       12      double-strand break repair via nonhomologous end joining
GO:0019321      0.000983602004949684    52.3054545454545        0.0473323645422462
2       12      pentose metabolic process
GO:0043968      0.000983602004949684    52.3054545454545        0.0473323645422462
2       12      histone H2A acetylation
GO:0018394      0.00101763507377363     9.89094685823092        0.445713099439485
4       113     peptidyl-lysine acetylation
GO:0006006      0.00107870204397061     7.07502989238741        0.780984014947062
5       198     glucose metabolic process
GO:0006475      0.00108629059233314     9.7113717491076 0.453601826863193       4
115     internal protein amino acid acetylation
GO:0071478      0.00153941452161595     14.4838383838384        0.228773095287523
3       58      cellular response to radiation
GO:0000726      0.00155297347453807     40.2265734265734        0.0591654556778078
2       15      non-recombinational repair
GO:0006473      0.00161393407662699     8.68533171028606        0.504878555117293
4       128     protein acetylation
GO:0022613      0.00189749896939257     6.19493006993007        0.887481835167116
5       225     ribonucleoprotein complex biogenesis
GO:0019318      0.00225138991968919     5.94768223043332        0.922981108573801
5       234     hexose metabolic process
GO:0018205      0.00229823412393509     7.85401459854015        0.556155283371393
4       141     peptidyl-lysine modification
GO:0071843      0.00246765333928066     5.81854043392505        0.94270292713307
5       239     cellular component biogenesis at cellular level
GO:0043543      0.00248066554433373     7.68409703504043        0.567988374506954
4       144     protein acylation
GO:0042254      0.00280649402421377     7.41652569941444        0.587710193066224
4       149     ribosome biogenesis
GO:0006260      0.0040314535482301      5.16634980988593        1.05708947477683
5       268     DNA replication
GO:0033044      0.00427607512846763     9.94027777777778        0.32738218808387
3       83      regulation of chromosome organization
GO:0035065      0.0043262629639112      22.7209486166008        0.0986090927963463
2       25      regulation of histone acetylation
GO:0000291      0.00467496492120553     21.7727272727273        0.1025534565082 2
26      nuclear-transcribed mRNA catabolic process, exonucleolytic
GO:0043928      0.00467496492120553     21.7727272727273        0.1025534565082 2
26      exonucleolytic nuclear-transcribed mRNA catabolic process involved in
deadenylation-dependent decay
GO:0070228      0.0050362322356854      20.9003636363636        0.106497820220054
2       27      regulation of lymphocyte apoptotic process
GO:2000756      0.0050362322356854      20.9003636363636        0.106497820220054
2       27      regulation of peptidyl-lysine acetylation
GO:0009411      0.0050366602528623      9.35228758169935        0.347104006643139
3       88      response to UV
GO:0034660      0.00522435135594807     4.84684065934066        1.12414365787835
5       285     ncRNA metabolic process
GO:0032508      0.00540996391986441     20.0951048951049        0.110442183931908
2       28      DNA duplex unwinding
GO:0006261      0.00587398483150878     8.82962962962963        0.366825825202408
3       93      DNA-dependent DNA replication
GO:0016568      0.00597030732275107     3.98262355789774        1.65268839526676
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6       419     chromatin modification
GO:0031058      0.00619441932858303     18.6571428571429        0.118330911355616
2       30      positive regulation of histone modification
GO:0016575      0.00660494395082142     18.012539184953 0.122275275067469       2
31      histone deacetylation
GO:0006302      0.00758079190010149     8.02188552188552        0.402325098609093
3       102     double-strand break repair
GO:0006271      0.00790852280964366     16.3204545454545        0.134108366203031
2       34      DNA strand elongation involved in DNA replication
GO:0034470      0.00793936756122365     5.46707739699653        0.78887274237077
4       200     ncRNA processing
GO:0006364      0.00799575748262253     7.86193619361936        0.4102138260328 3
104     rRNA processing
GO:0070227      0.00883660524121672     15.3582887700535        0.141997093626739
2       36      lymphocyte apoptotic process
GO:0022616      0.00931806605517473     14.9184415584416        0.145941457338592
2       37      DNA strand elongation
GO:0016072      0.00932016759081294     7.41796469366563        0.433880008303924
3       110     rRNA metabolic process
GO:2001252      0.00981101262259769     14.5030303030303        0.149885821050446
2       38      positive regulation of chromosome organization
Tissue: Skin_Sun_Exposed_Lower_leg=>Thyroid     Type:   cluster
SourceGene:     RP11-323D18.4(ENSG00000224625.2)
TargetGeneSet:  ZBTB48  LZIC    RP1     TCEB3   EYA3    EBNA1BP2        DPH2
PRKAA2  THEM4   PYGO2   FLAD1   HEATR1  SLC5A6  ASS1P2  CCDC142 POLR1A  POLR1B
CNOT10  TMEM39A TMEM41A GFM2    HARS    LARS    EEF1E1  PAK1IP1 RPL7L1  POLR1C  VTA1
MIOS    STOML2  FXN     RABEPK  ZNF79   TBC1D13 EXOSC2  NGB     ADO     POLR3A
ENTPD7  C10orf2 LZTS2   RP11    PDCD11  SPTY2D1 TMEM216 ZNF259  ZNF202  NOP2
PA2G4   UTP20   ATP6V0A2        PUS1    TTC5    PRMT5   LEO1    C15orf26
POLR3K  UBFD1   CTD     TSR1    TMEM199 CTB     PSME3   SNX11   METTL2A SIRT7   KRI1
ZNF433  NUDT19  ZNF461  ZNF576  OPA3    ZNF432  ZNF749  NOP56   RRP1B   PES1    GCAT
L3MBTL2 PPPDE2  UTP14A
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0071843      7.77522004347637e-15    20.3221524663677        1.09155075773303
16      239     cellular component biogenesis at cellular level
GO:0022613      6.37926985798725e-14    19.8529411764706        1.02761054598298
15      225     ribonucleoprotein complex biogenesis
GO:0042254      1.12063449901627e-13    25.6988068812431        0.680506539339838
13      149     ribosome biogenesis
GO:0034660      2.00245516060066e-12    15.3758169934641        1.30164002491177
15      285     ncRNA metabolic process
GO:0006364      3.61943461078362e-11    27.148556231003 0.474984430143243       10
104     rRNA processing
GO:0016072      6.36653164247794e-11    25.5089285714286        0.502387378036122
10      110     rRNA metabolic process
GO:0034470      1.49773832207879e-09    15.0222222222222        0.913431596429313
11      200     ncRNA processing
GO:0006354      5.80041871081762e-07    16.7793253901661        0.493253062071829
7       108     DNA-dependent transcription, elongation
GO:0006353      3.33910160873591e-05    15.4324849007765        0.369939796553872
5       81      DNA-dependent transcription, termination
GO:0006385      7.06983285707816e-05    45.6190476190476        0.0822088436786382
3       18      transcription elongation from RNA polymerase III promoter
GO:0006386      7.06983285707816e-05    45.6190476190476        0.0822088436786382
3       18      termination of RNA polymerase III transcription
GO:0006362      8.36803846565564e-05    42.7648809523809        0.0867760016607847
3       19      transcription elongation from RNA polymerase I promoter
GO:0009303      8.36803846565564e-05    42.7648809523809        0.0867760016607847
3       19      rRNA transcription
GO:0006363      0.000114107463271234    38.0079365079365        0.0959103176250778
3       21      termination of RNA polymerase I transcription
GO:0006361      0.00017195645465149 2    32.5714285714286        0.109611791571518
3       24      transcription initiation from RNA polymerase I promoter
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GO:0007000      0.000203629069863812    149.8125        0.0228357899107328      2
5       nucleolus organization
GO:0000466      0.000304542518136291    112.3515625     0.0274029478928794      2
6       maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S
rRNA, LSU-rRNA)
GO:0006360      0.000410539573718707    23.5730706075534        0.14614905542869
3       32      transcription from RNA polymerase I promoter
GO:0071826      0.00112000369305845     9.60282258064516        0.456715798214656
4       100     ribonucleoprotein complex subunit organization
GO:0000460      0.00131646899746473     44.921875       0.0548058957857588      2
12      maturation of 5.8S rRNA
GO:0006418      0.00135892751961416     15.1746031746032        0.219223583143035
3       48      tRNA aminoacylation for protein translation
GO:0043038      0.00162032020688437     14.2232142857143        0.232925057089475
3       51      amino acid activation
GO:0043039      0.00162032020688437     14.2232142857143        0.232925057089475
3       51      tRNA aminoacylation
GO:0006383      0.0017139455188221      13.9319727891156        0.237492215071621
3       52      transcription from RNA polymerase III promoter
GO:0006399      0.00254227009695544     7.60543854972007        0.57089474776832
4       125     tRNA metabolic process
GO:0016570      0.00674626543153756     4.52388575819672        1.19202823334025
5       261     histone modification
GO:0016569      0.00740867475787636     4.41840820923539        1.21943118123313
5       267     covalent chromatin modification
GO:0000387      0.00877135240453798     15.4698275862069        0.141581897446543
2       31      spliceosomal snRNP assembly
GO:0022618      0.00934004599905399     7.398033126294  0.433880008303924       3
95      ribonucleoprotein complex assembly
Tissue: Thyroid=>Skin_Sun_Exposed_Lower_leg     Type:   asymmetric
SourceGene:     RP11-473O4.3(ENSG00000253720.1)
TargetGeneSet:  TRIT1   RPS8    PRPF38A NEDD4   RPL5    BOLA1   DCST2   PAQR6   COPA
LYPLAL1 SRP9    C1orf35 RPS7    RP11    TMEM214 DDIT3   UBC     FIGLA   TPRKB   COA5
ARL6IP6 ASNSD1  SENP2   NOP58   EEF1B2  USP40   CRBN    GRM2    THOC7   RPL24   RYK
SNORA63 MRFAP1L1        COMMD8  EXOC7   RPL34   CDKN2AIP        PPWD1   TAF9    CTD
MAN2A1  NPM1    BOD1    TMEM14B TDP2    HIST1H1B        PRRT1   AGER    MAD2L1BP
COQ3    RP3     AIM1    ASF1A   GTF2H5  C6orf70 KLHL7   TAX1BP1 SBDS    C8orf40 FNTA
SGK3    PAF1    CKS1BP7 CA3     TTC35   C8orf76 C9orf123        RPS6    NDUFB6
CHMP5   C10orf31        COMMD3  CUL2    CHCHD1  RPS24   C10orf32        HRAS
C11orf58        C11orf46        IMMP1L  CCDC90B ZCRB1   NACA    C12orf47
MRP63   EFHA1   HMGB1   FRY-AS1 UFM1    WBP4    UPF3A   METTL17 EAPP    SNX6
SRSF5   RSL24D1 UBAP1L  MTHFS   WFIKKN1 RHBDL1  NUDT21  EDC4    FTLP14  PSMD7
MED11   RPL26   RPS7P1  C17orf75        ARHGAP27        CEP95   NOL11   RPL17
CIRBP   XAB2    CCDC130 SLC25A42        SUGP1   FAM98C  ZNF773  C21orf119
SPATA20P1       CTA     TBC1D8B VBP1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      9.63494194805802e-13    25.2284577993814        0.617604318040274
12      105     translational elongation
GO:0006614      2.38224892509629e-11    22.5692926969523        0.617604318040274
11      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      2.64556672883813e-11    22.3301564722617        0.623486263926372
11      106     cotranslational protein targeting to membrane
GO:0045047      2.64556672883813e-11    22.3301564722617        0.623486263926372
11      106     protein targeting to ER
GO:0072599      2.64556672883813e-11    22.3301564722617        0.623486263926372
11      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      8.604099912405e-11      19.8091689820662        0.694069614559546
11      118     protein localization to endoplasmic reticulum
GO:0000184      9.43576716288022e-11    19.6243743743744        0.699951560445644
11      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006415      1.2558277564126e-10     23.5144032921811        0.535257075634904
10      91      translational termination
GO:0072594      1.82545487122759e-10    13.3998691099476        1.19991696076396
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13      204     establishment of protein localization to organelle
GO:0000956      2.77698857692242e-10    14.8772358432947        0.994048854750536
12      169     nuclear-transcribed mRNA catabolic process
GO:0006402      5.06479339728e-10       14.0617263574847        1.04698636772542
12      178     mRNA catabolic process
GO:0022613      6.13784041834554e-10    12.0546383647799        1.32343782437202
13      225     ribonucleoprotein complex biogenesis
GO:0071843      1.28677545195209e-09    11.2967059980334        1.40578506677739
13      239     cellular component biogenesis at cellular level
GO:0006612      1.42124265995181e-09    14.8899885801294        0.899937720572971
11      153     protein targeting to membrane
GO:0043624      1.42124265995181e-09    14.8899885801294        0.899937720572971
11      153     cellular protein complex disassembly
GO:0043241      2.00077200951795e-09    14.3784703070417        0.92934745000346
11      158     protein complex disassembly
GO:0006401      2.55551489636779e-09    12.0715451770885        1.20579890665006
12      205     RNA catabolic process
GO:0034623      5.5419676658147e-09     12.9524954402255        1.02345858418103
11      174     cellular macromolecular complex disassembly
GO:0032984      7.45977842054639e-09    12.5625804375804        1.05286831361151
11      179     macromolecular complex disassembly
GO:0071845      1.03535434187357e-08    9.39088765887659        1.67047263165179
13      284     cellular component disassembly at cellular level
GO:0022411      1.22352049119903e-08    9.25166666666667        1.69400041519618
13      288     cellular component disassembly
GO:0042254      1.61989775956199e-08    13.6470023980815        0.876409937028579
10      149     ribosome biogenesis
GO:0019080      1.84113478799433e-08    13.451536643026 0.888173828800775       10
151     viral genome expression
GO:0019083      1.84113478799433e-08    13.451536643026 0.888173828800775       10
151     viral transcription
GO:0006413      1.96145897607643e-08    13.3558685446009        0.894055774686873
10      152     translational initiation
GO:0022415      3.66556342556424e-08    9.35793194874061        1.52930593038544
12      260     viral reproductive process
GO:0006364      1.66876313981007e-07    15.4437229437229        0.611722372154176
8       104     rRNA processing
GO:0016072      2.57978972112315e-07    14.5291571173924        0.647014047470763
8       110     rRNA metabolic process
GO:0016032      3.40853072402775e-07    6.28504206014117        2.65275759463013
14      451     viral reproduction
GO:0033365      6.04687279925659e-07    5.97434717235877        2.78216040412428
14      473     protein localization to organelle
GO:0006605      6.20176219177771e-07    5.96093080220453        2.78804235001038
14      474     protein targeting
GO:0019058      9.8363073351747e-07     8.53393665158371        1.3587294996886 10
231     viral infectious cycle
GO:0034470      2.58422186747729e-06    8.78857812069441        1.17638917721957
9       200     ncRNA processing
GO:0042274      3.20324942668156e-06    50.6243386243386        0.105875025949761
4       18      ribosomal small subunit biogenesis
GO:0008380      1.92025972464917e-05    5.9863684771033 1.8998685212096 10      323
RNA splicing
GO:0022618      1.98158317671353e-05    12.1834731901579        0.558784859179296
6       95      ribonucleoprotein complex assembly
GO:0071826      2.65503682587538e-05    11.5313762456235        0.588194588609785
6       100     ribonucleoprotein complex subunit organization
GO:0042273      4.15850860595777e-05    58.3617886178862        0.0705833506331742
3       12      ribosomal large subunit biogenesis
GO:0034660      4.41491830450558e-05    6.04548054919908        1.67635457753789
9       285     ncRNA metabolic process
GO:0042255      0.000104066430391483    40.3930581613508        0.094111341775656
3       16      ribosome assembly
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GO:0006397      0.000113667369892079    4.79074550128535        2.34689640855304
10      399     mRNA processing
GO:0000377      0.000196098658897105    6.45470519328387        1.19991696076396
7       204     RNA splicing, via transesterification reactions with bulged
adenosine as nucleophile
GO:0000398      0.000196098658897105    6.45470519328387        1.19991696076396
7       204     nuclear mRNA splicing, via spliceosome
GO:0000375      0.000227478789806445    6.29271388677329        1.22932669019445
7       209     RNA splicing, via transesterification reactions
GO:0000462      0.000505082847272706    86.5180722891566        0.0352916753165871
2       6       maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA,
5.8S rRNA, LSU-rRNA)
GO:0030490      0.000704412693740366    69.2096385542169        0.0411736212026849
2       7       maturation of SSU-rRNA
GO:0006511      0.00133476465735811     4.08872026849555        2.14102830253962
8       364     ubiquitin-dependent protein catabolic process
GO:0019941      0.00150602053313423     4.00787091696183        2.1822019237423 8
371     modification-dependent protein catabolic process
GO:0043632      0.00158456918102932     3.97416790859414        2.1998477614006 8
374     modification-dependent macromolecule catabolic process
GO:0006281      0.00183993437902993     3.87629437229437        2.25278527437548
8       383     DNA repair
GO:0051603      0.00202755986881313     3.81361420731499        2.28807694969206
8       389     proteolysis involved in cellular protein catabolic process
GO:0050930      0.00217192689908843     34.5927710843374        0.0705833506331742
2       12      induction of positive chemotaxis
GO:0030163      0.0024694876358983      3.38206627680312        2.91156321361843
9       495     protein catabolic process
GO:0044257      0.00248597939151822     3.68435625288417        2.36454224621134
8       402     cellular protein catabolic process
GO:0043620      0.00492094639463268     21.6114457831325        0.105875025949761
2       18      regulation of DNA-dependent transcription in response to stress
GO:0050927      0.00606459675869567     19.2074966532798        0.117638917721957
2       20      positive regulation of positive chemotaxis
GO:0050926      0.0066775058852177      18.1953075459734        0.123520863608055
2       21      regulation of positive chemotaxis
GO:0043161      0.00776631411310921     4.33884803921569        1.22932669019445
5       209     proteasomal ubiquitin-dependent protein catabolic process
GO:0065004      0.00823021901095836     5.36612948826689        0.794062694623209
4       135     protein-DNA complex assembly
GO:0007346      0.00885705081886503     3.59774964838256        1.78222960348765
6       303     regulation of mitotic cell cycle
GO:0010498      0.00888459433957299     4.1928317535545 1.27050031139714        5
216     proteasomal protein catabolic process
GO:0007093      0.00910002199762345     5.20566986739826        0.817590478167601
4       139     mitotic cell cycle checkpoint
Tissue: Thyroid=>Skin_Sun_Exposed_Lower_leg     Type:   cluster
SourceGene:     RP11-473O4.3(ENSG00000253720.1)
TargetGeneSet:  TRIT1   RPS8    PRPF38A NEDD4   RPL5    BOLA1   DCST2   PAQR6   COPA
LYPLAL1 SRP9    C1orf35 RPS7    RP11    TMEM214 DDIT3   UBC     FIGLA   TPRKB   COA5
ARL6IP6 ASNSD1  SENP2   NOP58   EEF1B2  USP40   CRBN    GRM2    THOC7   RPL24   RYK
SNORA63 MRFAP1L1        COMMD8  EXOC7   RPL34   CDKN2AIP        PPWD1   TAF9    CTD
MAN2A1  NPM1    BOD1    TMEM14B TDP2    HIST1H1B        PRRT1   AGER    MAD2L1BP
COQ3    RP3     AIM1    ASF1A   GTF2H5  C6orf70 KLHL7   TAX1BP1 SBDS    C8orf40 FNTA
SGK3    PAF1    CKS1BP7 CA3     TTC35   C8orf76 C9orf123        RPS6    NDUFB6
CHMP5   C10orf31        COMMD3  CUL2    CHCHD1  RPS24   C10orf32        HRAS
C11orf58        C11orf46        IMMP1L  CCDC90B ZCRB1   NACA    C12orf47
MRP63   EFHA1   HMGB1   FRY-AS1 UFM1    WBP4    UPF3A   METTL17 EAPP    SNX6
SRSF5   RSL24D1 UBAP1L  MTHFS   WFIKKN1 RHBDL1  NUDT21  EDC4    FTLP14  PSMD7
MED11   RPL26   RPS7P1  C17orf75        ARHGAP27        CEP95   NOL11   RPL17
CIRBP   XAB2    CCDC130 SLC25A42        SUGP1   FAM98C  ZNF773  C21orf119
SPATA20P1       CTA     TBC1D8B VBP1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
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GO:0006414      9.63494194805802e-13    25.2284577993814        0.617604318040274
12      105     translational elongation
GO:0006614      2.38224892509629e-11    22.5692926969523        0.617604318040274
11      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      2.64556672883813e-11    22.3301564722617        0.623486263926372
11      106     cotranslational protein targeting to membrane
GO:0045047      2.64556672883813e-11    22.3301564722617        0.623486263926372
11      106     protein targeting to ER
GO:0072599      2.64556672883813e-11    22.3301564722617        0.623486263926372
11      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      8.604099912405e-11      19.8091689820662        0.694069614559546
11      118     protein localization to endoplasmic reticulum
GO:0000184      9.43576716288022e-11    19.6243743743744        0.699951560445644
11      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006415      1.2558277564126e-10     23.5144032921811        0.535257075634904
10      91      translational termination
GO:0072594      1.82545487122759e-10    13.3998691099476        1.19991696076396
13      204     establishment of protein localization to organelle
GO:0000956      2.77698857692242e-10    14.8772358432947        0.994048854750536
12      169     nuclear-transcribed mRNA catabolic process
GO:0006402      5.06479339728e-10       14.0617263574847        1.04698636772542
12      178     mRNA catabolic process
GO:0022613      6.13784041834554e-10    12.0546383647799        1.32343782437202
13      225     ribonucleoprotein complex biogenesis
GO:0071843      1.28677545195209e-09    11.2967059980334        1.40578506677739
13      239     cellular component biogenesis at cellular level
GO:0006612      1.42124265995181e-09    14.8899885801294        0.899937720572971
11      153     protein targeting to membrane
GO:0043624      1.42124265995181e-09    14.8899885801294        0.899937720572971
11      153     cellular protein complex disassembly
GO:0043241      2.00077200951795e-09    14.3784703070417        0.92934745000346
11      158     protein complex disassembly
GO:0006401      2.55551489636779e-09    12.0715451770885        1.20579890665006
12      205     RNA catabolic process
GO:0034623      5.5419676658147e-09     12.9524954402255        1.02345858418103
11      174     cellular macromolecular complex disassembly
GO:0032984      7.45977842054639e-09    12.5625804375804        1.05286831361151
11      179     macromolecular complex disassembly
GO:0071845      1.03535434187357e-08    9.39088765887659        1.67047263165179
13      284     cellular component disassembly at cellular level
GO:0022411      1.22352049119903e-08    9.25166666666667        1.69400041519618
13      288     cellular component disassembly
GO:0042254      1.61989775956199e-08    13.6470023980815        0.876409937028579
10      149     ribosome biogenesis
GO:0019080      1.84113478799433e-08    13.451536643026 0.888173828800775       10
151     viral genome expression
GO:0019083      1.84113478799433e-08    13.451536643026 0.888173828800775       10
151     viral transcription
GO:0006413      1.96145897607643e-08    13.3558685446009        0.894055774686873
10      152     translational initiation
GO:0022415      3.66556342556424e-08    9.35793194874061        1.52930593038544
12      260     viral reproductive process
GO:0006364      1.66876313981007e-07    15.4437229437229        0.611722372154176
8       104     rRNA processing
GO:0016072      2.57978972112315e-07    14.5291571173924        0.647014047470763
8       110     rRNA metabolic process
GO:0016032      3.40853072402775e-07    6.28504206014117        2.65275759463013
14      451     viral reproduction
GO:0033365      6.04687279925659e-07    5.97434717235877        2.78216040412428
14      473     protein localization to organelle
GO:0006605      6.20176219177771e-07    5.96093080220453        2.78804235001038
14      474     protein targeting
GO:0019058      9.8363073351747e-07     8.53393665158371        1.3587294996886 10
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					231	viral infectious cycle
GO:0034470	2.58422186747729e-06	8.78857812069441	1.17638917721957	9	200	ncRNA processing
GO:0042274	3.20324942668156e-06	50.6243386243386	0.105875025949761	4	18	ribosomal small subunit biogenesis
GO:0008380	1.92025972464917e-05	5.9863684771033	1.8998685212096	10	323	RNA splicing
GO:0022618	1.98158317671353e-05	12.1834731901579	0.558784859179296	6	95	ribonucleoprotein complex assembly
GO:0071826	2.65503682587538e-05	11.5313762456235	0.588194588609785	6	100	ribonucleoprotein complex subunit organization
GO:0042273	4.15850860595777e-05	58.3617886178862	0.0705833506331742	3	12	ribosomal large subunit biogenesis
GO:0034660	4.41491830450558e-05	6.04548054919908	1.67635457753789	9	285	ncRNA metabolic process
GO:0042255	0.000104066430391483	40.3930581613508	0.0941111341775656	3	16	ribosome assembly
GO:0006397	0.000113667369892079	4.79074550128535	2.34689640855304	10	399	mRNA processing
GO:0000377	0.000196098658897105	6.45470519328387	1.19991696076396	7	204	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile
GO:0000398	0.000196098658897105	6.45470519328387	1.19991696076396	7	204	nuclear mRNA splicing, via spliceosome
GO:0000375	0.000227478789806445	6.29271388677329	1.22932669019445	7	209	RNA splicing, via transesterification reactions
GO:0000462	0.000505082847272706	86.5180722891566	0.0352916753165871	2	6	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
GO:0030490	0.000704412693740366	69.2096385542169	0.0411736212026849	2	7	maturation of SSU-rRNA
GO:0006511	0.00133476465735811	4.08872026849555	2.14102830253962	8	364	ubiquitin-dependent protein catabolic process
GO:0019941	0.00150602053313423	4.00787091696183	2.1822019237423	8	371	modification-dependent protein catabolic process
GO:0043632	0.00158456918102932	3.97416790859414	2.1998477614006	8	374	modification-dependent macromolecule catabolic process
GO:0006281	0.00183993437902993	3.87629437229437	2.25278527437548	8	383	DNA repair
GO:0051603	0.00202755986881313	3.81361420731499	2.28807694969206	8	389	proteolysis involved in cellular protein catabolic process
GO:0050930	0.00217192689908843	34.5927710843374	0.0705833506331742	2	12	induction of positive chemotaxis
GO:0030163	0.0024694876358983	3.38206627680312	2.91156321361843	9	495	protein catabolic process
GO:0044257	0.00248597939151822	3.68435625288417	2.36454224621134	8	402	cellular protein catabolic process
GO:0043620	0.00492094639463268	21.6114457831325	0.105875025949761	2	18	regulation of DNA-dependent transcription in response to stress
GO:0050927	0.00606459675869567	19.2074966532798	0.117638917721957	2	20	positive regulation of positive chemotaxis
GO:0050926	0.0066775058852177	18.1953075459734	0.123520863608055	2	21	regulation of positive chemotaxis
GO:0043161	0.00776631411310921	4.33884803921569	1.22932669019445	5	209	proteasomal ubiquitin-dependent protein catabolic process
GO:0065004	0.00823021901095836	5.36612948826689	0.794062694623209	4	135	protein-DNA complex assembly
GO:0007346	0.00885705081886503	3.59774964838256	1.78222960348765	6	303	regulation of mitotic cell cycle
GO:0010498	0.00888459433957299	4.1928317535545	1.27050031139714	5	216	proteasomal protein catabolic process
GO:0007093	0.0091002199762345	5.20566986739826	0.817590478167601	4	139	mitotic cell cycle checkpoint

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Tissue: Skin_Sun_Exposed_Lower_leg=>Thyroid     Type:   asymmetric
SourceGene:     SLC26A10(ENSG00000135502.12)
TargetGeneSet:  RP11    CACNA1S C1orf147        ACTA1   ACTN2   XIRP2   MYL1
VGLL2   TRDN    BPGM    MYPN    TNNI2   OR7E13P TBRG1   RP3     MYBPC1  C12orf73
TCHP    CATSPERB        MYH2    CKM     TNNT1   PCNT    MYO18B
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0030049      4.45877744890921e-14    242.290865384615        0.0539755034253685
7       39      muscle filament sliding
GO:0033275      4.45877744890921e-14    242.290865384615        0.0539755034253685
7       39      actin-myosin filament sliding
GO:0070252      7.80225094085748e-14    221.476923076923        0.0581274652273199
7       42      actin-mediated cell contraction
GO:0030048      9.73465781956882e-13    148.894970414201        0.0816552487717113
7       59      actin filament-based movement
GO:0006936      1.14193843371407e-11    50.5173913043478        0.330772956888797
9       239     muscle contraction
GO:0003012      2.98289607788242e-11    45.1241598868058        0.368140613106359
9       266     muscle system process
GO:0030029      2.20114025828332e-09    27.0947775628627        0.597882499481005
9       432     actin filament-based process
GO:0006941      3.04424438900589e-06    50.5633802816901        0.103799045048786
4       75      striated muscle contraction
GO:0010927      2.17896209326086e-05    30.0672268907563        0.170230433880008
4       123     cellular component assembly involved in morphogenesis
GO:0043501      6.51320731303245e-05    228.952380952381        0.0124558854058543
2       9       skeletal muscle adaptation
GO:0014888      0.000140651479709995    145.656565656566        0.0179918344751228
2       13      striated muscle adaptation
GO:0061061      0.000193326293867678    11.5734323432343        0.56605079233271
5       409     muscle structure development
GO:0003009      0.0003068190587918      94.2091503267974        0.0262957580790257
2       19      skeletal muscle contraction
GO:0055002      0.000410499840858156    24.3105203619909        0.148086637602934
3       107     striated muscle cell development
GO:0050879      0.000579757517178671    66.6990740740741        0.0359836689502457
2       26      multicellular organismal movement
GO:0050881      0.000579757517178671    66.6990740740741        0.0359836689502457
2       26      musculoskeletal movement
GO:0007517      0.00070401627756025     11.8160535117057        0.419348141997094
4       303     muscle organ development
GO:0055001      0.000708935535931096    20.0350140056022        0.178534357483911
3       129     muscle cell development
GO:0030239      0.000994130463345698    49.9965277777778        0.0470555670887828
2       34      myofibril assembly
GO:0007519      0.00109773164116792     17.1476590636255        0.207598090097571
3       150     skeletal muscle tissue development
GO:0043500      0.00117726471214678     45.7015873015873        0.0512075288907342
2       37      muscle adaptation
GO:0060538      0.00127518523706249     16.2535104364326        0.218669988236108
3       158     skeletal muscle organ development
GO:0051146      0.0015473561962559      15.1647767540751        0.233893848176597
3       169     striated muscle cell differentiation
GO:0031032      0.0017384182648659      37.1782945736434        0.0622794270292713
2       45      actomyosin structure organization
GO:0030031      0.00209851528895702     13.5891891891892        0.260189606255622
3       188     cell projection assembly
GO:0042384      0.00370160561663533     24.9427083333333        0.0913431596429313
2       66      cilium assembly
GO:0030035      0.00414650474202016     379.710526315789        0.00415196180195142
1       3       microspike assembly
GO:0032066      0.00414650474202016     379.710526315789        0.00415196180195142
1       3       nucleolus to nucleoplasm transport
GO:0042396      0.00414650474202016     379.710526315789        0.00415196180195142
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1       3       phosphagen biosynthetic process
GO:0048741      0.0041537626724066      23.468954248366 0.0968791087121998      2
70      skeletal muscle fiber development
GO:0042692      0.00438294808678494     10.3905296558457        0.337692893225382
3       244     muscle cell differentiation
GO:0048747      0.00525994507921223     20.7128427128427        0.109334994118054
2       79      muscle fiber development
GO:0014706      0.00534538779923922     9.65614353849648        0.362604664037091
3       262     striated muscle tissue development
GO:0003010      0.00552503948074912     253.122807017544        0.00553594906926856
1       4       voluntary skeletal muscle contraction
GO:0014721      0.00552503948074912     253.122807017544        0.00553594906926856
1       4       twitch skeletal muscle contraction
GO:0060537      0.00599176048850142     9.25555555555556        0.377828523977579
3       273     muscle tissue development
GO:0060271      0.00634458151023876     18.7529411764706        0.120406892256591
2       87      cilium morphogenesis
GO:0001778      0.00690176123684949     189.828947368421        0.0069199363365857
1       5       plasma membrane repair
GO:0030240      0.00690176123684949     189.828947368421        0.0069199363365857
1       5       skeletal muscle thin filament assembly
GO:0060315      0.00690176123684949     189.828947368421        0.0069199363365857
1       5       negative regulation of ryanodine-sensitive calcium-release channel
activity
GO:0032412      0.00798790870288432     16.5914351851852        0.13563075219708
2       98      regulation of ion transmembrane transporter activity
GO:0000244      0.00827667226933348     151.852631578947        0.00830392360390284
1       6       assembly of spliceosomal tri-snRNP
GO:0014866      0.00827667226933348     151.852631578947        0.00830392360390284
1       6       skeletal myofibril assembly
GO:0022898      0.00879180462379007     15.7645764576458        0.142550688533665
2       103     regulation of transmembrane transporter activity
GO:1901020      0.00964977483455431     126.535087719298        0.00968791087121998
1       7       negative regulation of calcium ion transmembrane transporter
activity
GO:0034765      0.0098025252408953      14.8743509865005        0.150854612137568
2       109     regulation of ion transmembrane transport
Tissue: Skin_Sun_Exposed_Lower_leg=>Thyroid     Type:   asymmetric
SourceGene:     TCF4(ENSG00000196628.7)
TargetGeneSet:  KCNAB2  WBP1    FTH1P22 RP4     IGKJ4   IGKV1-8 IGKV1-17
IGKV3-20        IGKV1-27        CD28    ICOS    ARL4C   PDCD1   SIDT1   DTHD1   U6
IGBP1P4 RP11    LHFPL3  PNOC    TCTN1   IGHG2   IGHGP   IGHG1   IGHV2-26
IGHV4-31        IGHV3-33        IGHV4-61        IGHV3-74        JMJD8   TBL3    GCSH
TNFRSF13B       PLD6    ATP9B   ZSCAN18 ZBP1    IGLV3-25        IGLV2-14
IGLC2   IGLC3   MIAT    TNFRSF13C       BEX2    MTCP1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006959      3.97227453570534e-11    52.8531855955679        0.227942702927133
8       122     humoral immune response
GO:0050778      1.16111174280658e-08    19.8154929577465        0.680091343159643
9       364     positive regulation of immune response
GO:0002449      1.77391227425219e-08    31.2025 0.312019929416649       7       167
lymphocyte mediated immunity
GO:0006958      3.0780705661675e-08     72.6212121212121        0.093419140543907
5       50      complement activation, classical pathway
GO:0002460      3.09440229672954e-08    28.6637931034483        0.338177288768943
7       181     adaptive immune response based on somatic recombination of immune
receptors built from immunoglobulin superfamily domains
GO:0016064      4.65226895787969e-08    38.9632653061225        0.207390492007474
6       111     immunoglobulin mediated immune response
GO:0019724      5.45911568725853e-08    37.8730158730159        0.212995640440108
6       114     B cell mediated immunity
GO:0002250      5.73973811363212e-08    26.0814136125654        0.369939796553872
7       198     adaptive immune response
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GO:0002443	8.87587889384766e-08	24.3970588235294	0.394228773095288	7	211	leukocyte mediated immunity
GO:0006956	1.00439134449161e-07	56.2931034482759	0.117708117085323	5	63	complement activation
GO:0002455	1.1773038054287e-07	54.4090909090909	0.121444882707079	5	65	humoral immune response mediated by circulating immunoglobulin
GO:0072376	3.80586713500269e-07	42.3465171192444	0.153207390492007	5	82	protein activation cascade
GO:0002252	5.14043064091848e-06	12.9703166226913	0.721195764998962	7	386	immune effector process
GO:0031294	1.07278252023149e-05	35.1573790569504	0.140128710815861	4	75	lymphocyte costimulation
GO:0031295	1.07278252023149e-05	35.1573790569504	0.140128710815861	4	75	T cell costimulation
GO:0050864	1.45726414017468e-05	32.4042913608131	0.151339007681129	4	81	regulation of B cell activation
GO:0002253	1.53118039550086e-05	13.7796196977084	0.558646460452564	6	299	activation of immune response
GO:0030888	0.000107522759101617	38.2367021276596	0.093419140543907	3	50	regulation of B cell proliferation
GO:0046649	0.00012146566979257	9.36567413850786	0.809009757110235	6	433	lymphocyte activation
GO:0050670	0.000138856518445971	17.744099378882	0.269047124766452	4	144	regulation of lymphocyte proliferation
GO:0032944	0.000142613770045866	17.6170212765957	0.27091550757733	4	145	regulation of mononuclear cell proliferation
GO:0051249	0.000157604446247797	11.5647482014388	0.528752335478514	5	283	regulation of lymphocyte activation
GO:0042100	0.000159123490207166	33.2638888888889	0.106497820220054	3	57	B cell proliferation
GO:0070663	0.000162515447931474	17.0077427039905	0.280257421631721	4	150	regulation of leukocyte proliferation
GO:0042113	0.00017538004703184	16.6618033265247	0.285862570064355	4	153	B cell activation
GO:0045066	0.000219333509983732	115.312	0.0224205937305377	2	12	regulatory T cell differentiation
GO:0030889	0.000258913610471625	104.821818181818	0.0242889765414158	2	13	negative regulation of B cell proliferation
GO:0050870	0.000268566108079728	14.8471752147878	0.319493460660162	4	171	positive regulation of T cell activation
GO:0046651	0.000274610196078045	14.7577639751553	0.32136184347104	4	172	lymphocyte proliferation
GO:0042110	0.000275018514558874	10.2127967573827	0.596014116670127	5	319	T cell activation
GO:0002694	0.000283079927967113	10.1467203682394	0.599750882291883	5	321	regulation of leukocyte activation
GO:0032943	0.000286991449531745	14.5820971867008	0.325098609092796	4	174	mononuclear cell proliferation
GO:0070661	0.000340560941099582	13.9189057156815	0.340045671579821	4	182	leukocyte proliferation
GO:0050865	0.000384162560432835	9.47149004841313	0.640855304131202	5	343	regulation of cell activation
GO:0001782	0.00050495018454502	72.04	0.0336308905958065	2	18	B cell homeostasis
GO:0042035	0.000633305008731961	20.3636363636364	0.170022835789911	3	91	regulation of cytokine biosynthetic process
GO:0051251	0.000639167222562705	11.714815577993	0.4017023043388	4	215	positive regulation of lymphocyte activation
GO:0050863	0.000708663573971892	11.3860949709477	0.412912601204069	4	221	regulation of T cell activation
GO:0042089	0.000833567862006689	18.4626288659794	0.186838281087814	3	100	cytokine biosynthetic process
GO:0002696	0.000863502941305667	10.780330358838	0.435333194934607	4		

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233     positive regulation of leukocyte activation
GO:0042107      0.000882920450586887    18.0871212121212        0.19057504670957
3       102     cytokine metabolic process
GO:0050867      0.00096413679721674     10.4554163596168        0.448411874610754
4       240     positive regulation of cell activation
GO:0050869      0.00106276642474843     48      0.0485779530828316      2       26
negative regulation of B cell activation
GO:0002260      0.00250987280221428     30.2863157894737        0.0747353124351256
2       40      lymphocyte homeostasis
GO:0001776      0.00374516579797624     24.4714893617021        0.0915507577330289
2       49      leukocyte homeostasis
GO:0032945      0.00374516579797624     24.4714893617021        0.0915507577330289
2       49      negative regulation of mononuclear cell proliferation
GO:0050672      0.00374516579797624     24.4714893617021        0.0915507577330289
2       49      negative regulation of lymphocyte proliferation
GO:0070664      0.00420833512253117     22.9984 0.0971559061656633      2       52
negative regulation of leukocyte proliferation
GO:0050871      0.00453115282243661     22.1107692307692        0.10089267178742
2       54      positive regulation of B cell activation
GO:0042108      0.00538673529853182     20.1642105263158        0.11023458584181
2       59      positive regulation of cytokine biosynthetic process
GO:0002636      0.00559506886110994     277.346153846154        0.00560514843263442
1       3       positive regulation of germinal center formation
GO:0015917      0.00559506886110994     277.346153846154        0.00560514843263442
1       3       aminophospholipid transport
GO:0016056      0.00559506886110994     277.346153846154        0.00560514843263442
1       3       rhodopsin mediated signaling pathway
GO:0045590      0.00559506886110994     277.346153846154        0.00560514843263442
1       3       negative regulation of regulatory T cell differentiation
GO:0042102      0.00669906381624608     17.95   0.123313265517957       2       66
positive regulation of T cell proliferation
GO:0002706      0.00814189961126811     16.1723943661972        0.136391945194104
2       73      regulation of lymphocyte mediated immunity
GO:0007028      0.00930835421207143     138.653846153846        0.0093419140543907
1       5       cytoplasm organization
GO:0070934      0.00930835421207143     138.653846153846        0.0093419140543907
1       5       CRD-mediated mRNA stabilization
GO:0002822      0.00971188231026789     14.7138461538462        0.149470624870251
2       80      regulation of adaptive immune response based on somatic
recombination of immune receptors built from immunoglobulin superfamily domains
Tissue: Skin_Sun_Exposed_Lower_leg=>Thyroid     Type:   cluster
SourceGene:     TCF4(ENSG00000196628.7)
TargetGeneSet:  KCNAB2  WBP1    FTH1P22 RP4     IGKJ4   IGKV1-8 IGKV1-17
IGKV3-20        IGKV1-27        CD28    ICOS    ARL4C   PDCD1   SIDT1   DTHD1   U6
IGBP1P4 RP11    LHFPL3  PNOC    TCTN1   IGHG2   IGHGP   IGHG1   IGHV2-26
IGHV4-31        IGHV3-33        IGHV4-61        IGHV3-74        JMJD8   TBL3    GCSH
TNFRSF13B       PLD6    ATP9B   ZSCAN18 ZBP1    IGLV3-25        IGLV2-14
IGLC2   IGLC3   MIAT    TNFRSF13C       BEX2    MTCP1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006959      3.97227453570534e-11    52.8531855955679        0.227942702927133
8       122     humoral immune response
GO:0050778      1.16111174280658e-08    19.8154929577465        0.680091343159643
9       364     positive regulation of immune response
GO:0002449      1.77391227425219e-08    31.2025 0.312019929416649       7       167
lymphocyte mediated immunity
GO:0006958      3.0780705661675e-08     72.6212121212121        0.093419140543907
5       50      complement activation, classical pathway
GO:0002460      3.09440229672954e-08    28.6637931034483        0.338177288768943
7       181     adaptive immune response based on somatic recombination of immune
receptors built from immunoglobulin superfamily domains
GO:0016064      4.65226895787969e-08    38.9632653061225        0.207390492007474
6       111     immunoglobulin mediated immune response
GO:0019724      5.45911568725853e-08    37.8730158730159        0.212995640440108
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6       114     B cell mediated immunity
GO:0002250      5.73973811363212e-08    26.0814136125654        0.369939796553872
7       198     adaptive immune response
GO:0002443      8.87587889384766e-08    24.3970588235294        0.394228773095288
7       211     leukocyte mediated immunity
GO:0006956      1.00439134449161e-07    56.2931034482759        0.117708117085323
5       63      complement activation
GO:0002455      1.1773038054287e-07     54.4090909090909        0.121444882707079
5       65      humoral immune response mediated by circulating immunoglobulin
GO:0072376      3.80586713500269e-07    42.3465171192444        0.153207390492007
5       82      protein activation cascade
GO:0002252      5.14043064091848e-06    12.9703166226913        0.721195764998962
7       386     immune effector process
GO:0031294      1.07278252023149e-05    35.1573790569504        0.140128710815861
4       75      lymphocyte costimulation
GO:0031295      1.07278252023149e-05    35.1573790569504        0.140128710815861
4       75      T cell costimulation
GO:0050864      1.45726414017468e-05    32.4042913608131        0.151339007681129
4       81      regulation of B cell activation
GO:0002253      1.53118039550086e-05    13.7796196977084        0.558646460452564
6       299     activation of immune response
GO:0030888      0.000107522759101617    38.2367021276596        0.093419140543907
3       50      regulation of B cell proliferation
GO:0046649      0.000121146566979257    9.36567413850786        0.809009757110235
6       433     lymphocyte activation
GO:0050670      0.000138856518445971    17.744099378882 0.269047124766452       4
144     regulation of lymphocyte proliferation
GO:0032944      0.000142613770045866    17.6170212765957        0.27091550757733
4       145     regulation of mononuclear cell proliferation
GO:0051249      0.000157604446247797    11.5647482014388        0.528752335478514
5       283     regulation of lymphocyte activation
GO:0042100      0.000159123490207166    33.2638888888889        0.106497820220054
3       57      B cell proliferation
GO:0070663      0.000162515447931474    17.0077427039905        0.280257421631721
4       150     regulation of leukocyte proliferation
GO:0042113      0.00017538004703184     16.6618033265247        0.285862570064355
4       153     B cell activation
GO:0045066      0.000219333509983732    115.312 0.0224205937305377      2       12
regulatory T cell differentiation
GO:0030889      0.000258913610471625    104.821818181818        0.0242889765414158
2       13      negative regulation of B cell proliferation
GO:0050870      0.000268566108079728    14.8471752147878        0.319493460660162
4       171     positive regulation of T cell activation
GO:0046651      0.000274610196078045    14.7577639751553        0.32136184347104
4       172     lymphocyte proliferation
GO:0042110      0.000275018514558874    10.2127967573827        0.596014116670127
5       319     T cell activation
GO:0002694      0.000283079927967113    10.1467203682394        0.599750882291883
5       321     regulation of leukocyte activation
GO:0032943      0.000286991449531745    14.5820971867008        0.325098609092796
4       174     mononuclear cell proliferation
GO:0070661      0.000340560941099582    13.9189057156815        0.340045671579821
4       182     leukocyte proliferation
GO:0050865      0.000384162560432835    9.47149004841313        0.640855304131202
5       343     regulation of cell activation
GO:0001782      0.00050495018454502     72.04   0.0336308905958065      2       18
B cell homeostasis
GO:0042035      0.000633305008731961    20.3636363636364        0.170022835789911
3       91      regulation of cytokine biosynthetic process
GO:0051251      0.000639167222562705    11.714815577993 0.4017023043388 4       215
positive regulation of lymphocyte activation
GO:0050863      0.000708663573971892    11.3860949709477        0.412912601204069
4       221     regulation of T cell activation
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GO:0042089      0.000833567862006689    18.4626288659794        0.186838281087814
3       100     cytokine biosynthetic process
GO:0002696      0.000863502941305667    10.780330358838 0.435333194934607       4
233     positive regulation of leukocyte activation
GO:0042107      0.000882920450586887    18.0871212121212        0.19057504670957
3       102     cytokine metabolic process
GO:0050867      0.00096413679721674     10.4554163596168        0.448411874610754
4       240     positive regulation of cell activation
GO:0050869      0.00106276642474843     48      0.0485779530828316      2       26
negative regulation of B cell activation
GO:0002260      0.00250987280221428     30.2863157894737        0.0747353124351256
2       40      lymphocyte homeostasis
GO:0001776      0.00374516579797624     24.4714893617021        0.0915507577330289
2       49      leukocyte homeostasis
GO:0032945      0.00374516579797624     24.4714893617021        0.0915507577330289
2       49      negative regulation of mononuclear cell proliferation
GO:0050672      0.00374516579797624     24.4714893617021        0.0915507577330289
2       49      negative regulation of lymphocyte proliferation
GO:0070664      0.00420833512253117     22.9984 0.0971559061656633      2       52
negative regulation of leukocyte proliferation
GO:0050871      0.00453115282243661     22.1107692307692        0.10089267178742
2       54      positive regulation of B cell activation
GO:0042108      0.00538673529853182     20.1642105263158        0.11023458584181
2       59      positive regulation of cytokine biosynthetic process
GO:0002636      0.00559506886110994     277.346153846154        0.00560514843263442
1       3       positive regulation of germinal center formation
GO:0015917      0.00559506886110994     277.346153846154        0.00560514843263442
1       3       aminophospholipid transport
GO:0016056      0.00559506886110994     277.346153846154        0.00560514843263442
1       3       rhodopsin mediated signaling pathway
GO:0045590      0.00559506886110994     277.346153846154        0.00560514843263442
1       3       negative regulation of regulatory T cell differentiation
GO:0042102      0.00669906381624608     17.95   0.123313265517957       2       66
positive regulation of T cell proliferation
GO:0002706      0.00814189961126811     16.1723943661972        0.136391945194104
2       73      regulation of lymphocyte mediated immunity
GO:0007028      0.00930835421207143     138.653846153846        0.0093419140543907
1       5       cytoplasm organization
GO:0070934      0.00930835421207143     138.653846153846        0.0093419140543907
1       5       CRD-mediated mRNA stabilization
GO:0002822      0.00971188231026789     14.7138461538462        0.149470624870251
2       80      regulation of adaptive immune response based on somatic
recombination of immune receptors built from immunoglobulin superfamily domains
Tissue: Whole_Blood=>Thyroid    Type:   asymmetric
SourceGene:     7SK(ENSG00000223039.1)
TargetGeneSet:  RP11    ERRFI1  NMNAT1  DFFA    DNAJC16 OTUD3   XKR8    MED18
PRDX3P2 FAM167B HDAC1   ZMYM1   RNF220  HHLA3   DDAH1   FRRS1   CYB561D1
DDX20   BCL9    GJA5    BOLA1   GOLPH3L ARNT    VPS72   SHE     LAMTOR2 MNDA
SLAMF8  USP21   FCGR3A  RNASEL  SMG7    TRMT1L  ZNF281  DISP1   MIXL1   C2orf44 PREB
EHD3    ARHGEF33        MSH6    PAPOLG  SPR     MRPL35  ZNF2    C2orf29 POLR1B  ORC2
ICA1L   PARD3B  IDH1    SPAG16  TMEM169 TNP1    MRPL44  EIF4E2  RNPEPL1 RPUSD3
CCRL1   ZNF619  ZNF620  CCR2    DUSP7   SCT     ABHD10  WDR52   ADPRH   MSL2
SLC25A36        ZBTB38  TRPC1   SIAH2   P2RY13  TACC3   SH3BP2  TMEM128 ZNF518B
NFXL1   UTP3    IL8     CASP6   ANKRD50 TIGD4   CCDC127 LPCAT1  BRIP1   DAP
C5orf51 SLC38A9 TRIM23  CD180   CETN3   SLC22A5 AFF4    SH3RF2  TCERG1  HMGXB3
C5orf54 NEURL1B DOK3    CTB     HIST1H3E        ZKSCAN4 ZKSCAN3 SCAND3  MICB    APOM
PFDN6   ZBTB9   NFYA    TAF8    C6orf203        TSPYL4  AKAP12  FAM103A2P
ELFN1   RNF216P1        COL28A1 TRA2A   VOPP1   LAT2    TMEM60  SLC12A9 GCC1
TNPO3   FAM131B EPHA1   ZNF786  ZNF398  GIMAP8  GIMAP7  GIMAP4  ESYT2   CTA
SH2D4A  CTD     INTS9   PDP1    WDR67   KLHL38  ZNF623  TONSL   ZNF250  RANBP6
KLHL9   DCAF10  C9orf85 C9orf40 RMI1    FOXE1   RNF20   C9orf80 ATP6V1G1
TRIM32  PSMD5   LHX6    ZBTB34  NAIF1   ABL1    GTF3C4  QSOX2   NUDT5   C10orf128
ERCC6   ADO     MSS51   AP3M1   ARHGAP19        HIF1AN  C10orf95        SUFU
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DUSP5   SMC3    CASC2   DUSP8   TPH1    SLC35C1 FAM180B HEXIM1  TMEM132A
TTC9C   ZBTB3   MEN1    EIF1AD  C11orf82        ANKRD42 PICALM  RDX     DPAGT1
ZNF202  HYLS1   KCNJ1   RAD52   NCAPD2  BCDIN3D SMUG1   ZC3H10  ZBTB39  DYRK2
ATXN7L3B        CSRP2   TMPO    RFC5    SRRM4   RNF34   ORAI1   RNF6    FAM48A
KBTBD6  KBTBD7  ARL11   SUGT1   FARP1-IT1       LIG4    RNASE2  ACIN1   C14orf119
SYNJ2BP MAP3K9  PROX2   VASH1   ZC3H14  RPS6KA5 BTBD7   PGBD4   ZFYVE19 ZFP106
ZSCAN29 HDC     RNF111  LACTB   DIS3L   ANP32A  PEX11A  C15orf38        NR2F2
LRRC28  ASB7    ZNF434  TFAP4   C16orf88        SPN     TAOK2   DDX19B  PLCG2
SLC16A13        TNK1    SNORA48 KRBA2   PIGL    BLMH    RNF135  CCT6B   PEX12
FAM134C GJC1    HIGD1B  TBKBP1  DLX3    PPP1R9B CHAD    HEATR6  APPBP2  FTSJ3
CD79B   QRICH2  CBX2    LIPG    ZNF555  PIAS4   TNFSF9  ZNF557  ZNF799  ZNF443
ZNF490  LYL1    JUND    LRRC25  SUGP1   ZNF90   ZNF486  KCTD15  ZNF792  U2AF1L4
LIN37   CAPNS1  ZFP82   ZNF260  ZNF420  ZFP36   EID2    LTBP4   MIA     ZNF526
ZNF284  ZNF225  BLOC1S3 RSPH6A  IGFL4   PPP1R15A        NAPSA   ZNF616  ZNF816
ZNF677  ZNF765  ZNF835  ZNF264  ZNF547  ZNF17   ZNF549  ZNF550  FAM110A ABHD12  NANP
DNMT3B  PXMP4   LBP     ZSWIM3  ZSWIM1  ZFP64   CSTF1   C20orf151       TCFL5
SOX18   RCAN1   C2CD2   C22orf29        CRKL    PPM1F   ZNF70   PRR14L  MFNG    TLR7
TLR8    SCML1   EIF1AX  ZFX     RBM3    FAM123B VSIG4   FHL1    IDS
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006469      0.000279990173208074    4.19201861130995        2.59414573385925
10      142     negative regulation of protein kinase activity
GO:0010332      0.000353325705541072    9.4248435627746 0.621133485571933       5
34      response to gamma radiation
GO:0033673      0.000457566102139861    3.92192997151952        2.75856342121652
10      151     negative regulation of kinase activity
GO:0033233      0.000466732731923299    27.1666666666667        0.164417687357276
3       9       regulation of protein sumoylation
GO:0071901      0.000742358201208229    5.12498054474708        1.49802781814407
7       82      negative regulation of protein serine/threonine kinase activity
GO:0051348      0.000831268473669817    3.61123977149915        2.97778700435956
10      163     negative regulation of transferase activity
GO:0045356      0.00194710386073015     54.1412213740458        0.073074527714345
2       4       positive regulation of interferon-alpha biosynthetic process
GO:0001933      0.00223963189042068     3.13417143879742        3.39796553871704
10      186     negative regulation of protein phosphorylation
GO:0000122      0.00240816445650831     2.29541912146729        7.85551172929209
17      430     negative regulation of transcription from RNA polymerase II promoter
GO:0002282      0.00320605995974029     36.0916030534351        0.0913431596429313
2       5       microglial cell activation involved in immune response
GO:0045349      0.00320605995974029     36.0916030534351        0.0913431596429313
2       5       interferon-alpha biosynthetic process
GO:0045354      0.00320605995974029     36.0916030534351        0.0913431596429313
2       5       regulation of interferon-alpha biosynthetic process
GO:0042326      0.00351530233284685     2.9316049589546 3.61718912186008        10
198     negative regulation of phosphorylation
GO:0010212      0.0036502089730963      3.7986670262357 1.97301224828732        7
108     response to ionizing radiation
GO:0045736      0.0040144883875776      10.8597701149425        0.328835374714553
3       18      negative regulation of cyclin-dependent protein kinase activity
GO:0010563      0.00419302704988163     2.85463669372935        3.70853228150301
10      203     negative regulation of phosphorus metabolic process
GO:0045936      0.00419302704988163     2.85463669372935        3.70853228150301
10      203     negative regulation of phosphate metabolic process
GO:0000244      0.00475121374870953     27.0667938931298        0.109611791571518
2       6       assembly of spliceosomal tri-snRNP
GO:0007256      0.00475121374870953     27.0667938931298        0.109611791571518
2       6       activation of JNKK activity
GO:0008630      0.00493330491000203     6.40407239819005        0.694208013286278
4       38      DNA damage response, signal transduction resulting in induction of
apoptosis
GO:0033235      0.00657176753387678     21.6519083969466        0.127880423500104
2       7       positive regulation of protein sumoylation
GO:0035970      0.00657176753387678     21.6519083969466        0.127880423500104
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2       7       peptidyl-threonine dephosphorylation
GO:0045359      0.00657176753387678     21.6519083969466        0.127880423500104
2       7       positive regulation of interferon-beta biosynthetic process
GO:0002263      0.00739237613492882     3.30393801153898        2.24704172721611
7       123     cell activation involved in immune response
GO:0002366      0.00739237613492882     3.30393801153898        2.24704172721611
7       123     leukocyte activation involved in immune response
GO:0000012      0.00865722004551591     18.0419847328244        0.14614905542869
2       8       single strand break repair
GO:0045350      0.00865722004551591     18.0419847328244        0.14614905542869
2       8       interferon-beta biosynthetic process
GO:0045357      0.00865722004551591     18.0419847328244        0.14614905542869
2       8       regulation of interferon-beta biosynthetic process
GO:0045416      0.00865722004551591     18.0419847328244        0.14614905542869
2       8       positive regulation of interleukin-8 biosynthetic process
GO:0031400      0.00926095629157091     2.29811507936508        5.48058957857588
12      300     negative regulation of protein modification process
GO:0002275      0.00973668034681133     5.18131868131868        0.840357068714968
4       46      myeloid cell activation involved in immune response
Tissue: Whole_Blood=>Thyroid    Type:   cluster
SourceGene:     7SK(ENSG00000223039.1)
TargetGeneSet:  RP11    ERRFI1  NMNAT1  DFFA    DNAJC16 OTUD3   XKR8    MED18
PRDX3P2 FAM167B HDAC1   ZMYM1   RNF220  HHLA3   DDAH1   FRRS1   CYB561D1
DDX20   BCL9    GJA5    BOLA1   GOLPH3L ARNT    VPS72   SHE     LAMTOR2 MNDA
SLAMF8  USP21   FCGR3A  RNASEL  SMG7    TRMT1L  ZNF281  DISP1   MIXL1   C2orf44 PREB
EHD3    ARHGEF33        MSH6    PAPOLG  SPR     MRPL35  ZNF2    C2orf29 POLR1B  ORC2
ICA1L   PARD3B  IDH1    SPAG16  TMEM169 TNP1    MRPL44  EIF4E2  RNPEPL1 RPUSD3
CCRL1   ZNF619  ZNF620  CCR2    DUSP7   SCT     ABHD10  WDR52   ADPRH   MSL2
SLC25A36        ZBTB38  TRPC1   SIAH2   P2RY13  TACC3   SH3BP2  TMEM128 ZNF518B
NFXL1   UTP3    IL8     CASP6   ANKRD50 TIGD4   CCDC127 LPCAT1  BRIP1   DAP
C5orf51 SLC38A9 TRIM23  CD180   CETN3   SLC22A5 AFF4    SH3RF2  TCERG1  HMGXB3
C5orf54 NEURL1B DOK3    CTB     HIST1H3E        ZKSCAN4 ZKSCAN3 SCAND3  MICB    APOM
PFDN6   ZBTB9   NFYA    TAF8    C6orf203        TSPYL4  AKAP12  FAM103A2P
ELFN1   RNF216P1        COL28A1 TRA2A   VOPP1   LAT2    TMEM60  SLC12A9 GCC1
TNPO3   FAM131B EPHA1   ZNF786  ZNF398  GIMAP8  GIMAP7  GIMAP4  ESYT2   CTA
SH2D4A  CTD     INTS9   PDP1    WDR67   KLHL38  ZNF623  TONSL   ZNF250  RANBP6
KLHL9   DCAF10  C9orf85 C9orf40 RMI1    FOXE1   RNF20   C9orf80 ATP6V1G1
TRIM32  PSMD5   LHX6    ZBTB34  NAIF1   ABL1    GTF3C4  QSOX2   NUDT5   C10orf128
ERCC6   ADO     MSS51   AP3M1   ARHGAP19        HIF1AN  C10orf95        SUFU
DUSP5   SMC3    CASC2   DUSP8   TPH1    SLC35C1 FAM180B HEXIM1  TMEM132A
TTC9C   ZBTB3   MEN1    EIF1AD  C11orf82        ANKRD42 PICALM  RDX     DPAGT1
ZNF202  HYLS1   KCNJ1   RAD52   NCAPD2  BCDIN3D SMUG1   ZC3H10  ZBTB39  DYRK2
ATXN7L3B        CSRP2   TMPO    RFC5    SRRM4   RNF34   ORAI1   RNF6    FAM48A
KBTBD6  KBTBD7  ARL11   SUGT1   FARP1-IT1       LIG4    RNASE2  ACIN1   C14orf119
SYNJ2BP MAP3K9  PROX2   VASH1   ZC3H14  RPS6KA5 BTBD7   PGBD4   ZFYVE19 ZFP106
ZSCAN29 HDC     RNF111  LACTB   DIS3L   ANP32A  PEX11A  C15orf38        NR2F2
LRRC28  ASB7    ZNF434  TFAP4   C16orf88        SPN     TAOK2   DDX19B  PLCG2
SLC16A13        TNK1    SNORA48 KRBA2   PIGL    BLMH    RNF135  CCT6B   PEX12
FAM134C GJC1    HIGD1B  TBKBP1  DLX3    PPP1R9B CHAD    HEATR6  APPBP2  FTSJ3
CD79B   QRICH2  CBX2    LIPG    ZNF555  PIAS4   TNFSF9  ZNF557  ZNF799  ZNF443
ZNF490  LYL1    JUND    LRRC25  SUGP1   ZNF90   ZNF486  KCTD15  ZNF792  U2AF1L4
LIN37   CAPNS1  ZFP82   ZNF260  ZNF420  ZFP36   EID2    LTBP4   MIA     ZNF526
ZNF284  ZNF225  BLOC1S3 RSPH6A  IGFL4   PPP1R15A        NAPSA   ZNF616  ZNF816
ZNF677  ZNF765  ZNF835  ZNF264  ZNF547  ZNF17   ZNF549  ZNF550  FAM110A ABHD12  NANP
DNMT3B  PXMP4   LBP     ZSWIM3  ZSWIM1  ZFP64   CSTF1   C20orf151       TCFL5
SOX18   RCAN1   C2CD2   C22orf29        CRKL    PPM1F   ZNF70   PRR14L  MFNG    TLR7
TLR8    SCML1   EIF1AX  ZFX     RBM3    FAM123B VSIG4   FHL1    IDS
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006469      0.000279990173208074    4.19201861130995        2.59414573385925
10      142     negative regulation of protein kinase activity
GO:0010332      0.000353325705541072    9.4248435627746 0.621133485571933       5
34      response to gamma radiation
GO:0033673      0.000457566102139861    3.92192997151952        2.75856342121652
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10      151     negative regulation of kinase activity
GO:0033233      0.000466732731923299    27.1666666666667        0.164417687357276
3       9       regulation of protein sumoylation
GO:0071901      0.000742358201208229    5.12498054474708        1.49802781814407
7       82      negative regulation of protein serine/threonine kinase activity
GO:0051348      0.000831268473669817    3.61123977149915        2.97778700435956
10      163     negative regulation of transferase activity
GO:0045356      0.00194710386073015     54.1412213740458        0.073074527714345
2       4       positive regulation of interferon-alpha biosynthetic process
GO:0001933      0.00223963189042068     3.13417143879742        3.39796553871704
10      186     negative regulation of protein phosphorylation
GO:0000122      0.00240816445650831     2.29541912146729        7.85551172929209
17      430     negative regulation of transcription from RNA polymerase II promoter
GO:0002282      0.00320605995974029     36.0916030534351        0.0913431596429313
2       5       microglial cell activation involved in immune response
GO:0045349      0.00320605995974029     36.0916030534351        0.0913431596429313
2       5       interferon-alpha biosynthetic process
GO:0045354      0.00320605995974029     36.0916030534351        0.0913431596429313
2       5       regulation of interferon-alpha biosynthetic process
GO:0042326      0.00351530233284685     2.9316049589546 3.61718912186008        10
198     negative regulation of phosphorylation
GO:0010212      0.0036502089730963      3.7986670262357 1.97301224828732        7
108     response to ionizing radiation
GO:0045736      0.0040144883875776      10.8597701149425        0.328835374714553
3       18      negative regulation of cyclin-dependent protein kinase activity
GO:0010563      0.00419302704988163     2.85463669372935        3.70853228150301
10      203     negative regulation of phosphorus metabolic process
GO:0045936      0.00419302704988163     2.85463669372935        3.70853228150301
10      203     negative regulation of phosphate metabolic process
GO:0000244      0.00475121374870953     27.0667938931298        0.109611791571518
2       6       assembly of spliceosomal tri-snRNP
GO:0007256      0.00475121374870953     27.0667938931298        0.109611791571518
2       6       activation of JNKK activity
GO:0008630      0.00493330491000203     6.40407239819005        0.694208013286278
4       38      DNA damage response, signal transduction resulting in induction of
apoptosis
GO:0033235      0.00657176753387678     21.6519083969466        0.127880423500104
2       7       positive regulation of protein sumoylation
GO:0035970      0.00657176753387678     21.6519083969466        0.127880423500104
2       7       peptidyl-threonine dephosphorylation
GO:0045359      0.00657176753387678     21.6519083969466        0.127880423500104
2       7       positive regulation of interferon-beta biosynthetic process
GO:0002263      0.00739237613492882     3.30393801153898        2.24704172721611
7       123     cell activation involved in immune response
GO:0002366      0.00739237613492882     3.30393801153898        2.24704172721611
7       123     leukocyte activation involved in immune response
GO:0000012      0.00865722004551591     18.0419847328244        0.14614905542869
2       8       single strand break repair
GO:0045350      0.00865722004551591     18.0419847328244        0.14614905542869
2       8       interferon-beta biosynthetic process
GO:0045357      0.00865722004551591     18.0419847328244        0.14614905542869
2       8       regulation of interferon-beta biosynthetic process
GO:0045416      0.00865722004551591     18.0419847328244        0.14614905542869
2       8       positive regulation of interleukin-8 biosynthetic process
GO:0031400      0.00926095629157091     2.29811507936508        5.48058957857588
12      300     negative regulation of protein modification process
GO:0002275      0.00973668034681133     5.18131868131868        0.840357068714968
4       46      myeloid cell activation involved in immune response
Tissue: Whole_Blood=>Thyroid    Type:   asymmetric
SourceGene:     AMFR(ENSG00000159461.9)
TargetGeneSet:  AKR7A2  C1QA    C1QC    C1QB    LAPTM5  AK2     ADORA3  RPRD2   RP11
SLAMF1  RRM2    CAPN14  PLEK    ZNF638-IT1      UBTFL6  WDR75   C3orf38 C3orf26
ILDR1   CD86    TFDP2   GP5     TADA2B  CTD     CD180   SERINC5 STARD4  APC
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CSF1R   HAVCR2  C5orf58 F13A1   C6orf47 ZBTB22  TBCC    SGK1    SRP72P2 CCZ1
NCF1B   TFEC    GCC1    TBXAS1  ZNF767  INSIG1  NAIF1   SETP5   IL2RA   HSD17B7P2
CEP55   O3FAR1  RHOG    MTRNR2L8        FAM111B MS4A6A  MS4A4E  MS4A7   YIF1A
FOLR2   CWF19L2 IL18    MCAM    CD163   ARID2   NCKAP1L C12orf56        KRT8P22
SELPLG  HVCN1   EXOSC8  RNASE6  ALDH6A1 PSTPIP1 C15orf58        IGSF6   APOBR
ITGAM   SHCBP1  AMFR    MT3     CTB     MLYCD   PIK3R5  CDK5RAP3        PDK2
GNA15   EBI3    VAV1    MYO1F   LRRC25  POU2F2  CD33    LILRA2  ZNF8    FKBP1A
CRLS1   7SK     NCOA3   ITGB2   TOB2    GPR34   RP6     WAS     ACTG1P10        ZXDB
VSIG4   RPSAP14 XIAP    SASH3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0046649      5.72667249465935e-07    6.54314574314574        2.36710262265587
13      433     lymphocyte activation
GO:0042110      1.21150996426741e-06    7.38655462184874        1.74389315618296
11      319     T cell activation
GO:0046635      3.51422065811752e-06    25.4871977240398        0.235070237353816
5       43      positive regulation of alpha-beta T cell activation
GO:0046634      1.20664215297118e-05    19.3540540540541        0.300671233824649
5       55      regulation of alpha-beta T cell activation
GO:0050865      1.67618630246928e-05    6.11002306654481        1.87509514912463
10      343     regulation of cell activation
GO:0042129      1.84692614533867e-05    12.3521268925739        0.552141720296173
6       101     regulation of T cell proliferation
GO:0050863      2.70602554461943e-05    7.49004827084573        1.2081516850045 8
221     regulation of T cell activation
GO:0042102      2.95788295713274e-05    15.8517944173682        0.360805480589579
5       66      positive regulation of T cell proliferation
GO:0002521      3.85262040908757e-05    6.17801072647489        1.65095841118262
9       302     leukocyte differentiation
GO:0050870      4.06885179853054e-05    8.42276422764228        0.934814199709363
7       171     positive regulation of T cell activation
GO:0042098      4.46166255895924e-05    10.4647749510763        0.645076465296519
6       118     T cell proliferation
GO:0002252      4.58983233867896e-05    5.39469626888683        2.11016538647844
10      386     immune effector process
GO:0050867      4.86618942058087e-05    6.86741136474016        1.31201992941665
8       240     positive regulation of cell activation
GO:0006959      5.3792325400273e-05     10.1010864430798        0.66694346412013
6       122     humoral immune response
GO:0002460      5.83890837826231e-05    7.9331098339719 0.98948169676839        7
181     adaptive immune response based on somatic recombination of immune receptors
built from immunoglobulin superfamily domains
GO:0007596      7.9140657730722e-05     4.6121210291098 2.72244135353955        11
498     blood coagulation
GO:0046631      8.43596319850862e-05    12.543875043875 0.448273475884022       5
82      alpha-beta T cell activation
GO:0072376      8.43596319850862e-05    12.543875043875 0.448273475884022       5
82      protein activation cascade
GO:0032623      9.51104621521364e-05    19.1093333333333        0.240536987059719
4       44      interleukin-2 production
GO:0043372      0.000101184972910591    40.4830827067669        0.092934745000346
3       17      positive regulation of CD4-positive, alpha-beta T cell
differentiation
GO:0002250      0.000102678435140264    7.21836823734729        1.08241644176874
7       198     adaptive immune response
GO:0050670      0.000134847218798117    8.47766527695057        0.78721195764999
6       144     regulation of lymphocyte proliferation
GO:0032944      0.000140061736785277    8.41608357149897        0.792678707355892
6       145     regulation of mononuclear cell proliferation
GO:2000516      0.000143056593367425    35.4177631578947        0.103868244412151
3       19      positive regulation of CD4-positive, alpha-beta T cell activation
GO:0002443      0.000152438472788205    6.75217864923747        1.15348418794547
7       211     leukocyte mediated immunity
GO:0051249      0.000153408109780161    5.7759795134443 1.54709016677047        8
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283     regulation of lymphocyte activation
GO:0050778      0.000160843711861014    5.07657947686117        1.98989689294858
9       364     positive regulation of immune response
GO:0070663      0.000168584536111386    8.12100456621005        0.820012455885406
6       150     regulation of leukocyte proliferation
GO:0051251      0.00017117417106622     6.6204594017094 1.17535118676908        7
215     positive regulation of lymphocyte activation
GO:0050671      0.000178056376220367    10.6036531036531        0.52480797176666
5       96      positive regulation of lymphocyte proliferation
GO:0030168      0.000181218179527848    6.55648148148148        1.18628468618089
7       217     platelet activation
GO:0032946      0.000186937031774168    10.4876615746181        0.530274721472562
5       97      positive regulation of mononuclear cell proliferation
GO:0045582      0.000197657353137294    15.5896598639456        0.289737734412843
4       53      positive regulation of T cell differentiation
GO:0006954      0.000202253503132725    4.46325509811466        2.52563836412705
10      462     inflammatory response
GO:0030097      0.000205812297407556    4.45308250951787        2.53110511383295
10      463     hemopoiesis
GO:0070665      0.000215617880731047    10.1543385490754        0.546674970590271
5       100     positive regulation of leukocyte proliferation
GO:0002253      0.000223274281062664    5.45220463675524        1.63455816206491
8       299     activation of immune response
GO:0002696      0.000279994646039632    6.08542281219272        1.27375268147533
7       233     positive regulation of leukocyte activation
GO:0048534      0.000351097338747098    4.14970865082922        2.70604110442184
10      495     hemopoietic or lymphoid organ development
GO:0046651      0.000353095449693844    7.03383396600099        0.940280949415265
6       172     lymphocyte proliferation
GO:0002694      0.000360174358177522    5.0610628627998 1.75482665559477        8
321     regulation of leukocyte activation
GO:0045621      0.000362790922793897    13.1622988505747        0.338938481765968
4       62      positive regulation of lymphocyte differentiation
GO:0032943      0.000375591082620152    6.94911937377691        0.951214448827071
6       174     mononuclear cell proliferation
GO:0006956      0.000385789434511847    12.9383050847458        0.34440523147187
4       63      complement activation
GO:0043370      0.00041843949134889     23.5986842105263        0.147602242059373
3       27      regulation of CD4-positive, alpha-beta T cell differentiation
GO:0070661      0.000477030694398031    6.62951432129514        0.994948446474292
6       182     leukocyte proliferation
GO:0007229      0.000516664230974918    11.9233333333333        0.371738980001384
4       68      integrin-mediated signaling pathway
GO:2000514      0.000518632478943084    21.7803643724696        0.158535741471178
3       29      regulation of CD4-positive, alpha-beta T cell activation
GO:0046638      0.000573997426413046    20.9722222222222        0.164002491177081
3       30      positive regulation of alpha-beta T cell differentiation
GO:0032515      0.000608769608858003    74.6337662337662        0.0382672479413189
2       7       negative regulation of phosphoprotein phosphatase activity
GO:0032101      0.000739919289285456    4.51412474849095        1.95709639471317
8       358     regulation of response to external stimulus
GO:0001817      0.00075347948560816     4.50094297981622        1.96256314441907
8       359     regulation of cytokine production
GO:0030098      0.000868287961127102    5.88376919883769        1.11521694000415
6       204     lymphocyte differentiation
GO:0045580      0.00104736885590511     9.77367521367521        0.448273475884022
4       82      regulation of T cell differentiation
GO:0032663      0.00124719428053958     15.719298245614 0.213203238530206       3
39      regulation of interleukin-2 production
GO:0046637      0.00134303976147446     15.2933854907539        0.218669988236108
3       40      regulation of alpha-beta T cell differentiation
GO:0001816      0.00139261489937974     4.07176911598792        2.15936613383157
8       395     cytokine production
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GO:0043367      0.00144339767295301     14.8898891966759        0.224136737942011
3       41      CD4-positive, alpha-beta T cell differentiation
GO:0030217      0.0016299378764811      6.36343296939323        0.852812954120822
5       156     T cell differentiation
GO:0006801      0.00165795990725779     14.1434210526316        0.235070237353816
3       43      superoxide metabolic process
GO:0035710      0.00165795990725779     14.1434210526316        0.235070237353816
3       43      CD4-positive, alpha-beta T cell activation
GO:0045619      0.00210180443756686     8.01515789473684        0.541208220884368
4       99      regulation of lymphocyte differentiation
GO:0002449      0.00219684706663474     5.92676009342676        0.912947200885752
5       167     lymphocyte mediated immunity
GO:0006958      0.0025619684878847      12.0310750279955        0.273337485295135
3       50      complement activation, classical pathway
GO:0006085      0.00257329522717421     31.0822510822511        0.0765344958826379
2       14      acetyl-CoA biosynthetic process
GO:0046641      0.00257329522717421     31.0822510822511        0.0765344958826379
2       14      positive regulation of alpha-beta T cell proliferation
GO:0030316      0.00286623451783341     11.5383995703545        0.284270984706941
3       52      osteoclast differentiation
GO:0016064      0.00318303113197412     7.11028037383178        0.6068092173552 4
111     immunoglobulin mediated immune response
GO:0019724      0.00350309245351609     6.91490909090909        0.623209466472908
4       114     B cell mediated immunity
GO:0030866      0.0038051697756915      24.8606060606061        0.092934745000346
2       17      cortical actin cytoskeleton organization
GO:0042095      0.0038051697756915      24.8606060606061        0.092934745000346
2       17      interferon-gamma biosynthetic process
GO:0045637      0.00396300212636255     6.67040935672515        0.645076465296519
4       118     regulation of myeloid cell differentiation
GO:0015949      0.0042656979540683      23.3051948051948        0.0984014947062487
2       18      nucleobase-containing small molecule interconversion
GO:0032620      0.0042656979540683      23.3051948051948        0.0984014947062487
2       18      interleukin-17 production
GO:0032660      0.0042656979540683      23.3051948051948        0.0984014947062487
2       18      regulation of interleukin-17 production
GO:0042104      0.0042656979540683      23.3051948051948        0.0984014947062487
2       18      positive regulation of activated T cell proliferation
GO:0046640      0.0042656979540683      23.3051948051948        0.0984014947062487
2       18      regulation of alpha-beta T cell proliferation
GO:0032649      0.00471707493739376     9.57604817127565        0.338938481765968
3       62      regulation of interferon-gamma production
GO:0030865      0.00475071458473899     21.9327731092437        0.103868244412151
2       19      cortical cytoskeleton organization
GO:0002573      0.00486334739263922     6.28143250688705        0.683343713237838
4       125     myeloid leukocyte differentiation
GO:0002455      0.00538456951437865     9.11078098471986        0.355338730883676
3       65      humoral immune response mediated by circulating immunoglobulin
GO:0046632      0.00538456951437865     9.11078098471986        0.355338730883676
3       65      alpha-beta T cell differentiation
GO:0002446      0.00579311705311845     19.6213260423787        0.114801743823957
2       21      neutrophil mediated immunity
GO:0031529      0.00579311705311845     19.6213260423787        0.114801743823957
2       21      ruffle organization
GO:0042094      0.00579311705311845     19.6213260423787        0.114801743823957
2       21      interleukin-2 biosynthetic process
GO:0046633      0.00579311705311845     19.6213260423787        0.114801743823957
2       21      alpha-beta T cell proliferation
GO:0032609      0.00585952701430043     8.82483552631579        0.366272230295481
3       67      interferon-gamma production
GO:0010543      0.00634996031081422     18.638961038961 0.12026849352986        2
22      regulation of platelet activation
GO:0030225      0.00634996031081422     18.638961038961 0.12026849352986        2
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22      macrophage differentiation
GO:0032673      0.00693020683008556     17.7501546072975        0.125735243235762
2       23      regulation of interleukin-4 production
GO:0042554      0.00693020683008556     17.7501546072975        0.125735243235762
2       23      superoxide anion generation
GO:0043029      0.00693020683008556     17.7501546072975        0.125735243235762
2       23      T cell homeostasis
GO:0002761      0.00743179406559731     8.06503759398496        0.399072728530898
3       73      regulation of myeloid leukocyte differentiation
GO:0071706      0.00743179406559731     8.06503759398496        0.399072728530898
3       73      tumor necrosis factor superfamily cytokine production
GO:0046006      0.00753359074695003     16.9421487603306        0.131201992941665
2       24      regulation of activated T cell proliferation
GO:0030099      0.00804466067507511     4.30667153640127        1.24095218323991
5       227     myeloid cell differentiation
GO:0030858      0.00815984834055658     16.2044042913608        0.136668742647568
2       25      positive regulation of epithelial cell differentiation
GO:0032855      0.00815984834055658     16.2044042913608        0.136668742647568
2       25      positive regulation of Rac GTPase activity
GO:0042092      0.00815984834055658     16.2044042913608        0.136668742647568
2       25      type 2 immune response
GO:0043666      0.00815984834055658     16.2044042913608        0.136668742647568
2       25      regulation of phosphoprotein phosphatase activity
GO:0050798      0.00880871801818296     15.5281385281385        0.14213549235347
2       26      activated T cell proliferation
GO:0051004      0.00880871801818296     15.5281385281385        0.14213549235347
2       26      regulation of lipoprotein lipase activity
GO:0032633      0.00947994030032968     14.905974025974 0.147602242059373       2
27      interleukin-4 production
GO:0032722      0.00947994030032968     14.905974025974 0.147602242059373       2
27      positive regulation of chemokine production
GO:0042113      0.00982247367293868     5.0910067114094 0.836412705003114       4
153     B cell activation
Tissue: Whole_Blood=>Thyroid    Type:   cluster
SourceGene:     AMFR(ENSG00000159461.9)
TargetGeneSet:  AKR7A2  C1QA    C1QC    C1QB    LAPTM5  AK2     ADORA3  RPRD2   RP11
SLAMF1  RRM2    CAPN14  PLEK    ZNF638-IT1      UBTFL6  WDR75   C3orf38 C3orf26
ILDR1   CD86    TFDP2   GP5     TADA2B  CTD     CD180   SERINC5 STARD4  APC
CSF1R   HAVCR2  C5orf58 F13A1   C6orf47 ZBTB22  TBCC    SGK1    SRP72P2 CCZ1
NCF1B   TFEC    GCC1    TBXAS1  ZNF767  INSIG1  NAIF1   SETP5   IL2RA   HSD17B7P2
CEP55   O3FAR1  RHOG    MTRNR2L8        FAM111B MS4A6A  MS4A4E  MS4A7   YIF1A
FOLR2   CWF19L2 IL18    MCAM    CD163   ARID2   NCKAP1L C12orf56        KRT8P22
SELPLG  HVCN1   EXOSC8  RNASE6  ALDH6A1 PSTPIP1 C15orf58        IGSF6   APOBR
ITGAM   SHCBP1  AMFR    MT3     CTB     MLYCD   PIK3R5  CDK5RAP3        PDK2
GNA15   EBI3    VAV1    MYO1F   LRRC25  POU2F2  CD33    LILRA2  ZNF8    FKBP1A
CRLS1   7SK     NCOA3   ITGB2   TOB2    GPR34   RP6     WAS     ACTG1P10        ZXDB
VSIG4   RPSAP14 XIAP    SASH3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0046649      5.72667249465935e-07    6.54314574314574        2.36710262265587
13      433     lymphocyte activation
GO:0042110      1.21150996426741e-06    7.38655462184874        1.74389315618296
11      319     T cell activation
GO:0046635      3.51422065811752e-06    25.4871977240398        0.235070237353816
5       43      positive regulation of alpha-beta T cell activation
GO:0046634      1.20664215297118e-05    19.3540540540541        0.300671233824649
5       55      regulation of alpha-beta T cell activation
GO:0050865      1.67618630246928e-05    6.11002306654481        1.87509514912463
10      343     regulation of cell activation
GO:0042129      1.84692614533867e-05    12.3521268925739        0.552141720296173
6       101     regulation of T cell proliferation
GO:0050863      2.70602554461943e-05    7.49004827084573        1.2081516850045 8
221     regulation of T cell activation
GO:0042102      2.95788295713274e-05    15.8517944173682        0.360805480589579
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5       66      positive regulation of T cell proliferation
GO:0002521      3.85262040908757e-05    6.17801072647489        1.65095841118262
9       302     leukocyte differentiation
GO:0050870      4.06885179853054e-05    8.42276422764228        0.934814199709363
7       171     positive regulation of T cell activation
GO:0042098      4.46166255895924e-05    10.4647749510763        0.645076465296519
6       118     T cell proliferation
GO:0002252      4.58983233867896e-05    5.39469626888683        2.11016538647844
10      386     immune effector process
GO:0050867      4.86618942058087e-05    6.86741136474016        1.31201992941665
8       240     positive regulation of cell activation
GO:0006959      5.3792325400273e-05     10.1010864430798        0.66694346412013
6       122     humoral immune response
GO:0002460      5.83890837826231e-05    7.9331098339719 0.98948169676839        7
181     adaptive immune response based on somatic recombination of immune receptors
built from immunoglobulin superfamily domains
GO:0007596      7.9140657730722e-05     4.6121210291098 2.72244135353955        11
498     blood coagulation
GO:0046631      8.43596319850862e-05    12.543875043875 0.448273475884022       5
82      alpha-beta T cell activation
GO:0072376      8.43596319850862e-05    12.543875043875 0.448273475884022       5
82      protein activation cascade
GO:0032623      9.51104621521364e-05    19.1093333333333        0.240536987059719
4       44      interleukin-2 production
GO:0043372      0.000101184972910591    40.4830827067669        0.092934745000346
3       17      positive regulation of CD4-positive, alpha-beta T cell
differentiation
GO:0002250      0.000102678435140264    7.21836823734729        1.08241644176874
7       198     adaptive immune response
GO:0050670      0.00013484721879811 7   8.47766527695057        0.78721195764999
6       144     regulation of lymphocyte proliferation
GO:0032944      0.00014006173678527 7   8.41608357149897        0.792678707355892
6       145     regulation of mononuclear cell proliferation
GO:2000516      0.000143056593367425    35.4177631578947        0.103868244412151
3       19      positive regulation of CD4-positive, alpha-beta T cell activation
GO:0002443      0.000152438472788205    6.75217864923747        1.15348418794547
7       211     leukocyte mediated immunity
GO:0051249      0.000153408109780161    5.7759795134443 1.54709016677047        8
283     regulation of lymphocyte activation
GO:0050778      0.000160843711861014    5.07657947686117        1.98989689294858
9       364     positive regulation of immune response
GO:0070663      0.000168584536111386    8.12100456621005        0.820012455885406
6       150     regulation of leukocyte proliferation
GO:0051251      0.00017117417106622     6.6204594017094 1.17535118676908        7
215     positive regulation of lymphocyte activation
GO:0050671      0.000178056376220367    10.6036531036531        0.52480797176666
5       96      positive regulation of lymphocyte proliferation
GO:0030168      0.000181218179527848    6.55648148148148        1.18628468618089
7       217     platelet activation
GO:0032946      0.000186937031774168    10.4876615746181        0.530274721472562
5       97      positive regulation of mononuclear cell proliferation
GO:0045582      0.000197657353137294    15.5896598639456        0.289737734412843
4       53      positive regulation of T cell differentiation
GO:0006954      0.000202253503132725    4.46325509811466        2.52563836412705
10      462     inflammatory response
GO:0030097      0.000205812297407556    4.45308250951787        2.53110511383295
10      463     hemopoiesis
GO:0070665      0.000215617880731047    10.1543385490754        0.546674970590271
5       100     positive regulation of leukocyte proliferation
GO:0002253      0.000223274281062664    5.45220463675524        1.63455816206491
8       299     activation of immune response
GO:0002696      0.000279994646039632    6.08542281219272        1.27375268147533
7       233     positive regulation of leukocyte activation
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GO:0048534	0.000351097338747098	4.14970865082922	2.70604110442184	10	495	hemopoietic or lymphoid organ development
GO:0046651	0.000353095449693844	7.03383396600099	0.940280949415265	6	172	lymphocyte proliferation
GO:0002694	0.000360174358177522	5.0610628627998	1.75482665559477	8	321	regulation of leukocyte activation
GO:0045621	0.000362790922793897	13.1622988505747	0.338938481765968	4	62	positive regulation of lymphocyte differentiation
GO:0032943	0.000375591082620152	6.94911937377691	0.951214448827071	6	174	mononuclear cell proliferation
GO:0006956	0.000385789434511847	12.9383050847458	0.34440523147187	4	63	complement activation
GO:0043370	0.00041843949134889	23.5986842105263	0.147602242059373	3	27	regulation of CD4-positive, alpha-beta T cell differentiation
GO:0070661	0.000477030694398031	6.62951432129514	0.994948446474292	6	182	leukocyte proliferation
GO:0007229	0.000516664230974918	11.9233333333333	0.371738980001384	4	68	integrin-mediated signaling pathway
GO:2000514	0.000518632478943084	21.7803643724696	0.158535741471178	3	29	regulation of CD4-positive, alpha-beta T cell activation
GO:0046638	0.000573997426413046	20.9722222222222	0.164002491177081	3	30	positive regulation of alpha-beta T cell differentiation
GO:0032515	0.000608769608858003	74.6337662337662	0.0382672479413189	2	7	negative regulation of phosphoprotein phosphatase activity
GO:0032101	0.000739919289285456	4.51412474849095	1.95709639471317	8	358	regulation of response to external stimulus
GO:0001817	0.00075347948560816	4.50094297981622	1.96256314441907	8	359	regulation of cytokine production
GO:0030098	0.000868287961127102	5.88376919883769	1.11521694000415	6	204	lymphocyte differentiation
GO:0045580	0.00104736885590511	9.77367521367521	0.448273475884022	4	82	regulation of T cell differentiation
GO:0032663	0.00124719428053958	15.719298245614	0.213203238530206	3	39	regulation of interleukin-2 production
GO:0046637	0.00134303976147446	15.2933854907539	0.218669988236108	3	40	regulation of alpha-beta T cell differentiation
GO:0001816	0.00139261489937974	4.07176911598792	2.15936613383157	8	395	cytokine production
GO:0043367	0.00144339767295301	14.8898891966759	0.224136737942011	3	41	CD4-positive, alpha-beta T cell differentiation
GO:0030217	0.0016299378764811	6.36343296939323	0.852812954120822	5	156	T cell differentiation
GO:0006801	0.00165795990725779	14.1434210526316	0.235070237353816	3	43	superoxide metabolic process
GO:0035710	0.00165795990725779	14.1434210526316	0.235070237353816	3	43	CD4-positive, alpha-beta T cell activation
GO:0045619	0.00210180443756686	8.01515789473684	0.541208220884368	4	99	regulation of lymphocyte differentiation
GO:0002449	0.00219684706663474	5.92676009342676	0.912947200885752	5	167	lymphocyte mediated immunity
GO:0006958	0.0025619684878847	12.0310750279955	0.273337485295135	3	50	complement activation, classical pathway
GO:0006085	0.00257329522717421	31.0822510822511	0.0765344958826379	2	14	acetyl-CoA biosynthetic process
GO:0046641	0.00257329522717421	31.0822510822511	0.0765344958826379	2	14	positive regulation of alpha-beta T cell proliferation
GO:0030316	0.00286623451783341	11.5383995703545	0.284270984706941	3	52	osteoclast differentiation
GO:0016064	0.00318303113197412	7.11028037383178	0.6068092173552	4	111	immunoglobulin mediated immune response
GO:0019724	0.00350309245351609	6.91490909090909	0.623209466472908	4	114	B cell mediated immunity
GO:0030866	0.0038051697756915	24.8606060606061	0.092934745000346			

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2       17      cortical actin cytoskeleton organization
GO:0042095      0.0038051697756915      24.8606060606061        0.092934745000346
2       17      interferon-gamma biosynthetic process
GO:0045637      0.00396300212636255     6.67040935672515        0.645076465296519
4       118     regulation of myeloid cell differentiation
GO:0015949      0.0042656979540683      23.3051948051948        0.0984014947062487
2       18      nucleobase-containing small molecule interconversion
GO:0032620      0.0042656979540683      23.3051948051948        0.0984014947062487
2       18      interleukin-17 production
GO:0032660      0.0042656979540683      23.3051948051948        0.0984014947062487
2       18      regulation of interleukin-17 production
GO:0042104      0.0042656979540683      23.3051948051948        0.0984014947062487
2       18      positive regulation of activated T cell proliferation
GO:0046640      0.0042656979540683      23.3051948051948        0.0984014947062487
2       18      regulation of alpha-beta T cell proliferation
GO:0032649      0.00471707493739376     9.57604817127565        0.338938481765968
3       62      regulation of interferon-gamma production
GO:0030865      0.00475071458473899     21.9327731092437        0.103868244412151
2       19      cortical cytoskeleton organization
GO:0002573      0.00486334739263922     6.28143250688705        0.683343713237838
4       125     myeloid leukocyte differentiation
GO:0002455      0.0053845695143786 5    9.11078098471986        0.355338730883676
3       65      humoral immune response mediated by circulating immunoglobulin
GO:0046632      0.0053845695143786 5    9.11078098471986        0.355338730883676
3       65      alpha-beta T cell differentiation
GO:0002446      0.00579311705311845     19.6213260423787        0.114801743823957
2       21      neutrophil mediated immunity
GO:0031529      0.00579311705311845     19.6213260423787        0.114801743823957
2       21      ruffle organization
GO:0042094      0.00579311705311845     19.6213260423787        0.114801743823957
2       21      interleukin-2 biosynthetic process
GO:0046633      0.00579311705311845     19.6213260423787        0.114801743823957
2       21      alpha-beta T cell proliferation
GO:0032609      0.00585952701430043     8.82483552631579        0.366272230295481
3       67      interferon-gamma production
GO:0010543      0.00634996031081422     18.638961038961 0.12026849352986        2
22      regulation of platelet activation
GO:0030225      0.00634996031081422     18.638961038961 0.12026849352986        2
22      macrophage differentiation
GO:0032673      0.00693020683008556     17.7501546072975        0.125735243235762
2       23      regulation of interleukin-4 production
GO:0042554      0.00693020683008556     17.7501546072975        0.125735243235762
2       23      superoxide anion generation
GO:0043029      0.00693020683008556     17.7501546072975        0.125735243235762
2       23      T cell homeostasis
GO:0002761      0.00743179406559731     8.06503759398496        0.399072728530898
3       73      regulation of myeloid leukocyte differentiation
GO:0071706      0.00743179406559731     8.06503759398496        0.399072728530898
3       73      tumor necrosis factor superfamily cytokine production
GO:0046006      0.00753359074695003     16.9421487603306        0.131201992941665
2       24      regulation of activated T cell proliferation
GO:0030099      0.00804466067507511     4.30667153640127        1.24095218323991
5       227     myeloid cell differentiation
GO:0030858      0.00815984834055658     16.2044042913608        0.136668742647568
2       25      positive regulation of epithelial cell differentiation
GO:0032855      0.00815984834055658     16.2044042913608        0.136668742647568
2       25      positive regulation of Rac GTPase activity
GO:0042092      0.00815984834055658     16.2044042913608        0.136668742647568
2       25      type 2 immune response
GO:0043666      0.00815984834055658     16.2044042913608        0.136668742647568
2       25      regulation of phosphoprotein phosphatase activity
GO:0050798      0.00880871801818296     15.5281385281385        0.14213549235347
2       26      activated T cell proliferation
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GO:0051004      0.00880871801818296     15.5281385281385        0.14213549235347
2       26      regulation of lipoprotein lipase activity
GO:0032633      0.00947994030032968     14.905974025974 0.147602242059373       2
27      interleukin-4 production
GO:0032722      0.00947994030032968     14.905974025974 0.147602242059373       2
27      positive regulation of chemokine production
GO:0042113      0.00982247367293868     5.0910067114094 0.836412705003114       4
153     B cell activation
Tissue: Whole_Blood=>Thyroid    Type:   asymmetric
SourceGene:     AMY2A(ENSG00000243480.3)
TargetGeneSet:  CELA3B  CELA3A  CRNN    SPRR3   CPB1    PRL     CLPS    CGA     CPA2
CPA1    PRSS1   PNLIP   PNLIPRP2        KRT4    PLA2G1B RP11    RHCG    GP2
CTRB2   CTRB1   KRTAP3-2        KRTAP11-1       BRD1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0007586      1.51426135092439e-12    87.3054074638233        0.158397342744447
8       109     digestion
GO:0044241      4.45140475278301e-09    308.427807486631        0.021797799460245
4       15      lipid digestion
GO:0022617      1.83105550247234e-05    72.7121212121212        0.0523147187045879
3       36      extracellular matrix disassembly
GO:0016042      0.000366898473453374    14.0306475531389        0.351671164625285
4       242     lipid catabolic process
GO:0008202      0.000586693720234097    12.3398692810458        0.398173136807141
4       274     steroid metabolic process
GO:0001523      0.0014428580814799      40.9473684210526        0.0566742785966369
2       39      retinoid metabolic process
GO:0030198      0.00155770974328471     15.0548523206751        0.233963047539963
3       161     extracellular matrix organization
GO:0043062      0.00158561961605076     14.9591194968553        0.235416234170646
3       162     extracellular structure organization
GO:0016101      0.0015938929661462 8    38.8421052631579        0.0595806518580029
2       41      diterpenoid metabolic process
GO:0006721      0.0023624467699341      31.5394736842105        0.0726593315341499
2       50      terpenoid metabolic process
GO:0032275      0.00435352854395898     360.7   0.00435955989204899     1       3
luteinizing hormone secretion
GO:0044240      0.00435352854395898     360.7   0.00435955989204899     1       3
multicellular organismal lipid catabolic process
GO:0070634      0.00435352854395898     360.7   0.00435955989204899     1       3
transepithelial ammonium transport
GO:0072488      0.00435352854395898     360.7   0.00435955989204899     1       3
ammonium transmembrane transport
GO:0006720      0.00483544160740886     21.593984962406 0.104629437409176       2
72      isoprenoid metabolic process
GO:0009791      0.00551129037912381     20.1473684210526        0.111895370562591
2       77      post-embryonic development
GO:0032431      0.00580068911293552     240.45  0.00581274652273199     1       4
activation of phospholipase A2 activity
GO:0006066      0.00641700421826788     8.97782002534854        0.386547643761677
3       266     alcohol metabolic process
GO:0032430      0.00724584627557323     180.325 0.00726593315341499     1       5
positive regulation of phospholipase A2 activity
GO:0030855      0.00753766248507537     8.45340501792115        0.409798629852605
3       282     epithelial cell differentiation
GO:0071845      0.0076854182153757      8.3920521945433 0.412705003113971       3
284     cellular component disassembly at cellular level
GO:0022411      0.00798610278699269     8.2719298245614 0.418517749636703       3
288     cellular component disassembly
GO:0000244      0.00868900266683825     144.25  0.00871911978409799     1       6
assembly of spliceosomal tri-snRNP
GO:0002385      0.00868900266683825     144.25  0.00871911978409799     1       6
mucosal immune response
GO:0015696      0.00868900266683825     144.25  0.00871911978409799     1       6
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ammonium transport
GO:0019374      0.00868900266683825     144.25  0.00871911978409799     1       6
galactolipid metabolic process
GO:0045056      0.00868900266683825     144.25  0.00871911978409799     1       6
transcytosis
Tissue: Whole_Blood=>Thyroid    Type:   asymmetric
SourceGene:     CASP10(ENSG00000003400.10)
TargetGeneSet:  SF3A3   SELRC1  SETDB1  ADAR    RP11    URB2    RHOB    WDR43
POLR1B  VPRBP   RP13    NOP14   SRP72   CCT6P1  MAK16   NCBP1   NGB     HNRNPF
NOLC1   BET1L   NAT10   WDR74   RERG    NUFIP1  EXOC5   NIP7    USP10   DPH1    TSR1
SEZ6    CCDC43  EFTUD2  KPNB1   ATCAY   TNFSF14 ZNF317  BRD4    AKAP8   ZNF8
BACH1   BRWD1-IT2       COL18A1 EP300
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0071843      2.21202167880767e-10    23.8259993281827        0.595391322399834
10      239     cellular component biogenesis at cellular level
GO:0022613      2.99435719193124e-09    21.912037037037 0.560514843263442       9
225     ribonucleoprotein complex biogenesis
GO:0022618      1.14307459859597e-07    32.1932584269663        0.236661822711231
6       95      ribonucleoprotein complex assembly
GO:0071826      1.55388656106245e-07    30.4702127659574        0.249117708117085
6       100     ribonucleoprotein complex subunit organization
GO:0000377      1.00603769758897e-05    14.3606060606061        0.508200124558854
6       204     RNA splicing, via transesterification reactions with bulged
adenosine as nucleophile
GO:0000398      1.00603769758897e-05    14.3606060606061        0.508200124558854
6       204     nuclear mRNA splicing, via spliceosome
GO:0000375      1.15505591914944e-05    14.0019704433498        0.520656009964708
6       209     RNA splicing, via transesterification reactions
GO:0042254      3.17423559617724e-05    15.9845430107527        0.371185385094457
5       149     ribosome biogenesis
GO:0006397      4.84742666700223e-05    8.63485221674877        0.99397965538717
7       399     mRNA processing
GO:0007000      6.0056443209649e-05     282.588235294118        0.0124558854058543
2       5       nucleolus organization
GO:0008380      0.000131646102897489    8.89463722397476        0.804650197218186
6       323     RNA splicing
GO:0090305      0.000508815473285125    21.75   0.156944156113764       3       63
nucleic acid phosphodiester bond hydrolysis
GO:0042255      0.000708352526025667    60.5084033613445        0.0398588332987337
2       16      ribosome assembly
GO:0006913      0.00107660461177516     7.2668246933938 0.792194311812331       5
318     nucleocytoplasmic transport
GO:0051169      0.00112263877896694     7.19630461412822        0.799667843055844
5       321     nuclear transport
GO:0006606      0.00135078207165987     9.30890052356021        0.485779530828316
4       195     protein import into nucleus
GO:0051170      0.0014289298286985      9.16301546391753        0.493253062071829
4       198     nuclear import
GO:0043388      0.00203655412226881     33.8588235294118        0.067261781191613
2       27      positive regulation of DNA binding
GO:0034504      0.0021716726600272 2    8.14048165137615        0.553041312019929
4       222     protein localization to nucleus
GO:0006354      0.0024225620784798 3    12.3896103896104        0.269047124766452
3       108     DNA-dependent transcription, elongation
GO:0000387      0.00268117418933943     29.1805273833671        0.0772264895162964
2       31      spliceosomal snRNP assembly
GO:0042306      0.00296692122864391     11.5060337892196        0.288976541415819
3       116     regulation of protein import into nucleus
GO:1900180      0.00296692122864391     11.5060337892196        0.288976541415819
3       116     regulation of protein localization to nucleus
GO:0000060      0.00380429496468588     24.1680672268908        0.0921735520033216
2       37      protein import into nucleus, translocation
GO:0017038      0.00405042757761231     6.80528846153846        0.657670749429105
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4       264     protein import
GO:0046822      0.00473504233258129     9.68860244233379        0.341291260120407
3       137     regulation of nucleocytoplasmic transport
GO:0033157      0.00502965251544117     9.47445255474453        0.348764791363919
3       140     regulation of intracellular protein transport
GO:0070301      0.0051099802034095     20.622668579627 0.107120614490347       2
43      cellular response to hydrogen peroxide
GO:0006997      0.00558484740037423     19.6607387140903        0.112102968652688
2       45      nucleus organization
GO:0043967      0.00582960250515155     19.2125668449198        0.114594145733859
2       46      histone H4 acetylation
GO:0033365      0.00599990723060243     4.80665839536807        1.17832675939381
5       473     protein localization to organelle
GO:0006605      0.00605302286071859     4.79606575417842        1.18081793647498
5       474     protein targeting
GO:0031047      0.00607920608121654     18.7843137254902        0.11708532281503
2       47      gene silencing by RNA
GO:0051098      0.00727676494327996     8.25593514765489        0.398588332987337
3       160     regulation of binding
GO:0000491      0.00745544346333527     205.9   0.00747353124351256     1       3
small nucleolar ribonucleoprotein complex assembly
GO:0000492      0.00745544346333527     205.9   0.00747353124351256     1       3
box C/D snoRNP assembly
GO:0044154      0.00745544346333527     205.9   0.00747353124351256     1       3
histone H3-K14 acetylation
GO:0050434      0.00824768231140087     15.9400665926748        0.137014739464397
2       55      positive regulation of viral transcription
GO:0032386      0.00973668760545556     7.3974025974026 0.443429520448412       3
178     regulation of intracellular transport
GO:0000447      0.00992856112912421     137.257142857143        0.00996470832468341
1       4       endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA
and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
GO:0000469      0.00992856112912421     137.257142857143        0.00996470832468341
1       4       cleavage involved in rRNA processing
GO:0000478      0.00992856112912421     137.257142857143        0.00996470832468341
1       4       endonucleolytic cleavage involved in rRNA processing
GO:0000479      0.00992856112912421     137.257142857143        0.00996470832468341
1       4       endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA,
5.8S rRNA, LSU-rRNA)
GO:0000966      0.00992856112912421     137.257142857143        0.00996470832468341
1       4       RNA 5'-end processing
GO:0006610      0.00992856112912421     137.257142857143        0.00996470832468341
1       4       ribosomal protein import into nucleus
GO:0008588      0.00992856112912421     137.257142857143        0.00996470832468341
1       4       release of cytoplasmic sequestered NF-kappaB
GO:0018076      0.00992856112912421     137.257142857143        0.00996470832468341
1       4       N-terminal peptidyl-lysine acetylation
GO:0060298      0.00992856112912421     137.257142857143        0.00996470832468341
1       4       positive regulation of sarcomere organization
GO:0061418      0.00992856112912421     137.257142857143        0.00996470832468341
1       4       regulation of transcription from RNA polymerase II promoter in
response to hypoxia
GO:2000171      0.00992856112912421     137.257142857143        0.00996470832468341
1       4       negative regulation of dendrite development
Tissue: Thyroid=>Whole_Blood    Type:   asymmetric
SourceGene:     CLPP(ENSG00000125656.3)
TargetGeneSet:  ATRX    KCNN3   TOR3A   BUB1    KIAA1524        NCAPG   CCNA2
RANBP3L TTK     RP11    FBXO5   EZH2    GINS4   MCM4    MCM10   RRM1    CHEK1
CCNB2   SHCBP1  C2CD2
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0000075      5.71053787162181e-09    42.2948936170213        0.284686180887136
7       242     cell cycle checkpoint
GO:0010564      8.22417850551875e-09    30.7126436781609        0.487025119368902
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8       414     regulation of cell cycle process
GO:0071156      1.04358611884653e-08    38.6143968871595        0.310566742785966
7       264     regulation of cell cycle arrest
GO:0045786      1.25557048159008e-08    29.018389018389 0.514082070444952       8
437     negative regulation of cell cycle
GO:0000280      7.26777836398913e-08    28.7571428571429        0.411736212026849
7       350     nuclear division
GO:0007067      7.26777836398913e-08    28.7571428571429        0.411736212026849
7       350     mitosis
GO:0000087      8.81243477332554e-08    27.9226628895184        0.423500103799045
7       360     M phase of mitotic cell cycle
GO:0007050      1.04321868816989e-07    27.2110497237569        0.434087606394021
7       369     cell cycle arrest
GO:0048285      1.06267944644013e-07    27.1341597796143        0.435263995571241
7       370     organelle fission
GO:0045839      1.16683968809599e-07    123.059829059829        0.0470555670887828
4       40      negative regulation of mitosis
GO:0051784      1.16683968809599e-07    123.059829059829        0.0470555670887828
4       40      negative regulation of nuclear division
GO:0051329      1.25211051332442e-07    26.460752688172 0.445851498166217       7
379     interphase of mitotic cell cycle
GO:0051325      1.44378048516681e-07    25.8889473684211        0.455262611583973
7       387     interphase
GO:0007088      2.87596821198805e-06    52.5641025641026        0.103522247595322
4       88      regulation of mitosis
GO:0051783      2.87596821198805e-06    52.5641025641026        0.103522247595322
4       88      regulation of nuclear division
GO:0010948      4.07345040441317e-06    47.9665551839465        0.112933361013079
4       96      negative regulation of cell cycle process
GO:0045841      8.64692470749185e-06    96.4419642857143        0.0411736212026849
3       35      negative regulation of mitotic metaphase/anaphase transition
GO:0006260      1.08952418588103e-05    22.4508871989861        0.315272299494845
5       268     DNA replication
GO:0030071      1.62097344171137e-05    77.1107142857143        0.0505847346204415
3       43      regulation of mitotic metaphase/anaphase transition
GO:0007091      1.86112825578916e-05    73.4285714285714        0.0529375129748806
3       45      mitotic metaphase/anaphase transition
GO:0007346      1.97254232303307e-05    19.7651006711409        0.35644592069753
5       303     regulation of mitotic cell cycle
GO:0010639      2.85819821851923e-05    28.7199597787833        0.184693100823472
4       157     negative regulation of organelle organization
GO:0051301      0.000132680453138237    13.0378448918717        0.531727908103245
5       452     cell division
GO:0051129      0.000341146021950791    14.7985347985348        0.350563974811432
4       298     negative regulation of cellular component organization
GO:0007093      0.000536490187489596    22.5283613445378        0.16351809563352
3       139     mitotic cell cycle checkpoint
GO:0051320      0.000582809827051627    21.8785714285714        0.168223652342398
3       143     S phase
GO:0031572      0.000593664129512498    66.2298850574713        0.0364680644938067
2       31      G2/M transition DNA damage checkpoint
GO:0000086      0.000594777118110322    21.7218844984802        0.169400041519618
3       144     G2/M transition of mitotic cell cycle
GO:0007094      0.000673164262056883    61.9483870967742        0.0388208428482458
2       33      mitotic cell cycle spindle assembly checkpoint
GO:0006271      0.000714742559025276    60.0083333333333        0.0399972320254654
2       34      DNA strand elongation involved in DNA replication
GO:0071173      0.000714742559025276    60.0083333333333        0.0399972320254654
2       34      spindle assembly checkpoint
GO:0071174      0.000801542709238449    56.4705882352941        0.0423500103799045
2       36      mitotic cell cycle spindle checkpoint
GO:0022616      0.000846759411781415    54.8533333333333        0.0435263995571241
2       37      DNA strand elongation
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GO:0031576      0.000989645204184707    50.5122807017544        0.0470555670887828
2       40      G2/M transition checkpoint
GO:0031577      0.00109090652425899     47.98   0.0494083454432219      2       42
spindle checkpoint
GO:0000082      0.00124909903274545     16.6873536299766        0.21880838696284
3       186     G1/S transition of mitotic cell cycle
GO:0033043      0.00148433095390793     9.85530716423165        0.51878762715383
4       441     regulation of organelle organization
GO:0046602      0.00352526115515339     451     0.00352916753165871     1       3
regulation of mitotic centrosome separation
GO:0000226      0.00357483858317044     11.4135338345865        0.316448688672064
3       269     microtubule cytoskeleton organization
GO:0000216      0.0038051697756915      24.8606060606061        0.09293474500346
2       79      M/G1 transition of mitotic cell cycle
GO:0007051      0.00390004462103452     24.5401709401709        0.094111341775656
2       80      spindle organization
GO:0000079      0.00419126352725067     23.6263374485597        0.0976403017092243
2       83      regulation of cyclin-dependent protein kinase activity
GO:0033044      0.00419126352725067     23.6263374485597        0.0976403017092243
2       83      regulation of chromosome organization
GO:0000212      0.00469774665905387     300.645833333333        0.00470555670887828
1       4       meiotic spindle organization
GO:0007144      0.00469774665905387     300.645833333333        0.00470555670887828
1       4       female meiosis I
GO:0060564      0.00469774665905387     300.645833333333        0.00470555670887828
1       4       negative regulation of mitotic anaphase-promoting complex activity
GO:0006261      0.00523270528103615     21.0153846153846        0.10940419348142
2       93      DNA-dependent DNA replication
GO:0000089      0.00586893363952024     225.46875       0.00588194588609785     1
5       mitotic metaphase
GO:0007100      0.00586893363952024     225.46875       0.00588194588609785     1
5       mitotic centrosome separation
GO:0035405      0.00586893363952024     225.46875       0.00588194588609785     1
5       histone-threonine phosphorylation
GO:0000244      0.00703882344487339     180.3625        0.00705833506331742     1
6       assembly of spliceosomal tri-snRNP
GO:0006975      0.00703882344487339     180.3625        0.00705833506331742     1
6       DNA damage induced protein phosphorylation
GO:0048096      0.00703882344487339     180.3625        0.00705833506331742     1
6       chromatin-mediated maintenance of transcription
GO:0051299      0.00703882344487339     180.3625        0.00705833506331742     1
6       centrosome separation
GO:0071313      0.00703882344487339     180.3625        0.00705833506331742     1
6       cellular response to caffeine
GO:0007095      0.00820741742212772     150.291666666667        0.00823472424053699
1       7       mitotic cell cycle G2/M transition DNA damage checkpoint
GO:0051290      0.00820741742212772     150.291666666667        0.00823472424053699
1       7       protein heterotetramerization
GO:0071415      0.00820741742212772     150.291666666667        0.00823472424053699
1       7       cellular response to purine-containing compound
GO:0043414      0.00829916638042183     16.4574712643678        0.138813922911909
2       118     macromolecule methylation
GO:0040029      0.00884940838944783     15.9044444444444        0.143519479620787
2       122     regulation of gene expression, epigenetic
GO:0000077      0.00999787074467132     14.9020833333333        0.152930593038544
2       130     DNA damage checkpoint
Tissue: Whole_Blood=>Thyroid    Type:   cluster
SourceGene:     ENSG00000238943.1
TargetGeneSet:  ERRFI1  SPSB1   NMNAT1  DNAJC16 ARHGEF19-AS1    NECAP2  OTUD3
LDLRAP1 XKR8    MED18   PRDX3P2 FAM167B HDAC1   ZMYM1   RNF220  FRRS1   CYB561D1
POLR3GL BCL9    BOLA1   GOLPH3L VPS72   U6      SHE     USP21   DUSP27  SELP
DARS2   RNASEL  SMG7    TRMT1L  PTGS2   SOX13   RP11    INTS7   ATF3    DISP1   SMC6
C2orf44 EHD3    CCDC75  PAPOLG  SPR     MRPL35  ZNF2    C2orf29 POLR1B  CHN1
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CASP10  CREB1   IDH1    TMEM169 EIF4E2  MSL3P1  COPS8   RNPEPL1 RPL15   TRANK1
ZNF619  ZNF620  NME6    NPRL2   DUSP7   SCT     ABHD10  ADPRH   GATA2   MSL2
SLC25A36        ZBTB38  HPS3    P2RY13  SERPINI2        TNFSF10 NAALADL2
GCNT1P3 TACC3   SORCS2  COX18   CASP6   ANKRD50 CCDC127 LPCAT1  DAP     C5orf51
SLC38A9 PTCD2   TNFAIP8 AFF4    HARS2   HMGXB3  DOK3    HIST1H3E        ZKSCAN4
ZKSCAN3 SCAND3  ZBTB9   TAF8    CAPN11  MCM3    DBIP1   UBE2J1  C6orf203
ASF1A   AKAP12  ELFN1   RNF216P1        VOPP1   ZNF107  TMEM60  CROT    SLC12A9
PIK3CG  TNPO3   FAM131B ZNF786  ZNF398  GIMAP8  GIMAP7  GIMAP4  SMARCD3 CTA
FUT10   PDP1    WDR67   KLHL38  ZNF696  ZNF623  TONSL   RANBP6  KLHL9   DCAF10
C9orf85 C9orf40 CEP78   RMI1    FOXE1   RNF20   C9orf80 LHX6    ZBTB34  NAIF1   GLE1
ABL1    NUDT5   C10orf136       C10orf128       ADO     MSS51   AP3M1   ARHGAP19
SUFU    SMC3    C10orf88        TTC9C   ZBTB3   MEN1    FOSL1   C11orf82
SLC36A4 RDX     RNF214  ABCG4   ZNF202  HYLS1   FLI1    RAD52   CD9     LRMP
BCDIN3D FAM186A KRT7    RP3     SMUG1   SUOX    TIMELESS        ZBTB39  ATXN7L3B
TMPO    ANAPC7  COQ5    RNF34   FAM48A  KBTBD6  KBTBD7  LPAR6   ARL11   TTC5
RNASE1  ACIN1   C14orf119       PROX2   VASH1   MIR656  ZFP106  ZSCAN29 CTD
CCNB2   DIS3L   SMAD6   IQCH    FEM1B   ANP32A  PEX11A  CHD2    NR2F2   ASB7
TFAP4   C16orf88        PLK1    TAOK2   HIRIP3  PLCG2   SPNS2   SLC16A13
WRAP53  ARHGEF15        PIGL    LLGL1   BLMH    CRLF3   RNF135  PEX12   PIP4K2B
FAM134C RUNDC1  GJC1    DLX3    PPP1R9B HEATR6  APPBP2  CD79B   QRICH2  USP36   CBX2
SIRT7   RNU5F-3P        ZNF555  PIAS4   ZNF627  ZNF625  ZNF799  ZNF443  ZNF490  LYL1
IL27RA  ANO8    RAB3A   SUGP1   KCTD15  ZNF792  THAP8   CAPNS1  ZNF420  ZNF573
SAMD4B  EID2    ZNF780A MAP3K10 LTBP4   MIA     ZNF526  ZNF221  ZNF284  ZNF225
PVRL2   GEMIN7  BLOC1S3 FBXO46  PPP1R15A        C19orf63        ZNF616  ZNF816
ZNF677  ZNF765  TMC4    ZNF264  ZNF547  ZNF549  SLC52A3 FAM110A PANK2   ANKRD5  NANP
C20orf160       RP1     DNMT3B  PXMP4   RBL1    SDC4    ZSWIM3  ZSWIM1  ZFP64
AURKA   CSTF1   TAF4    C20orf151       SOX18   RGS19   CYYR1   BACE2   C2CD2
C22orf29        CRKL    ZNF70   GTPBP1  EFCAB6  TLR8    TCEANC  SCML1   ZFX
GPR34   CXorf24 RPL23AP83       FAM123B VSIG4   MAGEC2
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0033261      0.00158554766356836     9.01398601398601        0.510691301640025
4       30      regulation of S phase
GO:0045736      0.00329117860132599     11.679012345679 0.306414780984015       3
18      negative regulation of cyclin-dependent protein kinase activity
GO:0010564      0.00494738674276267     2.24685089346743        7.04753996263234
15      414     regulation of cell cycle process
GO:0021700      0.00567986020378686     3.14957983193277        2.68964085530413
8       158     developmental maturation
GO:0007090      0.00590783962912106     9.21767381416504        0.374506954536018
3       22      regulation of S phase of mitotic cell cycle
GO:0045786      0.00800200296448542     2.12085308056872        7.43906996055636
15      437     negative regulation of cell cycle
GO:0033233      0.00960200448278314     16.6252927400468        0.153207390492007
2       9       regulation of protein sumoylation
Tissue: Whole_Blood=>Thyroid    Type:   cluster
SourceGene:     ING4(ENSG00000111653.15)
TargetGeneSet:  UBE2J2  DNAJC16 TXLNA   SF3A3   TOE1    USP1    RP11    KCND3
SCNM1   CELF3   CCT3    IQGAP3  CDC73   ASPM    URB2    HEATR1  EIF2B4  MSH6
PCBP1   NCAPH   POU3F3  SSB     NUP35   PTPRN   CLN5    CHCHD4  IFRD2   ACTR8
ZBTB11  GRPEL1  WDR36   RBM22   FBXW11  HRH2    BYSL    HDAC2   NKAIN2  FBXO5
SNORA29 EIF3B   RNF216P1        THAP5   CNOT4   U1      ABCF2   NEIL2   PPP2R2A
BAALC   PLAA    DCAF10  FRMD3   METTL11A        SURF6   NGB     BMS1    HNRNPF
NOLC1   ADRA2A  TSSC4   C11orf46        STIP1   NCAM1   MPP2    NOP2    DDX23
ZC3H10  INHBC   TBK1    C12orf29        SART3   NAA16   TPTE2P3 FAM70B  RBM23
SNORD116-15     BUB1B   GABPB1  IDH3A   FAM103A1        CTD     E2F4    CIRH1A
DHODH   USP10   CYBA    TSR1    COIL    FTSJ3   MRPL38  DOT1L   ZNF77   KHSRP
GATAD2A ZFP82   GRWD1   PRMT1   PEG3    NOP56   MCM3AP-AS1      PARP4P3 UBE2L3
MIR221  MAGEH1  EDA     FAM122C MAGEA8
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022613      1.90176179361749e-12    15.0948827292111        1.27672825410006
15      225     ribonucleoprotein complex biogenesis
GO:0071843      4.54980692536357e-12    14.137460021322 1.35616912324407        15
239     cellular component biogenesis at cellular level
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GO:0042254	7.21942106151792e-10	15.9768320065319	0.845477821604041	11	149	ribosome biogenesis
GO:0006397	4.75183889232843e-08	7.47807486631016	2.26406477060411	14	399	mRNA processing
GO:0008380	1.3928037721635e-05	6.23713170039049	1.83281433810809	10	323	RNA splicing
GO:0022618	1.6118246502793e-05	12.6670609107037	0.539063040620026	6	95	ribonucleoprotein complex assembly
GO:0071826	2.16151964470521e-05	11.9890817469205	0.567434779600028	6	100	ribonucleoprotein complex subunit organization
GO:0000375	2.38435884093652e-05	7.62027699341132	1.18593868936406	8	209	RNA splicing, via transesterification reactions
GO:0006364	2.70231486534987e-05	11.4965091299678	0.590132170784029	6	104	rRNA processing
GO:0016072	3.71277901418746e-05	10.8286943319838	0.62417825756003	6	110	rRNA metabolic process
GO:0032259	9.85669348900182e-05	8.99621052631579	0.743339561276036	6	131	methylation
GO:0034470	0.000138461507791272	6.85540587219344	1.13486955920006	7	200	ncRNA processing
GO:0000377	0.000156517181096764	6.71431472081218	1.15756695038406	7	204	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile
GO:0000398	0.000156517181096764	6.71431472081218	1.15756695038406	7	204	nuclear mRNA splicing, via spliceosome
GO:0060789	0.000189440581023968	179.5875	0.0226973911840011	2	4	hair follicle placode formation
GO:0043414	0.00055193127756544	8.1921618204804	0.669573039928033	5	118	macromolecule methylation
GO:0033120	0.00065573595463257	71.82	0.0397204345720019	2	7	positive regulation of RNA splicing
GO:0045292	0.00065573595463257	71.82	0.0397204345720019	2	7	nuclear mRNA cis splicing, via spliceosome
GO:0034660	0.00116037215425537	4.73079136690647	1.61718912186008	7	285	ncRNA metabolic process
GO:0050685	0.0016922542545246	39.8888888888889	0.062417825756003	2	11	positive regulation of mRNA processing
GO:0060788	0.00318343603243353	27.6076923076923	0.0851152169400042	2	15	ectodermal placode formation
GO:0071696	0.00318343603243353	27.6076923076923	0.0851152169400042	2	15	ectodermal placode development
GO:0071697	0.00318343603243353	27.6076923076923	0.0851152169400042	2	15	ectodermal placode morphogenesis
GO:0009749	0.00329993944260055	7.03402366863905	0.61282956196803	4	108	response to glucose stimulus
GO:0042255	0.00362485571722543	25.6339285714286	0.0907895647360044	2	16	ribosome assembly
GO:0017038	0.00385904213214055	4.31793145654835	1.49802781814407	6	264	protein import
GO:0009746	0.00388106150564039	6.70900964478946	0.641201300948031	4	113	response to hexose stimulus
GO:0034284	0.0041317453096702	6.58720258720259	0.652549996540032	4	115	response to monosaccharide stimulus
GO:0043484	0.00413297682835745	10.0668073136428	0.323437824372016	3	57	regulation of RNA splicing
GO:0045862	0.00434075830036303	9.88308400460299	0.329112172168016	3	58	positive regulation of proteolysis
GO:0048285	0.0049975243521611	3.6011753902663	2.0995086845201	7	370	organelle fission
GO:0031365	0.00510878432960978	21.1058823529412	0.107812608124005	2	19	N-terminal protein amino acid modification
GO:0031648	0.00510878432960978	21.1058823529412	0.107812608124005	2	19	protein destabilization

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GO:0009743      0.00671697810417207     5.70552884615385        0.749013909072037
4       132     response to carbohydrate stimulus
GO:0000083      0.00682576729509103     17.93625        0.124835651512006       2
22      regulation of transcription involved in G1/S phase of mitotic cell cycle
GO:0007090      0.00682576729509103     17.93625        0.124835651512006       2
22      regulation of S phase of mitotic cell cycle
GO:0030163      0.00694191987368296     3.08163605083523        2.80880215902014
8       495     protein catabolic process
GO:0033157      0.00823705393207931     5.36689291101056        0.794408691440039
4       140     regulation of intracellular protein transport
GO:0030162      0.00864950084488337     5.28836863619472        0.805757387032039
4       142     regulation of proteolysis
GO:0006479      0.00952863464021312     7.33578515224085        0.436924780292021
3       77      protein methylation
GO:0008213      0.00952863464021312     7.33578515224085        0.436924780292021
3       77      protein alkylation
Tissue: Thyroid=>Whole_Blood    Type:   asymmetric
SourceGene:     KRTAP3-2(ENSG00000212900.1)
TargetGeneSet:  CELA2B  CELA3A  AMY2A   SMCP    CPB1    SPINK1  CLPS    RP11    CPA2
CPA1    PRSS1   PNLIP   PNLIPRP2        KRT6A   KRT4    GP2     CTRB2   CTRB1
KRT13
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0007586      5.69496585169008e-13    103.193519351935        0.14331188153069
8       109     digestion
GO:0044241      8.68065653198509e-07    225.3125        0.0197218185592693      3
15      lipid digestion
GO:0022617      1.33863255514118e-05    81.8125 0.0473323645422462      3       36
extracellular matrix disassembly
GO:0030198      0.00115359192296497     16.939082278481 0.211680852536157       3
161     extracellular matrix organization
GO:0043062      0.00117438184385728     16.8313679245283        0.212995640440108
3       162     extracellular structure organization
GO:0001523      0.00117890899156601     45.7710651828299        0.0512767282541001
2       39      retinoid metabolic process
GO:0016101      0.00130255347491052     43.4177978883861        0.0539063040620026
2       41      diterpenoid metabolic process
GO:0006721      0.00193222176422744     35.2549019607843        0.0657393951975642
2       50      terpenoid metabolic process
GO:0016042      0.0036858273964719      11.1346757322176        0.318178672756211
3       242     lipid catabolic process
GO:0006720      0.00396282855922372     24.1378151260504        0.0946647290844924
2       72      isoprenoid metabolic process
GO:0009791      0.00451877459080465     22.5207843137255        0.101238668604249
2       77      post-embryonic development
GO:0008202      0.00521715255170248     9.79773985239852        0.360251885682652
3       274     steroid metabolic process
GO:0071845      0.00576367505250986     9.44239323843416        0.373399764722165
3       284     cellular component disassembly at cellular level
GO:0022411      0.00599161296939949     9.30723684210526        0.37865891633797
3       288     cellular component disassembly
GO:0007341      0.00655758079782431     200.388888888889        0.00657393951975642
1       5       penetration of zona pellucida
GO:0044245      0.00655758079782431     200.388888888889        0.00657393951975642
1       5       polysaccharide digestion
GO:0000244      0.00786419895958823     160.3   0.0078887274237077      1       6
assembly of spliceosomal tri-snRNP
GO:0002385      0.00786419895958823     160.3   0.0078887274237077      1       6
mucosal immune response
GO:0019374      0.00786419895958823     160.3   0.0078887274237077      1       6
galactolipid metabolic process
GO:0045056      0.00786419895958823     160.3   0.0078887274237077      1       6
transcytosis
Tissue: Whole_Blood=>Thyroid    Type:   asymmetric
```

```
SourceGene:     NCAN(ENSG00000130287.5)
TargetGeneSet:  NOC2L   RBP7    RP1     NUDC    NCDN    LRRC41  HIPK1   C1orf61
TROVE2  CDC73   RP11    ACBD3   URB2    SMPD4   GORASP2 MOBP    C3orf39 TMF1
GAP43   TMEM39A ZIC1    LETM1   TBC1D1  ANKRD17 SEC24D  ZBTB8OSP1       WDR36
SAR1B   SEC24A  CAMK2A  CPLX2   FAF2    SNCB    SSR1    PPARD   PGM3    SF3B5
EIF3B   C7orf26 ABCF2   SLC35G5 NEIL2   PRKDC   STMN2   UBQLN1  SURF4   SEC16A
SEC24C  NOLC1   GBF1    SEC23IP TSSC4   COPB1   SLC1A2  GANAB   STIP1   SYVN1
SLC22A20        ARCN1   RNF26   LEPREL2 CBX5    KIF5A   CAND1   SART3   GCN1L1
ATP6V0A2        STON2   RNF40   DNAJA2  EDC4    PRDM7   DPH1    ARHGDIA FOXK2
ST8SIA3 AP3D1   ELAVL1  P2RY11  RAVER1  ELAVL3  USE1    GATAD2A PSMC4   SMG9
GRWD1   PRMT1   CNOT3   FIZ1    PEG3    RPS18P1 SNAP25  SEC23B  RIMS4   RP4     PRR5
APEX2   MAGEH1  RP13    HCFC1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0048199      2.75977668969244e-12    75.4947368421053        0.164417687357276
8       27      vesicle targeting, to, from or within Golgi
GO:0006901      2.81246575646194e-11    53.0962962962963        0.21313403916684
8       35      vesicle coating
GO:0006900      4.56823424919053e-11    49.4275862068965        0.225313127119231
8       37      membrane budding
GO:0006903      4.56823424919053e-11    49.4275862068965        0.225313127119231
8       37      vesicle targeting
GO:0051650      4.22897738743914e-10    35.8075 0.29229811085738        8       48
establishment of vesicle localization
GO:0051648      5.20139281349438e-09    25.0982456140351        0.395820358452702
8       65      vesicle localization
GO:0051656      1.00269660814096e-08    17.6718492019813        0.615043941595737
9       101     establishment of organelle localization
GO:0048207      2.13662666113678e-08    86.4638554216867        0.0913431596429313
5       15      vesicle targeting, rough ER to cis-Golgi
GO:0048208      2.13662666113678e-08    86.4638554216867        0.0913431596429313
5       15      COPII vesicle coating
GO:0090114      2.13662666113678e-08    86.4638554216867        0.0913431596429313
5       15      COPII-coated vesicle budding
GO:0006888      3.90193650725047e-08    25.7728909465021        0.334924918690748
7       55      ER to Golgi vesicle-mediated transport
GO:0016050      7.70335352135787e-08    17.2048192771084        0.554148501833783
8       91      vesicle organization
GO:0048193      1.04763838398002e-07    11.031857031857 1.0656701958342 10      175
Golgi vesicle transport
GO:0051640      3.12625900674405e-07    11.4909776461083        0.913431596429313
9       150     organelle localization
GO:0018279      9.60119573805604e-07    15.4291666666667        0.529790325929001
7       87      protein N-linked glycosylation via asparagine
GO:0018196      1.03798281649526e-06    15.2376162170401        0.535879869905197
7       88      peptidyl-asparagine modification
GO:0006487      1.40452995019808e-06    14.5164851125635        0.560238045809979
7       92      protein N-linked glycosylation
GO:0035964      5.9714342159921e-05     50.6576470588235        0.0791640716905404
3       13      COPI-coated vesicle budding
GO:0048194      5.9714342159921e-05     50.6576470588235        0.0791640716905404
3       13      Golgi vesicle budding
GO:0048200      5.9714342159921e-05     50.6576470588235        0.0791640716905404
3       13      Golgi transport vesicle coating
GO:0048205      5.9714342159921e-05     50.6576470588235        0.0791640716905404
3       13      COPI coating of Golgi vesicle
GO:0016044      9.99787248871515e-05    4.86206656938364        2.30793716697806
10      379     cellular membrane organization
GO:0061024      0.000106687222457645    4.82182244279019        2.32620579890665
10      382     membrane organization
GO:0043687      0.00011634485631479     7.04718319852419        1.10220745969137
7       181     post-translational protein modification
GO:0019882      0.000326942268488207    7.12512529234881        0.925610684381704
6       152     antigen processing and presentation
```

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GO:0002474      0.000340633540317546    9.14445014098949        0.602864853643347
5       99      antigen processing and presentation of peptide antigen via MHC class
I
GO:0006890      0.0004026008062532      24.1042016806723        0.14614905542869
3       24      retrograde vesicle-mediated transport, Golgi to ER
GO:0048002      0.0005086228600119      8.34015674347877        0.657670749429105
5       108     antigen processing and presentation of peptide antigen
GO:0006486      0.000861910155642113    4.97989417989418        1.53456508200125
7       252     protein glycosylation
GO:0043413      0.000861910155642113    4.97989417989418        1.53456508200125
7       252     macromolecule glycosylation
GO:0070085      0.000923652236374787    4.91860812425329        1.55283371392983
7       255     glycosylation
GO:0071482      0.000952519709758408    17.4450304259635        0.194865407238253
3       32      cellular response to light stimulus
GO:0033523      0.00128371324468993     47.6943521594684        0.0548058957857588
2       9       histone H2B ubiquitination
GO:0007603      0.0019457472888171      37.0904392764858        0.0669849837381496
2       11      phototransduction, visible light
GO:0007030      0.00196791157521203     13.3049535603715        0.249671303024012
3       41      Golgi organization
GO:0009101      0.0024766349159052      4.10698198198198        1.84513182478721
7       303     glycoprotein biosynthetic process
GO:0010390      0.00526494139286236     20.8531976744186        0.109611791571518
2       18      histone monoubiquitination
GO:0071478      0.00528826764857013     9.18160427807487        0.353193550619334
3       58      cellular response to radiation
GO:0009100      0.00554123245301087     3.52185615848407        2.13742993564459
7       351     glycoprotein metabolic process
GO:0031648      0.00586116541092958     19.625170998632 0.115701335547713       2
19      protein destabilization
GO:0009584      0.00648676271591792     18.5335917312661        0.121790879523908
2       20      detection of visible light
GO:1901137      0.00754088878676143     3.3142567224759 2.2653103591447 7       372
carbohydrate derivative biosynthetic process
Tissue: Thyroid=>Whole_Blood    Type:   asymmetric
SourceGene:     OLIG1(ENSG00000184221.8)
TargetGeneSet:  BCAN    ATP1A4  CNTN2   KIF1A   MOBP    IMPG2   SOX2-OT SORCS2
CTNND2  TMEM130 PTPRZ1  OR2A9P  STMN2   NTRK2   OLFM1   GRIN1   SLCO1A2 FAIM2
PPM1H   CLIC1P1 FAM123A CYP46A1 C16orf13        MT3     AQP4    TUBB4A  MAG
LRRC4B  SHANK1  RP11    BCAS1   GPM6B   PLP1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0007612      2.42177573625753e-07    46.8101761252446        0.140336308905958
5       78      learning
GO:0007611      4.5936283323766e-06     25.015756302521 0.253684866099232       5
141     learning or memory
GO:0050890      7.0705225750299e-06     22.8124001278364        0.277074250916892
5       154     cognition
GO:0010975      1.86149100770493e-05    18.5297944314338        0.338246488132309
5       188     regulation of neuron projection development
GO:0050770      2.44408904771926e-05    28.3260869565217        0.172721610961179
4       96      regulation of axonogenesis
GO:0031344      4.89526522222706e-05    15.026455026455 0.413812192927825       5
230     regulation of cell projection organization
GO:0051960      5.56979163054521e-05    10.9111398963731        0.705279911424815
6       392     regulation of nervous system development
GO:0045664      0.000153540336941953    11.6873346560847        0.527160750121099
5       293     regulation of neuron differentiation
GO:0021782      0.000157213624916511    33.4681677018634        0.106151823403225
3       59      glial cell development
GO:0006707      0.000169504482655436    133.481481481481        0.0197910179226351
2       11      cholesterol catabolic process
GO:0016127      0.000169504482655436    133.481481481481        0.0197910179226351
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2       11      sterol catabolic process
GO:0022010      0.000169504482655436    133.481481481481        0.0197910179226351
2       11      central nervous system myelination
GO:0032291      0.000169504482655436    133.481481481481        0.0197910179226351
2       11      axon ensheathment in central nervous system
GO:2000463      0.000169504482655436    133.481481481481        0.0197910179226351
2       11      positive regulation of excitatory postsynaptic membrane potential
GO:0010769      0.000215767505636689    15.810421286031 0.302262819182064       4
168     regulation of cell morphogenesis involved in differentiation
GO:0031345      0.000229468490445889    29.2683423913043        0.120545290983323
3       67      negative regulation of cell projection organization
GO:0050804      0.000241400759633476    15.3372781065089        0.311258736419625
4       173     regulation of synaptic transmission
GO:0051969      0.000324821799205402    14.1500248385494        0.336447304684797
4       187     regulation of transmission of nerve impulse
GO:0045838      0.000367786810607516    85.7797619047619        0.0287869351601965
2       16      positive regulation of membrane potential
GO:0050767      0.000378772103909581    9.54687288020621        0.640509307314373
5       356     regulation of neurogenesis
GO:0048167      0.000401922738021126    23.9916387959866        0.145733859248495
3       81      regulation of synaptic plasticity
GO:0031644      0.000411323128239673    13.2680652680653        0.358037506054944
4       199     regulation of neurological system process
GO:0042391      0.000522441754386378    12.4274475524476        0.381426890872604
4       212     regulation of membrane potential
GO:0006706      0.000769435401192477    57.1587301587302        0.0413812192927825
2       23      steroid catabolic process
GO:0021953      0.000882121917511441    18.1367665681722        0.190713445436302
3       106     central nervous system neuron differentiation
GO:0060284      0.00102179355141063     7.6032833224614 0.797038267247941       5
443     regulation of cell development
GO:0014003      0.0011432530838012      46.150641025641 0.0503771365303439      2
28      oligodendrocyte development
GO:0007610      0.00128095959583095     7.21206486933168        0.838419486540724
5       466     behavior
GO:0010001      0.00138795476634237     15.4193316564858        0.223098747491523
3       124     glial cell differentiation
GO:0022604      0.00143497775342852     9.39017916390179        0.500172998408415
4       278     regulation of cell morphogenesis
GO:0043523      0.00145330451763101     15.1664899257688        0.226697114386548
3       126     regulation of neuron apoptotic process
GO:1901214      0.00145330451763101     15.1664899257688        0.226697114386548
3       126     regulation of neuron death
GO:0007409      0.00165913525184291     6.78547083455059        0.888796623071068
5       494     axonogenesis
GO:0060079      0.00178569731497192     36.3434343434343        0.0629714206629299
2       35      regulation of excitatory postsynaptic membrane potential
GO:0051129      0.00185168168737784     8.73902288188003        0.53615666735866
4       298     negative regulation of cellular component organization
GO:0051402      0.00188620277565234     13.8067632850242        0.248287315756695
3       138     neuron apoptotic process
GO:0050771      0.00188865069289165     35.2720588235294        0.0647706041104422
2       36      negative regulation of axonogenesis
GO:0044087      0.00196773891443697     8.58984493767102        0.545152584596222
4       303     regulation of cellular component biogenesis
GO:0070997      0.00204652761729825     13.4056928370347        0.255484049546744
3       142     neuron death
GO:0042063      0.00217219112194648     13.1197183098592        0.260881599889281
3       145     gliogenesis
GO:0048708      0.00221406413008979     32.4054054054054        0.070168154452979
2       39      astrocyte differentiation
GO:0021537      0.00225858286693251     12.9356884057971        0.264479966784306
3       147     telencephalon development
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GO:0048168	0.00232802143443588	31.5504385964912	0.0719673379004913
2	40	regulation of neuronal synaptic plasticity
GO:0060078	0.00232802143443588	31.5504385964912	0.0719673379004913
2	40	regulation of postsynaptic membrane potential
GO:0021954	0.0026862197063143б	29.2357723577236	0.0773648882430282
2	43	central nervous system neuron development
GO:0008206	0.0028110299456674l	28.5376984126984	0.0791640716905404
2	44	bile acid metabolic process
GO:0008306	0.00293852999747532	27.8720930232558	0.0809632551380527
2	45	associative learning
GO:0007215	0.00320156226858409	26.6296296296296	0.0845616220330773
2	47	glutamate receptor signaling pathway
GO:0010976	0.0037594958556273	24.4489795918367	0.0917583558231264
2	51	positive regulation of neuron projection development
GO:0048709	0.00405424962355107	23.4869281045752	0.095356722718151
2	53	oligodendrocyte differentiation
GO:0007017	0.00501252730018951	6.56041131105398	0.707079094872327
4	393	microtubule-based process
GO:0031117	0.00538821719050797	288.46	0.00539755034253685	1	3
positive regulation of microtubule depolymerization
GO:0031133	0.00538821719050797	288.46	0.00539755034253685	1	3
regulation of axon diameter
GO:0036003	0.00538821719050797	288.46	0.00539755034253685	1	3
positive regulation of transcription from RNA polymerase II promoter in response to
stress
GO:0045163	0.00538821719050797	288.46	0.00539755034253685	1	3
clustering of voltage-gated potassium channels
GO:0050893	0.00538821719050797	288.46	0.00539755034253685	1	3
sensory processing
GO:0051581	0.00538821719050797	288.46	0.00539755034253685	1	3
negative regulation of neurotransmitter uptake
GO:0051611	0.00538821719050797	288.46	0.00539755034253685	1	3
regulation of serotonin uptake
GO:0051612	0.00538821719050797	288.46	0.00539755034253685	1	3
negative regulation of serotonin uptake
GO:0071205	0.00538821719050797	288.46	0.00539755034253685	1	3
protein localization to juxtaparanode region of axon
GO:2000009	0.00538821719050797	288.46	0.00539755034253685	1	3
negative regulation of protein localization to cell surface
GO:0044057	0.00617586384696138	6.16861104996698	0.750259497612622
4	417	regulation of system process
GO:0042552	0.00659225990226509	18.1300505050505	0.122344474430835
2	68	myelination
GO:0032536	0.00717807781848756	192.293333333333	0.00719673379004913
1	4	regulation of cell projection size
GO:0042759	0.00717807781848756	192.293333333333	0.00719673379004913
1	4	long-chain fatty acid biosynthetic process
GO:0051610	0.00717807781848756	192.293333333333	0.00719673379004913
1	4	serotonin uptake
GO:0072592	0.00717807781848756	192.293333333333	0.00719673379004913
1	4	oxygen metabolic process
GO:0007272	0.00736424552645795	17.0892857142857	0.129541208220884
2	72	ensheathment of neurons
GO:0008366	0.00736424552645795	17.0892857142857	0.129541208220884
2	72	axon ensheathment
GO:0051899	0.00756335669081938	16.8474178403756	0.131340391668397
2	73	membrane depolarization
GO:0051494	0.00776489631219968	16.6122685185185	0.133139575115909
2	74	negative regulation of cytoskeleton organization
GO:0007420	0.00793004676512219	5.72522522522523	0.806034184485503
4	448	brain development
GO:0001764	0.00838399916751115	15.9444444444444	0.138537125458446
2	77	neuron migration
```

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GO:0097285      0.00847345213804796     7.94476581451763        0.424607293612899
3       236     cell-type specific apoptotic process
GO:0001973      0.0089648411587466 3     144.21  0.00899591723756141     1       5
adenosine receptor signaling pathway
GO:0021826      0.00896484115874663     144.21  0.00899591723756141     1       5
substrate-independent telencephalic tangential migration
GO:0021830      0.00896484115874663     144.21  0.00899591723756141     1       5
interneuron migration from the subpallium to the cortex
GO:0021843      0.00896484115874663     144.21  0.00899591723756141     1       5
substrate-independent telencephalic tangential interneuron migration
GO:0021853      0.00896484115874663     144.21  0.00899591723756141     1       5
cerebral cortex GABAergic interneuron migration
GO:0021894      0.00896484115874663     144.21  0.00899591723756141     1       5
cerebral cortex GABAergic interneuron development
GO:0031115      0.00896484115874663     144.21  0.00899591723756141     1       5
negative regulation of microtubule polymerization
GO:0033210      0.00896484115874663     144.21  0.00899591723756141     1       5
leptin-mediated signaling pathway
GO:0035418      0.00896484115874663     144.21  0.00899591723756141     1       5
protein localization to synapse
GO:0071625      0.00896484115874663     144.21  0.00899591723756141     1       5
vocalization behavior
GO:0043524      0.00924294353506946     15.1329113924051        0.145733859248495
2       81      negative regulation of neuron apoptotic process
GO:0050768      0.00924294353506946     15.1329113924051        0.145733859248495
2       81      negative regulation of neurogenesis
GO:1901215      0.00924294353506946     15.1329113924051        0.145733859248495
2       81      negative regulation of neuron death
GO:0030900      0.00959389310905019     7.58071988595866        0.444398311535534
3       247     forebrain development
GO:0051493      0.0096998565238327 5     7.54924578527063        0.446197494983046
3       248     regulation of cytoskeleton organization
GO:0019228      0.00991195731059808     14.5762195121951        0.151131409591032
2       84      regulation of action potential in neuron
Tissue: Whole_Blood=>Thyroid    Type:   cluster
SourceGene:     RP11-476C8.3(ENSG00000250163.1)
TargetGeneSet:  FNDC5   RP11    GPSM2   HMGB1P11        SIX2    IGKJ5   IGKC
IGKJ2   IGKV4-1 IGKV5-2 IGKV3-15        IGKV3-20        IGKV2-24        IGKV2-29
IGKV2D-24       MFSD6   SERPINE2        CCR4    BCHE    TXK     IGJ     TRIM2
ANXA10  NNT     PPP2R2A PNOC    POLR2K  PIP4K2A RPS24   ROBO3   APAF1   SPIC
IGHA2   IGHA1   IGHV3-13        IGHV1-46        IGHV1-69        IGHV3-73
LINC00324       PIEZO2  PNMAL2  DPM1    IGLV7-43        IGLV2-11        IGLL5
IGLC1   IGLC3   RN5-8S6
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006958      7.01309979723971e-10    81.6875 0.103799045048786       6       50
complement activation, classical pathway
GO:0006956      2.94353652635558e-09    63      0.13078679676147        6       63
complement activation
GO:0002455      3.56814685279044e-09    60.8559322033898        0.134938758563421
6       65      humoral immune response mediated by circulating immunoglobulin
GO:0072376      1.47636597233999e-08    47.1875 0.170230433880008       6       82
protein activation cascade
GO:0016064      9.15904609930835e-08    34.0857142857143        0.230433880008304
6       111     immunoglobulin mediated immune response
GO:0019724      1.07417590743408e-07    33.1319444444444        0.236661822711231
6       114     B cell mediated immunity
GO:0002250      1.27080174854711e-07    22.6747097655361        0.411044218393191
7       198     adaptive immune response
GO:0006959      1.60955212150291e-07    30.8297413793103        0.253269669919037
6       122     humoral immune response
GO:0002449      1.02719060191915e-06    22.1428571428571        0.346688810462944
6       167     lymphocyte mediated immunity
GO:0002460      1.64360542847173e-06    20.3514285714286        0.375752543076604
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6       181     adaptive immune response based on somatic recombination of immune
receptors built from immunoglobulin superfamily domains
GO:0002253      2.0475684111775e-06     14.7264740917213        0.620718289391738
7       299     activation of immune response
GO:0002443      3.99911101796174e-06    17.3365853658537        0.438031970105875
6       211     leukocyte mediated immunity
GO:0050778      7.49754686067186e-06    11.9897698209719        0.755657047955159
7       364     positive regulation of immune response
GO:0002252      0.000120432446390825    9.2375  0.801328627776625       6       386
immune effector process
GO:0090331      0.00621545179129268     248.603448275862        0.00622794270292713
1       3       negative regulation of platelet aggregation
GO:0010757      0.00827895791298872     165.724137931034        0.00830392360390284
1       4       negative regulation of plasminogen activation
GO:0035268      0.00827895791298872     165.724137931034        0.00830392360390284
1       4       protein mannosylation
GO:0035269      0.00827895791298872     165.724137931034        0.00830392360390284
1       4       protein O-linked mannosylation
GO:0060332      0.00827895791298872     165.724137931034        0.00830392360390284
1       4       positive regulation of response to interferon-gamma
GO:0060335      0.00827895791298872     165.724137931034        0.00830392360390284
1       4       positive regulation of interferon-gamma-mediated signaling pathway
Tissue: Whole_Blood=>Thyroid    Type:   cluster
SourceGene:     RP11-890B15.3(ENSG00000255455.1)
TargetGeneSet:  CEP104  RP4     DFFA    MED18   MFI2    AKIRIN1 MOB3C   ZFYVE9  USP1
ITGB3BP U6      ZNF644  AMIGO1  HIPK1   DENND4B UBQLN4  SMG5    RRNAD1  B4GALT3 POGK
GS1     CDC73   RP11    SLC5A6  MSH6    AMMECR1L        NDUFA10 CMC1    PRKAR2A NEK4
SLC25A36        MYNN    SENP2   CEP19   CCDC149 MTRR    ZFR     NIPBL   SEC24A
FBXW11  C5orf25 SRPK1   BRPF3   TAF8    RPL7L1  RARS2   FBXO5   C7orf26 PURB
TRIM56  CUL1    ZNF398  ABCF2   POLR3D  CHMP7   KAT6A   CTD     COX6C   DNAJA1  RGP1
BICD2   NUP188  METTL11A        TOR1B   FBXO18  TAF3    PHRF1   NUP98   BDNF-AS1
ETFA    MARK2   STIP1   TEX12   PAFAH1B2        SETP16  CBL     HYLS1   TMEM198B
RNF41   GCN1L1  RP13    MPHOSPH8        RANP8   PDS5B   NIPA2   HERC2   PLEKHO2
GOLGA6L5        ZNF592  SEC14L5 TBC1D10B        SRCAP   SETD1A  DNAJA2  NFATC3  TAT
GAN     VPS53   ALKBH5  LEPREL4 STAT5B  RUNDC1  NMT1    PPM1D   METTL2A FOXK2
ZBTB7A  FEM1A   ELAVL1  ZNF441  ZNF791  BRD4    U2AF2   ZNF264  ZNF587  ZSCAN22
TRIM28  RP5-1187M17.10  PHF20   TP53RK  GNAS-AS1        C22orf29        KRT18P5 CRKL
PPARA   DDX3X   SMC1A   MED12   RGAG4   MID2    CUL4B   XIAP
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0007064      4.94507727089692e-05    56.03125        0.0753581067054183      3
11      mitotic sister chromatid cohesion
GO:0007059      0.000397550402121733    6.84545016851228        0.959103176250778
6       140     chromosome segregation
GO:0016570      0.000422029338857773    4.8991008991009 1.78804235001038        8
261     histone modification
GO:0043543      0.000461953799762098    6.64516129032258        0.986506124143658
6       144     protein acylation
GO:0016569      0.000490697853596793    4.7835716407145 1.8291467718497 8       267
covalent chromatin modification
GO:0016573      0.000870290617365219    7.35850030985334        0.739879593107743
5       108     histone acetylation
GO:0018393      0.000945346314671262    7.21732522796353        0.753581067054183
5       110     internal peptidyl-lysine acetylation
GO:0018394      0.00106682760768211     7.01536643026005        0.774133277973843
5       113     peptidyl-lysine acetylation
GO:0006475      0.00115401297137377     6.88684719535783        0.787834751920282
5       115     internal protein amino acid acetylation
GO:0007062      0.00133918451408605     15.4342672413793        0.219223583143035
3       32      sister chromatid cohesion
GO:0006473      0.0018552255678164      6.15334717176959        0.87689433257214
5       128     protein acetylation
GO:0032968      0.00201721214730941     36.9690721649485        0.0685073697321985
2       10      positive regulation of transcription elongation from RNA polymerase
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II promoter
GO:0016568      0.00230075228150553     3.40048780487805        2.87045879177912
9       419     chromatin modification
GO:0001833      0.00245449245277618     32.8591065292096        0.0753581067054183
2       11      inner cell mass cell proliferation
GO:0050684      0.0027527937845859      11.7713815789474        0.280880215902014
3       41      regulation of mRNA processing
GO:0018205      0.00282738089969911     5.56007509386733        0.965953913223998
5       141     peptidyl-lysine modification
GO:0034243      0.00293226963861002     29.5711340206186        0.0822088436786382
2       12      regulation of transcription elongation from RNA polymerase II
promoter
GO:0043966      0.00336976613982241     10.9077743902439        0.301432426821673
3       44      histone H3 acetylation
GO:0001832      0.00344997965876219     26.8809746954077        0.089059580651858
2       13      blastocyst growth
GO:0006511      0.00350669296113077     3.45622916409433        2.49366825825202
8       364     ubiquitin-dependent protein catabolic process
GO:0008629      0.00365319924625485     6.82488038277512        0.630267801536226
4       92      induction of apoptosis by intracellular signals
GO:0019941      0.00393365268343782     3.3878848424303 2.54162341706456        8
371     modification-dependent protein catabolic process
GO:0051457      0.00400706415907981     24.639175257732 0.0959103176250778      2
14      maintenance of protein location in nucleus
GO:0043632      0.00412851483988718     3.359394703657  2.56217562798422        8
374     modification-dependent macromolecule catabolic process
GO:0032434      0.00431473509296612     9.93541666666667        0.328835374714553
3       48      regulation of proteasomal ubiquitin-dependent protein catabolic
process
GO:0000070      0.0045735241388741      9.71875 0.335686111687772       3       49
mitotic sister chromatid segregation
GO:0031146      0.00460297042707586     22.7422680412371        0.102761054598298
2       15      SCF-dependent proteasomal ubiquitin-dependent protein catabolic
process
GO:0051603      0.00521737929362048     3.22367396383144        2.66493668258252
8       389     proteolysis involved in cellular protein catabolic process
GO:0032786      0.00523715134210935     21.1163475699558        0.109611791571518
2       16      positive regulation of DNA-dependent transcription, elongation
GO:0000819      0.00540553901069568     9.1218112244898 0.356238322607432       3
52      sister chromatid segregation
GO:0006917      0.00570987006360094     3.17233154442457        2.70604110442184
8       395     induction of apoptosis
GO:0012502      0.00596907556326967     3.14725274725275        2.7265933153415 8
398     induction of programmed cell death
GO:0044257      0.00632855386116627     3.11440843420539        2.75399626323438
8       402     cellular protein catabolic process
GO:0061136      0.00698286457656797     8.27430555555556        0.390492007473531
3       57      regulation of proteasomal protein catabolic process
GO:0051028      0.00709591086384157     5.60550909985243        0.760431804027403
4       111     mRNA transport
GO:0006103      0.00736395360587303     17.3862947240752        0.130164002491177
2       19      2-oxoglutarate metabolic process
GO:0031365      0.00736395360587303     17.3862947240752        0.130164002491177
2       19      N-terminal protein amino acid modification
GO:0031648      0.00736395360587303     17.3862947240752        0.130164002491177
2       19      protein destabilization
GO:0045637      0.0087689923227001      5.25872576177285        0.808386962839942
4       118     regulation of myeloid cell differentiation
GO:0051052      0.00903878426481114     4.16451157869989        1.27423707701889
5       186     regulation of DNA metabolic process
Tissue: Whole_Blood=>Thyroid    Type:   asymmetric
SourceGene:     SREBF2(ENSG00000198911.6)
TargetGeneSet:  RPL22   C1QA    C1QC    C1QB    RP4     RPS27   HMGN2P18
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FCGR2B  RPS7    RNF181  RPL31   RPL32   TBC1D5  RPSA    RPL24   CD200R1 CD86
CHST13  TET2    AMACR   ERAP1   SKP1    CD14    CSF1R   CTB     RP11    RPL10A
GPR63   HMGB1P17        GATA4   RPL7    RPL35   SET     CARD9   RPL13AP5
FAM204A VENTX   MS4A6A  FOLR2   RPS25   NCKAP1L NACA    RNASE6  PLCB2   CTD
GTF2A2  PSTPIP1 SHCBP1  RPL17   RPL19   PHLPP1  VAV1    RPS11   RPL28   CRLS1
PXMP4   FAM176C ITGB2   WAS
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      5.46155160304568e-22    80.7800751879699        0.31485710331465
15      91      translational termination
GO:0006414      5.36924710258027e-21    68.147619047619 0.363296657670749       15
105     translational elongation
GO:0006614      5.36924710258027e-21    68.147619047619 0.363296657670749       15
105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      6.23999991538573e-21    67.3940345368917        0.366756625839042
15      106     cotranslational protein targeting to membrane
GO:0045047      6.23999991538573e-21    67.3940345368917        0.366756625839042
15      106     protein targeting to ER
GO:0072599      6.23999991538573e-21    67.3940345368917        0.366756625839042
15      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      3.38727394618744e-20    59.4923717059639        0.408276243858556
15      118     protein localization to endoplasmic reticulum
GO:0000184      3.86696228041177e-20    58.9162087912088        0.411736212026849
15      119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0034623      3.34592963438323e-19    42.421444527178 0.602034461282956       16
174     cellular macromolecular complex disassembly
GO:0032984      5.31378881271477e-19    41.1057380007218        0.61933430212442
16      179     macromolecular complex disassembly
GO:0019080      1.56537407444312e-18    44.952731092437 0.522455193412221       15
151     viral genome expression
GO:0019083      1.56537407444312e-18    44.952731092437 0.522455193412221       15
151     viral transcription
GO:0006413      1.73278747921261e-18    44.621480709072 0.525915161580513       15
152     translational initiation
GO:0006612      1.91673349877618e-18    44.2950310559006        0.529375129748806
15      153     protein targeting to membrane
GO:0043624      1.91673349877618e-18    44.2950310559006        0.529375129748806
15      153     cellular protein complex disassembly
GO:0043241      3.14143990266426e-18    42.7312687312687        0.546674970590271
15      158     protein complex disassembly
GO:0006401      4.80346781339796e-18    35.3862433862434        0.709293474500035
16      205     RNA catabolic process
GO:0000956      8.8021397121475e-18     39.6484230055659        0.584734620441492
15      169     nuclear-transcribed mRNA catabolic process
GO:0006402      1.9411925709822e-17     37.4355828220859        0.615874333956128
15      178     mRNA catabolic process
GO:0072594      1.52997242797413e-16    32.2267573696145        0.705833506331742
15      204     establishment of protein localization to organelle
GO:0071845      8.77764533169957e-16    24.8165057067603        0.98263095979517
16      284     cellular component disassembly at cellular level
GO:0019058      9.88046726504687e-16    28.1448412698413        0.799252646875649
15      231     viral infectious cycle
GO:0022411      1.09469512259589e-15    24.4446366782007        0.996470832468341
16      288     cellular component disassembly
GO:0022415      5.74240783472818e-15    24.7626822157434        0.899591723756141
15      260     viral reproductive process
GO:0016032      7.15927499949212e-14    16.5786203044268        1.56044564390008
17      451     viral reproduction
GO:0033365      3.34230472782977e-11    13.0470991890206        1.63656494360252
15      473     protein localization to organelle
GO:0006605      3.4434807145423e-11     13.0177404295051        1.64002491177081
15      474     protein targeting
GO:0042274      3.06614596131556e-05    61.2170212765957        0.0622794270292713
3       18      ribosomal small subunit biogenesis
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GO:0002253      7.05025891710982e-05    7.86580121057662        1.03453048231956
7       299     activation of immune response
GO:0000028      0.000174438093056294    149.96875       0.0207598090097571      2
6       ribosomal small subunit assembly
GO:0050778      0.000238634397527419    6.40401276789786        1.2594284132586 7
364     positive regulation of immune response
GO:0006958      0.000681278069094101    19.4938886373925        0.172998408414643
3       50      complement activation, classical pathway
GO:0022613      0.00104845951084384     7.16212121212121        0.778492837865892
5       225     ribonucleoprotein complex biogenesis
GO:0006956      0.00133742369874619     15.2563829787234        0.21797799460245
3       63      complement activation
GO:0042255      0.00136496319274614     42.8184523809524        0.0553594906926856
2       16      ribosome assembly
GO:0071843      0.00137103252344914     6.72697056030389        0.826932392221992
5       239     cellular component biogenesis at cellular level
GO:0001817      0.00142445078473875     5.42673190831831        1.24212857241713
6       359     regulation of cytokine production
GO:0002455      0.00146397411224734     14.7621825669183        0.224897930939035
3       65      humoral immune response mediated by circulating immunoglobulin
GO:0046632      0.00146397411224734     14.7621825669183        0.224897930939035
3       65      alpha-beta T cell differentiation
GO:0043372      0.00154354313670416     39.9611111111111        0.0588194588609785
2       17      positive regulation of CD4-positive, alpha-beta T cell
differentiation
GO:0042254      0.00172982013550401     8.54932533733133        0.515535257075635
4       149     ribosome biogenesis
GO:0045076      0.00193222176422743     35.2549019607843        0.0657393951975642
2       19      regulation of interleukin-2 biosynthetic process
GO:2000516      0.00193222176422743     35.2549019607843        0.0657393951975642
2       19      positive regulation of CD4-positive, alpha-beta T cell activation
GO:0071706      0.00204450628494989     13.0677811550152        0.252577676285378
3       73      tumor necrosis factor superfamily cytokine production
GO:0001816      0.00230931400200473     4.9118953026408 1.36668742647568        6
395     cytokine production
GO:0042094      0.00236244676993409     31.5394736842105        0.0726593315341499
2       21      interleukin-2 biosynthetic process
GO:0030225      0.00259296101324586     29.9604166666667        0.0761192997024427
2       22      macrophage differentiation
GO:0046631      0.00284836220456694     11.5717748451387        0.283717389800014
3       82      alpha-beta T cell activation
GO:0072376      0.00284836220456694     11.5717748451387        0.283717389800014
3       82      protein activation cascade
GO:0006909      0.00325985358161567     11.0110228146629        0.297557262473185
3       86      phagocytosis
GO:0002521      0.0037865254952186      5.2764683875795 1.04491038682444        5
302     leukocyte differentiation
GO:0043370      0.00389673425792935     23.96   0.093419140543907       2       27
regulation of CD4-positive, alpha-beta T cell differentiation
GO:0001819      0.00393115330481027     6.7559990496555 0.647014047470763       4
187     positive regulation of cytokine production
GO:0022618      0.00431401968990256     9.92761332099908        0.328696975987821
3       95      ribonucleoprotein complex assembly
GO:2000514      0.00448750684712852     22.1820987654321        0.100339076880493
2       29      regulation of CD4-positive, alpha-beta T cell activation
GO:0042110      0.00477401966054854     4.98478414720453        1.10372984568542
5       319     T cell activation
GO:0046638      0.00479746029912768     21.3883928571429        0.103799045048786
2       30      positive regulation of alpha-beta T cell differentiation
GO:0071826      0.00497922049308118     9.4125904803685 0.345996816829285       3
100     ribonucleoprotein complex subunit organization
GO:0030097      0.00504328122791284     4.16073204694649        1.60196526191959
6       463     hemopoiesis
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GO:0032760      0.0054461620521191      19.9597222222222        0.110718981385371
2       32      positive regulation of tumor necrosis factor production
GO:0006364      0.00555360540278177     9.03728670739414        0.359836689502457
3       104     rRNA processing
GO:0016072      0.0064872011323432      8.52694372638696        0.380596498512214
3       110     rRNA metabolic process
GO:0016064      0.0066513335552234      8.44739952718676        0.384056466680507
3       111     immunoglobulin mediated immune response
GO:0048534      0.00694240379473592     3.87953151143335        1.71268424330496
6       495     hemopoietic or lymphoid organ development
GO:0019724      0.00715855032465881     8.21736630247269        0.394436371185385
3       114     B cell mediated immunity
GO:0030099      0.0077615939744837      5.52856307272373        0.785412774202477
4       227     myeloid cell differentiation
GO:0032663      0.00801194098606083     16.1756756756757        0.134938758563421
2       39      regulation of interleukin-2 production
GO:0046637      0.00841510248029055     15.7489035087719        0.138398726731714
2       40      regulation of alpha-beta T cell differentiation
GO:0006959      0.00862134695839894     7.66064723761845        0.422116116531728
3       122     humoral immune response
GO:0002757      0.0087452078709616      5.33408620365142        0.81309251954882
4       235     immune response-activating signal transduction
GO:0043367      0.00882722417092368     15.3440170940171        0.141858694900007
2       41      CD4-positive, alpha-beta T cell differentiation
GO:0035710      0.00967809142555777     14.5934959349593        0.148778631236593
2       43      CD4-positive, alpha-beta T cell activation
GO:0046635      0.00967809142555777     14.5934959349593        0.148778631236593
2       43      positive regulation of alpha-beta T cell activation
Tissue: Whole_Blood=>Thyroid    Type:   cluster
SourceGene:     SST(ENSG00000157005.3)
TargetGeneSet:  LRRC47  KIAA0090        MFI2    UQCRH   RP4     GSTM3   NBPF10
PIAS3   ADAR    ZBTB7B  METTL13 QSOX1   DHX9    URB2    HEATR1  MORN2   MSH6
HMGA1P8 POLR1B  TMEM185B        ITGB6   GORASP2 7SK     FARP2   XCR1    RP11
LETM1   CNGA1   NUP155  CTD     SKIV2L2 PHAX    SEC24A  AFAP1L1 PRRC2A  ZBTB9   PGM3
LATS1   PRR18   HEATR2  C7orf26 POM121C MEPCE   ABCF2   MTMR9   PRKDC   UQCRB
ZFP41   STOML2  TLN1    UBQLN1  SEC16A  BMS1P7  SEC24C  SEC23IP NUP98   SPTY2D1
PRPF19  UBE4A   ARCN1   DDX6    CBX5    ANKRD52 CAND1   GCN1L1  ZIC2    PRMT5-AS1
PRMT5   TUBGCP4 TNFAIP8L3       RNF111  RNF40   POLR2C  EDC4    PIEZO1  TIMM22  RP13
DPH1    TP53    GRAP    LIG3    TEX34   CA10    GNA11   FEM1A   ZNF562  RAVER1
CHERP   MPV17L2 TOMM40  GRWD1   TRIM28  CDH22   SLC2A10 ADNP    GCNT7   PRPF6   PWP2
CRKL    SF3A1   BCOR    SMC1A   APEX2   HCFC1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0000377      1.15365543243125e-08    12.0624854999613        1.10110026987752
11      204     RNA splicing, via transesterification reactions with bulged
adenosine as nucleophile
GO:0000398      1.15365543243125e-08    12.0624854999613        1.10110026987752
11      204     nuclear mRNA splicing, via spliceosome
GO:0000375      1.48367893969954e-08    11.7537313432836        1.1280880215902 11
209     RNA splicing, via transesterification reactions
GO:0071843      5.96174559502445e-07    9.08296943231441        1.29001453186631
10      239     cellular component biogenesis at cellular level
GO:0022618      7.66284453746082e-07    16.0043213828425        0.512767282541001
7       95      ribonucleoprotein complex assembly
GO:0071826      1.08642122355679e-06    15.1385733757383        0.539755034253685
7       100     ribonucleoprotein complex subunit organization
GO:0008380      1.20153249783804e-06    7.39911021814007        1.7434087606394 11
323     RNA splicing
GO:0006397      1.39444324278229e-06    6.5708245243129 2.1536225866722 12      399
mRNA processing
GO:0022613      3.29035265921355e-06    8.54891304347826        1.21444882707079
9       225     ribonucleoprotein complex biogenesis
GO:0048199      1.2541880371997e-05     33.7250293772033        0.145733859248495
4       27      vesicle targeting, to, from or within Golgi
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GO:0000387      2.21207823724036e-05    28.7207207207207        0.167324060618642
4       31      spliceosomal snRNP assembly
GO:0006901      3.62128744856227e-05    25.0078465562337        0.18891426198879
4       35      vesicle coating
GO:0006900      4.53053923311206e-05    23.4889434889435        0.199709362673863
4       37      membrane budding
GO:0006903      4.53053923311206e-05    23.4889434889435        0.199709362673863
4       37      vesicle targeting
GO:0048207      6.56901663562067e-05    47.87   0.0809632551380527      3       15
vesicle targeting, rough ER to cis-Golgi
GO:0048208      6.56901663562067e-05    47.87   0.0809632551380527      3       15
COPII vesicle coating
GO:0090114      6.56901663562067e-05    47.87   0.0809632551380527      3       15
COPII-coated vesicle budding
GO:0051650      0.000127608563505716    17.6031941031941        0.259082416441769
4       48      establishment of vesicle localization
GO:0006122      0.000171364275136886    189.092105263158        0.0215902013701474
2       4       mitochondrial electron transport, ubiquinol to cytochrome c
GO:0006281      0.000213198878765418    4.88223668914206        2.06726178119161
9       383     DNA repair
GO:0002326      0.000284606396846764    126.052631578947        0.0269877517126842
2       5       B cell lineage commitment
GO:0051648      0.000414255240652964    12.6823216659282        0.350840772264895
4       65      vesicle localization
GO:0000244      0.000425414344459507    94.5328947368421        0.0323853020552211
2       6       assembly of spliceosomal tri-snRNP
GO:0007006      0.00073451305538224     19.124  0.178119161303716       3       33
mitochondrial membrane organization
GO:0051095      0.000788557041987128    63.0131578947368        0.0431804027402948
2       8       regulation of helicase activity
GO:0006403      0.000835014385006894    7.44640803095263        0.734066846585011
5       136     RNA localization
GO:0016044      0.000983353545347316    4.31328455910666        2.04567157982147
8       379     cellular membrane organization
GO:0000245      0.00102994617045959     16.8694117647059        0.199709362673863
3       37      spliceosomal complex assembly
GO:0061024      0.00103451672924188     4.277769289534  2.06186423084908        8
382     membrane organization
GO:0016050      0.00147111728672856     8.87604846225536        0.491177081170853
4       91      vesicle organization
GO:0006997      0.00182360238199878     13.6485714285714        0.242889765414158
3       45      nucleus organization
GO:0007007      0.00183288240692901     37.7973684210526        0.0647706041104422
2       12      inner mitochondrial membrane organization
GO:0008340      0.00183288240692901     37.7973684210526        0.0647706041104422
2       12      determination of adult lifespan
GO:0051656      0.00215795043950319     7.95541933686264        0.545152584596222
4       101     establishment of organelle localization
GO:0002360      0.00215856763415339     34.3588516746412        0.070168154452979
2       13      T cell lineage commitment
GO:0006486      0.00238648340456517     4.78556910569106        1.36018268631929
6       252     protein glycosylation
GO:0043413      0.00238648340456517     4.78556910569106        1.36018268631929
6       252     macromolecule glycosylation
GO:0070085      0.0025315329577764      4.72690763052209        1.3763753373469 6
255     glycosylation
GO:0006888      0.00324380592768268     11.0161538461538        0.296865268839527
3       55      ER to Golgi vesicle-mediated transport
GO:0051053      0.00377127759435451     10.4130909090909        0.313057919867137
3       58      negative regulation of DNA metabolic process
GO:0010390      0.00416076748304574     23.6134868421053        0.0971559061656633
2       18      histone monoubiquitination
GO:0009303      0.00463406501533718     22.2229102167183        0.1025534565082 2
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19      rRNA transcription
GO:0050657      0.00519506983914373     6.1612972972973 0.696283994187254       4
129     nucleic acid transport
GO:0050658      0.00519506983914373     6.1612972972973 0.696283994187254       4
129     RNA transport
GO:0051236      0.00519506983914373     6.1612972972973 0.696283994187254       4
129     establishment of RNA localization
GO:0006310      0.00541934970834893     4.75725221595487        1.1280880215902 5
209     DNA recombination
GO:0009101      0.00587069167689304     3.94949494949495        1.63545775378867
6       303     glycoprotein biosynthetic process
GO:0006471      0.0061948900365192      18.8855263157895        0.118746107535811
2       22      protein ADP-ribosylation
GO:0010259      0.00735028424056083     17.1662679425837        0.129541208220884
2       24      multicellular organismal aging
GO:0006289      0.00801726283746006     7.83561643835616        0.4102138260328 3
76      nucleotide-excision repair
GO:0000291      0.00859516597238188     15.7335526315789        0.140336308905958
2       26      nuclear-transcribed mRNA catabolic process, exonucleolytic
GO:0043928      0.00859516597238188     15.7335526315789        0.140336308905958
2       26      exonucleolytic nuclear-transcribed mRNA catabolic process involved
in deadenylation-dependent decay
GO:0015931      0.00878355991970019     5.26730840429471        0.809632551380527
4       150     nucleobase-containing compound transport
GO:0051640      0.00878355991970019     5.26730840429471        0.809632551380527
4       150     organelle localization
GO:0016925      0.0099275250191223      14.5212550607287        0.151131409591032
2       28      protein sumoylation
Tissue: Whole_Blood=>Thyroid    Type:   cluster
SourceGene:     TMEM191A(ENSG00000226287.3)
TargetGeneSet:  NOC2L   UBE2J2  SPEN    NUDC    EYA3    TXLNA   EIF2C3  STK40
AKIRIN1 TOE1    SELRC1  RP4     PYGO2   UBQLN4  CCT3    ETV3    TTC32   ERLEC1
PCBP1   TMEM127 RBP4    HSPD1   C2orf69 INHA    CLN5    NKIRAS1 TMEM158 TMEM115
FYTTD1  LETM1   GRPEL1  RP11    ANKRD17 EIF4E   CCRN4L  ANKRA2  PHAX    SLC35A4
RBM22   ABHD16A LY6G6E  DAXX    BRPF3   TBC1D22B        RPL7L1  RP13    ARID1B
TULP4   USP42   PURB    HUS1    BAZ1B   MEPCE   ABCF2   PINX1   LSM12P1 KAT6A
DNAJA1  TEX10   TBC1D13 TOR1B   RNLS    LZTS2   NOLC1   AFAP1L2 TSSC4   NUP98   NXF1
MARK2   STIP1   SF1     C11orf68        PAFAH1B2        C2CD2L  SC5DL   HSPA8
PKNOX2  FKBP4   NOP2    FMNL3   AVIL    GCN1L1  GPR133  PUS1    PDS5B   TARDBPP2
FAM70B  SALL2   RBM23   PRMT5   EIF2B2  DIO2    IDH3A   DNAJA4  CHRNA3  CD2BP2
TBC1D10B        RNF40   SETD1A  E2F4    CIRH1A  USP10   VPS53   TSR1    ALKBH5
USP22   GIT1    PPP1R9B MED13   SIRT7   RBBP8   NFIC    MAP2K2  FEM1A   ZNF562
ELOF1   DNAJB1  BRD4    ARMC6   GATAD2A IRF2BP1 GRWD1   KCNJ14  FIZ1    TRIM28
ZNF337  RP3     LINC00478       IGLC5   ST13    L3MBTL2 SMC1A
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0016570      3.6230625639836e-06     6.45975 1.93253062071829        11      261
histone modification
GO:0006457      4.49158677109177e-06    7.07536783104794        1.59933568611169
10      216     protein folding
GO:0016569      4.50585519221402e-06    6.3056640625    1.97695661199917        11
267     covalent chromatin modification
GO:0016568      1.29774902123674e-05    4.74777277014988        3.10241505778147
13      419     chromatin modification
GO:0000377      2.02722703576904e-05    6.66357927786499        1.51048370354993
9       204     RNA splicing, via transesterification reactions with bulged
adenosine as nucleophile
GO:0000398      2.02722703576904e-05    6.66357927786499        1.51048370354993
9       204     nuclear mRNA splicing, via spliceosome
GO:0000375      2.45554717631266e-05    6.49469387755102        1.54750536295066
9       209     RNA splicing, via transesterification reactions
GO:0000087      7.19801848441197e-05    4.59482449856733        2.66555947685281
11      360     M phase of mitotic cell cycle
GO:0000387      7.663344165069e-05      20.5925925925926        0.229534288284548
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4       31      spliceosomal snRNP assembly
GO:0042026      8.27114288575499e-05    45.9455128205128        0.0888519825617604
3       12      protein refolding
GO:0008380      0.00013985244034312     4.62138928230295        2.39159919728738
10      323     RNA splicing
GO:0006397      0.000178321613870727    4.12145618556701        2.95432842017853
11      399     mRNA processing
GO:0006986      0.000389673072422535    6.86838927795219        0.955158812538925
6       129     response to unfolded protein
GO:0061077      0.000476344630755438    22.9583333333333        0.155490969483081
3       21      chaperone-mediated protein folding
GO:0035966      0.000516382493018023    6.4953541507997 1.00698913569995        6
136     response to topologically incorrect protein
GO:0006458      0.000543270386402793    11.8132617227845        0.377620925887482
4       51      'de novo' protein folding
GO:0022618      0.000691968692341552    7.7636165577342 0.703411528613937       5
95      ribonucleoprotein complex assembly
GO:0000244      0.00079907177952278     68.2857142857143        0.0444259912808802
2       6       assembly of spliceosomal tri-snRNP
GO:0048096      0.00079907177952278     68.2857142857143        0.0444259912808802
2       6       chromatin-mediated maintenance of transcription
GO:0070389      0.00079907177952278     68.2857142857143        0.0444259912808802
2       6       chaperone cofactor-dependent protein refolding
GO:0071826      0.000873285052963591    7.35242518059855        0.74043318801467
5       100     ribonucleoprotein complex subunit organization
GO:0030521      0.00113948759308705     9.56545028456645        0.459068576569096
4       62      androgen receptor signaling pathway
GO:0000280      0.00115389361514591     3.77123107307439        2.59151615805135
9       350     nuclear division
GO:0007067      0.00115389361514591     3.77123107307439        2.59151615805135
9       350     mitosis
GO:0016573      0.00123404834008591     6.77755568246716        0.799667843055844
5       108     histone acetylation
GO:0018393      0.0013392704885431      6.64752567693744        0.814476506816137
5       110     internal peptidyl-lysine acetylation
GO:0022613      0.00141082096378194     4.53587155963303        1.66597467303301
7       225     ribonucleoprotein complex biogenesis
GO:0018394      0.00150933750578905     6.46151053013798        0.836689502456577
5       113     peptidyl-lysine acetylation
GO:0006475      0.00163122169908091     6.34313725490196        0.851498166216871
5       115     internal protein amino acid acetylation
GO:0048285      0.00169383049192516     3.55721069591271        2.73960279565428
9       370     organelle fission
GO:0006405      0.0016973727916986      8.531142643764  0.510898899730122       4
69      RNA export from nucleus
GO:0045931      0.00183206250357425     13.7634615384615        0.244342952044841
3       33      positive regulation of mitotic cell cycle
GO:0071843      0.00199011420128346     4.25793103448276        1.76963531935506
7       239     cellular component biogenesis at cellular level
GO:0051085      0.00235123801475254     34.1333333333333        0.074043318801467
2       10      chaperone mediated protein folding requiring cofactor
GO:0044419      0.00259200549074806     3.32973760932945        2.9173067607778 9
394     interspecies interaction between organisms
GO:0006473      0.00260718603424917     5.66754344014028        0.947754480658778
5       128     protein acetylation
GO:0051169      0.00263737072435057     3.62242230612838        2.37679053352709
8       321     nuclear transport
GO:0050657      0.00269660187948411     5.62144212523719        0.955158812538925
5       129     nucleic acid transport
GO:0050658      0.00269660187948411     5.62144212523719        0.955158812538925
5       129     RNA transport
GO:0051236      0.00269660187948411     5.62144212523719        0.955158812538925
5       129     establishment of RNA localization
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GO:0007064      0.00285987547293078     30.3386243386243        0.0814476506816137
2       11      mitotic sister chromatid cohesion
GO:0006403      0.00338597480719715     5.31844035324053        1.00698913569995
5       136     RNA localization
GO:0018205      0.00395043290127815     5.12110726643599        1.04401079510069
5       141     peptidyl-lysine modification
GO:0043966      0.00419286621707235     10.06308630394  0.325790602726455       3
44      histone H3 acetylation
GO:0043543      0.00431979414912155     5.00952179432924        1.06622379074113
5       144     protein acylation
GO:0045815      0.00466373673300363     22.7492063492064        0.103660646322054
2       14      positive regulation of gene expression, epigenetic
GO:0051084      0.0047547071160943      9.59369409660107        0.340599266486748
3       46      'de novo' posttranslational protein folding
GO:0015931      0.00513145534617908     4.80020283975659        1.11064978202201
5       150     nucleobase-containing compound transport
GO:0000070      0.00567913236572984     8.96613712374582        0.362812262127188
3       49      mitotic sister chromatid segregation
GO:0010458      0.00609095393581712     19.4965986394558        0.118469310082347
2       16      exit from mitosis
GO:0030518      0.00669499024630151     5.70393354018617        0.747837519894817
4       101     intracellular steroid hormone receptor signaling pathway
GO:0000819      0.00670414535134251     8.41542386185243        0.385025257767629
3       52      sister chromatid segregation
GO:0006302      0.00692927868272914     5.64533386170002        0.755241851774964
4       102     double-strand break repair
GO:0007346      0.00727626059367854     3.32216216216216        2.24351255968445
7       303     regulation of mitotic cell cycle
GO:0006281      0.00755558402172471     3.01015488215488        2.83585911009619
8       383     DNA repair
GO:0051168      0.00872236616921661     5.26638927415626        0.807072174935991
4       109     nuclear export
GO:0071478      0.00906605014910685     7.49423076923077        0.429451249048509
3       58      cellular response to radiation
GO:0051028      0.00928533524098818     5.16722620451865        0.821880838696284
4       111     mRNA transport
GO:0006913      0.00936147059222981     3.15855305466238        2.35457753788665
7       318     nucleocytoplasmic transport
GO:0016571      0.00950107513571365     7.35989010989011        0.436855580928655
3       59      histone methylation
GO:0006406      0.00994811026184323     7.23026315789474        0.444259912808802
3       60      mRNA export from nucleus
Tissue: Whole_Blood=>Thyroid    Type:   cluster
SourceGene:     TMEM64(ENSG00000180694.9)
TargetGeneSet:  FCRL3   RP11    FCRL2   IGKJ5   IGKC    IGKJ4   IGKJ3   IGKJ2
IGKV1-6 IGKV3-7 IGKV1-9 IGKV1-13        IGKV1-17        IGKV2-26        IGKV1-27
IGKV2-28        IGKV2-29        IGKV1-33        IGKV1-39        IGKV2-40
IGKV1D-33       IGKV2D-29       IGKV2D-28       IGKV3D-20       IGKV1D-16
IGKV1D-13       IGKV3D-7        IGJ     CTD     CTB     DNAH8   RGS17   ARHGEF10
CENPP   RIN1    AMOTL1  GS1     IGHG3   KIAA0125        IGHV1-3 IGHV4-4 IGHV3-13
IGHV1-18        IGHV4-28        IGHV4-31        IGHV3-33        IGHV3-43
IGHV1-46        IGHV5-51        IGHV4-55        IGHV2-70        IGHV3-73
IGHV3-74        IGHV5-78        DOC2B   TNFRSF13B       CD79A   LINC00176
PPM1F   IGLV9-49        IGLV1-47        IGLV5-45        IGLV1-40        IGLV3-25
IGLV3-21        IGLV3-1 IGLL5   IGLC1   IGLC3   IGLC7   PHF21B
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006958      4.17272448412705e-17    210.526829268293        0.0830392360390284
9       50      complement activation, classical pathway
GO:0006956      3.89403027699151e-16    159.7   0.104629437409176       9       63
complement activation
GO:0002455      5.24961254567502e-16    153.975 0.107951006850737       9       65
humoral immune response mediated by circulating immunoglobulin
GO:0072376      4.73636565626121e-15    117.978082191781        0.136184347104007
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9       82      protein activation cascade
GO:0016064      7.94729347232045e-14    84.2647058823529        0.184347104006643
9       111     immunoglobulin mediated immune response
GO:0019724      1.01656580271012e-13    81.84   0.189329458168985       9       114
B cell mediated immunity
GO:0006959      1.89850781575545e-13    76.0035398230089        0.202615735935229
9       122     humoral immune response
GO:0002449      3.33579003599497e-12    54.1860759493671        0.277351048370355
9       167     lymphocyte mediated immunity
GO:0002460      6.91206296908552e-12    49.7267441860465        0.300602034461283
9       181     adaptive immune response based on somatic recombination of immune
receptors built from immunoglobulin superfamily domains
GO:0002250      1.55296624225031e-11    45.2    0.328835374714553       9       198
adaptive immune response
GO:0002253      1.87926130523349e-11    34.9431537320811        0.49657463151339
10      299     activation of immune response
GO:0002443      2.75033885290613e-11    42.2524752475247        0.3504255760847 9
211     leukocyte mediated immunity
GO:0050778      1.3027059467683e-10     28.3958837772397        0.604525638364127
10      364     positive regulation of immune response
GO:0002252      5.78430500835518e-09    22.3607427055703        0.6410629022213 9
386     immune effector process
GO:0051496      0.000838456291624716    54.5568181818182        0.0431804027402948
2       26      positive regulation of stress fiber assembly
GO:0032233      0.0011177006176441      46.75   0.0498235416234171      2       30
positive regulation of actin filament bundle assembly
GO:0051492      0.00169914447007782     37.3818181818182        0.061449034668881
2       37      regulation of stress fiber assembly
GO:0032231      0.00228983935999548     31.8980044345898        0.0714137429935645
2       43      regulation of actin filament bundle assembly
GO:0043149      0.00239645191615069     31.1363636363636        0.073074527714345
2       44      stress fiber assembly
GO:0010638      0.00332423105454637     11.3071428571429        0.303923603902844
3       183     positive regulation of organelle organization
GO:0042100      0.00399022793096356     23.7553719008264        0.0946647290844924
2       57      B cell proliferation
GO:0031585      0.00497442779656243     313.586956521739        0.00498235416234171
1       3       regulation of inositol 1,4,5-trisphosphate-sensitive calcium-release
channel activity
GO:0031987      0.00497442779656243     313.586956521739        0.00498235416234171
1       3       locomotion involved in locomotory behavior
GO:0048791      0.00497442779656243     313.586956521739        0.00498235416234171
1       3       calcium ion-dependent exocytosis of neurotransmitter
GO:0051643      0.00497442779656243     313.586956521739        0.00498235416234171
1       3       endoplasmic reticulum localization
GO:0042552      0.00563234430661618     19.7809917355372        0.112933361013079
2       68      myelination
GO:0051017      0.00579461598130192     19.4843962008141        0.114594145733859
2       69      actin filament bundle assembly
GO:0007272      0.00629421014504686     18.6454545454545        0.119576499896201
2       72      ensheathment of neurons
GO:0008366      0.00629421014504686     18.6454545454545        0.119576499896201
2       72      axon ensheathment
GO:0009313      0.0066272941955714      209.04347826087 0.00664313888312228     1
4       oligosaccharide catabolic process
GO:0031340      0.0066272941955714      209.04347826087 0.00664313888312228     1
4       positive regulation of vesicle fusion
GO:0042759      0.0066272941955714      209.04347826087 0.00664313888312228     1
4       long-chain fatty acid biosynthetic process
GO:0019228      0.0084809763532936      15.9035476718404        0.139505916545568
2       84      regulation of action potential in neuron
GO:0051495      0.00927550456992079     15.1596194503171        0.14614905542869
2       88      positive regulation of cytoskeleton organization
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GO:0000244      0.00992513678201701     125.408695652174        0.00996470832468341
1       6       assembly of spliceosomal tri-snRNP
Tissue: Whole_Blood=>Nerve_Tibial       Type:   asymmetric
SourceGene:     CTD-2313J17.1(ENSG00000258922.1)
TargetGeneSet:  CHCHD2P6        HSPB7   CCT8P1  RP11    CHRNB2  DPT     ACVR1C
KRT8P15 GPBAR1  DES     SLC19A3 TIMP4   ADIPOQ  ADIPOQ-AS1      LVRN    PPARGC1B
MLXIPL  AQP9    LRRC37A5P       AGPAT2  C10orf71        RBP4    GPAM    ACSL5
LGALS12 RPS3AP40        MYEOV   GPD1    PPP1R1A ACACB   MYH7    PLIN1   TUSC5
STAT5A  CA4     SCN4A   CIDEA   PLIN4   PLIN5   SLC7A10 LIPE    FTCD-AS1
SULT4A1 GYG2    PFKFB1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006641      7.95965961852856e-08    34.6038647342995        0.223790741125182
6       98      triglyceride metabolic process
GO:0006639      1.07255759533129e-07    32.8087056128293        0.235208636080548
6       103     acylglycerol metabolic process
GO:0006638      1.13639611300147e-07    32.4716553287982        0.237492215071621
6       104     neutral lipid metabolic process
GO:0019216      2.24183935298213e-07    20.4888934594817        0.443014324268217
7       194     regulation of lipid metabolic process
GO:0009749      4.26731426718578e-06    24.8179611650485        0.246626531035914
5       108     response to glucose stimulus
GO:0009746      5.33018893176607e-06    23.6607142857143        0.258044425991281
5       113     response to hexose stimulus
GO:0034284      5.80925195704711e-06    23.2272727272727        0.262611583973427
5       115     response to monosaccharide stimulus
GO:0019432      6.09748631581001e-06    40.4475721323012        0.121029686526884
4       53      triglyceride biosynthetic process
GO:0046460      7.07899897634248e-06    38.8559837728195        0.125596844509031
4       55      neutral lipid biosynthetic process
GO:0046463      7.07899897634248e-06    38.8559837728195        0.125596844509031
4       55      acylglycerol biosynthetic process
GO:0010876      8.00881384652893e-06    15.1079213184476        0.490969483080756
6       215     lipid localization
GO:0009743      1.13902959533377e-05    20.0942069741282        0.301432426821673
5       132     response to carbohydrate stimulus
GO:0043434      2.01369832473102e-05    10.0821538461538        0.872327174589994
7       382     response to peptide hormone stimulus
GO:0046486      2.30751876697959e-05    12.4418093983311        0.59144695868798
6       259     glycerolipid metabolic process
GO:0006112      3.25040083304447e-05    16.0141509433962        0.374506954536018
5       164     energy reserve metabolic process
GO:0006091      4.17181105858948e-05    8.95112369815458        0.977371808179365
7       428     generation of precursor metabolites and energy
GO:0006631      4.18734110600985e-05    11.1394799054374        0.657670749429105
6       288     fatty acid metabolic process
GO:0045834      5.46501790211906e-05    22.4608150470219        0.210089267178742
4       92      positive regulation of lipid metabolic process
GO:0044262      7.06567202148421e-05    13.5163373860182        0.440730745277143
5       193     cellular carbohydrate metabolic process
GO:0006006      7.97540034018014e-05    13.1615470022206        0.45214864023251
5       198     glucose metabolic process
GO:0046889      0.00013480857295596     35.0658536585366        0.100477475607224
3       44      positive regulation of lipid biosynthetic process
GO:0019318      0.00017482274792078     11.0644104803493        0.534357483911148
5       234     hexose metabolic process
GO:0009744      0.000180239911948168    132.820276497696        0.0205522109196595
2       9       response to sucrose stimulus
GO:0034285      0.000180239911948168    132.820276497696        0.0205522109196595
2       9       response to disaccharide stimulus
GO:0055089      0.000180239911948168    132.820276497696        0.0205522109196595
2       9       fatty acid homeostasis
GO:0019915      0.000186082374057382    31.2434782608696        0.111895370562591
3       49      lipid storage
```

GO:0010867	0.00022497792689792	116.209677419355	0.0228357899107328	2	10	positive regulation of triglyceride biosynthetic process
GO:0032868	0.000246715170641447	10.2450838635049	0.575461905750467	5	252	response to insulin stimulus
GO:0032787	0.000257958470179801	7.88917018284107	0.915715175420386	6	401	monocarboxylic acid metabolic process
GO:0005996	0.000260608018732448	10.12	0.582312642723687	5	255	monosaccharide metabolic process
GO:0033032	0.000274580123993068	103.290322580645	0.0251193689018061	2	11	regulation of myeloid cell apoptotic process
GO:0006094	0.000307315513526828	26.1145454545455	0.13244758148225	3	58	gluconeogenesis
GO:0016024	0.000329025405415394	92.9548387096774	0.0274029478928794	2	12	CDP-diacylglycerol biosynthetic process
GO:0019319	0.000374340354630484	24.3372881355932	0.141581897446543	3	62	hexose biosynthetic process
GO:0033028	0.000388292739320376	84.4985337243402	0.0296865268839527	2	13	myeloid cell apoptotic process
GO:0046341	0.000388292739320376	84.4985337243402	0.0296865268839527	2	13	CDP-diacylglycerol metabolic process
GO:0045017	0.000418976347448355	12.94555353902	0.356238322607432	4	156	glycerolipid biosynthetic process
GO:0040014	0.000430331682137595	23.1548387096774	0.148432634419763	3	65	regulation of multicellular organism growth
GO:0046364	0.000450123790556485	22.7857142857143	0.150716213410837	3	66	monosaccharide biosynthetic process
GO:0010866	0.000452361159660209	77.4516129032258	0.031970105875026	2	14	regulation of triglyceride biosynthetic process
GO:0070293	0.000452361159660209	77.4516129032258	0.031970105875026	2	14	renal absorption
GO:0003014	0.000470491835915483	22.428125	0.15299979240191	3	67	renal system process
GO:0010906	0.000470491835915483	22.428125	0.15299979240191	3	67	regulation of glucose metabolic process
GO:0019217	0.000470491835915483	22.428125	0.15299979240191	3	67	regulation of fatty acid metabolic process
GO:0051240	0.000506655532519243	6.91363523880228	1.03902844093834	6	455	positive regulation of multicellular organismal process
GO:0090208	0.000594817723377894	66.3778801843318	0.0365372638571725	2	16	positive regulation of triglyceride metabolic process
GO:0002761	0.000605182306922169	20.4971428571429	0.16670126634835	3	73	regulation of myeloid leukocyte differentiation
GO:0015980	0.000609943471952853	8.34673604541154	0.701058750259498	5	307	energy derivation by oxidation of organic compounds
GO:0016051	0.000718327161609398	11.1614420062696	0.411044218393191	4	180	carbohydrate biosynthetic process
GO:0042104	0.000756228677422032	58.0725806451613	0.0411044218393191	2	18	positive regulation of activated T cell proliferation
GO:0010675	0.000880251032037665	17.9225	0.189537056259082	3	83	regulation of cellular carbohydrate metabolic process
GO:0042493	0.000916446693937499	7.59980578334053	0.767282541000623	5	336	response to drug
GO:0006109	0.00100918327127551	17.0642857142857	0.198671372223376	3	87	regulation of carbohydrate metabolic process
GO:0090207	0.00113525328177882	46.4451612903226	0.0502387378036122	2	22	regulation of triglyceride metabolic process
GO:0031667	0.0011718462077691	7.17755102040816	0.810670541831015	5	355	response to nutrient levels
GO:0006732	0.00118699078097754	9.70706725844998	0.470417272161096	4	206	coenzyme metabolic process
GO:0046890	0.00122405919835558	15.92	0.212372846169815	3	93	regulation of lipid biosynthetic process
GO:0001817	0.00123174727611219	7.09443099273608	0.819804857795308			

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5       359     regulation of cytokine production
GO:0019433      0.00124159877728433     44.2304147465438        0.0525223167946855
2       23      triglyceride catabolic process
GO:0032370      0.00124159877728433     44.2304147465438        0.0525223167946855
2       23      positive regulation of lipid transport
GO:0043029      0.00124159877728433     44.2304147465438        0.0525223167946855
2       23      T cell homeostasis
GO:0045471      0.00126245280254452     15.743956043956 0.214656425160889       3
94      response to ethanol
GO:0097305      0.00130159908001424     15.5717391304348        0.216940004151962
3       95      response to alcohol
GO:0008016      0.00134150364896893     15.4032258064516        0.219223583143035
3       96      regulation of heart contraction
GO:0050671      0.00134150364896893     15.4032258064516        0.219223583143035
3       96      positive regulation of lymphocyte proliferation
GO:0046006      0.00135253927893591     42.217008797654 0.0548058957857588      2
24      regulation of activated T cell proliferation
GO:0046461      0.00135253927893591     42.217008797654 0.0548058957857588      2
24      neutral lipid catabolic process
GO:0046464      0.00135253927893591     42.217008797654 0.0548058957857588      2
24      acylglycerol catabolic process
GO:0032946      0.00138217208181276     15.2382978723404        0.221507162134108
3       97      positive regulation of mononuclear cell proliferation
GO:0070665      0.00150881560490668     14.7639175257732        0.228357899107328
3       100     positive regulation of leukocyte proliferation
GO:0009991      0.00154789068584402     6.7239563385676 0.863192858625701       5
378     response to extracellular stimulus
GO:0040018      0.00158812434901315     38.6935483870968        0.0593730537679053
2       26      positive regulation of multicellular organism growth
GO:0050798      0.00158812434901315     38.6935483870968        0.0593730537679053
2       26      activated T cell proliferation
GO:0045923      0.0017127286007007      37.1432258064516        0.0616566327589786
2       27      positive regulation of fatty acid metabolic process
GO:0032844      0.00172440672777148     8.74014778325123        0.520656009964708
4       228     regulation of homeostatic process
GO:0032720      0.00184184722471557     35.712158808933 0.0639402117500519      2
28      negative regulation of tumor necrosis factor production
GO:0033865      0.00184184722471557     35.712158808933 0.0639402117500519      2
28      nucleoside bisphosphate metabolic process
GO:0001816      0.00187841568405204     6.42307692307692        0.902013701473946
5       395     cytokine production
GO:0006936      0.00204818652604451     8.32457813646368        0.545775378866514
4       239     muscle contraction
GO:0051048      0.00208751363034533     13.1275229357798        0.255760847000208
3       112     negative regulation of secretion
GO:0016042      0.00214332846222422     8.21790785279629        0.552626115839734
4       242     lipid catabolic process
GO:0051186      0.00224149476476971     8.11389326083846        0.559476852812954
4       245     cofactor metabolic process
GO:0051046      0.00228223744714 8      6.13182773109244        0.943118123313265
5       413     regulation of secretion
GO:0003015      0.00230708936296899     12.6592920353982        0.264895162964501
3       116     heart process
GO:0060047      0.00230708936296899     12.6592920353982        0.264895162964501
3       116     heart contraction
GO:0044057      0.00237998888247377     6.07056171983356        0.952252439277559
5       417     regulation of system process
GO:0046503      0.00240306638746981     30.941935483871 0.073074527714345       2
32      glycerolipid catabolic process
GO:0045637      0.00242205427147634     12.4373913043478        0.269462320946647
3       118     regulation of myeloid cell differentiation
GO:0002763      0.00271024518725041     29.0040322580645        0.0776416856964916
2       34      positive regulation of myeloid leukocyte differentiation
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GO:0002573	0.00285223938865716	11.7180327868852	0.28544737388416	3	125	myeloid leukocyte differentiation
GO:0003012	0.00301746110844096	7.45248749670966	0.607432011625493	4	266	muscle system process
GO:0051384	0.00339833948917098	10.9907692307692	0.303716005812747	3	133	response to glucocorticoid stimulus
GO:0071375	0.0034896220308333	7.14664645699128	0.632551380527299	4	277	cellular response to peptide hormone stimulus
GO:0015909	0.00355442549303487	25.075850043592	0.089059580651858	2	39	long-chain fatty acid transport
GO:0030049	0.00355442549303487	25.075850043592	0.089059580651858	2	39	muscle filament sliding
GO:0033275	0.00355442549303487	25.075850043592	0.089059580651858	2	39	actin-myosin filament sliding
GO:0044242	0.00369380886083433	10.6597014925373	0.31285032177704	3	137	cellular lipid catabolic process
GO:0002260	0.00373617448509086	24.4142614601019	0.0913431596429313	2	40	lymphocyte homeostasis
GO:0006637	0.00373617448509086	24.4142614601019	0.0913431596429313	2	40	acyl-CoA metabolic process
GO:0035383	0.00373617448509086	24.4142614601019	0.0913431596429313	2	40	thioester metabolic process
GO:0007565	0.00392542749391757	10.4240875912409	0.31970105875026	3	140	female pregnancy
GO:0031960	0.00408466676056487	10.2726618705036	0.324268216732406	3	142	response to corticosteroid stimulus
GO:0070252	0.00411243099306515	23.1903225806452	0.0959103176250778	2	42	actin-mediated cell contraction
GO:0050670	0.00424780202510783	10.1255319148936	0.328835374714553	3	144	regulation of lymphocyte proliferation
GO:0046888	0.00430690018207738	22.6231313926043	0.0981938966161511	2	43	negative regulation of hormone secretion
GO:0032944	0.00433083971768706	10.0535211267606	0.331118953705626	3	145	regulation of mononuclear cell proliferation
GO:0048871	0.00433083971768706	10.0535211267606	0.331118953705626	3	145	multicellular organismal homeostasis
GO:0032623	0.00450557121108316	22.0829493087558	0.10047747560722‌4	2	44	interleukin-2 production
GO:0070663	0.00476087008678795	9.70816326530612	0.342536848660992	3	150	regulation of leukocyte proliferation
GO:0008015	0.00480145424207656	6.51320493599354	0.691924434295204	4	303	blood circulation
GO:0048545	0.00480145424207656	6.51320493599354	0.691924434295204	4	303	response to steroid hormone stimulus
GO:0003013	0.00485769549577889	6.49103448275862	0.694208013286278	4	304	circulatory system process
GO:0010565	0.0051229100949274	9.44834437086093	0.351671164625285	3	154	regulation of cellular ketone metabolic process
GO:0015850	0.00534189439482383	20.1570827489481	0.109611791571518	2	48	organic alcohol transport
GO:0016052	0.00550119277722173	9.20193548387097	0.360805480589579	3	158	carbohydrate catabolic process
GO:0001776	0.00556129065102666	19.7268359643102	0.111895370562591	2	49	leukocyte homeostasis
GO:0015908	0.00647957616206189	18.1745730550285	0.121029686526884	2	53	fatty acid transport
GO:0044275	0.00671922984530893	17.8238213399504	0.123313265517957	2	54	cellular carbohydrate catabolic process
GO:0045638	0.00671922984530893	17.8238213399504	0.123313265517957	2	54	negative regulation of myeloid cell differentiation
GO:0050871	0.00671922984530893	17.8238213399504	0.123313265517957	2	54	positive regulation of B cell activation
GO:0009756	0.00683557664080414	225.25	0.00685073697321985	1	3	

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carbohydrate mediated signaling
GO:0015825      0.00683557664080414     225.25  0.00685073697321985     1       3
L-serine transport
GO:0021562      0.00683557664080414     225.25  0.00685073697321985     1       3
vestibulocochlear nerve development
GO:0032226      0.00683557664080414     225.25  0.00685073697321985     1       3
positive regulation of synaptic transmission, dopaminergic
GO:0033026      0.00683557664080414     225.25  0.00685073697321985     1       3
negative regulation of mast cell apoptotic process
GO:0033034      0.00683557664080414     225.25  0.00685073697321985     1       3
positive regulation of myeloid cell apoptotic process
GO:0033211      0.00683557664080414     225.25  0.00685073697321985     1       3
adiponectin-mediated signaling pathway
GO:0045715      0.00683557664080414     225.25  0.00685073697321985     1       3
negative regulation of low-density lipoprotein particle receptor biosynthetic
process
GO:0045759      0.00683557664080414     225.25  0.00685073697321985     1       3
negative regulation of action potential
GO:0046544      0.00683557664080414     225.25  0.00685073697321985     1       3
development of secondary male sexual characteristics
GO:0060084      0.00683557664080414     225.25  0.00685073697321985     1       3
synaptic transmission involved in micturition
GO:0060375      0.00683557664080414     225.25  0.00685073697321985     1       3
regulation of mast cell differentiation
GO:0070666      0.00683557664080414     225.25  0.00685073697321985     1       3
regulation of mast cell proliferation
GO:0070668      0.00683557664080414     225.25  0.00685073697321985     1       3
positive regulation of mast cell proliferation
GO:0071639      0.00683557664080414     225.25  0.00685073697321985     1       3
positive regulation of monocyte chemotactic protein-1 production
GO:0072244      0.00683557664080414     225.25  0.00685073697321985     1       3
metanephric glomerular epithelium development
GO:0072248      0.00683557664080414     225.25  0.00685073697321985     1       3
metanephric glomerular visceral epithelial cell differentiation
GO:0072249      0.00683557664080414     225.25  0.00685073697321985     1       3
metanephric glomerular visceral epithelial cell development
GO:0072312      0.00683557664080414     225.25  0.00685073697321985     1       3
metanephric glomerular epithelial cell differentiation
GO:0072313      0.00683557664080414     225.25  0.00685073697321985     1       3
metanephric glomerular epithelial cell development
GO:1901164      0.00683557664080414     225.25  0.00685073697321985     1       3
negative regulation of trophoblast cell migration
GO:2000467      0.00683557664080414     225.25  0.00685073697321985     1       3
positive regulation of glycogen (starch) synthase activity
GO:0006790      0.00695592397448554     8.43136094674556        0.392775586464605
3       172     sulfur compound metabolic process
GO:0046651      0.00695592397448554     8.43136094674556        0.392775586464605
3       172     lymphocyte proliferation
GO:0032368      0.00696287953114553     17.4863055386488        0.125596844509031
2       55      regulation of lipid transport
GO:0045639      0.00696287953114553     17.4863055386488        0.125596844509031
2       55      positive regulation of myeloid cell differentiation
GO:0032943      0.00718064994085068     8.33157894736842        0.397342744446751
3       174     mononuclear cell proliferation
GO:0030048      0.00797707204132772     16.2546689303905        0.134731160473324
2       59      actin filament-based movement
GO:0046942      0.008001113998289       8       0.413327797384264       3       181
carboxylic acid transport
GO:0070661      0.00812266346310296     7.95474860335196        0.415611376375337
3       182     leukocyte proliferation
GO:0015849      0.00824530508517664     7.91    0.417894955366411       3       183
organic acid transport
GO:0030856      0.00850766980920513     15.7014762165118        0.13929831845547
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2       61      regulation of epithelial cell differentiation
GO:0005977      0.00877878079102428     15.4387096774194        0.141581897446543
2       62      glycogen metabolic process
GO:0006096      0.00877878079102428     15.4387096774194        0.141581897446543
2       62      glycolysis
GO:0006869      0.00887497436532377     7.69351351351351        0.429312850321777
3       188     lipid transport
GO:0006073      0.00905374255208205     15.1845584346906        0.143865476437617
2       63      cellular glucan metabolic process
GO:0007588      0.00905374255208205     15.1845584346906        0.143865476437617
2       63      excretion
GO:0044042      0.00905374255208205     15.1845584346906        0.143865476437617
2       63      glucan metabolic process
GO:0000255      0.00910401697654961     150.15625       0.00913431596429313     1
4       allantoin metabolic process
GO:0001661      0.00910401697654961     150.15625       0.00913431596429313     1
4       conditioned taste aversion
GO:0006003      0.00910401697654961     150.15625       0.00913431596429313     1
4       fructose 2,6-bisphosphate metabolic process
GO:0006549      0.00910401697654961     150.15625       0.00913431596429313     1
4       isoleucine metabolic process
GO:0010694      0.00910401697654961     150.15625       0.00913431596429313     1
4       positive regulation of alkaline phosphatase activity
GO:0015793      0.00910401697654961     150.15625       0.00913431596429313     1
4       glycerol transport
GO:0021631      0.00910401697654961     150.15625       0.00913431596429313     1
4       optic nerve morphogenesis
GO:0032329      0.00910401697654961     150.15625       0.00913431596429313     1
4       serine transport
GO:0033023      0.00910401697654961     150.15625       0.00913431596429313     1
4       mast cell homeostasis
GO:0033024      0.00910401697654961     150.15625       0.00913431596429313     1
4       mast cell apoptotic process
GO:0033025      0.00910401697654961     150.15625       0.00913431596429313     1
4       regulation of mast cell apoptotic process
GO:0035788      0.00910401697654961     150.15625       0.00913431596429313     1
4       cell migration involved in metanephros development
GO:0035789      0.00910401697654961     150.15625       0.00913431596429313     1
4       metanephric mesenchymal cell migration
GO:0046449      0.00910401697654961     150.15625       0.00913431596429313     1
4       creatinine metabolic process
GO:0061450      0.00910401697654961     150.15625       0.00913431596429313     1
4       trophoblast cell migration
GO:0070662      0.00910401697654961     150.15625       0.00913431596429313     1
4       mast cell proliferation
GO:0070970      0.00910401697654961     150.15625       0.00913431596429313     1
4       interleukin-2 secretion
GO:1901163      0.00910401697654961     150.15625       0.00913431596429313     1
4       regulation of trophoblast cell migration
GO:2000589      0.00910401697654961     150.15625       0.00913431596429313     1
4       regulation of metanephric mesenchymal cell migration
GO:0048511      0.00913456471449922     7.61016042780749        0.433880008303924
3       190     rhythmic process
GO:0042102      0.00990155387085299     14.4697580645161        0.150716213410837
2       66      positive regulation of T cell proliferation
Tissue: Whole_Blood=>Nerve_Tibial       Type:   cluster
SourceGene:     CTD-2313J17.1(ENSG00000258922.1)
TargetGeneSet:  CHCHD2P6        HSPB7   CCT8P1  RP11    CHRNB2  DPT     ACVR1C
KRT8P15 GPBAR1  DES     SLC19A3 TIMP4   ADIPOQ  ADIPOQ-AS1      LVRN    PPARGC1B
MLXIPL  AQP9    LRRC37A5P       AGPAT2  C10orf71        RBP4    GPAM    ACSL5
LGALS12 RPS3AP40        MYEOV   GPD1    PPP1R1A ACACB   MYH7    PLIN1   TUSC5
STAT5A  CA4     SCN4A   CIDEA   PLIN4   PLIN5   SLC7A10 LIPE    FTCD-AS1
SULT4A1 GYG2    PFKFB1
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GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0006641	7.95965961852856e-08	34.6038647342995	0.223790741125182	6	98	triglyceride metabolic process
GO:0006639	1.07255759533129e-07	32.8087056128293	0.235208636080548	6	103	acylglycerol metabolic process
GO:0006638	1.13639611300147e-07	32.4716553287982	0.237492215071621	6	104	neutral lipid metabolic process
GO:0019216	2.24183935298213e-07	20.4888934594817	0.443014324268217	7	194	regulation of lipid metabolic process
GO:0009749	4.26731426718578e-06	24.8179611650485	0.246626531035914	5	108	response to glucose stimulus
GO:0009746	5.33018893176607e-06	23.6607142857143	0.258044425991281	5	113	response to hexose stimulus
GO:0034284	5.80925195704711e-06	23.2272727272727	0.262611583973427	5	115	response to monosaccharide stimulus
GO:0019432	6.09748631581001e-06	40.4475721323012	0.121029686526884	4	53	triglyceride biosynthetic process
GO:0046460	7.07899897634248e-06	38.8559837728195	0.125596844509031	4	55	neutral lipid biosynthetic process
GO:0046463	7.07899897634248e-06	38.8559837728195	0.125596844509031	4	55	acylglycerol biosynthetic process
GO:0010876	8.00881384652893e-06	15.1079213184476	0.490969483080756	6	215	lipid localization
GO:0009743	1.13902959533377e-05	20.0942069741282	0.301432426821673	5	132	response to carbohydrate stimulus
GO:0043434	2.01369832473102e-05	10.0821538461538	0.872327174589994	7	382	response to peptide hormone stimulus
GO:0046486	2.30751876697959e-05	12.4418093983311	0.59144695868798	6	259	glycerolipid metabolic process
GO:0006112	3.25040083304447e-05	16.0141509433962	0.374506954536018	5	164	energy reserve metabolic process
GO:0006091	4.17181105858948e-05	8.95112369815458	0.977371808179365	7	428	generation of precursor metabolites and energy
GO:0006631	4.18734110600985e-05	11.1394799054374	0.657670749429105	6	288	fatty acid metabolic process
GO:0045834	5.46501790211906e-05	22.4608150470219	0.210089267178742	4	92	positive regulation of lipid metabolic process
GO:0044262	7.06567202148421e-05	13.5163373860182	0.440730745277143	5	193	cellular carbohydrate metabolic process
GO:0006006	7.97540034018014e-05	13.1615470022206	0.45214864023251	5	198	glucose metabolic process
GO:0046889	0.00013480857295596	35.0658536585366	0.100477475607224	3	44	positive regulation of lipid biosynthetic process
GO:0019318	0.00017482274792078	11.0644104803493	0.534357483911148	5	234	hexose metabolic process
GO:0009744	0.000180239911948168	132.820276497696	0.0205522109196595	2	9	response to sucrose stimulus
GO:0034285	0.000180239911948168	132.820276497696	0.0205522109196595	2	9	response to disaccharide stimulus
GO:0055089	0.000180239911948168	132.820276497696	0.0205522109196595	2	9	fatty acid homeostasis
GO:0019915	0.000186082374057382	31.2434782608696	0.111895370562591	3	49	lipid storage
GO:0010867	0.00022497792689792	116.209677419355	0.0228357899107328	2	10	positive regulation of triglyceride biosynthetic process
GO:0032868	0.000246715170641447	10.2450838635049	0.575461905750467	5	252	response to insulin stimulus
GO:0032787	0.000257958470179801	7.88917018284107	0.915715175420386	6	401	monocarboxylic acid metabolic process
GO:0005996	0.000260608018732448	10.12	0.582312642723687	5	255	monosaccharide metabolic process
GO:0033032	0.000274580123993068	103.290322580645	0.0251193689018061	2	11	regulation of myeloid cell apoptotic process

GO:0006094	0.000307315513526828	26.1145454545455	0.13244758148225	3	58	gluconeogenesis
GO:0016024	0.000329025405415394	92.9548387096774	0.0274029478928794	2	12	CDP-diacylglycerol biosynthetic process
GO:0019319	0.000374340354630484	24.3372881355932	0.141581897446543	3	62	hexose biosynthetic process
GO:0033028	0.000388292739320376	84.4985337243402	0.0296865268839527	2	13	myeloid cell apoptotic process
GO:0046341	0.000388292739320376	84.4985337243402	0.0296865268839527	2	13	CDP-diacylglycerol metabolic process
GO:0045017	0.000418976347448355	12.94555353902	0.356238322607432	4	156	glycerolipid biosynthetic process
GO:0040014	0.000430331682137595	23.1548387096774	0.148432634419763	3	65	regulation of multicellular organism growth
GO:0046364	0.000450123790556485	22.7857142857143	0.150716213410837	3	66	monosaccharide biosynthetic process
GO:0010866	0.000452361159660209	77.4516129032258	0.031970105875026	2	14	regulation of triglyceride biosynthetic process
GO:0070293	0.000452361159660209	77.4516129032258	0.031970105875026	2	14	renal absorption
GO:0003014	0.000470491835915483	22.428125	0.15299979240191	3	67	renal system process
GO:0010906	0.000470491835915483	22.428125	0.15299979240191	3	67	regulation of glucose metabolic process
GO:0019217	0.000470491835915483	22.428125	0.15299979240191	3	67	regulation of fatty acid metabolic process
GO:0051240	0.000506655532519243	6.91363523880228	1.03902844093834	6	455	positive regulation of multicellular organismal process
GO:0090208	0.000594817723377894	66.3778801843318	0.0365372638571725	2	16	positive regulation of triglyceride metabolic process
GO:0002761	0.000605182306922169	20.4971428571429	0.16670126634835	3	73	regulation of myeloid leukocyte differentiation
GO:0015980	0.000609943471952853	8.34673604541154	0.701058750259498	5	307	energy derivation by oxidation of organic compounds
GO:0016051	0.000718327161609398	11.1614420062696	0.411044218393191	4	180	carbohydrate biosynthetic process
GO:0042104	0.000756228677422032	58.0725806451613	0.0411044218393191	2	18	positive regulation of activated T cell proliferation
GO:0010675	0.00088025103203765	17.9225	0.189537056259082	3	83	regulation of cellular carbohydrate metabolic process
GO:0042493	0.000916446693937499	7.59980578334053	0.767282541000623	5	336	response to drug
GO:0006109	0.00100918327127551	17.0642857142857	0.198671372223376	3	87	regulation of carbohydrate metabolic process
GO:0090207	0.00113525328177882	46.4451612903226	0.0502387378036122	2	22	regulation of triglyceride metabolic process
GO:0031667	0.0011718462077691	7.17755102040816	0.810670541831015	5	355	response to nutrient levels
GO:0006732	0.00118699078097754	9.70706725844998	0.470417272161096	4	206	coenzyme metabolic process
GO:0046890	0.00122405919835558	15.92	0.212372846169815	3	93	regulation of lipid biosynthetic process
GO:0001817	0.00123174727611219	7.09443099273608	0.819804857795308	5	359	regulation of cytokine production
GO:0019433	0.00124159877728433	44.2304147465438	0.0525223167946855	2	23	triglyceride catabolic process
GO:0032370	0.00124159877728433	44.2304147465438	0.0525223167946855	2	23	positive regulation of lipid transport
GO:0043029	0.00124159877728433	44.2304147465438	0.0525223167946855	2	23	T cell homeostasis
GO:0045471	0.00126245280254452	15.743956043956	0.214656425160889	3	94	response to ethanol
GO:0097305	0.00130159908001424	15.5717391304348	0.216940004151962			

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3       95      response to alcohol
GO:0008016      0.00134150364896893     15.4032258064516        0.219223583143035
3       96      regulation of heart contraction
GO:0050671      0.00134150364896893     15.4032258064516        0.219223583143035
3       96      positive regulation of lymphocyte proliferation
GO:0046006      0.00135253927893591     42.217008797654 0.0548058957857588      2
24      regulation of activated T cell proliferation
GO:0046461      0.00135253927893591     42.217008797654 0.0548058957857588      2
24      neutral lipid catabolic process
GO:0046464      0.00135253927893591     42.217008797654 0.0548058957857588      2
24      acylglycerol catabolic process
GO:0032946      0.00138217208181276     15.2382978723404        0.221507162134108
3       97      positive regulation of mononuclear cell proliferation
GO:0070665      0.00150881560490668     14.7639175257732        0.228357899107328
3       100     positive regulation of leukocyte proliferation
GO:0009991      0.00154789068584402     6.7239563385676 0.863192858625701       5
378     response to extracellular stimulus
GO:0040018      0.00158812434901315     38.6935483870968        0.0593730537679053
2       26      positive regulation of multicellular organism growth
GO:0050798      0.00158812434901315     38.6935483870968        0.0593730537679053
2       26      activated T cell proliferation
GO:0045923      0.0017127286007007      37.1432258064516        0.0616566327589786
2       27      positive regulation of fatty acid metabolic process
GO:0032844      0.00172440672777148     8.74014778325123        0.520656009964708
4       228     regulation of homeostatic process
GO:0032720      0.00184184722471557     35.712158808933 0.0639402117500519      2
28      negative regulation of tumor necrosis factor production
GO:0033865      0.00184184722471557     35.712158808933 0.0639402117500519      2
28      nucleoside bisphosphate metabolic process
GO:0001816      0.00187841568405204     6.42307692307692        0.902013701473946
5       395     cytokine production
GO:0006936      0.00204818652604451     8.32457813646368        0.545775378866514
4       239     muscle contraction
GO:0051048      0.00208751363034533     13.1275229357798        0.255760847000208
3       112     negative regulation of secretion
GO:0016042      0.00214332846222422     8.21790785279629        0.552626115839734
4       242     lipid catabolic process
GO:0051186      0.00224149476476971     8.11389326083846        0.559476852812954
4       245     cofactor metabolic process
GO:0051046      0.002282237447148       6.13182773109244        0.943118123313265
5       413     regulation of secretion
GO:0003015      0.00230708936296899     12.6592920353982        0.264895162964501
3       116     heart process
GO:0060047      0.00230708936296899     12.6592920353982        0.264895162964501
3       116     heart contraction
GO:0044057      0.00237998888247377     6.07056171983356        0.952252439277559
5       417     regulation of system process
GO:0046503      0.00240306638746981     30.941935483871 0.073074527714345       2
32      glycerolipid catabolic process
GO:0045637      0.00242205427147634     12.4373913043478        0.269462320946647
3       118     regulation of myeloid cell differentiation
GO:0002763      0.00271024518725041     29.0040322580645        0.0776416856964916
2       34      positive regulation of myeloid leukocyte differentiation
GO:0002573      0.00285223938865716     11.7180327868852        0.28544737388416
3       125     myeloid leukocyte differentiation
GO:0003012      0.00301746110844096     7.45248749670966        0.607432011625493
4       266     muscle system process
GO:0051384      0.00339833948917098     10.9907692307692        0.303716005812747
3       133     response to glucocorticoid stimulus
GO:0071375      0.0034896220308333      7.14664645699128        0.632551380527299
4       277     cellular response to peptide hormone stimulus
GO:0015909      0.00355442549303487     25.075850043592 0.089059580651858       2
39      long-chain fatty acid transport
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GO:0030049	0.00355442549303487	25.075850043592	0.089059580651858	2	39	muscle filament sliding
GO:0033275	0.00355442549303487	25.075850043592	0.089059580651858	2	39	actin-myosin filament sliding
GO:0044242	0.00369380886083433	10.6597014925373	0.31285032177704	3	137	cellular lipid catabolic process
GO:0002260	0.00373617448509086	24.4142614601019	0.0913431596429313	2	40	lymphocyte homeostasis
GO:0006637	0.00373617448509086	24.4142614601019	0.0913431596429313	2	40	acyl-CoA metabolic process
GO:0035383	0.00373617448509086	24.4142614601019	0.0913431596429313	2	40	thioester metabolic process
GO:0007565	0.00392542749391757	10.4240875912409	0.31970105875026	3	140	female pregnancy
GO:0031960	0.00408466676056487	10.2726618705036	0.324268216732406	3	142	response to corticosteroid stimulus
GO:0070252	0.00411243099306515	23.1903225806452	0.0959103176250778	2	42	actin-mediated cell contraction
GO:0050670	0.00424780202510783	10.1255319148936	0.328835374714553	3	144	regulation of lymphocyte proliferation
GO:0046888	0.00430690018207738	22.6231313926043	0.0981938966161511	2	43	negative regulation of hormone secretion
GO:0032944	0.00433083971768706	10.0535211267606	0.331118953705626	3	145	regulation of mononuclear cell proliferation
GO:0048871	0.00433083971768706	10.0535211267606	0.331118953705626	3	145	multicellular organismal homeostasis
GO:0032623	0.00450557121108316	22.0829493087558	0.100477475607224	2	44	interleukin-2 production
GO:0070663	0.00476087008678795	9.70816326530612	0.342536848660992	3	150	regulation of leukocyte proliferation
GO:0008015	0.00480145424207656	6.51320493599354	0.691924434295204	4	303	blood circulation
GO:0048545	0.00480145424207656	6.51320493599354	0.691924434295204	4	303	response to steroid hormone stimulus
GO:0003013	0.00485769549577889	6.49103448275862	0.694208013286278	4	304	circulatory system process
GO:0010565	0.0051229100949274	9.44834437086093	0.351671164625285	3	154	regulation of cellular ketone metabolic process
GO:0015850	0.00534189439482383	20.1570827489481	0.109611791571518	2	48	organic alcohol transport
GO:0016052	0.00550119277722173	9.20193548387097	0.360805480589579	3	158	carbohydrate catabolic process
GO:0001776	0.00556129065102666	19.7268359643102	0.111895370562591	2	49	leukocyte homeostasis
GO:0015908	0.00647957616206189	18.1745730550285	0.121029686526884	2	53	fatty acid transport
GO:0044275	0.00671922984530893	17.8238213399504	0.123313265517957	2	54	cellular carbohydrate catabolic process
GO:0045638	0.00671922984530893	17.8238213399504	0.123313265517957	2	54	negative regulation of myeloid cell differentiation
GO:0050871	0.00671922984530893	17.8238213399504	0.123313265517957	2	54	positive regulation of B cell activation
GO:0009756	0.00683557664080414	225.25	0.00685073697321985	1	3	carbohydrate mediated signaling
GO:0015825	0.00683557664080414	225.25	0.00685073697321985	1	3	L-serine transport
GO:0021562	0.00683557664080414	225.25	0.00685073697321985	1	3	vestibulocochlear nerve development
GO:0032226	0.00683557664080414	225.25	0.00685073697321985	1	3	positive regulation of synaptic transmission, dopaminergic
GO:0033026	0.00683557664080414	225.25	0.00685073697321985	1	3	negative regulation of mast cell apoptotic process
GO:0033034	0.00683557664080414	225.25	0.00685073697321985	1	3	

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positive regulation of myeloid cell apoptotic process
GO:0033211	0.00683557664080414	225.25	0.00685073697321985	1	3
adiponectin-mediated signaling pathway
GO:0045715	0.00683557664080414	225.25	0.00685073697321985	1	3
negative regulation of low-density lipoprotein particle receptor biosynthetic
process
GO:0045759	0.00683557664080414	225.25	0.00685073697321985	1	3
negative regulation of action potential
GO:0046544	0.00683557664080414	225.25	0.00685073697321985	1	3
development of secondary male sexual characteristics
GO:0060084	0.00683557664080414	225.25	0.00685073697321985	1	3
synaptic transmission involved in micturition
GO:0060375	0.00683557664080414	225.25	0.00685073697321985	1	3
regulation of mast cell differentiation
GO:0070666	0.00683557664080414	225.25	0.00685073697321985	1	3
regulation of mast cell proliferation
GO:0070668	0.00683557664080414	225.25	0.00685073697321985	1	3
positive regulation of mast cell proliferation
GO:0071639	0.00683557664080414	225.25	0.00685073697321985	1	3
positive regulation of monocyte chemotactic protein-1 production
GO:0072244	0.00683557664080414	225.25	0.00685073697321985	1	3
metanephric glomerular epithelium development
GO:0072248	0.00683557664080414	225.25	0.00685073697321985	1	3
metanephric glomerular visceral epithelial cell differentiation
GO:0072249	0.00683557664080414	225.25	0.00685073697321985	1	3
metanephric glomerular visceral epithelial cell development
GO:0072312	0.00683557664080414	225.25	0.00685073697321985	1	3
metanephric glomerular epithelial cell differentiation
GO:0072313	0.00683557664080414	225.25	0.00685073697321985	1	3
metanephric glomerular epithelial cell development
GO:1901164	0.00683557664080414	225.25	0.00685073697321985	1	3
negative regulation of trophoblast cell migration
GO:2000467	0.00683557664080414	225.25	0.00685073697321985	1	3
positive regulation of glycogen (starch) synthase activity
GO:0006790	0.00695592397448554	8.43136094674556	0.392775586464605
3	172	sulfur compound metabolic process
GO:0046651	0.00695592397448554	8.43136094674556	0.392775586464605
3	172	lymphocyte proliferation
GO:0032368	0.00696287953114553	17.4863055386488	0.125596844509031
2	55	regulation of lipid transport
GO:0045639	0.00696287953114553	17.4863055386488	0.125596844509031
2	55	positive regulation of myeloid cell differentiation
GO:0032943	0.00718064994085068	8.33157894736842	0.397342744446751
3	174	mononuclear cell proliferation
GO:0030048	0.00797707204132772	16.2546689303905	0.134731160473324
2	59	actin filament-based movement
GO:0046942	0.008001113998289	8	0.413327797384264	3	181
carboxylic acid transport
GO:0070661	0.00812266346310296	7.95474860335196	0.415611376375337
3	182	leukocyte proliferation
GO:0015849	0.00824530508517664	7.91	0.417894955366411	3	183
organic acid transport
GO:0030856	0.00850766980920513	15.7014762165118	0.13929831845547
2	61	regulation of epithelial cell differentiation
GO:0005977	0.00877878079102428	15.4387096774194	0.141581897446543
2	62	glycogen metabolic process
GO:0006096	0.00877878079102428	15.4387096774194	0.141581897446543
2	62	glycolysis
GO:0006869	0.00887497436532377	7.69351351351351	0.429312850321777
3	188	lipid transport
GO:0006073	0.00905374255208205	15.1845584346906	0.143865476437617
2	63	cellular glucan metabolic process
GO:0007588	0.00905374255208205	15.1845584346906	0.143865476437617
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2       63      excretion
GO:0044042      0.00905374255208205     15.1845584346906        0.143865476437617
2       63      glucan metabolic process
GO:0000255      0.00910401697654961     150.15625       0.00913431596429313     1
4       allantoin metabolic process
GO:0001661      0.00910401697654961     150.15625       0.00913431596429313     1
4       conditioned taste aversion
GO:0006003      0.00910401697654961     150.15625       0.00913431596429313     1
4       fructose 2,6-bisphosphate metabolic process
GO:0006549      0.00910401697654961     150.15625       0.00913431596429313     1
4       isoleucine metabolic process
GO:0010694      0.00910401697654961     150.15625       0.00913431596429313     1
4       positive regulation of alkaline phosphatase activity
GO:0015793      0.00910401697654961     150.15625       0.00913431596429313     1
4       glycerol transport
GO:0021631      0.00910401697654961     150.15625       0.00913431596429313     1
4       optic nerve morphogenesis
GO:0032329      0.00910401697654961     150.15625       0.00913431596429313     1
4       serine transport
GO:0033023      0.00910401697654961     150.15625       0.00913431596429313     1
4       mast cell homeostasis
GO:0033024      0.00910401697654961     150.15625       0.00913431596429313     1
4       mast cell apoptotic process
GO:0033025      0.00910401697654961     150.15625       0.00913431596429313     1
4       regulation of mast cell apoptotic process
GO:0035788      0.00910401697654961     150.15625       0.00913431596429313     1
4       cell migration involved in metanephros development
GO:0035789      0.00910401697654961     150.15625       0.00913431596429313     1
4       metanephric mesenchymal cell migration
GO:0046449      0.00910401697654961     150.15625       0.00913431596429313     1
4       creatinine metabolic process
GO:0061450      0.00910401697654961     150.15625       0.00913431596429313     1
4       trophoblast cell migration
GO:0070662      0.00910401697654961     150.15625       0.00913431596429313     1
4       mast cell proliferation
GO:0070970      0.00910401697654961     150.15625       0.00913431596429313     1
4       interleukin-2 secretion
GO:1901163      0.00910401697654961     150.15625       0.00913431596429313     1
4       regulation of trophoblast cell migration
GO:2000589      0.00910401697654961     150.15625       0.00913431596429313     1
4       regulation of metanephric mesenchymal cell migration
GO:0048511      0.00913456471449922     7.61016042780749        0.433880008303924
3       190     rhythmic process
GO:0042102      0.00990155387085299     14.4697580645161        0.150716213410837
2       66      positive regulation of T cell proliferation
Tissue: Whole_Blood=>Nerve_Tibial       Type:   asymmetric
SourceGene:     CUL4A(ENSG00000139842.10)
TargetGeneSet:  KIF17   RPL11   RPS8    CELSR2  WDR3    DISC1   UBC     EIF4G1
RPL37   CTB     RPS14   PAQR8   C7orf59 C8orf22 RPS6    RP11    PLXDC2  OGDHL
OPALIN  AFAP1L2 RPL27A  RNY4P12 PFDN5   RPS2P5  LGALS3  UACA    RPS15A  CTD
USP10   RPL13   RPS4XP17        DHX33   ALOX12  SLC4A1  ST8SIA3 RPL36   RPS19   RPS5
C20orf7 EEF1A1P34       TOP1    DGCR6L  RPS2P55 RPL39
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0000184      1.24897502355414e-21    106.02962962963 0.263511175697184       14
119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006415      3.16171307186085e-21    125.798245614035        0.201508546121376
13      91      translational termination
GO:0006414      2.26310575893594e-20    106.550915331808        0.23250986090928
13      105     translational elongation
GO:0006614      2.26310575893594e-20    106.550915331808        0.23250986090928
13      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      2.5762848558257e-20     105.397849462366        0.234724240536987
13      106     cotranslational protein targeting to membrane
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GO:0045047      2.5762848558257e-20     105.397849462366        0.234724240536987
13      106     protein targeting to ER
GO:0072599      2.5762848558257e-20     105.397849462366        0.234724240536987
13      106     establishment of protein localization to endoplasmic reticulum
GO:0006413      4.41839364815424e-20    80.4887278582931        0.336585703411529
14      152     translational initiation
GO:0070972      1.10974300524213e-19    93.2741854636592        0.261296796069476
13      118     protein localization to endoplasmic reticulum
GO:0000956      2.03667109337544e-19    71.5756272401434        0.374230157082555
14      169     nuclear-transcribed mRNA catabolic process
GO:0006402      4.28813336523965e-19    67.6050135501355        0.394159573731922
14      178     mRNA catabolic process
GO:0019080      3.06758669200438e-18    70.8058733790999        0.334371323783821
13      151     viral genome expression
GO:0019083      3.06758669200438e-18    70.8058733790999        0.334371323783821
13      151     viral transcription
GO:0006401      3.21991973746047e-18    57.9383362420012        0.453947823680022
14      205     RNA catabolic process
GO:0006612      3.65694427156894e-18    69.7845864661654        0.338800083039236
13      153     protein targeting to membrane
GO:0043624      3.65694427156894e-18    69.7845864661654        0.338800083039236
13      153     cellular protein complex disassembly
GO:0043241      5.61566052569289e-18    67.3546279491833        0.349871981177773
13      158     protein complex disassembly
GO:0034623      2.0239181888553e-17     60.5930042497548        0.385302055221092
13      174     cellular macromolecular complex disassembly
GO:0032984      2.94558056497476e-17    58.7473050095117        0.396373953359629
13      179     macromolecular complex disassembly
GO:0072594      1.65240705598338e-16    50.9683108294296        0.451733444052315
13      204     establishment of protein localization to organelle
GO:0019058      8.42480598174367e-16    44.5709802028006        0.511521694000415
13      231     viral infectious cycle
GO:0022415      3.93172573517223e-15    39.2576177285319        0.575738703203931
13      260     viral reproductive process
GO:0071845      1.23449504183135e-14    35.7203340454457        0.628883814268909
13      284     cellular component disassembly at cellular level
GO:0022411      1.47911356394452e-14    35.1908133971292        0.637741332779738
13      288     cellular component disassembly
GO:0033365      3.68090591887531e-13    23.6552892762043        1.04740156390561
14      473     protein localization to organelle
GO:0006605      3.78839596302438e-13    23.6021739130435        1.04961594353332
14      474     protein targeting
GO:0016032      4.54313354767063e-12    21.8400624849796        0.998685212096049
13      451     viral reproduction
GO:0042274      5.92798374568652e-08    146.989795918367        0.0398588332987337
4       18      ribosomal small subunit biogenesis
GO:0006364      3.02375370973492e-06    26.7863823419379        0.230295481281572
5       104     rRNA processing
GO:0016072      3.98675482202562e-06    25.2451499118166        0.243581759047817
5       110     rRNA metabolic process
GO:0022613      8.60790909856727e-06    14.9631190727081        0.498235416234171
6       225     ribonucleoprotein complex biogenesis
GO:0071843      1.21469877748305e-05    14.0501815780786        0.529236731022075
6       239     cellular component biogenesis at cellular level
GO:0042254      1.75278236072245e-05    18.3577674897119        0.329942564528406
5       149     ribosome biogenesis
GO:0000028      7.08649346705689e-05    240.25  0.0132862777662446      2       6
ribosomal small subunit assembly
GO:0034470      7.17649374984581e-05    13.5080721747388        0.442875925541485
5       200     ncRNA processing
GO:0030490      9.90736496479359e-05    192.186666666667        0.015500657393952
2       7       maturation of SSU-rRNA
GO:0034660      0.000374834957853287    9.35119047619048        0.631098193896616
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5       285     ncRNA metabolic process
GO:0042255      0.000559129016773945    68.5952380952381        0.0354300740433188
2       16      ribosome assembly
GO:0022618      0.00118890525093476     16.109820089955 0.210366064632205       3
95      ribonucleoprotein complex assembly
GO:0071826      0.00137853377482935     15.2740846071809        0.221437962770743
3       100     ribonucleoprotein complex subunit organization
GO:0009311      0.00270053835413189     29.0626262626263        0.0775032869697599
2       35      oligosaccharide metabolic process
GO:0042770      0.00359380637828664     10.7842939843947        0.310013147879039
3       140     signal transduction in response to DNA damage
GO:0006417      0.00722953372170327     8.32378725891292        0.398588332987337
3       180     regulation of translation
GO:0009313      0.00882905451161087     155.010752688172        0.0088575185108297
1       4       oligosaccharide catabolic process
GO:0042058      0.00905849143105096     15.1915343915344        0.143934675800983
2       65      regulation of epidermal growth factor receptor signaling pathway
GO:1901184      0.00905849143105096     15.1915343915344        0.143934675800983
2       65      regulation of ERBB signaling pathway
Tissue: Whole_Blood=>Nerve_Tibial       Type:   cluster
SourceGene:     ENSG00000215692.2
TargetGeneSet:  MMEL1   RHD     MRPS21  ILF2    LAMTOR2 TOR1AIP1        CYB5R1
MRPL33  TXNDC9  CCDC115 NIF3L1  GPBAR1  SLC19A3 NEU4    ABHD5   GLT8D1  SPCS1   ATG3
COPS4   CCRN4L  PDCD6   CTD     HINT1   UQCRQ   UBE2D2  COX7A2  HMGN3   RSPH4A
PSMB1   NDUFA5  RP11    DCTN3   ATP5C1  NDUFB8  NDUFS3  MRPL16  POLR2G  NDUFA9  POMP
ACTR10  ERH     GTF2A2  COX5A   IMP3    WDR61   PSMA4   MRPL28  NDUFB10 MT1A
C17orf75        MAPT    NT5C    MYL12B  CIDEA   C19orf10        C19orf70
NR2F6   LIPE    PFDN4   ATP5J   RP13    SLC25A14
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022904      7.14548993627377e-11    32.8965517241379        0.358729499688603
9       96      respiratory electron transport chain
GO:0045333      1.00921237123601e-10    24.5609504132231        0.530620718289392
10      142     cellular respiration
GO:0022900      1.44440940593033e-09    22.8352 0.500726593315342       9       134
electron transport chain
GO:0015980      1.41230806753552e-08    12.1865964802011        1.14718704587918
11      307     energy derivation by oxidation of organic compounds
GO:0006119      7.13260775497814e-08    34.4831730769231        0.216732406061864
6       58      oxidative phosphorylation
GO:0006120      2.08094257316656e-07    47.2876892692561        0.134523562383226
5       36      mitochondrial electron transport, NADH to ubiquinone
GO:0006091      4.11010024982092e-07    8.57620880040154        1.59933568611169
11      428     generation of precursor metabolites and energy
GO:0042773      8.20775950669017e-07    34.8760932944606        0.175627984222545
5       47      ATP synthesis coupled electron transport
GO:0042775      8.20775950669017e-07    34.8760932944606        0.175627984222545
5       47      mitochondrial ATP synthesis coupled electron transport
GO:0010889      0.000485187089209365    79.0659340659341        0.0336308905958065
2       9       regulation of sequestering of triglyceride
GO:0030730      0.000883135281802382    55.3346153846154        0.0448411874610754
2       12      sequestering of triglyceride
GO:0042776      0.00104120748370045     50.3006993006993        0.0485779530828316
2       13      mitochondrial ATP synthesis coupled proton transport
GO:0015985      0.00201806400550782     34.5697115384615        0.067261781191613
2       18      energy coupled proton transport, down electrochemical gradient
GO:0015986      0.00201806400550782     34.5697115384615        0.067261781191613
2       18      ATP synthesis coupled proton transport
GO:0006368      0.00285995989622136     11.5423045930701        0.283994187253477
3       76      transcription elongation from RNA polymerase II promoter
GO:0019433      0.00329739848003617     26.3296703296703        0.0859456093003944
2       23      triglyceride catabolic process
GO:0046461      0.00358857698598804     25.1311188811189        0.0896823749221507
2       24      neutral lipid catabolic process
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GO:0046464      0.00358857698598804     25.1311188811189        0.0896823749221507
2       24      acylglycerol catabolic process
GO:0010883      0.00594578868574476     19.0557029177719        0.115839734274445
2       31      regulation of lipid storage
GO:0046503      0.00632706927272287     18.4192307692308        0.119576499896201
2       32      glycerolipid catabolic process
GO:0006839      0.00688407507148582     8.32615026208503        0.388623624662653
3       104     mitochondrial transport
GO:0006213      0.00712218686936403     17.265625       0.127050031139714       2
34      pyrimidine nucleoside metabolic process
GO:0006354      0.00763737610691479     8.00672268907563        0.403570687149678
3       108     DNA-dependent transcription, elongation
GO:0050994      0.0097620332936343      14.5334008097166        0.149470624870251
2       40      regulation of lipid catabolic process
Tissue: Whole_Blood=>Nerve_Tibial       Type:   asymmetric
SourceGene:     ENSG00000223427.1
TargetGeneSet:  RPL11   BEND5   RP11    RPS3A   RPL37   RPS14   RP1     RPL7
RPL30   SLC25A16        RP3     C12orf57        ESYT1   LINC00284       RPS15A
FAM195B PLAUR   RPS9
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      2.2645856743272e-15     276.722891566265        0.0818628468618089
8       91      translational termination
GO:0006414      7.39737806616546e-15    236.552577319588        0.0944571309943949
8       105     translational elongation
GO:0006614      7.39737806616546e-15    236.552577319588        0.0944571309943949
8       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      7.99876945837285e-15    234.122448979592        0.095356722718151
8       106     cotranslational protein targeting to membrane
GO:0045047      7.99876945837285e-15    234.122448979592        0.095356722718151
8       106     protein targeting to ER
GO:0072599      7.99876945837285e-15    234.122448979592        0.095356722718151
8       106     establishment of protein localization to endoplasmic reticulum
GO:0070972      1.93301394887444e-14    208.407272727273        0.106151823403225
8       118     protein localization to endoplasmic reticulum
GO:0000184      2.07168843987525e-14    206.515315315315        0.107051415126981
8       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      1.45197876836852e-13    159.944055944056        0.135838350287177
8       151     viral genome expression
GO:0019083      1.45197876836852e-13    159.944055944056        0.135838350287177
8       151     viral transcription
GO:0006413      1.53216865161122e-13    158.822222222222        0.136737942010934
8       152     translational initiation
GO:0006612      1.61620037654147e-13    157.715862068966        0.13763753373469
8       153     protein targeting to membrane
GO:0043624      1.61620037654147e-13    157.715862068966        0.13763753373469
8       153     cellular protein complex disassembly
GO:0043241      2.09964281985463e-13    152.405333333333        0.14213549235347
8       158     protein complex disassembly
GO:0000956      3.62799703186586e-13    141.883229813665        0.152031001314788
8       169     nuclear-transcribed mRNA catabolic process
GO:0034623      4.59644970334229e-13    137.561445783133        0.156528959933569
8       174     cellular macromolecular complex disassembly
GO:0006402      5.52669097790648e-13    134.287058823529        0.160127326828593
8       178     mRNA catabolic process
GO:0032984      5.78345150665467e-13    133.492397660819        0.161026918552349
8       179     macromolecular complex disassembly
GO:0072594      1.66562301569108e-12    116.261224489796        0.183516711646253
8       204     establishment of protein localization to organelle
GO:0006401      1.73272298658867e-12    115.662944162437        0.184416303370009
8       205     RNA catabolic process
GO:0019058      4.53847616254241e-12    101.991031390135        0.207805688187669
8       231     viral infectious cycle
GO:0022415      1.17453174807e-11       90.0698412698413        0.233893848176597
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8       260     viral reproductive process
GO:0071845      2.3844783469826e-11     82.0985507246377        0.255484049546744
8       284     cellular component disassembly at cellular level
GO:0022411      2.66715589585514e-11    80.9028571428571        0.259082416441769
8       288     cellular component disassembly
GO:0016032      9.49610229002725e-10    50.5462753950339        0.40571586741402
8       451     viral reproduction
GO:0033365      1.38442515114239e-09    48.0791397849462        0.425506885336655
8       473     protein localization to organelle
GO:0006605      1.40774668848207e-09    47.9725321888412        0.426406477060411
8       474     protein targeting
GO:0022613      3.66390468420667e-05    28.5912518853695        0.202408137845132
4       225     ribonucleoprotein complex biogenesis
GO:0071843      4.63911088316707e-05    26.8614657210402        0.215002421977718
4       239     cellular component biogenesis at cellular level
GO:0042273      4.90566804345865e-05    262.327272727273        0.0107951006850737
2       12      ribosomal large subunit biogenesis
GO:0006364      9.82729892449382e-05    42.5851485148515        0.0935575392706387
3       104     rRNA processing
GO:0016072      0.000116104888066178    40.1803738317757        0.0989550896131756
3       110     rRNA metabolic process
GO:0042254      0.000284810388586126    29.3671232876712        0.134039166839665
3       149     ribosome biogenesis
GO:0034470      0.000674215310389172    21.6868020304569        0.179918344751228
3       200     ncRNA processing
GO:0034660      0.00187474148387098     15.0595744680851        0.2563836412705 3
285     ncRNA metabolic process
GO:0035845      0.00269653454263397     601.5   0.00269877517126842     1       3
photoreceptor cell outer segment organization
GO:0022618      0.00318190779670647     28.0449657869013        0.0854612137568334
2       95      ribonucleoprotein complex assembly
GO:0071826      0.00351860284161307     26.6048237476809        0.0899591723756141
2       100     ribonucleoprotein complex subunit organization
GO:0000028      0.00538635572456225     240.55  0.00539755034253685     1       6
ribosomal small subunit assembly
GO:0000244      0.00538635572456225     240.55  0.00539755034253685     1       6
assembly of spliceosomal tri-snRNP
GO:0046548      0.00538635572456225     240.55  0.00539755034253685     1       6
retinal rod cell development
GO:0016255      0.00628147357680053     200.444444444444        0.00629714206629299
1       7       attachment of GPI anchor to protein
GO:0030490      0.00628147357680053     200.444444444444        0.00629714206629299
1       7       maturation of SSU-rRNA
GO:0042670      0.00717584776978741     171.797619047619        0.00719673379004913
1       8       retinal cone cell differentiation
GO:0046549      0.00717584776978741     171.797619047619        0.00719673379004913
1       8       retinal cone cell development
GO:0035082      0.00806947886990461     150.3125        0.00809632551380527     1
9       axoneme assembly
GO:0007603      0.00985451405509652     120.233333333333        0.00989550896131756
1       11      phototransduction, visible light
GO:0015939      0.00985451405509652     120.233333333333        0.00989550896131756
1       11      pantothenate metabolic process
Tissue: Whole_Blood=>Nerve_Tibial       Type:   asymmetric
SourceGene:     ENSG00000239868.1
TargetGeneSet:  RPL11   PTP4A2  SPATA1  PKP4    STXBP5L RPL37   RPS14   RPL30   RPS6
MLLT3   FAU     SSH3    RP11    BRCA1   TEN1    H2AFB1  TSPY2
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      1.52134492269554e-10    126.635294117647        0.0881599889281019
6       91      translational termination
GO:0006414      3.64866860971662e-10    108.621212121212        0.10172306414781
6       105     translational elongation
GO:0006614      3.64866860971662e-10    108.621212121212        0.10172306414781
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6       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      3.86574351311955e-10    107.5275        0.102691855234932       6
106     cotranslational protein targeting to membrane
GO:0045047      3.86574351311955e-10    107.5275        0.102691855234932       6
106     protein targeting to ER
GO:0072599      3.86574351311955e-10    107.5275        0.102691855234932       6
106     establishment of protein localization to endoplasmic reticulum
GO:0070972      7.4244611047915e-10     95.9263392857143        0.114317348280396
6       118     protein localization to endoplasmic reticulum
GO:0000184      7.81494755081527e-10    95.070796460177 0.115286139367518       6
119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      3.30213632810986e-09    73.9241379310345        0.146287454155422
6       151     viral genome expression
GO:0019083      3.30213632810986e-09    73.9241379310345        0.146287454155422
6       151     viral transcription
GO:0006413      3.43619654365752e-09    73.4126712328767        0.147256245242544
6       152     translational initiation
GO:0006612      3.57473907535994e-09    72.9081632653061        0.148225036329666
6       153     protein targeting to membrane
GO:0043624      3.57473907535994e-09    72.9081632653061        0.148225036329666
6       153     cellular protein complex disassembly
GO:0043241      4.33889801528491e-09    70.4851973684211        0.153068991765276
6       158     protein complex disassembly
GO:0000956      6.50453295792254e-09    65.6779141104294        0.163725693723618
6       169     nuclear-transcribed mRNA catabolic process
GO:0034623      7.74967672713448e-09    63.7008928571429        0.168569649159228
6       174     cellular macromolecular complex disassembly
GO:0006402      8.88250406825206e-09    62.2020348837209        0.172444813507716
6       178     mRNA catabolic process
GO:0032984      9.18616671947224e-09    61.8381502890173        0.173413604594838
6       179     macromolecular complex disassembly
GO:0072594      2.00974441671439e-08    53.9356060606061        0.197633381772888
6       204     establishment of protein localization to organelle
GO:0006401      2.06934699435073e-08    53.6608040201005        0.19860217286001
6       205     RNA catabolic process
GO:0019058      4.21891608217816e-08    47.3733333333333        0.223790741125182
6       231     viral infectious cycle
GO:0022415      8.521368995048e-08      41.878937007874 0.25188568265172        6
260     viral reproductive process
GO:0071845      1.43783632651427e-07    38.1987410071942        0.275136668742648
6       284     cellular component disassembly at cellular level
GO:0022411      1.56185396868913e-07    37.6462765957447        0.279011833091136
6       288     cellular component disassembly
GO:0016032      2.16953986617778e-06    23.5820224719101        0.436924780292021
6       451     viral reproduction
GO:0033365      2.86094470380534e-06    22.4357601713062        0.458238184208705
6       473     protein localization to organelle
GO:0006605      2.89621490432341e-06    22.3862179487179        0.459206975295827
6       474     protein targeting
GO:0000028      1.30447221048509e-05    601.375 0.00581274652273199     2       6
ribosomal small subunit assembly
GO:0022613      5.06695558328355e-05    25.7303167420814        0.21797799460245
4       225     ribonucleoprotein complex biogenesis
GO:0071843      6.41061779079662e-05    24.1736170212766        0.231541069822158
4       239     cellular component biogenesis at cellular level
GO:0022618      9.50589881477697e-05    42.5247035573123        0.0920351532765899
3       95      ribonucleoprotein complex assembly
GO:0042255      0.000103781500201939    171.702380952381        0.015500657393952
2       16      ribosome assembly
GO:0071826      0.000110733184868375    40.3186504217432        0.0968791087121998
3       100     ribonucleoprotein complex subunit organization
GO:0006364      0.000124420910820782    38.7110711071107        0.100754273060688
3       104     rRNA processing
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GO:0042274	0.000132174965241725	150.21875	0.017438239568196	2	18	ribosomal small subunit biogenesis
GO:0016072	0.000146951707561641	36.5250637213254	0.10656701958342	3	110	rRNA metabolic process
GO:0042254	0.000359751295570921	26.6955168119552	0.144349871981178	3	149	ribosome biogenesis
GO:0034470	0.000849373375463598	19.713890170743	0.1937582174244	3	200	ncRNA processing
GO:0034660	0.00235143837695017	13.6895551257253	0.27610545982977	3	285	ncRNA metabolic process
GO:0090240	0.00290375925494735	555.192307692308	0.002906373261366	1	3	positive regulation of histone H4 acetylation
GO:2000052	0.00290375925494735	555.192307692308	0.002906373261366	1	3	positive regulation of non-canonical Wnt receptor signaling pathway
GO:0070925	0.00354549173861422	26.2747252747253	0.0900975711023459	2	93	organelle assembly
GO:0034770	0.00386993778280076	370.102564102564	0.00387516434848799	1	4	histone H4-K20 methylation
GO:0051573	0.00386993778280076	370.102564102564	0.00387516434848799	1	4	negative regulation of histone H3-K9 methylation
GO:2000095	0.00386993778280076	370.102564102564	0.00387516434848799	1	4	regulation of Wnt receptor signaling pathway, planar cell polarity pathway
GO:0006334	0.00466373673300363	22.7492063492064	0.103660646322054	2	107	nucleosome assembly
GO:0009048	0.00483524690379789	277.557692307692	0.00484395543560999	1	5	dosage compensation by inactivation of X chromosome
GO:0071680	0.00483524690379789	277.557692307692	0.00484395543560999	1	5	response to indole-3-methanol
GO:0071681	0.00483524690379789	277.557692307692	0.00484395543560999	1	5	cellular response to indole-3-methanol
GO:0090239	0.00483524690379789	277.557692307692	0.00484395543560999	1	5	regulation of histone H4 acetylation
GO:0031497	0.00554993442191808	20.7565217391304	0.113348557193274	2	117	chromatin assembly
GO:0000244	0.00579968734013603	222.030769230769	0.00581274652273199	1	6	assembly of spliceosomal tri-snRNP
GO:2000050	0.00579968734013603	222.030769230769	0.00581274652273199	1	6	regulation of non-canonical Wnt receptor signaling pathway
GO:0034728	0.00640862140835673	19.2379032258065	0.122067676977372	2	126	nucleosome organization
GO:0007506	0.00676325981346515	185.012820512821	0.00678153760985399	1	7	gonadal mesoderm development
GO:0007549	0.00676325981346515	185.012820512821	0.00678153760985399	1	7	dosage compensation
GO:0030490	0.00676325981346515	185.012820512821	0.00678153760985399	1	7	maturation of SSU-rRNA
GO:0031061	0.00676325981346515	185.012820512821	0.00678153760985399	1	7	negative regulation of histone methylation
GO:0051570	0.00676325981346515	185.012820512821	0.00678153760985399	1	7	regulation of histone H3-K9 methylation
GO:0085020	0.00676325981346515	185.012820512821	0.00678153760985399	1	7	protein K6-linked ubiquitination
GO:0065004	0.00732424844092379	17.9248120300752	0.13078679676147	2	135	protein-DNA complex assembly
GO:0006333	0.00764195344331103	17.5257352941176	0.133693170022836	2	138	chromatin assembly or disassembly
GO:0046599	0.0077259650448841	158.571428571429	0.00775032869697599	1	8	regulation of centriole replication
GO:0051571	0.0077259650448841	158.571428571429	0.00775032869697599	1	8	positive regulation of histone H3-K4 methylation
GO:0045717	0.00868780375494249	138.740384615385	0.00871911978409799	1	9	negative regulation of fatty acid biosynthetic process

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GO:0071824      0.00897436294612409     16.0912162162162        0.1453186630683 2
150     protein-DNA complex subunit organization
GO:0090068      0.0090898026421742      15.9821029082774        0.146287454155422
2       151     positive regulation of cell cycle process
GO:0006323      0.0093226970572125 5    15.7682119205298        0.148225036329666
2       153     DNA packaging
Tissue: Nerve_Tibial=>Whole_Blood       Type:   cluster
SourceGene:     ENSG00000241115.1
TargetGeneSet:  C1orf135        RP11    C1orf173        RP4-788L13.1    CELF3
HAPLN2  BCAN    KCNJ9   CNTN2   AGT     VSNL1   DPYSL5  TMEM178 CTNNA2  IGKV1-9
SCN2A   CHN1    CDK5R2  KIF1A   SLC6A1  MOBP    CAMKV   SYNPR   CADM2   GAP43
STXBP5L TF      ZIC1    SOX2-OT NAT8L   UCHL1   GABRG1  PCDH10  GRIA2   CTNND2  LIX1
SOWAHA  SLC6A7  CAMK2A  GABRB2  GABRA1  CPLX2   SNCB    MOG     GRM4    PACSIN1
BEND6   SNAP91  DGKB    ADCY1   VSTM2A  CALN1   KCND2   DPP6    PHYHIP  PENK
STMN2   GLDC    GABBR2  DBC1    USP20   GRIN1   GPR158  GAD2    OGDHL   PHYHIPL
OPALIN  LDB1    PTPN5   SLC1A2  SYT13   C11orf87        DDX25   OPCML   KCNA1
CNTN1   FAIM2   SYT1    SLC6A15 SRRM4   SYNDIG1L        CYP46A1 IGHA1   GABRA5
UNC13C  ARHGDIG ASPHD1  NDRG4   VAT1L   EFNB3   PPP1R1B GFAP    RIT2    SYT4
ST8SIA3 CNDP1   CTXN1   MAG     APLP1   SLC8A2  CACNG7  TTYH1   PEG3    CHGB
SNAP25  NNAT    SLC32A1 ZNF334  MYT1    DONSON  PCP4    HIRA    IGLC2   DERL3   PISD
PLP1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006836      3.22352373267445e-10    17.2760141093474        0.782298802851014
11      119     neurotransmitter transport
GO:0001505      7.57284467015395e-09    14.8287350338365        0.808594560930039
10      123     regulation of neurotransmitter levels
GO:0007214      8.84060676375253e-08    61.2948717948718        0.118330911355616
5       18      gamma-aminobutyric acid signaling pathway
GO:0007269      9.01340808494988e-08    16.832301797819 0.565358798699052       8
86      neurotransmitter secretion
GO:0007610      3.50225574868082e-07    5.78090354767184        3.06345581620649
15      466     behavior
GO:0007611      3.57801976966592e-07    11.276955602537 0.926925472285655       9
141     learning or memory
GO:0050890      7.54632827819174e-07    10.2565356856455        1.01238668604249
9       154     cognition
GO:0007612      7.66284453746082e-07    16.0043213828425        0.512767282541001
7       78      learning
GO:0048167      1.50178445608087e-05    12.8368539325843        0.53248910110027
6       81      regulation of synaptic plasticity
GO:0050804      1.7989914108355e-05     7.90860327412052        1.13729153691786
8       173     regulation of synaptic transmission
GO:0051969      3.14941270370074e-05    7.28286136261478        1.22932669019445
8       187     regulation of transmission of nerve impulse
GO:0031644      4.90265461726867e-05    6.81952217608473        1.30821396443153
8       199     regulation of neurological system process
GO:0003001      0.00023043956499334     4.78906900992349        2.07736488824303
9       316     generation of a signal involved in cell-cell signaling
GO:0023061      0.00023043956499334     4.78906900992349        2.07736488824303
9       316     signal release
GO:0007215      0.000251762796820982    14.6312292358804        0.308975157428552
4       47      glutamate receptor signaling pathway
GO:0001504      0.000443071924855114    23.3739130434783        0.151200608954398
3       23      neurotransmitter uptake
GO:0021782      0.000604910193909431    11.4293706293706        0.387862431665629
4       59      glial cell development
GO:0007420      0.000712119083303174    3.73838302444265        2.94512490485088
10      448     brain development
GO:0051932      0.000800324303079237    18.6926086956522        0.18407030655318
3       28      synaptic transmission, GABAergic
GO:0034220      0.000853027950025637    4.38293395675044        1.99190367448619
8       303     ion transmembrane transport
GO:0015824      0.000878974733991001    61.7247311827957        0.0460175766382949
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2       7       proline transport
GO:0008038      0.000888434997150001    17.9724080267559        0.190644246072936
3       29      neuron recognition
GO:0001508      0.000921715321858788    7.26146788990826        0.749429105252232
5       114     regulation of action potential
GO:0016079      0.0009824687037171      17.3055555555556        0.197218185592693
3       30      synaptic vesicle exocytosis
GO:0035235      0.0011669497299605      51.4336917562724        0.0525915161580513
2       8       ionotropic glutamate receptor signaling pathway
GO:0060384      0.0011669497299605      51.4336917562724        0.0525915161580513
2       8       innervation
GO:0007632      0.0014207979963508      15.0683730715288        0.223513943671718
3       34      visual behavior
GO:0007409      0.00149153115209424     3.37190082644628        3.24752612275967
10      494     axonogenesis
GO:0021692      0.00185944535970675     38.5698924731183        0.0657393951975642
2       10      cerebellar Purkinje cell layer morphogenesis
GO:0021694      0.00185944535970675     38.5698924731183        0.0657393951975642
2       10      cerebellar Purkinje cell layer formation
GO:0021702      0.00185944535970675     38.5698924731183        0.0657393951975642
2       10      cerebellar Purkinje cell differentiation
GO:0051580      0.00185944535970675     38.5698924731183        0.0657393951975642
2       10      regulation of neurotransmitter uptake
GO:0048708      0.0021190320054723      12.9710144927536        0.2563836412705 3
39      astrocyte differentiation
GO:0014002      0.00226294172378252     34.2819593787336        0.0723133347173206
2       11      astrocyte development
GO:0022010      0.00226294172378252     34.2819593787336        0.0723133347173206
2       11      central nervous system myelination
GO:0032291      0.00226294172378252     34.2819593787336        0.0723133347173206
2       11      axon ensheathment in central nervous system
GO:0019228      0.00226336961890837     7.84395604395604        0.552210919659539
4       84      regulation of action potential in neuron
GO:0048168      0.0022800120647534      12.6195652173913        0.262957580790257
3       40      regulation of neuronal synaptic plasticity
GO:0007270      0.00268139628558388     7.4683411826269 0.578506677738565       4
88      neuron-neuron synaptic transmission
GO:0043092      0.00270392915930431     30.8516129032258        0.078887274237077
2       12      L-amino acid import
GO:0042391      0.00273118996427797     4.63074070033817        1.39367517818836
6       212     regulation of membrane potential
GO:0007193      0.00280774809709358     11.670652173913 0.282679399349526       3
43      adenylate cyclase-inhibiting G-protein coupled receptor signaling pathway
GO:0051952      0.00280774809709358     11.670652173913 0.282679399349526       3
43      regulation of amine transport
GO:0043090      0.00318190779670647     28.0449657869013        0.0854612137568334
2       13      amino acid import
GO:0008306      0.00319799789027677     11.1133540372671        0.295827278389039
3       45      associative learning
GO:0048489      0.00384306604173459     10.3702898550725        0.315549096948308
3       48      synaptic vesicle transport
GO:0031344      0.00407703421607728     4.25321027287319        1.51200608954398
6       230     regulation of cell projection organization
GO:0006865      0.00455770999128027     6.39515586454362        0.670541831015155
4       102     amino acid transport
GO:0021697      0.00483286445549882     22.0307219662058        0.105183032316103
2       16      cerebellar cortex formation
GO:0021680      0.00545390522836393     20.5605734767025        0.111756971835859
2       17      cerebellar Purkinje cell layer development
GO:0051954      0.00545390522836393     20.5605734767025        0.111756971835859
2       17      positive regulation of amine transport
GO:0001662      0.00610950951902399     19.2741935483871        0.118330911355616
2       18      behavioral fear response
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GO:0060119      0.00610950951902399     19.2741935483871        0.118330911355616
2       18      inner ear receptor cell development
GO:0044057      0.0061336734011772      3.13565466655425        2.74133277973843
8       417     regulation of system process
GO:0002209      0.00679920584201408     18.1391524351676        0.124904850875372
2       19      behavioral defense response
GO:0015800      0.00679920584201408     18.1391524351676        0.124904850875372
2       19      acidic amino acid transport
GO:0015804      0.00679920584201408     18.1391524351676        0.124904850875372
2       19      neutral amino acid transport
GO:0021533      0.00679920584201408     18.1391524351676        0.124904850875372
2       19      cell differentiation in hindbrain
GO:0007616      0.00752252730331821     17.1302270011947        0.131478790395128
2       20      long-term memory
GO:0021696      0.00752252730331821     17.1302270011947        0.131478790395128
2       20      cerebellar cortex morphogenesis
GO:0010975      0.00797003349712608     4.302671523983  1.23590062971421        5
188     regulation of neuron projection development
GO:0015807      0.008279011561416       16.2275042444822        0.138052729914885
2       21      L-amino acid transport
GO:0010001      0.00902158742785589     5.21465201465201        0.815168500449796
4       124     glial cell differentiation
GO:0042596      0.00906820078863467     15.4150537634409        0.144626669434641
2       22      fear response
GO:0031345      0.00973198144254681     7.28192934782609        0.44045394782368
3       67      negative regulation of cell projection organization
Tissue: Whole_Blood=>Nerve_Tibial       Type:   asymmetric
SourceGene:     FAM184B(ENSG00000047662.4)
TargetGeneSet:  RP11    RPS8    CTB     RP4     SEMA4A  CREG1   RABGAP1L
IVNS1ABP        PLXNA2  XIRP2   KCTD18  RPL15   ZDHHC3  RPL29   NDUFB5  EXOC3
HNRNPAB RPL15P3 HEBP2   PPP1R35 CCT8L1P DNAJB6  ADAMDEC1        VCPIP1  POP1    MPDZ
GHITM   C10orf129       OR52N4  EIF3F   RPL27A  ALKBH3  VWA5A   SIAE    SNX19
H2AFJ   RPL18AP3        RPLP0   LGALS3  TIMM9   POMT2   CTD     SLC7A5  RYKP1
C17orf103       TCAP    SUPT4H1 KPNA2   CDR2L   RPL36   RPS19   FTL     C19orf76
ZNF350  RPS5    FTLP3   PLTP    RPL10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      9.45543999605251e-12    42.4874752801582        0.289668535049478
9       91      translational termination
GO:0019080      3.39485264796329e-11    28.1008668242711        0.480658777939243
10      151     viral genome expression
GO:0019083      3.39485264796329e-11    28.1008668242711        0.480658777939243
10      151     viral transcription
GO:0006414      3.50962897900514e-11    36.2559121621622        0.334232925057089
9       105     translational elongation
GO:0006614      3.50962897900514e-11    36.2559121621622        0.334232925057089
9       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006413      3.62563997705517e-11    27.9010172143975        0.483841948654072
10      152     translational initiation
GO:0006613      3.82638812841948e-11    35.8796322095291        0.337416095771919
9       106     cotranslational protein targeting to membrane
GO:0045047      3.82638812841948e-11    35.8796322095291        0.337416095771919
9       106     protein targeting to ER
GO:0072599      3.82638812841948e-11    35.8796322095291        0.337416095771919
9       106     establishment of protein localization to endoplasmic reticulum
GO:0006612      3.87033476992069e-11    27.7039627039627        0.487025119368902
10      153     protein targeting to membrane
GO:0070972      1.01321662815343e-10    31.9028018844533        0.375614144349872
9       118     protein localization to endoplasmic reticulum
GO:0000184      1.09357799215139e-10    31.6105651105651        0.378797315064701
9       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0072594      6.60160849558824e-10    20.3479381443299        0.649366825825202
10      204     establishment of protein localization to organelle
GO:0006401      6.92428979245824e-10    20.2421652421652        0.652549996540032
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10      205     RNA catabolic process
GO:0043624      1.04085252522312e-09    24.089527027027 0.487025119368902       9
153     cellular protein complex disassembly
GO:0043241      1.38482698952076e-09    23.2729911119173        0.502940972943049
9       158     protein complex disassembly
GO:0019058      2.20880145392951e-09    17.8280542986425        0.735312435125597
10      231     viral infectious cycle
GO:0000956      2.51212482621704e-09    21.65625        0.537955850806173       9
169     nuclear-transcribed mRNA catabolic process
GO:0034623      3.24869864435553e-09    20.992628992629 0.55387170438032        9
174     cellular macromolecular complex disassembly
GO:0006402      3.96822887559517e-09    20.4900047976971        0.566604387239637
9       178     mRNA catabolic process
GO:0032984      4.16861405576208e-09    20.3680445151033        0.569787557954467
9       179     macromolecular complex disassembly
GO:0022415      6.89585216681102e-09    15.7277777777778        0.82762438585565
10      260     viral reproductive process
GO:0006605      1.90497117833022e-08    10.6516424751719        1.50882291882915
12      474     protein targeting
GO:0033365      1.94678745871024e-07    9.48503401360544        1.50563974811432
11      473     protein localization to organelle
GO:0071845      2.24471404131612e-07    12.4982800982801        0.904020483011556
9       284     cellular component disassembly at cellular level
GO:0022411      2.5267118288185e-07     12.3156059285092        0.916753165870874
9       288     cellular component disassembly
GO:0016032      1.18043890244333e-06    8.79566641471403        1.43560999238807
10      451     viral reproduction
GO:0071526      0.00115623520727482     46.724025974026 0.0509307314372708      2
16      semaphorin-plexin signaling pathway
GO:0042274      0.00146823796056917     40.8778409090909        0.0572970728669296
2       18      ribosomal small subunit biogenesis
GO:0022613      0.00559728734870538     6.11247575953458        0.71621341083662
4       225     ribonucleoprotein complex biogenesis
GO:0071843      0.00691069135170613     5.74265450861196        0.760777800844232
4       239     cellular component biogenesis at cellular level
GO:0016056      0.00951980336629987     160.033333333333        0.00954951214448827
1       3       rhodopsin mediated signaling pathway
GO:0030241      0.00951980336629987     160.033333333333        0.00954951214448827
1       3       skeletal muscle myosin thick filament assembly
GO:0031034      0.00951980336629987     160.033333333333        0.00954951214448827
1       3       myosin filament assembly
GO:0035511      0.00951980336629987     160.033333333333        0.00954951214448827
1       3       oxidative DNA demethylation
GO:0048769      0.00951980336629987     160.033333333333        0.00954951214448827
1       3       sarcomerogenesis
GO:0071688      0.00951980336629987     160.033333333333        0.00954951214448827
1       3       striated muscle myosin thick filament assembly
Tissue: Whole_Blood=>Nerve_Tibial       Type:   cluster
SourceGene:     GCHFR(ENSG00000137880.4)
TargetGeneSet:  ZCCHC17 UQCRH   RBBP5   TTC32   NFU1    TEX261  RANBP2  MZT2B
UBE2E3  KCTD18  SLC23A3 TPRXL   UBE2E1  QARS    FAM194A EIF4G1  RP11    CEP135
SDAD1   CTD     PRRC2A  C6orf226        C7orf59 PPP1R35 PUS7    NOM1    C8orf59
COX6C   SPAG1   CTHRC1  CCL19   MSANTD3 RALGAPA1P       FAM208B RRP12   PPRC1
NOLC1   NUP98   FXC1    EIF3F   RPL27A  ALKBH3  MRPL16  GANAB   FAU     CNIH2
DPAGT1  TBCEL   ZCRB1   MARCH9  PXN     RLIMP1  LPAR6   OGFOD1P1        DIAPH3
RPS19P3 RPS29   GSTZ1   IFI27L1 IFI27   SRP14   MGA     NDUFB10 MIR4519 NAE1
COX4I1  RP13    MYBBP1A RPAIN   LIG3    USP36   NFIC    RPL36   ZNF85   RPS19
ROMO1   KRT18P4 RAB22A  BTG3    URB1    CBR3    BCR     RP3     TIMP1   SSR4    DKC1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0033365      1.20134575662999e-07    7.71743393009378        2.09480312781122
13      473     protein localization to organelle
GO:0006605      1.23108498008295e-07    7.70014035983157        2.09923188706664
13      474     protein targeting
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GO:0006612	3.52145543466475e-07	14.0315270935961	0.677600166078472	8	153	protein targeting to membrane
GO:0006614	3.86324505995467e-07	17.906015037594	0.465019721818559	7	105	SRP-dependent cotranslational protein targeting to membrane
GO:0006613	4.12211475722716e-07	17.7239057239057	0.469448481073974	7	106	cotranslational protein targeting to membrane
GO:0045047	4.12211475722716e-07	17.7239057239057	0.469448481073974	7	106	protein targeting to ER
GO:0072599	4.12211475722716e-07	17.7239057239057	0.469448481073974	7	106	establishment of protein localization to endoplasmic reticulum
GO:0070972	8.55506659094507e-07	15.7945313734787	0.522593592138952	7	118	protein localization to endoplasmic reticulum
GO:0072594	3.09035552486539e-06	10.3432944606414	0.903466888104629	8	204	establishment of protein localization to organelle
GO:0006413	4.66368805778185e-06	12.0621899576528	0.673171406823057	7	152	translational initiation
GO:0006414	6.7893325699112e-06	14.9299895506792	0.465019721818559	6	105	translational elongation
GO:0000184	1.39505800833643e-05	13.0674397314617	0.527022351394367	6	119	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006415	5.04180280683979e-05	14.0924320063067	0.403017092242751	5	91	translational termination
GO:0000956	0.000100130385091518	9.02729003596361	0.74846031416511	6	169	nuclear-transcribed mRNA catabolic process
GO:0006402	0.000133143355828662	8.54951884522855	0.788319147463843	6	178	mRNA catabolic process
GO:0006401	0.000286379882659833	7.37549818055796	0.907895647360044	6	205	RNA catabolic process
GO:0019080	0.000541196550747747	8.26619456698398	0.668742647567642	5	151	viral genome expression
GO:0019083	0.000541196550747747	8.26619456698398	0.668742647567642	5	151	viral transcription
GO:0043624	0.000574604898230805	8.15334402198809	0.677600166078472	5	153	cellular protein complex disassembly
GO:0043241	0.000664906819794072	7.88412540157306	0.699743962355546	5	158	protein complex disassembly
GO:0022904	0.000856585958792658	10.3586956521739	0.425160888519826	4	96	respiratory electron transport chain
GO:0034623	0.00102631382156598	7.12967606057567	0.770604110442184	5	174	cellular macromolecular complex disassembly
GO:0017038	0.00108468856513763	5.66519647153168	1.16919244342952	6	264	protein import
GO:0032984	0.00116456552965098	6.92236508864212	0.792747906719258	5	179	macromolecular complex disassembly
GO:0006260	0.00117194164689777	5.57712555935773	1.18690748045118	6	268	DNA replication
GO:0071845	0.00157605540551523	5.25018605805011	1.25776762853782	6	284	cellular component disassembly at cellular level
GO:0022411	0.00169194020664487	5.17424798239178	1.27548266555948	6	288	cellular component disassembly
GO:0006606	0.00170061809690906	6.33229259589652	0.863608054805896	5	195	protein import into nucleus
GO:0051170	0.00181844717923496	6.23254588565908	0.87689433257214	5	198	nuclear import
GO:0001522	0.00251577557013646	30.9075268817204	0.0752889073420525	2	17	pseudouridine synthesis
GO:0006913	0.00278049316678448	4.66677718832891	1.40834544322192	6	318	nucleocytoplasmic transport
GO:0051169	0.00291287820909797	4.62134646962233	1.42163172098817	6	321	nuclear transport
GO:0022900	0.00292135387194807	7.31128205128205	0.59345374022559	4	134	electron transport chain
GO:0034504	0.00298785610276722	5.53385925173787	0.983184554702097			

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5       222     protein localization to nucleus
GO:0022613      0.00316502475062341     5.45724191063174        0.996470832468341
5       225     ribonucleoprotein complex biogenesis
GO:0019058      0.00354197520513652     5.31010949452527        1.02304338800083
5       231     viral infectious cycle
GO:0045333      0.0035975749800384      6.88357487922705        0.628883814268909
4       142     cellular respiration
GO:0016032      0.00368654062782827     3.85652758021179        1.9973704241921 7
451     viral reproduction
GO:0071843      0.00409356502531015     5.12566999855135        1.05847346204415
5       239     cellular component biogenesis at cellular level
GO:0042254      0.00427061379286768     6.54804597701149        0.659885129056813
4       149     ribosome biogenesis
GO:0022415      0.00583111270544326     4.69657693585909        1.15147740640786
5       260     viral reproductive process
GO:0034660      0.00851298648710429     4.26967312348668        1.26219638779323
5       285     ncRNA metabolic process
Tissue: Whole_Blood=>Nerve_Tibial       Type:   cluster
SourceGene:     MTND2P28(ENSG00000225630.1)
TargetGeneSet:  MTND1P23        ZNF593  RP11    WASF2   LSM10   MACF1   LEPRE1  EVI5
PBXIP1  TKT     PRRC2C  TOR1AIP1        OR11L1  TSSC1   EPT1    C1D     GMCL1
PRADC1  MOGS    REG1B   REG1A   REG3A   C2orf55 EIF5B   SCN9A   UBE2V1  UBE2E3
FBXO36  CRTAP   SEC22C  NDUFAF3 AMT     SEMA3B  C3orf45 PCBP4   PRICKLE2        ATG3
NDUFB4  SHOX2   PDCD10  SEC62   TNK2    RAB28   CCNI    ENOPH1  DNAJB14 AP1AR
AADAT   PDCD6   MYO10   ITGA2   SREK1IP1        FAM174A CTB     MTND5P11
HCG11   HNRNPC  MTRNR2L9        ATG5    HDAC2   SFT2D1  PSMB1   STARD3NL
PPP1R35 TRIM56  POLR2J  ARMC10  PSMC2   FAM3C   PRSS3P1 PRSS3P2 DRP2    PABPC1
PUF60   EXOSC4  NFIB    PRSS3   SPTLC1  PSMB7   RABEPK  DNM1    WDR34   GPSM1
DCLRE1C PRINS   RBP4    PGAM1   MRPL43  PNLIPRP1        TOLLIP  MTRNR2L8
PDE3B   AMBRA1  POLR2G  ANKRD13D        SPCS2   ANGPTL5 CWF19L2 SIDT2   C12orf39
TWF1    ACVR1B  RPL14P1 CPM     RAN     MPHOSPH8        MRP63   POMP    RPL13AP25
MRPL52  PSME2   PSMA3   ITPK1   SIVA1   AHNAK2  GOLGA8IP        ITGA11  ADAMTSL3
CIB1    RHBDF1  MRPL28  CCP110  ITFG1   KATNB1  ZFHX3   CTRB2   CTRB1   TMEM231
PSMB6   TXNDC17 TRAPPC1 NCOR1   ERAL1   PSMB3   STAT5A  MAPT    ATP5G1  SLC35B1
CHMP6   CTD     AATK    SNRPD1  RPRD1A  C18orf32        LMAN1   SERPINB3
WDR18   NFIC    PIN1    OLFM2   SHKBP1  IDH3B   MRPS26  ADRM1   RANBP1  CTA
ZMAT5   ATXN10  HSD17B10        RP1     DOCK11  RBMX2   PHF6    MT
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0009308      3.2300547524198e-07     7.43631578947368        1.84513182478721
12      202     amine metabolic process
GO:0051443      7.9144848636653e-07     12.4193548387097        0.749013909072037
8       82      positive regulation of ubiquitin-protein ligase activity
GO:0006521      8.17606168415014e-07    15.98128        0.520656009964708       7
57      regulation of cellular amino acid metabolic process
GO:0044106      9.11107806810204e-07    7.47727272727273        1.67157982146564
11      183     cellular amine metabolic process
GO:0051351      1.14279621976077e-06    11.7791563275434        0.785551172929209
8       86      positive regulation of ligase activity
GO:0031397      1.91496597064058e-06    10.9331797235023        0.840357068714968
8       92      negative regulation of protein ubiquitination
GO:0000209      2.16587899756182e-06    7.69080447291282        1.47062487025119
10      161     protein polyubiquitination
GO:0006977      2.24967712570452e-06    13.5349152542373        0.602864853643347
7       66      DNA damage response, signal transduction by p53 class mediator
resulting in cell cycle arrest
GO:0072413      2.24967712570452e-06    13.5349152542373        0.602864853643347
7       66      signal transduction involved in mitotic cell cycle checkpoint
GO:0072431      2.24967712570452e-06    13.5349152542373        0.602864853643347
7       66      signal transduction involved in mitotic cell cycle G1/S transition
DNA damage checkpoint
GO:0072474      2.24967712570452e-06    13.5349152542373        0.602864853643347
7       66      signal transduction involved in mitotic cell cycle G1/S checkpoint
GO:0051436      2.49319001535254e-06    13.3084 0.61199916960764        7       67
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						negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
GO:0072401	2.49319001535254e-06	13.3084	0.61199916960764	7	67	signal transduction involved in DNA integrity checkpoint
GO:0072404	2.49319001535254e-06	13.3084	0.61199916960764	7	67	signal transduction involved in G1/S transition checkpoint
GO:0072422	2.49319001535254e-06	13.3084	0.61199916960764	7	67	signal transduction involved in DNA damage checkpoint
GO:0051438	2.64597126997556e-06	10.433284457478	0.87689433257214	8	96	regulation of ubiquitin-protein ligase activity
GO:0072395	2.75833066532783e-06	13.0893114754098	0.621133485571933	7	68	signal transduction involved in cell cycle checkpoint
GO:0051340	3.60160964550797e-06	9.97685834502104	0.913431596429313	8	100	regulation of ligase activity
GO:0033238	4.06638598950683e-06	12.2803692307692	0.657670749429105	7	72	regulation of cellular amine metabolic process
GO:0051352	4.06638598950683e-06	12.2803692307692	0.657670749429105	7	72	negative regulation of ligase activity
GO:0051437	4.06638598950683e-06	12.2803692307692	0.657670749429105	7	72	positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
GO:0051444	4.06638598950683e-06	12.2803692307692	0.657670749429105	7	72	negative regulation of ubiquitin-protein ligase activity
GO:0031571	4.46375747690041e-06	12.0934545454545	0.666805065393398	7	73	mitotic cell cycle G1/S transition DNA damage checkpoint
GO:0002479	5.35595246197984e-06	11.7361176470588	0.685073697321985	7	75	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent
GO:0051439	6.9690287729351e-06	11.2378591549296	0.712476645214864	7	78	regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
GO:0000216	7.58894447175862e-06	11.081	0.721610961179157	7	79	M/G1 transition of mitotic cell cycle
GO:0042590	7.58894447175862e-06	11.081	0.721610961179157	7	79	antigen processing and presentation of exogenous peptide antigen via MHC class I
GO:0071158	8.25397729617176e-06	10.9284383561644	0.73074527714345	7	80	positive regulation of cell cycle arrest
GO:0031575	9.72969962179052e-06	10.63552	0.749013909072037	7	82	mitotic cell cycle G1/S transition checkpoint
GO:0002478	1.0545797823155e-05	10.4948421052632	0.75814822503633	7	83	antigen processing and presentation of exogenous peptide antigen
GO:0031145	1.0545797823155e-05	10.4948421052632	0.75814822503633	7	83	anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process
GO:0019884	1.2348780939804e-05	10.2243076923077	0.776416856964916	7	85	antigen processing and presentation of exogenous antigen
GO:0071779	1.33417162947446e-05	10.0941772151899	0.785551172929209	7	86	G1/S transition checkpoint
GO:0031398	2.11135326875629e-05	7.69856329628626	1.16005812746523	8	127	positive regulation of protein ubiquitination
GO:0031396	2.33881804703795e-05	6.51633686148182	1.53456508200125	9	168	regulation of protein ubiquitination
GO:0000084	3.1117553475766e-05	7.26728110599078	1.22399833921528	8	134	S phase of mitotic cell cycle
GO:0002474	3.3505884625402e-05	8.65991304347826	0.90429728046502	7	99	antigen processing and presentation of peptide antigen via MHC class I
GO:2000045	3.3505884625402e-05	8.65991304347826	0.90429728046502	7	99	regulation of G1/S transition of mitotic cell cycle
GO:0051320	4.9546107212198e-05	6.77849462365591	1.30620718289392	8	143	S phase
GO:0048002	5.86332202170577e-05	7.88324752475248	0.986506124143658	7	108	antigen processing and presentation of peptide antigen

GO:0090068	7.28366097597503e-05	6.39566884728175	1.37928171060826	8	151	positive regulation of cell cycle process
GO:0030330	9.74419026646147e-05	7.23367272727273	1.0687149678223	7	117	DNA damage response, signal transduction by p53 class mediator
GO:0072331	0.000133376112443408	6.85662068965517	1.12352086360805	7	123	signal transduction by p53 class mediator
GO:0008380	0.000183354386938273	4.08129370629371	2.95038405646668	11	323	RNA splicing
GO:0000077	0.000188178727971676	6.46321951219512	1.18746107535811	7	130	DNA damage checkpoint
GO:0031570	0.000248492339210058	6.16	1.24226697114387	7	136	DNA integrity checkpoint
GO:0007093	0.000284007391518704	6.01872727272727	1.26966991903674	7	139	mitotic cell cycle checkpoint
GO:0042770	0.000296713203023757	5.97305263157895	1.27880423500104	7	140	signal transduction in response to DNA damage
GO:0000082	0.000306677544547471	5.12540775643349	1.69898276935852	8	186	G1/S transition of mitotic cell cycle
GO:2000602	0.000399011227893075	5.6716	1.34274444675109	7	147	regulation of interphase of mitotic cell cycle
GO:0007346	0.0004637358429957	3.92379566944553	2.76769773718082	10	303	regulation of mitotic cell cycle
GO:0019882	0.000488022457234222	5.47409655172414	1.38841602657256	7	152	antigen processing and presentation
GO:0010565	0.000527778174940012	5.39885714285714	1.40668465850114	7	154	regulation of cellular ketone metabolic process
GO:0006103	0.00064857552590479	20.7892441860465	0.173552003321569	3	19	2-oxoglutarate metabolic process
GO:0006520	0.000662694940194059	3.26917647058824	3.9916960763961	12	437	cellular amino acid metabolic process
GO:0010498	0.0008253890747478	4.37686104218362	1.97301224828732	8	216	proteasomal protein catabolic process
GO:0016032	0.00087261490862344	3.16173120728929	4.1195764998962	12	451	viral reproduction
GO:0006397	0.00107896583633829	3.26405810684161	3.64459206975296	11	399	mRNA processing
GO:0070534	0.00115415851015086	16.6267441860465	0.210089267178742	3	23	protein K63-linked ubiquitination
GO:0043248	0.00168753685903514	44.0430769230769	0.0639402117500519	2	7	proteasome assembly
GO:0051329	0.00250295854651677	3.09876049580168	3.4619057504671	10	379	interphase of mitotic cell cycle
GO:0006370	0.00252543883506868	12.3100775193798	0.274029478928794	3	30	7-methylguanosine mRNA capping
GO:0000377	0.00268690710758518	4.01437563451777	1.8634004567158	7	204	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile
GO:0000398	0.00268690710758518	4.01437563451777	1.8634004567158	7	204	nuclear mRNA splicing, via spliceosome
GO:0051325	0.00290852238268156	3.03126494760186	3.53498027818144	10	387	interphase
GO:0000375	0.0030741047744301	3.91362376237624	1.90907203653726	7	209	RNA splicing, via transesterification reactions
GO:0043161	0.0030741047744301	3.91362376237624	1.90907203653726	7	209	proteasomal ubiquitin-dependent protein catabolic process
GO:0009452	0.00332683107053226	11.0767441860465	0.301432426821673	3	33	7-methylguanosine RNA capping
GO:0036260	0.00332683107053226	11.0767441860465	0.301432426821673	3	33	RNA capping
GO:0022617	0.00426786976508781	10.0676532769556	0.328835374714553	3	36	extracellular matrix disassembly
GO:0006368	0.00513762425203364	6.18359375	0.694208013286278	4	76	transcription elongation from RNA polymerase II promoter

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GO:0000460      0.00514729089384574     22.0138461538462        0.109611791571518
2       12      maturation of 5.8S rRNA
GO:0031400      0.00628679521827653     3.09920459566947        2.74029478928794
8       300     negative regulation of protein modification process
GO:0000075      0.00680008138583364     3.35618723404255        2.21050446335894
7       242     cell cycle checkpoint
GO:0031112      0.00804353459532168     16.9301775147929        0.137014739464397
2       15      positive regulation of microtubule polymerization or
depolymerization
GO:0006283      0.00849285001853911     7.72093023255814        0.420178534357484
3       46      transcription-coupled nucleotide-excision repair
GO:2000243      0.00893067385808007     5.23308823529412        0.812954120822088
4       89      positive regulation of reproductive process
GO:0032886      0.009640765345223       5.11206896551724        0.831222752750675
4       91      regulation of microtubule-based process
Tissue: Whole_Blood=>Nerve_Tibial       Type:   asymmetric
SourceGene:     NEK6(ENSG00000119408.11)
TargetGeneSet:  RNF19B  KCNQ4   OSBPL9  LPHN2   CAPZA1  VPS45   DARC    NUF2    RP11
TOMM20  TP53I3  FAM179A ACTR2   PCBP1   PKP4    CCDC141 SH3BP5  KIAA1143
WDR82P1 ALDH1L1-AS1     AFAP1   RELL1   IL8     SEPT11  TBCK    RAB33B  PTGER4
SCAMP1  POU5F2  H2AFJ   PCDHB4  ZNF165  C6orf203        GNAI1   ORAI2   THAP5
AKR1B10 SOX7    UBXN8   GPR124  LSM1    SNAI2   KIAA1432        GALT    FAM214B
RAPGEF1 ZNF438  HNRNPF  CHCHD1  EMILIN3 ZNF518A HOGA1   FAM196A SF3B2   LRP5    PGR
MSANTD4 MCAM    ESAM    PKNOX2  APPL2   WBP11   ABCD2   RACGAP1 PCBP2   SLC7A1  KL
MTRF1   EFNB2   MYH6    BATF    IRF2BPL RPS2P4  CTD     SNUPN   BLM     CDR2
TSNAXIP1        TERF2   CMIP    GALNS   ARHGAP23        C17orf98        LRRC37A3
SYNGR2  ARHGDIA FN3K    ATP8B1  POLR2E  LRG1    SEMA6B  KHSRP   HNRNPUL1
SIGLEC10        CRLS1   TSHZ2   ERG     ICOSLG  CLTCL1  CCDC116 RP1     CSF2RB
SMCR7L  CXorf36 RPSAP14 PCDH19  IDS
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0000375      1.95112202809718e-07    10.3218993518316        1.14255068853367
10      209     RNA splicing, via transesterification reactions
GO:0008380      1.36842157637575e-06    7.28978129713424        1.76576015500657
11      323     RNA splicing
GO:0006397      1.037040984638e-05      5.83020012128563        2.18123313265518
11      399     mRNA processing
GO:0000377      1.52014142646623e-05    8.14946823799943        1.11521694000415
8       204     RNA splicing, via transesterification reactions with bulged
adenosine as nucleophile
GO:0000398      1.52014142646623e-05    8.14946823799943        1.11521694000415
8       204     nuclear mRNA splicing, via spliceosome
GO:2000104      0.00187962251482867     37.3038961038961        0.0656009964708325
2       12      negative regulation of DNA-dependent DNA replication
GO:0071775      0.00221351136977795     33.9102715466352        0.0710677461767352
2       13      regulation of cell cycle cytokinesis
GO:0071777      0.00221351136977795     33.9102715466352        0.0710677461767352
2       13      positive regulation of cell cycle cytokinesis
GO:0032467      0.00295868824346752     28.6893106893107        0.0820012455885406
2       15      positive regulation of cytokinesis
GO:0090329      0.00634996031081422     18.638961038961 0.12026849352986        2
22      regulation of DNA-dependent DNA replication
GO:0060444      0.00693020683008556     17.7501546072975        0.125735243235762
2       23      branching involved in mammary gland duct morphogenesis
GO:0045600      0.00753359074695003     16.9421487603306        0.131201992941665
2       24      positive regulation of fat cell differentiation
GO:0006200      0.00800599764520436     7.83991228070175        0.410006227942703
3       75      ATP catabolic process
GO:0032465      0.00815984834055658     16.2044042913608        0.136668742647568
2       25      regulation of cytokinesis
GO:0030278      0.00816878626080113     5.3828841607565 0.792678707355892       4
145     regulation of ossification
Tissue: Whole_Blood=>Nerve_Tibial       Type:   cluster
SourceGene:     NEK6(ENSG00000119408.11)
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TargetGeneSet:  RNF19B  KCNQ4   OSBPL9  LPHN2   CAPZA1  VPS45   DARC    NUF2    RP11
TOMM20  TP53I3  FAM179A ACTR2   PCBP1   PKP4    CCDC141 SH3BP5  KIAA1143
WDR82P1 ALDH1L1-AS1     AFAP1   RELL1   IL8     SEPT11  TBCK    RAB33B  PTGER4
SCAMP1  POU5F2  H2AFJ   PCDHB4  ZNF165  C6orf203        GNAI1   ORAI2   THAP5
AKR1B10 SOX7    UBXN8   GPR124  LSM1    SNAI2   KIAA1432        GALT    FAM214B
RAPGEF1 ZNF438  HNRNPF  CHCHD1  EMILIN3 ZNF518A HOGA1   FAM196A SF3B2   LRP5    PGR
MSANTD4 MCAM    ESAM    PKNOX2  APPL2   WBP11   ABCD2   RACGAP1 PCBP2   SLC7A1  KL
MTRF1   EFNB2   MYH6    BATF    IRF2BPL RPS2P4  CTD     SNUPN   BLM     CDR2
TSNAXIP1        TERF2   CMIP    GALNS   ARHGAP23        C17orf98        LRRC37A3
SYNGR2  ARHGDIA FN3K    ATP8B1  POLR2E  LRG1    SEMA6B  KHSRP   HNRNPUL1
SIGLEC10        CRLS1   TSHZ2   ERG     ICOSLG  CLTCL1  CCDC116 RP1     CSF2RB
SMCR7L  CXorf36 RPSAP14 PCDH19  IDS
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0000375      1.95112202809718e-07    10.3218993518316        1.14255068853367
10      209     RNA splicing, via transesterification reactions
GO:0008380      1.36842157637575e-06    7.28978129713424        1.76576015500657
11      323     RNA splicing
GO:0006397      1.037040984638e-05      5.83020012128563        2.18123313265518
11      399     mRNA processing
GO:0000377      1.52014142646623e-05    8.14946823799943        1.11521694000415
8       204     RNA splicing, via transesterification reactions with bulged
adenosine as nucleophile
GO:0000398      1.52014142646623e-05    8.14946823799943        1.11521694000415
8       204     nuclear mRNA splicing, via spliceosome
GO:2000104      0.0018796225148286 7    37.3038961038961        0.0656009964708325
2       12      negative regulation of DNA-dependent DNA replication
GO:0071775      0.00221351136977795     33.9102715466352        0.0710677461767352
2       13      regulation of cell cycle cytokinesis
GO:0071777      0.00221351136977795     33.9102715466352        0.0710677461767352
2       13      positive regulation of cell cycle cytokinesis
GO:0032467      0.00295868824346752     28.6893106893107        0.0820012455885406
2       15      positive regulation of cytokinesis
GO:0090329      0.0063499603108142 2    18.638961038961 0.12026849352986        2
22      regulation of DNA-dependent DNA replication
GO:0060444      0.00693020683008556     17.7501546072975        0.125735243235762
2       23      branching involved in mammary gland duct morphogenesis
GO:0045600      0.00753359074695003     16.9421487603306        0.131201992941665
2       24      positive regulation of fat cell differentiation
GO:0006200      0.00800599764520436     7.83991228070175        0.410006227942703
3       75      ATP catabolic process
GO:0032465      0.00815984834055658     16.2044042913608        0.136668742647568
2       25      regulation of cytokinesis
GO:0030278      0.00816878626080113     5.3828841607565 0.792678707355892       4
145     regulation of ossification
Tissue: Whole_Blood=>Nerve_Tibial       Type:   asymmetric
SourceGene:     RP11-253A20.1(ENSG00000238140.1)
TargetGeneSet:  OTUD3   GNG12   LHX4    SRSF7   ASS1P2  CYP8B1  ZNF595  LYAR
ZDHHC11 TMCO6   ZFP2    ID4     SP4     FAM133B ZNF767  ASPH    CTA     NOL8
TEX10   SUSD1   ZFP37   C9orf114        WDR85   ZNF485  RP11    C10orf107
MRVI1-AS1       CCDC34  TTC17   FNBP4   EED     SNORA18 HINFP   ZNF202  ENO2
DDX23   PA2G4   RSRC2   ZNF140  ST6GALNAC4P1    FTH1P7  RNASEH2B-AS1    NGDN
ZBTB1   ZNF434  LYRM1   NPIPL3  SNORA67 TADA2A  GJD3    ZNF271  IZUMO4  CTD
ELOF1   ZNF724P ZNF540  ZNF227  ZNF347  ZNF17   NOP56   ESF1    RP4     ZNF337
KRT18P4 EIF4ENIF1       NOL12   DMD-AS2 LAS1L   UPF3B   FRMD7
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022613      5.73777302553661e-05    10.2292718096611        0.685073697321985
6       225     ribonucleoprotein complex biogenesis
GO:0071843      8.0168192862928e-05     9.60515021459227        0.727700505155353
6       239     cellular component biogenesis at cellular level
GO:0006364      0.000275421458510974    14.307  0.316656286762162       4       104
rRNA processing
GO:0016072      0.000341253307514782    13.4915094339623        0.334924918690748
4       110     rRNA metabolic process
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GO:0042254      0.00106953144821759     9.83586206896552        0.453671026226559
4       149     ribosome biogenesis
GO:0034470      0.00313555516419719     7.25051020408163        0.608954397619542
4       200     ncRNA processing
GO:0000377      0.00336630188842736     7.1035  0.621133485571933       4       204
RNA splicing, via transesterification reactions with bulged adenosine as nucleophile
GO:0000398      0.00336630188842736     7.1035  0.621133485571933       4       204
nuclear mRNA splicing, via spliceosome
GO:0000375      0.00367072633441748     6.92780487804878        0.636357345512421
4       209     RNA splicing, via transesterification reactions
GO:0006369      0.00790323900060192     16.2868480725624        0.133969967476299
2       44      termination of RNA polymerase II transcription
GO:0016056      0.00910716059984296     167.5   0.00913431596429313     1       3
rhodopsin mediated signaling pathway
GO:0021523      0.00910716059984296     167.5   0.00913431596429313     1       3
somatic motor neuron differentiation
GO:0031585      0.00910716059984296     167.5   0.00913431596429313     1       3
regulation of inositol 1,4,5-trisphosphate-sensitive calcium-release channel
activity
Tissue: Whole_Blood=>Nerve_Tibial       Type:   cluster
SourceGene:     RP11-253A20.1(ENSG00000238140.1)
TargetGeneSet:  OTUD3   GNG12   LHX4    SRSF7   ASS1P2  CYP8B1  ZNF595  LYAR
ZDHHC11 TMCO6   ZFP2    ID4     SP4     FAM133B ZNF767  ASPH    CTA     NOL8
TEX10   SUSD1   ZFP37   C9orf114        WDR85   ZNF485  RP11    C10orf107
MRVI1-AS1       CCDC34  TTC17   FNBP4   EED     SNORA18 HINFP   ZNF202  ENO2
DDX23   PA2G4   RSRC2   ZNF140  ST6GALNAC4P1    FTH1P7  RNASEH2B-AS1    NGDN
ZBTB1   ZNF434  LYRM1   NPIPL3  SNORA67 TADA2A  GJD3    ZNF271  IZUMO4  CTD
ELOF1   ZNF724P ZNF540  ZNF227  ZNF347  ZNF17   NOP56   ESF1    RP4     ZNF337
KRT18P4 EIF4ENIF1       NOL12   DMD-AS2 LAS1L   UPF3B   FRMD7
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022613      5.73777302553661e-05    10.2292718096611        0.685073697321985
6       225     ribonucleoprotein complex biogenesis
GO:0071843      8.0168192862928e-05     9.6051502145922 7       0.727700505155353
6       239     cellular component biogenesis at cellular level
GO:0006364      0.000275421458510974    14.307  0.316656286762162       4       104
rRNA processing
GO:0016072      0.000341253307514782    13.4915094339623        0.334924918690748
4       110     rRNA metabolic process
GO:0042254      0.00106953144821759     9.83586206896552        0.453671026226559
4       149     ribosome biogenesis
GO:0034470      0.00313555516419719     7.25051020408163        0.608954397619542
4       200     ncRNA processing
GO:0000377      0.00336630188842736     7.1035  0.621133485571933       4       204
RNA splicing, via transesterification reactions with bulged adenosine as nucleophile
GO:0000398      0.00336630188842736     7.1035  0.621133485571933       4       204
nuclear mRNA splicing, via spliceosome
GO:0000375      0.00367072633441748     6.92780487804878        0.636357345512421
4       209     RNA splicing, via transesterification reactions
GO:0006369      0.00790323900060192     16.2868480725624        0.133969967476299
2       44      termination of RNA polymerase II transcription
GO:0016056      0.00910716059984296     167.5   0.00913431596429313     1       3
rhodopsin mediated signaling pathway
GO:0021523      0.00910716059984296     167.5   0.00913431596429313     1       3
somatic motor neuron differentiation
GO:0031585      0.00910716059984296     167.5   0.00913431596429313     1       3
regulation of inositol 1,4,5-trisphosphate-sensitive calcium-release channel
activity
Tissue: Whole_Blood=>Nerve_Tibial       Type:   asymmetric
SourceGene:     RP11-475O23.3(ENSG00000244383.1)
TargetGeneSet:  MIR214  TFB2M   PTRHD1  THSD7B  NELL2   ZDHHC23 RP11    CLDN18
HADHAP1 NREP    GPX3    RP1     HCG21   VEGFA   CLDN12  ZNF252  FREM1   AVPI1
CALHM3  NARS2   SNORA18 AMN1    CPSF6   PPP2R5C SMAD6   SRSF1   RNF165  NFKBID
TMEM145 PVR     ZNF444  ZIK1    FTLP3   MAPRE1  TMSB15B KIAA1210        TMEM185AL
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GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0031333	9.42063618146793e-05	40.5253759398496	0.0898207736488824	3	59	negative regulation of protein complex assembly
GO:0034329	0.000104514900157854	19.5706447187929	0.25271607501211	4	166	cell junction assembly
GO:0043254	0.000114598647833307	19.0937081659973	0.258805618988305	4	170	regulation of protein complex assembly
GO:0034330	0.000165493359798409	17.2993321190043	0.284686180887136	4	187	cell junction organization
GO:0016338	0.000501734720478402	72.045	0.0334924918690748	2	22	calcium-independent cell-cell adhesion
GO:0042462	0.000549012540182405	68.6095238095238	0.0350148778631237	2	23	eye photoreceptor cell development
GO:0045216	0.000729779281246389	19.6530892448513	0.179641547297765	3	118	cell-cell junction organization
GO:0042461	0.000758870007195971	57.616	0.0411044218393191	2	27	photoreceptor cell development
GO:0001754	0.000876164647072688	53.3407407407407	0.0441491938274168	2	29	eye photoreceptor cell differentiation
GO:0044087	0.00102840008996212	10.5016722408027	0.461282956196803	4	303	regulation of cellular component biogenesis
GO:0046530	0.00135082481415997	42.3382352941176	0.0548058957857588	2	36	photoreceptor cell differentiation
GO:0070830	0.00135082481415997	42.3382352941176	0.0548058957857588	2	36	tight junction assembly
GO:0032272	0.00158444278089746	38.8972972972973	0.0593730537679053	2	39	negative regulation of protein polymerization
GO:0043297	0.00192373965511358	35.0926829268293	0.0654625977441008	2	43	apical junction assembly
GO:0043154	0.00324177451759776	26.6203703703704	0.0852536156667359	2	56	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process
GO:0031589	0.00340655627254603	11.2906638455435	0.307521970797869	3	202	cell-substrate adhesion
GO:2000117	0.00359181154536618	25.2140350877193	0.0898207736488824	2	59	negative regulation of cysteine-type endopeptidase activity
GO:0007043	0.00434240655972103	22.8031746031746	0.0989550896131756	2	65	cell-cell junction assembly
GO:0000395	0.00456052365236981	343.5	0.00456715798214656	1	3	nuclear mRNA 5'-splice site recognition
GO:0006391	0.00456052365236981	343.5	0.00456715798214656	1	3	transcription initiation from mitochondrial promoter
GO:0006421	0.00456052365236981	343.5	0.00456715798214656	1	3	asparaginyl-tRNA aminoacylation
GO:0006982	0.00456052365236981	343.5	0.00456715798214656	1	3	response to lipid hydroperoxide
GO:0007352	0.00456052365236981	343.5	0.00456715798214656	1	3	zygotic specification of dorsal/ventral axis
GO:0010990	0.00456052365236981	343.5	0.00456715798214656	1	3	regulation of SMAD protein complex assembly
GO:0010991	0.00456052365236981	343.5	0.00456715798214656	1	3	negative regulation of SMAD protein complex assembly
GO:0035845	0.00456052365236981	343.5	0.00456715798214656	1	3	photoreceptor cell outer segment organization
GO:0038086	0.00456052365236981	343.5	0.00456715798214656	1	3	VEGF-activated platelet-derived growth factor receptor signaling pathway
GO:0038091	0.00456052365236981	343.5	0.00456715798214656	1	3	positive regulation of cell proliferation by VEGF-activated platelet derived growth factor receptor signaling pathway
GO:0042271	0.00456052365236981	343.5	0.00456715798214656	1	3	susceptibility to natural killer cell mediated cytotoxicity
GO:2001028	0.00456052365236981	343.5	0.00456715798214656	1	3	positive regulation of endothelial cell chemotaxis

GO:0017015	0.00474267137576785	21.7621212121212	0.103522247595322	2	68	regulation of transforming growth factor beta receptor signaling pathway
GO:0051494	0.00559240931166944	19.9402777777778	0.112656563559615	2	74	negative regulation of cytoskeleton organization
GO:0031124	0.00604159453228434	19.1386666666667	0.117223721541762	2	77	mRNA 3'-end processing
GO:0035372	0.00607628143750583	228.984126984127	0.00608954397619542	1	4	protein localization to microtubule
GO:0072698	0.00607628143750583	228.984126984127	0.00608954397619542	1	4	protein localization to microtubule cytoskeleton
GO:0048593	0.00634996031081421	18.638961038961	0.12026849352986	2	79	camera-type eye morphogenesis
GO:0051262	0.0066654041753842	18.1645569620253	0.123313265517957	2	81	protein tetramerization
GO:0002238	0.00758983593382867	171.72619047619	0.00761192997024427	1	5	response to molecule of fungal origin
GO:0031077	0.00758983593382867	171.72619047619	0.00761192997024427	1	5	post-embryonic camera-type eye development
GO:0031115	0.00758983593382867	171.72619047619	0.00761192997024427	1	5	negative regulation of microtubule polymerization
GO:0033085	0.00758983593382867	171.72619047619	0.00761192997024427	1	5	negative regulation of T cell differentiation in thymus
GO:0038083	0.00758983593382867	171.72619047619	0.00761192997024427	1	5	peptidyl-tyrosine autophosphorylation
GO:0043117	0.00758983593382867	171.72619047619	0.00761192997024427	1	5	positive regulation of vascular permeability
GO:0045750	0.00758983593382867	171.72619047619	0.00761192997024427	1	5	positive regulation of S phase of mitotic cell cycle
GO:0060394	0.00758983593382867	171.72619047619	0.00761192997024427	1	5	negative regulation of pathway-restricted SMAD protein phosphorylation
GO:0060753	0.00758983593382867	171.72619047619	0.00761192997024427	1	5	regulation of mast cell chemotaxis
GO:0060754	0.00758983593382867	171.72619047619	0.00761192997024427	1	5	positive regulation of mast cell chemotaxis
GO:2001026	0.00758983593382867	171.72619047619	0.00761192997024427	1	5	regulation of endothelial cell chemotaxis
GO:0031123	0.00834733482324249	16.1123595505618	0.138537125458446	2	91	RNA 3'-end processing
GO:0032271	0.00852500309646574	15.9322222222222	0.140059511452495	2	92	regulation of protein polymerization
GO:0043623	0.00902660910221944	7.86415863602669	0.436924780292021	3	287	cellular protein complex assembly
GO:0001657	0.00906820078863467	15.4150537634409	0.144626669434641	2	95	ureteric bud development
GO:0022618	0.00906820078863467	15.4150537634409	0.144626669434641	2	95	ribonucleoprotein complex assembly
GO:0000244	0.00910119019171707	137.371428571429	0.00913431596429313	1	6	assembly of spliceosomal tri-snRNP
GO:0002420	0.00910119019171707	137.371428571429	0.00913431596429313	1	6	natural killer cell mediated cytotoxicity directed against tumor cell target
GO:0002423	0.00910119019171707	137.371428571429	0.00913431596429313	1	6	natural killer cell mediated immune response to tumor cell
GO:0002855	0.00910119019171707	137.371428571429	0.00913431596429313	1	6	regulation of natural killer cell mediated immune response to tumor cell
GO:0002857	0.00910119019171707	137.371428571429	0.00913431596429313	1	6	positive regulation of natural killer cell mediated immune response to tumor cell
GO:0002858	0.00910119019171707	137.371428571429	0.00913431596429313	1	6	regulation of natural killer cell mediated cytotoxicity directed against tumor cell target

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GO:0002860      0.00910119019171707     137.371428571429        0.00913431596429313
1       6       positive regulation of natural killer cell mediated cytotoxicity
directed against tumor cell target
GO:0044380      0.00910119019171707     137.371428571429        0.00913431596429313
1       6       protein localization to cytoskeleton
GO:0046548      0.00910119019171707     137.371428571429        0.00913431596429313
1       6       retinal rod cell development
GO:0060215      0.00910119019171707     137.371428571429        0.00913431596429313
1       6       primitive hemopoiesis
GO:0070245      0.00910119019171707     137.371428571429        0.00913431596429313
1       6       positive regulation of thymocyte apoptotic process
GO:0090050      0.00910119019171707     137.371428571429        0.00913431596429313
1       6       positive regulation of cell migration involved in sprouting
angiogenesis
Tissue: Whole_Blood=>Nerve_Tibial       Type:   asymmetric
SourceGene:     SNORA42(ENSG00000207217.1)
TargetGeneSet:  HSPB7   MACF1   NEXN    C1orf61 F5      B3GALT2 RP11    RYR2
OR2L2   YPEL5   KCNG3   REEP1   POU3F3  SOWAHC  ACVR1C  GAD1    ERBB4   PPARG
C3orf23 MYLK    KALRN   ROPN1B  LPP     GPR125  SGCB    SPARCL1 CISD2   UGT8
USP38   RBM46   SORBS2  CTD     RCAN2   STXBP2  KLHL32  PLN     HEBP2   SFT2D1  ISPD
KIAA0895        DLX6    RP4     SERPINE1        ZMAT4   LYNX1   TPM2    PTPN3
GRIN1   ITGA8   PLXDC2  GAD2    CHAF1B  PRKG1   CAMK2G  VCL     EMX2OS  EMX2
STIM1   TMEM9B  MRVI1   TAGLN   RERGL   KRT18   ITGA5   S100G   CPNE6   C14orf180
SHC4    UNC13C  TPM1    MYH11   TMEM159 CRYM    RRAD    AOC3    ST8SIA3 OLFM2   CNN1
PDE4C   SLC8A2  ANGPT4  SNAP25  JAG1    DSTN    JPH2    SLC12A5 PTCHD1  COL4A6  FHL1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0030334      1.24366162339142e-05    6.37164925034075        1.81855926925472
10      365     regulation of cell migration
GO:0006816      1.65191485751477e-05    8.08219178082192        1.13099439485157
8       227     calcium ion transport
GO:2000145      1.97204030167133e-05    6.02322580645161        1.91820635250156
10      385     regulation of cell motility
GO:1901021      3.27250896480795e-05    62.4739130434783        0.0647706041104422
3       13      positive regulation of calcium ion transmembrane transporter
activity
GO:2001259      3.27250896480795e-05    62.4739130434783        0.0647706041104422
3       13      positive regulation of cation channel activity
GO:0051270      3.30671364212874e-05    5.65122483628426        2.03778285239776
10      409     regulation of cellular component movement
GO:0061061      3.30671364212874e-05    5.65122483628426        2.03778285239776
10      409     muscle structure development
GO:0040012      3.51836711008842e-05    5.60784785748676        2.05272991488478
10      412     regulation of locomotion
GO:0070838      4.36360576692067e-05    7.00744047619048        1.29541208220884
8       260     divalent metal ion transport
GO:0072511      4.86120467755844e-05    6.89599609375   1.31534149885821        8
264     divalent inorganic cation transport
GO:0003012      5.12724691109473e-05    6.84156976744186        1.32530620718289
8       266     muscle system process
GO:0051924      8.02470593050958e-05    9.38142292490119        0.717458999377206
6       144     regulation of calcium ion transport
GO:0050890      0.000116255886589071    8.74140049140049        0.767282541000623
6       154     cognition
GO:0060316      0.00014593752567850l    205.385714285714        0.0199294166493668
2       4       positive regulation of ryanodine-sensitive calcium-release channel
activity
GO:0006936      0.000183062333882884    6.56690981432361        1.19078264479967
7       239     muscle contraction
GO:1901019      0.000195520351876022    31.2152173913043        0.114594145733859
3       23      regulation of calcium ion transmembrane transporter activity
GO:0010959      0.000248159509690897    7.55342902711324        0.881876686734482
6       177     regulation of metal ion transport
GO:0048738      0.000267587318979812    9.68046132971506        0.572970728669296
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5       115     cardiac muscle tissue development
GO:0030336      0.000301549867017015    9.42147668735966        0.587917791156321
5       118     negative regulation of cell migration
GO:0006887      0.000313294925230738    5.98879466989703        1.30039443637119
7       261     exocytosis
GO:0032414      0.00031833981772063     26.0054347826087        0.134523562383226
3       27      positive regulation of ion transmembrane transporter activity
GO:2000146      0.000325944259850793    9.25632706035042        0.597882499481005
5       120     negative regulation of cell motility
GO:0060537      0.000410825282283638    5.71376518218623        1.36018268631929
7       273     muscle tissue development
GO:0051271      0.000423261922807407    8.72094445803768        0.632758978617397
5       127     negative regulation of cellular component movement
GO:0006538      0.000505853434055779    82.1371428571429        0.0348764791363919
2       7       glutamate catabolic process
GO:0040013      0.000541074983732698    8.24366539396043        0.667635457753789
5       134     negative regulation of locomotion
GO:0032411      0.000635189876702784    20.1234221598878        0.169400041519618
3       34      positive regulation of transporter activity
GO:2001257      0.000635189876702784    20.1234221598878        0.169400041519618
3       34      regulation of cation channel activity
GO:0007611      0.000682014930807697    7.81551799824407        0.702511936890181
5       141     learning or memory
GO:0043269      0.000750251098573927    6.07504288164666        1.08615320739049
6       218     regulation of ion transport
GO:0007517      0.000763333622590759    5.1237525987526 1.50965331118954        7
303     muscle organ development
GO:0007596      0.000787887600007132    4.0578439964943 2.48121237284617        9
498     blood coagulation
GO:0005513      0.000861595699690728    58.6612244897959        0.0448411874610754
2       9       detection of calcium ion
GO:0072070      0.000861595699690728    58.6612244897959        0.0448411874610754
2       9       loop of Henle development
GO:0006105      0.00107352482666513     51.325  0.0498235416234171      2       10
succinate metabolic process
GO:0072017      0.00107352482666513     51.325  0.0498235416234171      2       10
distal tubule development
GO:0008016      0.0013201158944733      9.1349104859335 0.478305999584804       4
96      regulation of heart contraction
GO:0031032      0.0014483355998319      14.8416149068323        0.224205937305377
3       45      actomyosin structure organization
GO:0007507      0.00154058927103041     4.5147187141217 1.70396512352086        7
342     heart development
GO:0031000      0.00156437954967697     41.0542857142857        0.0597882499481005
2       12      response to caffeine
GO:0060314      0.00184286217877313     37.3194805194805        0.0647706041104422
2       13      regulation of ryanodine-sensitive calcium-release channel activity
GO:0090257      0.00191891216477087     8.23356401384083        0.528129541208221
4       106     regulation of muscle system process
GO:0042136      0.00214308900724139     34.2071428571429        0.0697529582727839
2       14      neurotransmitter biosynthetic process
GO:0003015      0.00266461688964211     7.49317226890756        0.577953082831638
4       116     heart process
GO:0032409      0.00266461688964211     7.49317226890756        0.577953082831638
4       116     regulation of transporter activity
GO:0060047      0.00266461688964211     7.49317226890756        0.577953082831638
4       116     heart contraction
GO:0006688      0.00280790683681906     29.3163265306122        0.0797176665974673
2       16      glycosphingolipid biosynthetic process
GO:0043001      0.00280790683681906     29.3163265306122        0.0797176665974673
2       16      Golgi to plasma membrane protein transport
GO:0014074      0.0031720675533789 8     27.36   0.084700020759809       2       17
response to purine-containing compound
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GO:0009247      0.00355711188038176     25.6482142857143        0.0896823749221507
2       18      glycolipid biosynthetic process
GO:0008015      0.00396248498461866     4.31037649219467        1.50965331118954
6       303     blood circulation
GO:0048745      0.00396282855922372     24.1378151260504        0.0946647290844924
2       19      smooth muscle tissue development
GO:0003013      0.0040265969460125      4.29560707748627        1.51463566535188
6       304     circulatory system process
GO:0007613      0.00415249566492265     10.0399719495091        0.323853020552211
3       65      memory
GO:0006893      0.00438900786712372     22.7952380952381        0.0996470832468341
2       20      Golgi to plasma membrane transport
GO:0009914      0.00442666229475119     5.01096413666266        1.07618849906581
5       216     hormone transport
GO:0044057      0.00464974491020803     3.66915572232645        2.07764168569649
7       417     regulation of system process
GO:0003001      0.00485744321269216     4.1258064516129 1.57442391529998        6
316     generation of a signal involved in cell-cell signaling
GO:0023061      0.00485744321269216     4.1258064516129 1.57442391529998        6
316     signal release
GO:0021846      0.00530192309985648     20.5128571428571        0.109611791571518
2       22      cell proliferation in forebrain
GO:0043462      0.00530192309985648     20.5128571428571        0.109611791571518
2       22      regulation of ATPase activity
GO:0009065      0.00578824717109272     19.534693877551 0.114594145733859       2
23      glutamine family amino acid catabolic process
GO:0046676      0.00578824717109272     19.534693877551 0.114594145733859       2
23      negative regulation of insulin secretion
GO:0007160      0.00590201814857251     5.93992490613267        0.722441353539547
4       145     cell-matrix adhesion
GO:0021537      0.00619186632081811     5.85602632661456        0.732406061864231
4       147     telencephalon development
GO:0006939      0.00619594598024957     8.63949275362319        0.373676562175628
3       75      smooth muscle contraction
GO:0060402      0.00619594598024957     8.63949275362319        0.373676562175628
3       75      calcium ion transport into cytosol
GO:0006536      0.00629421014504686     18.6454545454545        0.119576499896201
2       24      glutamate metabolic process
GO:0060401      0.00642779079595319     8.52054794520548        0.37865891633797
3       76      cytosolic calcium ion transport
GO:0051050      0.0064317917407265      3.4439308398024 2.20718289391738        7
443     positive regulation of transport
GO:0042493      0.00651425162205806     3.8702479338843 1.67407099854681        6
336     response to drug
GO:0042133      0.00681960983346149     17.8335403726708        0.124558854058543
2       25      neurotransmitter metabolic process
GO:0090278      0.00681960983346149     17.8335403726708        0.124558854058543
2       25      negative regulation of peptide hormone secretion
GO:0055074      0.00699154709930207     4.47223627624589        1.20074735312435
5       241     calcium ion homeostasis
GO:0061041      0.00715417588426707     8.1824942791762 0.393605978824995       3
79      regulation of wound healing
GO:0002792      0.00736424552645795     17.0892857142857        0.129541208220884
2       26      negative regulation of peptide secretion
GO:0030073      0.0076135643941621      5.50580495356037        0.777247249325306
4       156     insulin secretion
GO:0030900      0.00773543425806473     4.3595041322314 1.2306414780984 5       247
forebrain development
GO:0006904      0.00792791798315694     16.4045714285714        0.134523562383226
2       27      vesicle docking involved in exocytosis
GO:0002576      0.00819567359848294     7.77119565217391        0.413535395474362
3       83      platelet degranulation
GO:0010035      0.00889084358501993     3.6121555498326 1.78866514428067        6
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359     response to inorganic substance
GO:0072507      0.008952363897252       4.20051138728667        1.27548266555948
5       256     divalent inorganic cation homeostasis
GO:0007269      0.00903239820985746     7.48873755893138        0.428482457961387
3       86      neurotransmitter secretion
GO:0048278      0.00911158351324811     15.1873015873016        0.144488270707909
2       29      vesicle docking
GO:0034329      0.00942866610108447     5.16230936819172        0.82707079094872З
4       166     cell junction assembly
GO:0055024      0.00973118536622807     14.6438775510204        0.149470624870251
2       30      regulation of cardiac muscle tissue development
GO:0014706      0.00983373807336037     4.10070271212033        1.30537679053353
5       262     striated muscle tissue development
GO:0006937      0.00991744843816333     7.22598584428716        0.443429520448412
3       89      regulation of muscle contraction
Tissue: Whole_Blood=>Nerve_Tibial       Type:   cluster
SourceGene:     SNORA42(ENSG00000207217.1)
TargetGeneSet:  HSPB7   MACF1   NEXN    C1orf61 F5      B3GALT2 RP11    RYR2
OR2L2   YPEL5   KCNG3   REEP1   POU3F3  SOWAHC  ACVR1C  GAD1    ERBB4   PPARG
C3orf23 MYLK    KALRN   ROPN1B  LPP     GPR125  SGCB    SPARCL1 CISD2   UGT8
USP38   RBM46   SORBS2  CTD     RCAN2   STXBP2  KLHL32  PLN     HEBP2   SFT2D1  ISPD
KIAA0895        DLX6    RP4     SERPINE1        ZMAT4   LYNX1   TPM2    PTPN3
GRIN1   ITGA8   PLXDC2  GAD2    CHAF1B  PRKG1   CAMK2G  VCL     EMX2OS  EMX2
STIM1   TMEM9B  MRVI1   TAGLN   RERGL   KRT18   ITGA5   S100G   CPNE6   C14orf180
SHC4    UNC13C  TPM1    MYH11   TMEM159 CRYM    RRAD    AOC3    ST8SIA3 OLFM2   CNN1
PDE4C   SLC8A2  ANGPT4  SNAP25  JAG1    DSTN    JPH2    SLC12A5 PTCHD1  COL4A6  FHL1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0030334      1.24366162339142e-05    6.37164925034075        1.81855926925472
10      365     regulation of cell migration
GO:0006816      1.65191485751477e-05    8.08219178082192        1.13099439485157
8       227     calcium ion transport
GO:2000145      1.97204030167133e-05    6.02322580645161        1.91820635250156
10      385     regulation of cell motility
GO:1901021      3.27250896480795e-05    62.4739130434783        0.0647706041104422
3       13      positive regulation of calcium ion transmembrane transporter
activity
GO:2001259      3.27250896480795e-05    62.4739130434783        0.0647706041104422
3       13      positive regulation of cation channel activity
GO:0051270      3.30671364212874e-05    5.65122483628426        2.03778285239776
10      409     regulation of cellular component movement
GO:0061061      3.30671364212874e-05    5.65122483628426        2.03778285239776
10      409     muscle structure development
GO:0040012      3.51836711008842e-05    5.60784785748676        2.05272991488478
10      412     regulation of locomotion
GO:0070838      4.36360576692067e-05    7.00744047619048        1.29541208220884
8       260     divalent metal ion transport
GO:0072511      4.86120467755844e-05    6.89599609375   1.31534149885821        8
264     divalent inorganic cation transport
GO:0003012      5.12724691109473e-05    6.84156976744186        1.32530620718289
8       266     muscle system process
GO:0051924      8.02470593050958e-05    9.38142292490119        0.717458999377206
6       144     regulation of calcium ion transport
GO:0050890      0.000116255886589071    8.74140049140049        0.767282541000623
6       154     cognition
GO:0060316      0.00014593752567850l    205.385714285714        0.0199294166493668
2       4       positive regulation of ryanodine-sensitive calcium-release channel
activity
GO:0006936      0.000183062333882884    6.56690981432361        1.19078264479967
7       239     muscle contraction
GO:1901019      0.000195520351876022    31.2152173913043        0.114594145733859
3       23      regulation of calcium ion transmembrane transporter activity
GO:0010959      0.000248159509690897    7.55342902711324        0.881876686734482
6       177     regulation of metal ion transport
```

GO:0048738	0.000267587318979812	9.68046132971506	0.572970728669296	5	115	cardiac muscle tissue development
GO:0030336	0.000301549867017015	9.42147668735966	0.587917791156321	5	118	negative regulation of cell migration
GO:0006887	0.000313294925230738	5.98879466989703	1.30039443637119	7	261	exocytosis
GO:0032414	0.00031833981772063	26.0054347826087	0.134523562383226	3	27	positive regulation of ion transmembrane transporter activity
GO:2000146	0.000325944259850793	9.25632706035042	0.597882499481005	5	120	negative regulation of cell motility
GO:0060537	0.000410825282283638	5.71376518218623	1.36018268631929	7	273	muscle tissue development
GO:0051271	0.000423261922807407	8.72094445803768	0.632758978617397	5	127	negative regulation of cellular component movement
GO:0006538	0.000505853434055779	82.1371428571429	0.0348764791363919	2	7	glutamate catabolic process
GO:0040013	0.000541074983732698	8.24366539396043	0.667635457753789	5	134	negative regulation of locomotion
GO:0032411	0.000635189876702784	20.1234221598878	0.169400041519618	3	34	positive regulation of transporter activity
GO:2001257	0.000635189876702784	20.1234221598878	0.169400041519618	3	34	regulation of cation channel activity
GO:0007611	0.00068201493080769	7.81551799824407	0.702511936890181	5	141	learning or memory
GO:0043269	0.000750251098573927	6.07504288164666	1.08615320739049	6	218	regulation of ion transport
GO:0007517	0.000763333622590759	5.1237525987526	1.50965331118954	7	303	muscle organ development
GO:0007596	0.000787887600007132	4.0578439964943	2.48121237284617	9	498	blood coagulation
GO:0005513	0.000861595699690728	58.6612244897959	0.0448411874610754	2	9	detection of calcium ion
GO:0072070	0.000861595699690728	58.6612244897959	0.0448411874610754	2	9	loop of Henle development
GO:0006105	0.00107352482666513	51.325	0.0498235416234171	2	10	succinate metabolic process
GO:0072017	0.00107352482666513	51.325	0.0498235416234171	2	10	distal tubule development
GO:0008016	0.0013320115894473	9.1349104859335	0.478305999584804	4	96	regulation of heart contraction
GO:0031032	0.0014483355998319	14.8416149068323	0.224205937305377	3	45	actomyosin structure organization
GO:0007507	0.00154058927103041	4.5147187141217	1.70396512352086	7	342	heart development
GO:0031000	0.00156437954967697	41.0542857142857	0.0597882499481005	2	12	response to caffeine
GO:0060314	0.00184286217877313	37.3194805194805	0.0647706041104422	2	13	regulation of ryanodine-sensitive calcium-release channel activity
GO:0090257	0.00191891216477087	8.23356401384083	0.528129541208221	4	106	regulation of muscle system process
GO:0042136	0.00214308900724139	34.2071428571429	0.0697529582727839	2	14	neurotransmitter biosynthetic process
GO:0003015	0.00266461688964211	7.49317226890756	0.577953082831638	4	116	heart process
GO:0032409	0.00266461688964211	7.49317226890756	0.577953082831638	4	116	regulation of transporter activity
GO:0060047	0.00266461688964211	7.49317226890756	0.577953082831638	4	116	heart contraction
GO:0006688	0.00280790683681906	29.3163265306122	0.0797176665974673	2	16	glycosphingolipid biosynthetic process
GO:0043001	0.00280790683681906	29.3163265306122	0.0797176665974673	2	16	Golgi to plasma membrane protein transport
GO:0014074	0.0031720675533789 8	27.36	0.084700020759809	2	17	

response to purine-containing compound

GO:0009247	0.00355711188038176	25.6482142857143	0.0896823749221507	2	18	glycolipid biosynthetic process
GO:0008015	0.00396248498461866	4.31037649219467	1.50965331118954	6	303	blood circulation
GO:0048745	0.00396282855922372	24.1378151260504	0.0946647290844924	2	19	smooth muscle tissue development
GO:0003013	0.0040265969460125	4.29560707748627	1.51463566535188	6	304	circulatory system process
GO:0007613	0.00415249566492265	10.0399719495091	0.323853020552211	3	65	memory
GO:0006893	0.00438900786712372	22.7952380952381	0.0996470832468341	2	20	Golgi to plasma membrane transport
GO:0009914	0.00442666229475119	5.01096413666266	1.07618849906581	5	216	hormone transport
GO:0044057	0.00464974491020803	3.66915572232645	2.07764168569649	7	417	regulation of system process
GO:0003001	0.00485744321269216	4.1258064516129	1.57442391529998	6	316	generation of a signal involved in cell-cell signaling
GO:0023061	0.00485744321269216	4.1258064516129	1.57442391529998	6	316	signal release
GO:0021846	0.00530192309985648	20.5128571428571	0.109611791571518	2	22	cell proliferation in forebrain
GO:0043462	0.00530192309985648	20.5128571428571	0.109611791571518	2	22	regulation of ATPase activity
GO:0009065	0.00578824717109272	19.534693877551	0.114594145733859	2	23	glutamine family amino acid catabolic process
GO:0046676	0.00578824717109272	19.534693877551	0.114594145733859	2	23	negative regulation of insulin secretion
GO:0007160	0.0059020181485725 1	5.93992490613267	0.722441353539547	4	145	cell-matrix adhesion
GO:0021537	0.00619186632081811	5.85602632661456	0.732406061864231	4	147	telencephalon development
GO:0006939	0.00619594598024957	8.63949275362319	0.373676562175628	3	75	smooth muscle contraction
GO:0060402	0.00619594598024957	8.63949275362319	0.373676562175628	3	75	calcium ion transport into cytosol
GO:0006536	0.00629421014504686	18.6454545454545	0.119576499896201	2	24	glutamate metabolic process
GO:0060401	0.00642779079595319	8.52054794520548	0.37865891633797	3	76	cytosolic calcium ion transport
GO:0051050	0.0064317917407265	3.4439308398024	2.20718289391738	7	443	positive regulation of transport
GO:0042493	0.00651425162205806	3.8702479338843	1.67407099854681	6	336	response to drug
GO:0042133	0.00681960983346149	17.8335403726708	0.124558854058543	2	25	neurotransmitter metabolic process
GO:0090278	0.00681960983346149	17.8335403726708	0.124558854058543	2	25	negative regulation of peptide hormone secretion
GO:0055074	0.00699154709930207	4.47223627624589	1.20074735312435	5	241	calcium ion homeostasis
GO:0061041	0.00715417588426707	8.1824942791762	0.393605978824995	3	79	regulation of wound healing
GO:0002792	0.00736424552645795	17.0892857142857	0.129541208220884	2	26	negative regulation of peptide secretion
GO:0030073	0.0076135643941621	5.50580495356037	0.777247249325306	4	156	insulin secretion
GO:0030900	0.00773543425806473	4.3595041322314	1.2306414780984	5	247	forebrain development
GO:0006904	0.00792791798315694	16.4045714285714	0.134523562383226	2	27	vesicle docking involved in exocytosis
GO:0002576	0.00819567359848294	7.77119565217391	0.413535395474362	3	83	platelet degranulation

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GO:0010035      0.00889084358501993     3.6121555498326 1.78866514428067        6
359     response to inorganic substance
GO:0072507      0.008952363897252       4.20051138728667        1.27548266555948
5       256     divalent inorganic cation homeostasis
GO:0007269      0.00903239820985746     7.48873755893138        0.428482457961387
3       86      neurotransmitter secretion
GO:0048278      0.00911158351324811     15.1873015873016        0.144488270707909
2       29      vesicle docking
GO:0034329      0.00942866610108447     5.16230936819172        0.827070790948723
4       166     cell junction assembly
GO:0055024      0.00973118536622807     14.6438775510204        0.149470624870251
2       30      regulation of cardiac muscle tissue development
GO:0014706      0.00983373807336037     4.10070271212033        1.30537679053353
5       262     striated muscle tissue development
GO:0006937      0.00991744843816333     7.22598584428716        0.443429520448412
3       89      regulation of muscle contraction
Tissue: Whole_Blood=>Nerve_Tibial       Type:   cluster
SourceGene:     TNKS2(ENSG00000107854.5)
TargetGeneSet:  ACTA1   ACTN2   ADSS    HPCAL1  WDR92   PROM2   XIRP2   HHATL
LMOD3   RP11    GBA3    PCDHGA10        PLAC8L1 SCARNA15        RP1     GATS
ANKRD7  LMOD2   PARP12  CTA     JAK2    C9orf123        VSIG2   TIMELESS
ATP2B1  MYBPC1  CORO1C  MYL2    WDR66   STX2    TEX26-AS1       VPS36   MYH7    CTD
ACYP1   ATXN3   MESP2   HDDC3   MYLPF   NQO1    SERPINF2        MYH2    MYH1    TCAP
ASB16   PODNL1  SAMD1   MAST3   CKM     EBF4    DEFB124 PVALB   RP13
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0030049      3.7567733468774e-12     112.375 0.0944571309943949      7       39
muscle filament sliding
GO:0033275      3.7567733468774e-12     112.375 0.0944571309943949      7       39
actin-myosin filament sliding
GO:0070252      6.55590847956634e-12    102.721428571429        0.10172306414781
7       42      actin-mediated cell contraction
GO:0030048      8.05397457089499e-11    69.0576923076923        0.142896685350495
7       59      actin filament-based movement
GO:0030029      1.95846619359972e-10    17.3863354037267        1.04629437409176
12      432     actin filament-based process
GO:0006936      7.97107515811943e-08    18.1946448613115        0.578852674555394
8       239     muscle contraction
GO:0003012      1.81534971904396e-07    16.2595463680735        0.644246072936129
8       266     muscle system process
GO:0030036      3.19301154275041e-06    10.9147467677651        0.942149332226143
8       389     actin cytoskeleton organization
GO:0030240      5.67278352594166e-05    291.171717171717        0.012109888589025
2       5       skeletal muscle thin filament assembly
GO:0030239      7.39750452420471e-05    43.5030241935484        0.0823472424053699
3       34      myofibril assembly
GO:0014866      8.49622464313458e-05    218.363636363636        0.01453186630683
2       6       skeletal myofibril assembly
GO:0031032      0.00017224636867096     32.0848214285714        0.108988997301225
3       45      actomyosin structure organization
GO:0055008      0.00017224636867096     32.0848214285714        0.108988997301225
3       45      cardiac muscle tissue morphogenesis
GO:0060415      0.000235951485266959    28.6615691489362        0.12109888589025
3       50      muscle tissue morphogenesis
GO:0048644      0.000330399990462283    25.40625        0.13563075219708        3
56      muscle organ morphogenesis
GO:0014706      0.000392217106967774    9.1822308690013 0.634558162064909       5
262     striated muscle tissue development
GO:0007512      0.000437120856360053    79.366391184573 0.031485710331465       2
13      adult heart development
GO:0060537      0.000473391710426235    8.79850746268657        0.661199916960764
5       273     muscle tissue development
GO:0055003      0.000509199036496687    72.7474747474748        0.0339076880492699
2       14      cardiac myofibril assembly
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GO:0009582	0.000611186812061313	20.3835227272727	0.167116462528545	3	69	detection of abiotic stimulus
GO:0007517	0.000759638955051211	7.89597315436242	0.733859248494914	5	303	muscle organ development
GO:0006941	0.000779905647422016	18.6770833333333	0.181648328835375	3	75	striated muscle contraction
GO:0003009	0.000949598362949957	51.3333333333333	0.0460175766382949	2	19	skeletal muscle contraction
GO:0007015	0.00121336722967996	9.60986319878399	0.472285654971974	4	195	actin filament organization
GO:0050879	0.00178569731497192	36.3434343434343	0.0629714206629299	2	26	multicellular organismal movement
GO:0050881	0.00178569731497192	36.3434343434343	0.0629714206629299	2	26	musculoskeletal movement
GO:0055002	0.00217429696375201	12.9014423076923	0.259151615805135	3	107	striated muscle cell development
GO:0055006	0.00237561555054854	31.1428571428571	0.0726593315341499	2	30	cardiac cell development
GO:0055013	0.00237561555054854	31.1428571428571	0.0726593315341499	2	30	cardiac muscle cell development
GO:0048738	0.00266920318368344	11.9732142857143	0.278527437547575	3	115	cardiac muscle tissue development
GO:0048729	0.00270899736842517	5.85505430242272	0.978478997993218	5	404	tissue morphogenesis
GO:0003015	0.00273554558956226	11.8664269911504	0.28094941526538	3	116	heart process
GO:0060047	0.00273554558956226	11.8664269911504	0.28094941526538	3	116	heart contraction
GO:0061061	0.00285682197027174	5.78052805280528	0.990588886582243	5	409	muscle structure development
GO:0055010	0.00287040793370604	28.1231671554252	0.0799252646875649	2	33	ventricular cardiac muscle tissue morphogenesis
GO:0010927	0.00322860047606374	11.16875	0.297903259290015	3	123	cellular component assembly involved in morphogenesis
GO:0003229	0.00340936807507379	25.6363636363636	0.0871911978409799	2	36	ventricular cardiac muscle tissue development
GO:0055001	0.00369204463956754	10.6324404761905	0.312435125596844	3	129	muscle cell development
GO:0008015	0.0059460696451267	6.09213507390225	0.733859248494914	4	303	blood circulation
GO:0003013	0.0060150705329335	6.07139784946237	0.736281226212719	4	304	circulatory system process
GO:0003007	0.00638223642454908	8.68222402597403	0.380250501695384	3	157	heart morphogenesis
GO:0030035	0.00724884985550822	211.970588235294	0.00726593315341499	1	3	microspike assembly
GO:0030241	0.00724884985550822	211.970588235294	0.00726593315341499	1	3	skeletal muscle myosin thick filament assembly
GO:0031034	0.00724884985550822	211.970588235294	0.00726593315341499	1	3	myosin filament assembly
GO:0035722	0.00724884985550822	211.970588235294	0.00726593315341499	1	3	interleukin-12-mediated signaling pathway
GO:0035845	0.00724884985550822	211.970588235294	0.00726593315341499	1	3	photoreceptor cell outer segment organization
GO:0035962	0.00724884985550822	211.970588235294	0.00726593315341499	1	3	response to interleukin-13
GO:0042396	0.00724884985550822	211.970588235294	0.00726593315341499	1	3	phosphagen biosynthetic process
GO:0044208	0.00724884985550822	211.970588235294	0.00726593315341499	1	3	'de novo' AMP biosynthetic process
GO:0048769	0.00724884985550822	211.970588235294	0.00726593315341499	1	3	sarcomerogenesis
GO:0071349	0.00724884985550822	211.970588235294	0.00726593315341499			

```
1       3       cellular response to interleukin-12
GO:0071688      0.00724884985550822     211.970588235294        0.00726593315341499
1       3       striated muscle myosin thick filament assembly
GO:0001756      0.0072677375634005      17.0707070707071        0.128364819043665
2       53      somitogenesis
GO:0003208      0.0072677375634005      17.0707070707071        0.128364819043665
2       53      cardiac ventricle morphogenesis
GO:0051146      0.00781536665211651     8.04781626506024        0.409314234309044
3       169     striated muscle cell differentiation
GO:0055007      0.00808537298117971     16.1189674523008        0.13563075219708
2       56      cardiac muscle cell differentiation
GO:0007507      0.00904992431093262     5.37430807405994        0.828316379489309
4       342     heart development
GO:0000920      0.00965377027737002     141.303921568627        0.00968791087121998
1       4       cytokinetic cell separation
GO:0002034      0.00965377027737002     141.303921568627        0.00968791087121998
1       4       regulation of blood vessel size by renin-angiotensin
GO:0003010      0.00965377027737002     141.303921568627        0.00968791087121998
1       4       voluntary skeletal muscle contraction
GO:0003072      0.00965377027737002     141.303921568627        0.00968791087121998
1       4       renal control of peripheral vascular resistance involved in
regulation of systemic arterial blood pressure
GO:0006498      0.00965377027737002     141.303921568627        0.00968791087121998
1       4       N-terminal protein lipidation
GO:0007509      0.00965377027737002     141.303921568627        0.00968791087121998
1       4       mesoderm migration involved in gastrulation
GO:0010757      0.00965377027737002     141.303921568627        0.00968791087121998
1       4       negative regulation of plasminogen activation
GO:0014721      0.00965377027737002     141.303921568627        0.00968791087121998
1       4       twitch skeletal muscle contraction
GO:0031033      0.00965377027737002     141.303921568627        0.00968791087121998
1       4       myosin filament organization
GO:0060398      0.00965377027737002     141.303921568627        0.00968791087121998
1       4       regulation of growth hormone receptor signaling pathway
GO:0070671      0.00965377027737002     141.303921568627        0.00968791087121998
1       4       response to interleukin-12
GO:0061053      0.00983857231101985     14.5010101010101        0.15016261850391
2       62      somite development
Tissue: Whole_Blood=>Skin_Sun_Exposed_Lower_leg Type:   cluster
SourceGene:     7SK(ENSG00000222448.1)
TargetGeneSet:  RP4     TRAF3IP3        RP11    HYAL2   IQCF1   BAP1    ZCCHC9
YWHAZP4 RP3     CNKSR3  BRAF    ZNF214  RP1     RNU4-2  RPL29P24        FAM155A
RN7SL1  HMGB1P14        SNORD3A RAMP2   ZNF446  ZNF585A RPS27AP2        CTD
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0071482      2.77877873389443e-06    149.058620689655        0.0287869351601965
3       32      cellular response to light stimulus
GO:0071478      1.70546908144403e-05    78.4527272727273        0.0521763199778562
3       58      cellular response to radiation
GO:0007603      4.09013235940024e-05    291.494949494949        0.00989550896131756
2       11      phototransduction, visible light
GO:0009584      0.000140651479709995    145.656565656566        0.0179918344751228
2       20      detection of visible light
GO:0071214      0.000199261435692489    33.2767441860465        0.118746107535811
3       132     cellular response to abiotic stimulus
GO:0007602      0.000388292739320376    84.4985337243402        0.0296865268839527
2       33      phototransduction
GO:0009416      0.000537138568596664    23.4989010989011        0.166424468894886
3       185     response to light stimulus
GO:0009583      0.0005715802987313      68.8995215311005        0.0359836689502457
2       40      detection of light stimulus
GO:0033135      0.00063029672839942     65.4454545454546        0.0377828523977579
2       42      regulation of peptidyl-serine phosphorylation
GO:0007601      0.000714204087430938    21.2492537313433        0.183516711646253
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3       204     visual perception
GO:0050953      0.000724433314894387    21.1425742574257        0.184416303370009
3       205     sensory perception of light stimulus
GO:0071363      0.0015052671564208 6    16.2954022988506        0.237492215071621
3       264     cellular response to growth factor stimulus
GO:0009582      0.0016940292028643 8    38.9986431478969        0.0620718289391738
2       69      detection of abiotic stimulus
GO:0070848      0.0018373297757535 4    15.1692857142857        0.254584457822988
3       283     response to growth factor stimulus
GO:0009314      0.0020490314227549      14.5845360824742        0.264479966784306
3       294     response to radiation
GO:0009581      0.0026165897153662 7    31.0692640692641        0.0773648882430282
2       86      detection of external stimulus
GO:0010764      0.0026965345426339 7    601.5   0.0026987751712684 2     1       3
negative regulation of fibroblast migration
GO:0016056      0.0026965345426339 7    601.5   0.0026987751712684 2     1       3
rhodopsin mediated signaling pathway
GO:0035845      0.0026965345426339 7    601.5   0.0026987751712684 2     1       3
photoreceptor cell outer segment organization
GO:0060041      0.0031165001936935 4    28.3517786561265        0.0845616220330773
2       94      retina development in camera-type eye
GO:0019087      0.0035938867748424      400.972222222222        0.00359836689502457
1       4       transformation of host cell by virus
GO:0071711      0.0035938867748424      400.972222222222        0.00359836689502457
1       4       basement membrane organization
GO:0097084      0.0035938867748424      400.972222222222        0.00359836689502457
1       4       vascular smooth muscle cell development
GO:2000482      0.0035938867748424      400.972222222222        0.00359836689502457
1       4       regulation of interleukin-8 secretion
GO:2000484      0.0035938867748424      400.972222222222        0.00359836689502457
1       4       positive regulation of interleukin-8 secretion
GO:2000778      0.0035938867748424      400.972222222222        0.00359836689502457
1       4       positive regulation of interleukin-6 secretion
GO:0018105      0.0036577682801468 5    26.0690909090909        0.0917583558231264
2       102     peptidyl-serine phosphorylation
GO:0070372      0.0040168287004258 3    24.8190476190476        0.0962563144419071
2       107     regulation of ERK1 and ERK2 cascade
GO:0071493      0.0044904936462987 2    300.708333333333        0.00449795861878071
1       5       cellular response to UV-B
GO:0072604      0.0044904936462987 2    300.708333333333        0.00449795861878071
1       5       interleukin-6 secretion
GO:0072606      0.0044904936462987 2    300.708333333333        0.00449795861878071
1       5       interleukin-8 secretion
GO:2001214      0.0044904936462987 2    300.708333333333        0.00449795861878071
1       5       positive regulation of vasculogenesis
GO:0010741      0.0045460658391705 9    23.2564935064935        0.1025534565082 2
114     negative regulation of intracellular protein kinase cascade
GO:0018209      0.0045460658391705 9    23.2564935064935        0.1025534565082 2
114     peptidyl-serine modification
GO:0070371      0.0053552247311478 7    21.3353204172876        0.111549373745762
2       124     ERK1 and ERK2 cascade
GO:0000244      0.0053863557245622 5    240.55  0.0053975503425368 5     1       6
assembly of spliceosomal tri-snRNP
GO:0009586      0.0053863557245622 5    240.55  0.0053975503425368 5     1       6
rhodopsin mediated phototransduction
GO:0030214      0.0053863557245622 5    240.55  0.0053975503425368 5     1       6
hyaluronan catabolic process
GO:0046548      0.0053863557245622 5    240.55  0.0053975503425368 5     1       6
retinal rod cell development
GO:0070295      0.0053863557245622 5    240.55  0.0053975503425368 5     1       6
renal water absorption
GO:2001212      0.0053863557245622 5    240.55  0.0053975503425368 5     1       6
regulation of vasculogenesis
```

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GO:0034333      0.00628147357680053     200.444444444444        0.00629714206629299
1       7       adherens junction assembly
GO:0035518      0.00628147357680053     200.444444444444        0.00629714206629299
1       7       histone H2A monoubiquitination
GO:0042117      0.00628147357680053     200.444444444444        0.00629714206629299
1       7       monocyte activation
GO:0033137      0.00717584776978741     171.797619047619        0.00719673379004913
1       8       negative regulation of peptidyl-serine phosphorylation
GO:0042670      0.00717584776978741     171.797619047619        0.00719673379004913
1       8       retinal cone cell differentiation
GO:0043116      0.00717584776978741     171.797619047619        0.00719673379004913
1       8       negative regulation of vascular permeability
GO:0046549      0.00717584776978741     171.797619047619        0.00719673379004913
1       8       retinal cone cell development
GO:0044344      0.00794527228135684     17.3187878787879        0.136737942010934
2       152     cellular response to fibroblast growth factor stimulus
GO:0071774      0.00794527228135684     17.3187878787879        0.136737942010934
2       152     response to fibroblast growth factor stimulus
GO:0003097      0.00806947886990461     150.3125        0.00809632551380527     1
9       renal water transport
GO:0010762      0.00806947886990461     150.3125        0.00809632551380527     1
9       regulation of fibroblast migration
GO:0035082      0.00806947886990461     150.3125        0.00809632551380527     1
9       axoneme assembly
GO:0035886      0.00806947886990461     150.3125        0.00809632551380527     1
9       vascular smooth muscle cell differentiation
GO:2000352      0.00806947886990461     150.3125        0.00809632551380527     1
9       negative regulation of endothelial cell apoptotic process
GO:0007600      0.00812273753351948     8.78050314465409        0.431804027402948
3       480     sensory perception
GO:0035810      0.00896236744314161     133.601851851852        0.00899591723756141
1       10      positive regulation of urine volume
GO:0050908      0.00985451405509652     120.233333333333        0.00989550896131756
1       11      detection of light stimulus involved in visual perception
GO:0050962      0.00985451405509652     120.233333333333        0.00989550896131756
1       11      detection of light stimulus involved in sensory perception
Tissue: Whole_Blood=>Skin_Sun_Exposed_Lower_leg Type:   asymmetric
SourceGene:     CELF4(ENSG00000101489.10)
TargetGeneSet:  GNB1    RPL11   FAM176B BTBD19  RP4     RP11    LINC00568
NCSTN   SYT2    THPO    RPS7    UBC     RPL31   BTF3L4P2        MYEOV2  CCDC72
RPL24   RPL35A  RPL37   NSA2    CTD     TOMM7   AKR1B10 TCEB1   TXN     RPS24
USMG5   RPS13   COMMD6  NDUFB1  RPS3AP6 EME2    NOMO1   RPS7P1  RPL17   RPL27
POLR2E  CAPNS1  KDELR1  ZNFX1-AS1       EEF1B2P3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0019080      6.1554212472483e-19     84.0996376811594        0.303024012179088
13      151     viral genome expression
GO:0019083      6.1554212472483e-19     84.0996376811594        0.303024012179088
13      151     viral transcription
GO:0070972      2.28826561363151e-18    95.3340732519423        0.236800221437963
12      118     protein localization to endoplasmic reticulum
GO:0006415      1.04293495901498e-17    109.556944444444        0.182617119922497
11      91      translational termination
GO:0006414      5.40296037411533e-17    93.1489361702128        0.210712061449035
11      105     translational elongation
GO:0006614      5.40296037411533e-17    93.1489361702128        0.210712061449035
11      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      6.02164137774053e-17    92.1619883040936        0.212718842986645
11      106     cotranslational protein targeting to membrane
GO:0045047      6.02164137774053e-17    92.1619883040936        0.212718842986645
11      106     protein targeting to ER
GO:0072599      6.02164137774053e-17    92.1619883040936        0.212718842986645
11      106     establishment of protein localization to endoplasmic reticulum
GO:0019058      1.71709935812202e-16    52.9392201834862        0.463566535187876
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13	231	viral infectious cycle
GO:0000184	2.2498105684425e-16	80.9948559670782	0.238807002975573
11	119	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0022415	8.05900844682899e-16	46.6282894736842	0.521763199778562
13	260	viral reproductive process
GO:0072594	1.90328976671369e-15	52.3161764705882	0.40938343367241
12	204	establishment of protein localization to organelle
GO:0006413	3.55563203017854e-15	61.8955870764381	0.305030793716698
11	152	translational initiation
GO:0006612	3.82665601067179e-15	61.4553990610329	0.307037575254308
11	153	protein targeting to membrane
GO:0043624	3.82665601067179e-15	61.4553990610329	0.307037575254308
11	153	cellular protein complex disassembly
GO:0043241	5.48420494375765e-15	59.3442932728647	0.317071482942357
11	158	protein complex disassembly
GO:0000956	1.16255646827721e-14	55.1701828410689	0.339146079856065
11	169	nuclear-transcribed mRNA catabolic process
GO:0034623	1.60854144364843e-14	53.459100204499 0.349179987544115	11
174	cellular macromolecular complex disassembly
GO:0006402	2.0711872234438e-14	52.164005322688 0.357207113694554	11
178	mRNA catabolic process
GO:0032984	2.20425535631333e-14	51.8498677248677	0.359213895232164
11	179	macromolecular complex disassembly
GO:0033365	6.62768263607272e-14	28.3924473493101	0.949207667289461
14	473	protein localization to organelle
GO:0006401	9.9014971193746e-14	44.8190148911798	0.41139021521002
11	205	RNA catabolic process
GO:0016032	9.66873001902579e-13	25.9406392694064	0.905058473462044
13	451	viral reproduction
GO:0006605	1.81693803399836e-12	24.6058839479393	0.951214448827071
13	474	protein targeting
GO:0071845	3.5201848940134e-12	31.6725681725682	0.569925956681198
11	284	cellular component disassembly at cellular level
GO:0022411	4.09790316936296e-12	31.2063778580024	0.577953082831638
11	288	cellular component disassembly
GO:0006364	1.81397986870106e-06	30.1409932659933	0.208705279911425
5	104	rRNA processing
GO:0016072	2.39417513374434e-06	28.406746031746 0.220745969137084	5
110	rRNA metabolic process
GO:0022613	4.69180297661919e-06	16.9184038117927	0.451525845962217
6	225	ribonucleoprotein complex biogenesis
GO:0071843	6.63733170336328e-06	15.8861727934316	0.479620787488755
6	239	cellular component biogenesis at cellular level
GO:0042254	1.05971600280302e-05	20.6568287037037	0.299010449103868
5	149	ribosome biogenesis
GO:0034470	4.37716726698017e-05	15.1997863247863	0.401356307521971
5	200	ncRNA processing
GO:0034660	0.000231990509370735	10.5223214285714	0.571932738218808
5	285	ncRNA metabolic process
GO:0042273	0.000253467985720606	106.755555555556	0.0240813784513182
2	12	ribosomal large subunit biogenesis
GO:0042274	0.000583212288892517	66.6944444444444	0.0361220676769774
2	18	ribosomal small subunit biogenesis
GO:0007220	0.00072245030302257	59.2757201646091	0.0401356307521971
2	20	Notch receptor processing
GO:0035872	0.00414243345232755	23.1497584541063	0.096325513805273
2	48	nucleotide-binding domain, leucine rich repeat containing receptor
signaling pathway
GO:0050434	0.0054063355297355	20.0824598183089	0.110372984568542
2	55	positive regulation of viral transcription
GO:0016056	0.00600868615951344	257.5	0.00602034461282956	1	3
rhodopsin mediated signaling pathway
GO:0046782	0.00793065877349068	16.3612535612536	0.13445436301986
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2       67      regulation of viral transcription
GO:0008300      0.00800382376342956     171.654761904762        0.00802712615043942
1       4       isoprenoid catabolic process
GO:0048524      0.00985562566301913     14.5601217656012        0.150508615320739
2       75      positive regulation of viral reproduction
GO:0046826      0.00999509455396486     128.732142857143        0.0100339076880493
1       5       negative regulation of protein export from nucleus
Tissue: Whole_Blood=>Skin_Sun_Exposed_Lower_leg Type:   cluster
SourceGene:     CLNK(ENSG00000109684.9)
TargetGeneSet:  PADI1   CDC20   KIF2C   PSRC1   CENPF   EXO1    ODC1    BUB1
STEAP3  RP11    SIAH2   ECT2    TACC3   FAM50B  PSORS1C1        CSNK2B  GPSM3
GRIK2   LDHAP4  PTGS1   CDK1    KIF20B  MKI67   HBD     E2F8    SLC36A4 CDCA3
FZD10   BUB1B   PLCB2   CASC5   KIF23   CCNF    VWA3A   ORC6    SPAG5   SYNRG
TOP2A   KIF18B  USP32   NDC80   MAN2B1  UBE2S   TPX2    NTSR1   GTSE1   RP3
KIF4A
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0051301      1.21075483065493e-17    24.5271131639723        1.37623693862016
19      452     cell division
GO:0000087      1.40197949215378e-16    25.8166504697117        1.09611791571518
17      360     M phase of mitotic cell cycle
GO:0000280      2.24557936903206e-15    24.0769888793841        1.0656701958342 16
350     nuclear division
GO:0007067      2.24557936903206e-15    24.0769888793841        1.0656701958342 16
350     mitosis
GO:0048285      5.3648323216949e-15     22.6844229217111        1.12656563559615
16      370     organelle fission
GO:0007017      1.37540521879979e-14    21.2656309208033        1.1965953913224 16
393     microtubule-based process
GO:0010564      6.01653234092679e-13    18.1591910811512        1.26053560307245
15      414     regulation of cell cycle process
GO:0000226      1.68316174189478e-11    20.6468871595331        0.819043664798284
12      269     microtubule cytoskeleton organization
GO:0007059      3.08458184360342e-10    28.0226826608506        0.426268078333679
9       140     chromosome segregation
GO:0007051      3.96260831573879e-09    37.1484635320252        0.243581759047817
7       80      spindle organization
GO:0000236      6.08811110417298e-09    34.7550242550243        0.258805618988305
7       85      mitotic prometaphase
GO:0007346      1.869974447837e-08      14.1678377835776        0.922565912393606
10      303     regulation of mitotic cell cycle
GO:0000075      3.79823293767637e-08    15.6426732066217        0.736834821119646
9       242     cell cycle checkpoint
GO:0071173      5.39393193852549e-08    63.5632183908046        0.103522247595322
5       34      spindle assembly checkpoint
GO:0033043      5.83467262148604e-08    10.8348837209302        1.34274444675109
11      441     regulation of organelle organization
GO:0071156      8.01901196423996e-08    14.2709243697479        0.803819804857795
9       264     regulation of cell cycle arrest
GO:0007050      1.19431519081556e-07    11.5090938882517        1.12352086360805
10      369     cell cycle arrest
GO:0031577      1.61956069275609e-07    49.7920997920998        0.127880423500104
5       42      spindle checkpoint
GO:0008608      1.72823685853093e-07    110.723076923077        0.0517611237976611
4       17      attachment of spindle microtubules to kinetochore
GO:0007093      1.86368464392659e-07    20.4596642096642        0.423223306345582
7       139     mitotic cell cycle checkpoint
GO:0051313      2.80210845088583e-07    95.9466666666667        0.0578506677738565
4       19      attachment of spindle microtubules to chromosome
GO:0032886      3.07331770700919e-07    26.6043343653251        0.277074250916892
6       91      regulation of microtubule-based process
GO:0045786      5.69710459173975e-07    9.62942554070809        1.3305653587987 10
437     negative regulation of cell cycle
GO:0051983      7.59729081247084e-07    71.935  0.073074527714345       4       24
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regulation of chromosome segregation
GO:0007052      2.86790487866996e-06    49.5793103448276        0.100477475607224
4       33      mitotic spindle organization
GO:0007094      2.86790487866996e-06    49.5793103448276        0.100477475607224
4       33      mitotic cell cycle spindle assembly checkpoint
GO:0070507      3.25815398589644e-06    25.8866016612495        0.231402671095426
5       76      regulation of microtubule cytoskeleton organization
GO:0034453      3.65346320691979e-06    46.3741935483871        0.1065670195834 2
4       35      microtubule anchoring
GO:0045841      3.65346320691979e-06    46.3741935483871        0.1065670195834 2
4       35      negative regulation of mitotic metaphase/anaphase transition
GO:0071174      4.10105227245656e-06    44.921875       0.109611791571518       4
36      mitotic cell cycle spindle checkpoint
GO:0045839      6.30658648157389e-06    39.9194444444444        0.121790879523908
4       40      negative regulation of mitosis
GO:0051784      6.30658648157389e-06    39.9194444444444        0.121790879523908
4       40      negative regulation of nuclear division
GO:0007088      6.72475418879287e-06    22.1254247760272        0.267939934952598
5       88      regulation of mitosis
GO:0051783      6.72475418879287e-06    22.1254247760272        0.267939934952598
5       88      regulation of nuclear division
GO:0030071      8.45981383992258e-06    36.8410256410256        0.130925195488202
4       43      regulation of mitotic metaphase/anaphase transition
GO:0032507      9.79035488740564e-06    20.3945868945869        0.289253338869282
5       95      maintenance of protein location in cell
GO:0007091      1.01685457206719e-05    35.0390243902439        0.137014739464397
4       45      mitotic metaphase/anaphase transition
GO:0051651      1.74845489906267e-05    17.9801407742584        0.325790602726455
5       107     maintenance of location in cell
GO:0000819      1.81921946525286e-05    29.9145833333333        0.158328143381081
4       52      sister chromatid segregation
GO:0045185      1.91284276287608e-05    17.6319033530572        0.33188014670265
5       109     maintenance of protein location
GO:0007018      6.8113014651684e-05     13.3539210181546        0.432357622309875
5       142     microtubule-based movement
GO:0060236      9.0080051161491e-05     228.634920634921        0.0152238599404885
2       5       regulation of mitotic spindle organization
GO:0051493      9.82844315264563e-05    9.24206176598521        0.755103453048232
6       248     regulation of cytoskeleton organization
GO:0010389      0.000100957416931335    38.970189701897 0.0913431596429313      3
30      regulation of G2/M transition of mitotic cell cycle
GO:0006511      0.00010421123777288     7.44568097509274        1.10829700366757
7       364     ubiquitin-dependent protein catabolic process
GO:0010639      0.000109550369726576    12.0234480431849        0.47802920213134
5       157     negative regulation of organelle organization
GO:0031145      0.000115299689295311    18.1367088607595        0.25271607501211
4       83      anaphase-promoting complex-dependent proteasomal ubiquitin-dependent
protein catabolic process
GO:0019941      0.00011733408102932     7.29885654885655        1.12961040758425
7       371     modification-dependent protein catabolic process
GO:0043632      0.000123355982829683    7.23764636571176        1.13874472354854
7       374     modification-dependent macromolecule catabolic process
GO:0034501      0.000134858384279777    171.464285714286        0.0182686319285863
2       6       protein localization to kinetochore
GO:0051603      0.000157368710410237    6.9460166973256 1.18441630337001        7
389     proteolysis involved in cellular protein catabolic process
GO:0051235      0.000163579020883428    10.998609823911 0.520656009964708       5
171     maintenance of location
GO:0051488      0.000188436148093084    137.161904761905        0.021313403916684
2       7       activation of anaphase-promoting complex activity
GO:0090224      0.000188436148093084    137.161904761905        0.021313403916684
2       7       regulation of spindle organization
GO:0044257      0.000192682918905938    6.71118713650359        1.22399833921528
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7       402     cellular protein catabolic process
GO:0010948      0.000202529156755743    15.5597826086957        0.29229811085738
4       96      negative regulation of cell cycle process
GO:0051438      0.000202529156755743    15.5597826086957        0.29229811085738
4       96      regulation of ubiquitin-protein ligase activity
GO:0051340      0.000236960782968079    14.9072916666667        0.304477198809771
4       100     regulation of ligase activity
GO:0051988      0.000250761781355739    114.293650793651        0.0243581759047817
2       8       regulation of attachment of spindle microtubules to kinetochore
GO:0043161      0.000414060716645826    8.92596782302665        0.636357345512421
5       209     proteasomal ubiquitin-dependent protein catabolic process
GO:0000070      0.000440019098798648    22.8435843054083        0.149193827416788
3       49      mitotic sister chromatid segregation
GO:0010498      0.000481338980778608    8.62559241706161        0.657670749429105
5       216     proteasomal protein catabolic process
GO:0000085      0.000489713582063037    76.1798941798942        0.0334924918690748
2       11      G2 phase of mitotic cell cycle
GO:0051319      0.000489713582063037    76.1798941798942        0.0334924918690748
2       11      G2 phase
GO:0071780      0.000489713582063037    76.1798941798942        0.0334924918690748
2       11      mitotic cell cycle G2/M transition checkpoint
GO:0048015      0.000571105863466488    11.7090163934426        0.383641270500311
4       126     phosphatidylinositol-mediated signaling
GO:0048017      0.000571105863466488    11.7090163934426        0.383641270500311
4       126     inositol lipid-mediated signaling
GO:0030163      0.00067657689176099     5.39615640230394        1.50716213410837
7       495     protein catabolic process
GO:0071775      0.000691818707593643    62.3203463203463        0.0395820358452702
2       13      regulation of cell cycle cytokinesis
GO:0071777      0.000691818707593643    62.3203463203463        0.0395820358452702
2       13      positive regulation of cell cycle cytokinesis
GO:0032467      0.00092769643147102     52.7252747252747        0.0456715798214656
2       15      positive regulation of cytokinesis
GO:2000602      0.00101716443896408     9.97482517482517        0.447581482250363
4       147     regulation of interphase of mitotic cell cycle
GO:0051640      0.00109641375977974     9.76780821917808        0.456715798214656
4       150     organelle localization
GO:0051310      0.0011969473098622      45.6888888888889        0.0517611237976611
2       17      metaphase plate congression
GO:0031396      0.00166536096463478     8.68475609756098        0.511521694000415
4       168     regulation of protein ubiquitination
GO:0051439      0.00170862344283546     13.9824390243902        0.237492215071621
3       78      regulation of ubiquitin-protein ligase activity involved in mitotic
cell cycle
GO:0043623      0.00171933122862262     6.42162211311148        0.873849560584043
5       287     cellular protein complex assembly
GO:0050000      0.00183398782323813     36.0601503759398        0.0639402117500519
2       21      chromosome localization
GO:0051303      0.00183398782323813     36.0601503759398        0.0639402117500519
2       21      establishment of chromosome localization
GO:0051302      0.00197224465543193     13.2707625810435        0.249671303024012
3       82      regulation of cell division
GO:0051443      0.00197224465543193     13.2707625810435        0.249671303024012
3       82      positive regulation of ubiquitin-protein ligase activity
GO:0051129      0.00202708400405556     6.17572416207229        0.907342052453117
5       298     negative regulation of cellular component organization
GO:0034502      0.00220099556319947     32.6213151927438        0.0700297557262473
2       23      protein localization to chromosome
GO:0051351      0.00225992739481469     12.6276814575375        0.261850390976403
3       86      positive regulation of ligase activity
GO:0032465      0.00259981261753148     29.7805383022774        0.0761192997024427
2       25      regulation of cytokinesis
GO:0032855      0.00259981261753148     29.7805383022774        0.0761192997024427
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2       25      positive regulation of Rac GTPase activity
GO:0033205      0.00349134755729705     25.3615520282187        0.0882983876548336
2       29      cell cycle cytokinesis
GO:0051656      0.00356524281848327     10.6836734693878        0.307521970797869
3       101     establishment of organelle localization
GO:0030261      0.00373351828160888     24.4540816326531        0.0913431596429313
2       30      chromosome condensation
GO:0042306      0.00525349251927208     9.25577379667602        0.353193550619334
3       116     regulation of protein import into nucleus
GO:1900180      0.00525349251927208     9.25577379667602        0.353193550619334
3       116     regulation of protein localization to nucleus
GO:0051329      0.00566545348042037     4.81043466337584        1.15396858348903
5       379     interphase of mitotic cell cycle
GO:0051325      0.00618084301721672     4.70700765203383        1.17832675939381
5       387     interphase
GO:0031576      0.00656677947216334     18.0062656641604        0.121790879523908
2       40      G2/M transition checkpoint
GO:0031398      0.00675157317073719     8.42820613690008        0.386686042488409
3       127     positive regulation of protein ubiquitination
GO:0007098      0.00689025778493647     17.5433455433455        0.124835651512006
2       41      centrosome cycle
GO:0070301      0.00755853177685014     16.68524970964  0.130925195488202       2
43      cellular response to hydrogen peroxide
GO:0046822      0.00831327291252606     7.79377502730251        0.417133762369386
3       137     regulation of nucleocytoplasmic transport
GO:0031109      0.00861357420988902     15.5443722943723        0.140059511452495
2       46      microtubule polymerization or depolymerization
GO:0006260      0.0087746421073058      5.35719696969697        0.815998892810186
4       268     DNA replication
GO:0033157      0.0088198247624466      7.62150614206872        0.426268078333679
3       140     regulation of intracellular protein transport
GO:0010826      0.00910716059984296     167.5   0.00913431596429313     1       3
negative regulation of centrosome duplication
GO:0014038      0.00910716059984296     167.5   0.00913431596429313     1       3
regulation of Schwann cell differentiation
GO:0015808      0.00910716059984296     167.5   0.00913431596429313     1       3
L-alanine transport
GO:0030263      0.00910716059984296     167.5   0.00913431596429313     1       3
apoptotic chromosome condensation
GO:0030951      0.00910716059984296     167.5   0.00913431596429313     1       3
establishment or maintenance of microtubule cytoskeleton polarity
GO:0030953      0.00910716059984296     167.5   0.00913431596429313     1       3
astral microtubule organization
GO:0033211      0.00910716059984296     167.5   0.00913431596429313     1       3
adiponectin-mediated signaling pathway
GO:0038030      0.00910716059984296     167.5   0.00913431596429313     1       3
non-canonical Wnt receptor signaling pathway via MAPK cascade
GO:0000086      0.00952295802356474     7.40321743642968        0.43844716628607
3       144     G2/M transition of mitotic cell cycle
Tissue: Skin_Sun_Exposed_Lower_leg=>Whole_Blood Type:   asymmetric
SourceGene:     CTD-2561B21.10(ENSG00000262098.1)
TargetGeneSet:  CYP4A22 HAO2    APCS    APOA2   SERPINC1        AGXT    UGT2B10 RP13
HOXA11  PON1    AMBP    ITIH2   FRAT1   GLYATL1 RP11    APOC3   APOA1   MED6
RAB8A
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0010903      1.3522488597058e-09     Inf     0.00352916753165871     3       3
negative regulation of very-low-density lipoprotein particle remodeling
GO:0010901      1.35028408915895e-08    1546.28571428571        0.00588194588609785
3       5       regulation of very-low-density lipoprotein particle remodeling
GO:0035376      2.69860552913237e-08    1030.78571428571        0.00705833506331742
3       6       sterol import
GO:0035382      2.69860552913237e-08    1030.78571428571        0.00705833506331742
3       6       sterol transmembrane transport
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GO:0070508	2.69860552913237e-08	1030.78571428571	0.00705833506331742	3	6	cholesterol import
GO:0032371	4.61781324607167e-08	158.307692307692	0.0376444536710262	4	32	regulation of sterol transport
GO:0032374	4.61781324607167e-08	158.307692307692	0.0376444536710262	4	32	regulation of cholesterol transport
GO:0033344	7.54252620415058e-08	138.480769230769	0.0423500103799045	4	36	cholesterol efflux
GO:0034384	1.13094494321647e-07	515.285714285714	0.0105875025949761	3	9	high-density lipoprotein particle clearance
GO:0033700	1.61446143118067e-07	441.642857142857	0.0117638917721957	3	10	phospholipid efflux
GO:0034370	2.21827110259013e-07	386.410714285714	0.0129402809494153	3	11	triglyceride-rich lipoprotein particle remodeling
GO:0034372	2.21827110259013e-07	386.410714285714	0.0129402809494153	3	11	very-low-density lipoprotein particle remodeling
GO:0034377	3.83941628398622e-07	309.085714285714	0.0152930593038544	3	13	plasma lipoprotein particle assembly
GO:0065005	3.83941628398622e-07	309.085714285714	0.0152930593038544	3	13	protein-lipid complex assembly
GO:0032368	4.30764736795057e-07	86.7752639517345	0.0647014047470763	4	55	regulation of lipid transport
GO:0034375	4.88297831702514e-07	280.967532467532	0.016469448481074	3	14	high-density lipoprotein particle remodeling
GO:0015918	6.56275688479771e-07	77.608636977058	0.0717597398103937	4	61	sterol transport
GO:0030301	6.56275688479771e-07	77.608636977058	0.0717597398103937	4	61	cholesterol transport
GO:0043691	9.10217205166957e-07	220.714285714286	0.0199986160127327	3	17	reverse cholesterol transport
GO:0034367	2.3602611781074e-06	154.435714285714	0.0270569510760501	3	23	macromolecular complex remodeling
GO:0034368	2.3602611781074e-06	154.435714285714	0.0270569510760501	3	23	protein-lipid complex remodeling
GO:0034369	2.3602611781074e-06	154.435714285714	0.0270569510760501	3	23	plasma lipoprotein particle remodeling
GO:0071825	3.88690786963359e-06	128.660714285714	0.0317625077849284	3	27	protein-lipid complex subunit organization
GO:0071827	3.88690786963359e-06	128.660714285714	0.0317625077849284	3	27	plasma lipoprotein particle organization
GO:0018158	3.9050242570584e-06	1924.4	0.00352916753165871	2	3	protein oxidation
GO:0060620	3.9050242570584e-06	1924.4	0.00352916753165871	2	3	regulation of cholesterol import
GO:2000909	3.9050242570584e-06	1924.4	0.00352916753165871	2	3	regulation of sterol import
GO:0051346	4.64937173304342e-06	26.9204545454545	0.264687564874403	5	225	negative regulation of hydrolase activity
GO:0034381	5.38340488293117e-06	114.34126984127	0.0352916753165871	3	30	plasma lipoprotein particle clearance
GO:0015914	5.95586594228601e-06	110.25	0.0364680644938067	3	31	phospholipid transport
GO:0046470	6.56721295709553e-06	106.440886699507	0.0376444536710262	3	32	phosphatidylcholine metabolic process
GO:0008203	7.52834268934527e-06	40.8148148148148	0.131755587848592	4	112	cholesterol metabolic process
GO:0032488	7.80464344963398e-06	962.133333333333	0.00470555670887828	2	4	Cdc42 protein signal transduction
GO:0016125	9.57670561999659e-06	38.3117056856187	0.139990312089129	4	119	sterol metabolic process
GO:0002740	1.29987371887955e-05	641.377777777778	0.00588194588609785	2	5	negative regulation of cytokine secretion involved in immune response

GO:0030300	1.94846127555476e-05	481	0.00705833506331742	2	6	regulation of intestinal cholesterol absorption
GO:0034380	1.94846127555476e-05	481	0.00705833506331742	2	6	high-density lipoprotein particle assembly
GO:0097006	1.98952708483494e-05	71.7159468438538	0.0541139021521002	3	46	regulation of plasma lipoprotein particle levels
GO:0042439	2.40943119459989e-05	67.0248447204969	0.0576430696837589	3	49	ethanolamine-containing compound metabolic process
GO:0002374	2.72595813477165e-05	384.773333333333	0.00823472424053699	2	7	cytokine secretion involved in immune response
GO:0002739	2.72595813477165e-05	384.773333333333	0.00823472424053699	2	7	regulation of cytokine secretion involved in immune response
GO:0010873	2.72595813477165e-05	384.773333333333	0.00823472424053699	2	7	positive regulation of cholesterol esterification
GO:0018206	2.72595813477165e-05	384.773333333333	0.00823472424053699	2	7	peptidyl-methionine modification
GO:0042632	4.00892270692846e-05	56.0220779220779	0.068230572278735	3	58	cholesterol homeostasis
GO:0055092	4.00892270692846e-05	56.0220779220779	0.068230572278735	3	58	sterol homeostasis
GO:0010872	4.66660619555133e-05	274.8	0.0105875025949761	2	9	regulation of cholesterol esterification
GO:0006869	5.78309668742603e-05	23.8294314381271	0.221161165317279	4	188	lipid transport
GO:0060192	5.82922159086122e-05	240.433333333333	0.0117638917721957	2	10	negative regulation of lipase activity
GO:0030299	8.53769851992569e-05	192.32	0.0141166701266348	2	12	intestinal cholesterol absorption
GO:0032372	8.53769851992569e-05	192.32	0.0141166701266348	2	12	negative regulation of sterol transport
GO:0032375	8.53769851992569e-05	192.32	0.0141166701266348	2	12	negative regulation of cholesterol transport
GO:0034433	8.53769851992569e-05	192.32	0.0141166701266348	2	12	steroid esterification
GO:0034434	8.53769851992569e-05	192.32	0.0141166701266348	2	12	sterol esterification
GO:0034435	8.53769851992569e-05	192.32	0.0141166701266348	2	12	cholesterol esterification
GO:0010876	9.73990908507416e-05	20.7407947502734	0.252923673102207	4	215	lipid localization
GO:0055088	0.00010901190307642	39.4395604395604	0.0952875233547851	3	81	lipid homeostasis
GO:0044241	0.000135545311571209	147.907692307692	0.0176458376582935	2	15	lipid digestion
GO:0050995	0.000175320638318622	128.168888888889	0.0199986160127327	2	17	negative regulation of lipid catabolic process
GO:0046486	0.000199633252261023	17.1088989441931	0.304684796899869	4	259	glycerolipid metabolic process
GO:0042157	0.000203765598651705	31.6723122238586	0.117638917721957	3	100	lipoprotein metabolic process
GO:0006656	0.000220135062408993	113.074509803922	0.0223513943671718	2	19	phosphatidylcholine biosynthetic process
GO:0044058	0.000220135062408993	113.074509803922	0.0223513943671718	2	19	regulation of digestive system process
GO:0006066	0.000221117517056833	16.6435701702877	0.312919521140405	4	266	alcohol metabolic process
GO:0050892	0.00024442533295198	106.785185185185	0.0235277835443914	2	20	intestinal absorption
GO:0008202	0.000247666698828858	16.1413105413105	0.322330634558162	4	274	steroid metabolic process
GO:0045940	0.000269967461932187	101.157894736842	0.024704172721611	2	21	positive regulation of steroid metabolic process
GO:0070328	0.000269967461932187	101.157894736842	0.024704172721611			

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2       21      triglyceride homeostasis
GO:0032369      0.000296758818738297    96.0933333333333        0.0258805618988305
2       22      negative regulation of lipid transport
GO:0050710      0.000296758818738297    96.0933333333333        0.0258805618988305
2       22      negative regulation of cytokine secretion
GO:0046461      0.00035407871258923     87.3454545454545        0.0282333402532697
2       24      neutral lipid catabolic process
GO:0046464      0.00035407871258923     87.3454545454545        0.0282333402532697
2       24      acylglycerol catabolic process
GO:0006576      0.00045110696199473 6   23.9497767857143        0.154106982215764
3       131     cellular biogenic amine metabolic process
GO:0030258      0.000631622485874444    21.264880952381 0.17292920905127 7      3
147     lipid modification
GO:0046503      0.000632803923949525    64.0177777777778        0.0376444536710262
2       32      glycerolipid catabolic process
GO:0050709      0.000801542709238449    56.4705882352941        0.0423500103799045
2       36      negative regulation of protein secretion
GO:0002718      0.000893183771772659    53.3259259259259        0.0447027887343436
2       38      regulation of cytokine production involved in immune response
GO:0006650      0.000947064446731535    18.4182444061962        0.198809770950107
3       169     glycerophospholipid metabolic process
GO:0050994      0.000989645204184707    50.5122807017544        0.0470555670887828
2       40      regulation of lipid catabolic process
GO:0002367      0.00114333075790981     46.8065040650406        0.0505847346204415
2       43      cytokine production involved in immune response
GO:0044106      0.00119191032005846     16.9690476190476        0.215279219431181
3       183     cellular amine metabolic process
GO:0019216      0.0014100229618061      15.9794315632012        0.228219500380596
3       194     regulation of lipid metabolic process
GO:0022600      0.00154354313670417     39.9611111111111        0.0588194588609785
2       50      digestive system process
GO:0009308      0.00158348809063928     15.3284278535535        0.237630613798353
3       202     amine metabolic process
GO:0006954      0.00176185480686079     9.38931810547531        0.543491799875441
4       462     inflammatory response
GO:0034763      0.001798132633664       36.8769230769231        0.0635250155698568
2       54      negative regulation of transmembrane transport
GO:0045833      0.001798132633664       36.8769230769231        0.0635250155698568
2       54      negative regulation of lipid metabolic process
GO:0002700      0.00243884182336189     31.416393442623 0.0741125181648329      2
63      regulation of production of molecular mediator of immune response
GO:0019218      0.00243884182336189     31.416393442623 0.0741125181648329      2
63      regulation of steroid metabolic process
GO:0050728      0.00251577557013646     30.9075268817204        0.0752889073420525
2       64      negative regulation of inflammatory response
GO:0006644      0.0026202087052885 1    12.781512605042 0.283509791709916       3
241     phospholipid metabolic process
GO:0051051      0.00300684492669438     12.1577142857143        0.297626461836551
3       253     negative regulation of transport
GO:0009895      0.00325917000526778     26.9727699530516        0.0858764099370286
2       73      negative regulation of catabolic process
GO:0050707      0.00343672534671266     26.2301369863014        0.0882291882914677
2       75      regulation of cytokine secretion
GO:0009436      0.00352526115515339     451     0.00352916753165871     1       3
glyoxylate catabolic process
GO:0010982      0.00352526115515339     451     0.00352916753165871     1       3
regulation of high-density lipoprotein particle clearance
GO:0010989      0.00352526115515339     451     0.00352916753165871     1       3
negative regulation of low-density lipoprotein particle clearance
GO:0019532      0.00352526115515339     451     0.00352916753165871     1       3
oxalate transport
GO:0050711      0.00352526115515339     451     0.00352916753165871     1       3
negative regulation of interleukin-1 secretion
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GO:0031348	0.0038051697756915	24.8606060606061	0.092934745000346
2	79	negative regulation of defense response
GO:0006524	0.00469774665905387	300.645833333333	0.00470555670887828
1	4	alanine catabolic process
GO:0009080	0.00469774665905387	300.645833333333	0.00470555670887828
1	4	pyruvate family amino acid catabolic process
GO:0010915	0.00469774665905387	300.645833333333	0.00470555670887828
1	4	regulation of very-low-density lipoprotein particle clearance
GO:0010916	0.00469774665905387	300.645833333333	0.00470555670887828
1	4	negative regulation of very-low-density lipoprotein particle
clearance
GO:0042851	0.00469774665905387	300.645833333333	0.00470555670887828
1	4	L-alanine metabolic process
GO:0042853	0.00469774665905387	300.645833333333	0.00470555670887828
1	4	L-alanine catabolic process
GO:0090209	0.00469774665905387	300.645833333333	0.00470555670887828
1	4	negative regulation of triglyceride metabolic process
GO:0050663	0.00469846554697515	22.2449612403101	0.103522247595322
2	88	cytokine secretion
GO:0051129	0.00476380627719108	10.2704600484262	0.350563974811432
3	298	negative regulation of cellular component organization
GO:0045834	0.00512370858432933	21.2503703703704	0.1082278043042 2
92	positive regulation of lipid metabolic process
GO:0031647	0.00556610375852272	20.3404255319149	0.112933361013079
2	96	regulation of protein stability
GO:0051224	0.00567936485189403	20.1249122807018	0.114109750190298
2	97	negative regulation of protein transport
GO:0006641	0.00579368615702643	19.9138888888889	0.115286139367518
2	98	triglyceride metabolic process
GO:0006522	0.0058689336395202 4	225.46875	0.00588194588609785	1
5	alanine metabolic process
GO:0009078	0.0058689336395202 4	225.46875	0.00588194588609785	1
5	pyruvate family amino acid metabolic process
GO:0042866	0.0058689336395202 4	225.46875	0.00588194588609785	1
5	pyruvate biosynthetic process
GO:0051005	0.0058689336395202 4	225.46875	0.00588194588609785	1
5	negative regulation of lipoprotein lipase activity
GO:0002440	0.00602550001428533	19.5047619047619	0.117638917721957
2	100	production of molecular mediator of immune response
GO:0051241	0.00606434498783987	9.39130434782609	0.38232648259636
3	325	negative regulation of multicellular organismal process
GO:0006639	0.00638111380335713	18.9214521452145	0.121168085253616
2	103	acylglycerol metabolic process
GO:0006638	0.00650174719451049	18.7346405228758	0.122344474430835
2	104	neutral lipid metabolic process
GO:0060191	0.00650174719451049	18.7346405228758	0.122344474430835
2	104	regulation of lipase activity
GO:0002526	0.00662342443514267	18.5514563106796	0.123520863608055
2	105	acute inflammatory response
GO:0046474	0.00674614320171622	18.3717948717949	0.124697252785274
2	106	glycerophospholipid biosynthetic process
GO:0000244	0.00703882344487339	180.3625	0.00705833506331742	1
6	assembly of spliceosomal tri-snRNP
GO:0006545	0.00703882344487339	180.3625	0.00705833506331742	1
6	glycine biosynthetic process
GO:0006642	0.00703882344487339	180.3625	0.00705833506331742	1
6	triglyceride mobilization
GO:0006787	0.00703882344487339	180.3625	0.00705833506331742	1
6	porphyrin-containing compound catabolic process
GO:0010804	0.00703882344487339	180.3625	0.00705833506331742	1
6	negative regulation of tumor necrosis factor-mediated signaling pathway
GO:0010985	0.00703882344487339	180.3625	0.00705833506331742	1
6	negative regulation of lipoprotein particle clearance
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GO:0010988	0.00703882344487339	180.3625	0.00705833506331742	1
6	regulation of low-density lipoprotein particle clearance
GO:0033015	0.00703882344487339	180.3625	0.00705833506331742	1
6	tetrapyrrole catabolic process
GO:0034115	0.00703882344487339	180.3625	0.00705833506331742	1
6	negative regulation of heterotypic cell-cell adhesion
GO:0034379	0.00703882344487339	180.3625	0.00705833506331742	1
6	very-low-density lipoprotein particle assembly
GO:0034447	0.00703882344487339	180.3625	0.00705833506331742	1
6	very-low-density lipoprotein particle clearance
GO:0042167	0.00703882344487339	180.3625	0.00705833506331742	1
6	heme catabolic process
GO:0046149	0.00703882344487339	180.3625	0.00705833506331742	1
6	pigment catabolic process
GO:0046185	0.00703882344487339	180.3625	0.00705833506331742	1
6	aldehyde catabolic process
GO:0007586	0.00712052547373714	17.8529595015576	0.128226420316933
2	109	digestion
GO:0051048	0.00750419816453199	17.3624242424242	0.131755587848592
2	112	negative regulation of secretion
GO:0007266	0.00803010609168622	16.7485380116959	0.13646114455747
2	116	Rho protein signal transduction
GO:0032409	0.00803010609168622	16.7485380116959	0.13646114455747
2	116	regulation of transporter activity
GO:0050708	0.00803010609168622	16.7485380116959	0.13646114455747
2	116	regulation of protein secretion
GO:0034382	0.00820741742212772	150.291666666667	0.00823472424053699
1	7	chylomicron remnant clearance
GO:0071830	0.00820741742212772	150.291666666667	0.00823472424053699
1	7	triglyceride-rich lipoprotein particle clearance
GO:0032102	0.00857227320936868	16.1762711864407	0.141166701266348
2	120	negative regulation of response to external stimulus
GO:0010951	0.00898948094198444	15.7719008264463	0.144695868798007
2	123	negative regulation of endopeptidase activity
GO:0006835	0.00937471691699199	128.8125	0.00941111341775656	1
8	dicarboxylic acid transport
GO:0010896	0.00937471691699199	128.8125	0.00941111341775656	1
8	regulation of triglyceride catabolic process
GO:0032691	0.00937471691699199	128.8125	0.00941111341775656	1
8	negative regulation of interleukin-1 beta production
GO:0045416	0.00937471691699199	128.8125	0.00941111341775656	1
8	positive regulation of interleukin-8 biosynthetic process
GO:0046487	0.00937471691699199	128.8125	0.00941111341775656	1
8	glyoxylate metabolic process
GO:0048261	0.00937471691699199	128.8125	0.00941111341775656	1
8	negative regulation of receptor-mediated endocytosis
GO:0010466	0.00941569131911977	15.3870967741935	0.148225036329666
2	126	negative regulation of peptidase activity
GO:0007369	0.00955975150155423	15.2629333333333	0.149401425506885
2	127	gastrulation
Tissue: Whole_Blood=>Skin_Sun_Exposed_Lower_leg Type:	asymmetric
SourceGene:	EFNB2(ENSG00000125266.5)
TargetGeneSet:	TMEM222	PTPRU	FCGR1A	IQGAP3	CHRND	HACL1	QTRTD1	TACC3
PGBD1	KIFC1	SRPK1	BET3L	EPO	C7orf34	RP11	PTGS1	MKI67	TMEM80
NALCN-AS1	CTD	CASC5	KIF23	PRMT7	KIF18B	SKA1	UBE2S
GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0000087	9.06337916393127e-06	15.9050847457627	0.523147187045879
6	360	M phase of mitotic cell cycle
GO:0007017	1.49419123300948e-05	14.5147286821705	0.571102345858418
6	393	microtubule-based process
GO:0051301	3.29497714564307e-05	12.5417040358744	0.656840357068715
6	452	cell division
GO:0007059	4.44325215119729e-05	24.7301038062284	0.20344612829562
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4       140     chromosome segregation
GO:0000280      0.000119704517526048    12.758152173913 0.508615320739049       5
350     nuclear division
GO:0007067      0.000119704517526048    12.758152173913 0.508615320739049       5
350     mitosis
GO:0048285      0.000155361824498736    12.0419520547945        0.537679053352709
5       370     organelle fission
GO:0000226      0.000547386671293492    12.5771365149834        0.390907203653726
4       269     microtubule cytoskeleton organization
GO:0000387      0.000911800213719304    52.2722323049002        0.0450487855511729
2       31      spliceosomal snRNP assembly
GO:0007018      0.00108513254464467     17.1354916067146        0.206352501556986
3       142     microtubule-based movement
GO:0000377      0.00305627430583342     11.7985074626866        0.296450072659332
3       204     RNA splicing, via transesterification reactions with bulged
adenosine as nucleophile
GO:0000398      0.00305627430583342     11.7985074626866        0.296450072659332
3       204     nuclear mRNA splicing, via spliceosome
GO:0000375      0.00327241733481647     11.5080906148867        0.303716005812747
3       209     RNA splicing, via transesterification reactions
GO:0030953      0.00435352854395898     360.7   0.00435955989204899     1       3
astral microtubule organization
GO:0007286      0.0051008350516861 8    20.9912280701754        0.107535810670542
2       74      spermatid development
GO:0051051      0.00558547112112292     9.45333333333333        0.367656217562798
3       253     negative regulation of transport
GO:0048515      0.00565138779423199     19.8808864265928        0.113348557193274
2       78      spermatid differentiation
GO:0008617      0.0058006891129355 2    240.45  0.00581274652273199     1       4
guanosine metabolic process
GO:0010766      0.0058006891129355 2    240.45  0.00581274652273199     1       4
negative regulation of sodium ion transport
GO:0033601      0.0058006891129355 2    240.45  0.00581274652273199     1       4
positive regulation of mammary gland epithelial cell proliferation
GO:0035519      0.0058006891129355 2    240.45  0.00581274652273199     1       4
protein K29-linked ubiquitination
GO:0044314      0.0058006891129355 2    240.45  0.00581274652273199     1       4
protein K27-linked ubiquitination
GO:0051256      0.0058006891129355 2    240.45  0.00581274652273199     1       4
spindle midzone assembly involved in mitosis
GO:0071474      0.0058006891129355 2    240.45  0.00581274652273199     1       4
cellular hyperosmotic response
GO:0007051      0.00593647358341864     19.3684210526316        0.11625493045464
2       80      spindle organization
GO:0051302      0.0062280502125474      18.8815789473684        0.119161303716006
2       82      regulation of cell division
GO:0000236      0.0066775058852177      18.1953075459734        0.123520863608055
2       85      mitotic prometaphase
GO:0010700      0.00724584627557323     180.325 0.00726593315341499     1       5
negative regulation of norepinephrine secretion
GO:0032811      0.00724584627557323     180.325 0.00726593315341499     1       5
negative regulation of epinephrine secretion
GO:0035247      0.00724584627557323     180.325 0.00726593315341499     1       5
peptidyl-arginine omega-N-methylation
GO:0043985      0.00724584627557323     180.325 0.00726593315341499     1       5
histone H4-R3 methylation
GO:0051255      0.00724584627557323     180.325 0.00726593315341499     1       5
spindle midzone assembly
GO:0032886      0.00761949636656151     16.9615612063868        0.132239983392153
2       91      regulation of microtubule-based process
GO:0022618      0.00827901156141599     16.2275042444822        0.138052729914885
2       95      ribonucleoprotein complex assembly
GO:0032507      0.00827901156141599     16.2275042444822        0.138052729914885
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2       95      maintenance of protein location in cell
GO:0000244      0.0086890026683825      144.25  0.00871911978409799     1       6
assembly of spliceosomal tri-snRNP
GO:0001561      0.0086890026683825      144.25  0.00871911978409799     1       6
fatty acid alpha-oxidation
GO:0014060      0.0086890026683825      144.25  0.00871911978409799     1       6
regulation of epinephrine secretion
GO:0035092      0.0086890026683825      144.25  0.00871911978409799     1       6
sperm chromatin condensation
GO:0048630      0.0086890026683825      144.25  0.00871911978409799     1       6
skeletal muscle tissue growth
GO:0071826      0.00913836677595833     15.3941997851772        0.1453186630683 2
100     ribonucleoprotein complex subunit organization
Tissue: Whole_Blood=>Skin_Sun_Exposed_Lower_leg Type:   asymmetric
SourceGene:     ENSG00000201678.1
TargetGeneSet:  CTSS    APOA1BP F5      RP11    RNF187  STEAP3  VDAC1   VEGFA
SUMO2P8 SND1    SNX18P8 SPAG6   TMEM123 CASP7   LDHA    C11orf34        GAPDH   TPI1
ITPR2   CCDC59  MTHFD1  THBS1   PKM2    ATP6V0CP1       NGFR    ZFP161  ST8SIA5 GPI
ZNF155  SLC1A5  TNNC2   C20orf166       PGK1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006096      1.7034681239111e-09     69.9691558441558        0.120130094803128
6       62      glycolysis
GO:0006007      5.48555831129968e-09    56.7351778656126        0.1453186630683 6
75      glucose catabolic process
GO:0019320      1.66317054988727e-08    46.5551948051948        0.17438239568196
6       90      hexose catabolic process
GO:0046365      2.16362420271596e-08    44.426652892562 0.182132724378936       6
94      monosaccharide catabolic process
GO:0016052      4.79604883791271e-07    25.6058612440191        0.306137983530551
6       158     carbohydrate catabolic process
GO:0006006      1.79729684751679e-06    20.2144886363636        0.383641270500311
6       198     glucose metabolic process
GO:0006094      4.45119409156979e-06    44.3487654320988        0.112379766106152
4       58      gluconeogenesis
GO:0019318      4.72619195946909e-06    16.9796650717703        0.453394228773095
6       234     hexose metabolic process
GO:0019319      5.82153242119713e-06    41.2787356321839        0.120130094803128
4       62      hexose biosynthetic process
GO:0046364      7.48134892633618e-06    38.6048387096774        0.127880423500104
4       66      monosaccharide biosynthetic process
GO:0005996      7.74068860155788e-06    15.5246440306681        0.494083454432219
6       255     monosaccharide metabolic process
GO:0006091      1.31419964030225e-05    11.0863024544735        0.829285170576431
7       428     generation of precursor metabolites and energy
GO:0040037      0.000161361374145993    138.605769230769        0.01937582174244
2       10      negative regulation of fibroblast growth factor receptor signaling
pathway
GO:0016051      0.000377289487555806    13.4914772727273        0.348764791363919
4       180     carbohydrate biosynthetic process
GO:0002576      0.000539581552864316    21.5145 0.160819320462252       3       83
platelet degranulation
GO:0043536      0.000673184465959876    61.5598290598291        0.0387516434848799
2       20      positive regulation of blood vessel endothelial cell migration
GO:0030168      0.000763050545273834    11.1189358372457        0.420455331810947
4       217     platelet activation
GO:0040036      0.000816491689859045    55.3961538461538        0.0426268078333679
2       22      regulation of fibroblast growth factor receptor signaling pathway
GO:0051893      0.00105657514328283     48.1605351170569        0.0484395543560999
2       25      regulation of focal adhesion assembly
GO:0090109      0.00105657514328283     48.1605351170569        0.0484395543560999
2       25      regulation of cell-substrate junction assembly
GO:0009266      0.00109970566046966     16.6834951456311        0.205383710469864
3       106     response to temperature stimulus
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GO:0071363	0.00157815493339972	9.07884615384615	0.511521694000415	4	264	cellular response to growth factor stimulus
GO:0070848	0.00203506583769419	8.44922341696535	0.548335755311051	4	283	response to growth factor stimulus
GO:0043535	0.00218978410065928	32.5542986425339	0.0697529582727839	2	36	regulation of blood vessel endothelial cell migration
GO:0008543	0.0022957669888139	12.7961194029851	0.265448757871428	3	137	fibroblast growth factor receptor signaling pathway
GO:0010595	0.0026982209398674	29.1194331983806	0.0775032869697599	2	40	positive regulation of endothelial cell migration
GO:0002040	0.00297130648490636	27.6596153846154	0.0813784513182479	2	42	sprouting angiogenesis
GO:0048041	0.00297130648490636	27.6596153846154	0.0813784513182479	2	42	focal adhesion assembly
GO:0044344	0.00308196496660673	11.4958389261745	0.294512490485088	3	152	cellular response to fibroblast growth factor stimulus
GO:0071774	0.00308196496660673	11.4958389261745	0.294512490485088	3	152	response to fibroblast growth factor stimulus
GO:0043281	0.00381707674728929	10.6300621118012	0.317763476576016	3	164	regulation of cysteine-type endopeptidase activity involved in apoptotic process
GO:0010811	0.00402455770380558	23.5286415711948	0.0949415265379558	2	49	positive regulation of cell-substrate adhesion
GO:2000116	0.00415234104609564	10.306265060241	0.327451387447236	3	169	regulation of cysteine-type endopeptidase activity
GO:0002690	0.00418724208946625	23.036858974359	0.0968791087121998	2	50	positive regulation of leukocyte chemotaxis
GO:0043154	0.00522637642588173	20.468660968661	0.108504601757664	2	56	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process
GO:0001952	0.00540996391986441	20.0951048951049	0.110442183931908	2	57	regulation of cell-matrix adhesion
GO:0007044	0.00540996391986441	20.0951048951049	0.110442183931908	2	57	cell-substrate junction assembly
GO:0043534	0.00540996391986441	20.0951048951049	0.110442183931908	2	57	blood vessel endothelial cell migration
GO:0002688	0.00559649222465406	19.7348901098901	0.112379766106152	2	58	regulation of leukocyte chemotaxis
GO:2000117	0.00578595009340963	19.387314439946	0.114317348280396	2	59	negative regulation of cysteine-type endopeptidase activity
GO:0017014	0.00580189185011537	267.055555555556	0.00581274652273199	1	3	protein nitrosylation
GO:0018119	0.00580189185011537	267.055555555556	0.00581274652273199	1	3	peptidyl-cysteine S-nitrosylation
GO:0019682	0.00580189185011537	267.055555555556	0.00581274652273199	1	3	glyceraldehyde-3-phosphate metabolic process
GO:0038086	0.00580189185011537	267.055555555556	0.00581274652273199	1	3	VEGF-activated platelet-derived growth factor receptor signaling pathway
GO:0038091	0.00580189185011537	267.055555555556	0.00581274652273199	1	3	positive regulation of cell proliferation by VEGF-activated platelet derived growth factor receptor signaling pathway
GO:2001028	0.00580189185011537	267.055555555556	0.00581274652273199	1	3	positive regulation of endothelial cell chemotaxis
GO:0002687	0.00597832630913533	19.051724137931	0.11625493045464	2	60	positive regulation of leukocyte migration
GO:0010594	0.00762106028238352	16.7331002331002	0.131755587848592	2	68	regulation of endothelial cell migration
GO:0006868	0.00772863236978594	178.024691358025	0.00775032869697599	1	4	glutamine transport
GO:0010748	0.00772863236978594	178.024691358025	0.00775032869697599	1	4	negative regulation of plasma membrane long-chain fatty acid transport

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GO:0010757      0.00772863236978594     178.024691358025        0.00775032869697599
1       4       negative regulation of plasminogen activation
GO:0032914      0.00772863236978594     178.024691358025        0.00775032869697599
1       4       positive regulation of transforming growth factor beta1 production
GO:0001936      0.00806015101635253     16.2386877828054        0.13563075219708
2       70      regulation of endothelial cell proliferation
GO:0050921      0.00828389719599944     16.0022296544036        0.137568334371324
2       71      positive regulation of chemotaxis
GO:0001666      0.00840043789092221     7.93004651162791        0.422392913985191
3       218     response to hypoxia
GO:0036293      0.00861263490302064     7.85585253456221        0.426268078333679
3       220     response to decreased oxygen levels
GO:0010746      0.00965177200387202     133.509259259259        0.00968791087121998
1       5       regulation of plasma membrane long-chain fatty acid transport
GO:0031077      0.00965177200387202     133.509259259259        0.00968791087121998
1       5       post-embryonic camera-type eye development
GO:0038083      0.00965177200387202     133.509259259259        0.00968791087121998
1       5       peptidyl-tyrosine autophosphorylation
GO:0043117      0.00965177200387202     133.509259259259        0.00968791087121998
1       5       positive regulation of vascular permeability
GO:0060753      0.00965177200387202     133.509259259259        0.00968791087121998
1       5       regulation of mast cell chemotaxis
GO:0060754      0.00965177200387202     133.509259259259        0.00968791087121998
1       5       positive regulation of mast cell chemotaxis
GO:2001026      0.00965177200387202     133.509259259259        0.00968791087121998
1       5       regulation of endothelial cell chemotaxis
GO:0045766      0.00992752501912228     14.5212550607287        0.151131409591032
2       78      positive regulation of angiogenesis
Tissue: Whole_Blood=>Skin_Sun_Exposed_Lower_leg Type:   cluster
SourceGene:     ENSG00000201678.1
TargetGeneSet:  CTSS    APOA1BP F5      RP11    RNF187  STEAP3  VDAC1   VEGFA
SUMO2P8 SND1    SNX18P8 SPAG6   TMEM123 CASP7   LDHA    C11orf34        GAPDH   TPI1
ITPR2   CCDC59  MTHFD1  THBS1   PKM2    ATP6V0CP1       NGFR    ZFP161  ST8SIA5 GPI
ZNF155  SLC1A5  TNNC2   C20orf166       PGK1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006096      1.7034681239111e-09     69.9691558441558        0.120130094803128
6       62      glycolysis
GO:0006007      5.48555831129968e-09    56.7351778656126        0.1453186630683 6
75      glucose catabolic process
GO:0019320      1.66317054988727e-08    46.5551948051948        0.17438239568196
6       90      hexose catabolic process
GO:0046365      2.16362420271596e-08    44.426652892562 0.182132724378936       6
94      monosaccharide catabolic process
GO:0016052      4.79604883791271e-07    25.6058612440191        0.306137983530551
6       158     carbohydrate catabolic process
GO:0006006      1.79729684751679e-06    20.2144886363636        0.383641270500311
6       198     glucose metabolic process
GO:0006094      4.45119409156979e-06    44.3487654320988        0.112379766106152
4       58      gluconeogenesis
GO:0019318      4.72619195946909e-06    16.9796650717703        0.453394228773095
6       234     hexose metabolic process
GO:0019319      5.82153242119713e-06    41.2787356321839        0.120130094803128
4       62      hexose biosynthetic process
GO:0046364      7.48134892633618e-06    38.6048387096774        0.127880423500104
4       66      monosaccharide biosynthetic process
GO:0005996      7.74068860155788e-06    15.5246440306681        0.494083454432219
6       255     monosaccharide metabolic process
GO:0006091      1.31419964030225e-05    11.0863024544735        0.829285170576431
7       428     generation of precursor metabolites and energy
GO:0040037      0.000161361374145993    138.605769230769        0.01937582174244
2       10      negative regulation of fibroblast growth factor receptor signaling
pathway
GO:0016051      0.000377289487555806    13.4914772727273        0.348764791363919
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4       180     carbohydrate biosynthetic process
GO:0002576      0.000539581552864316    21.5145 0.160819320462252       3       83
platelet degranulation
GO:0043536      0.000673184465959876    61.5598290598291        0.0387516434848799
2       20      positive regulation of blood vessel endothelial cell migration
GO:0030168      0.000763050545273834    11.1189358372457        0.420455331810947
4       217     platelet activation
GO:0040036      0.000816491689859045    55.3961538461538        0.0426268078333679
2       22      regulation of fibroblast growth factor receptor signaling pathway
GO:0051893      0.00105657514328283     48.1605351170569        0.0484395543560999
2       25      regulation of focal adhesion assembly
GO:0090109      0.00105657514328283     48.1605351170569        0.0484395543560999
2       25      regulation of cell-substrate junction assembly
GO:0009266      0.00109970566046966     16.6834951456311        0.205383710469864
3       106     response to temperature stimulus
GO:0071363      0.00157815493339972     9.07884615384615        0.511521694000415
4       264     cellular response to growth factor stimulus
GO:0070848      0.00203506583769419     8.44922341696535        0.548335755311051
4       283     response to growth factor stimulus
GO:0043535      0.00218978410065928     32.5542986425339        0.0697529582727839
2       36      regulation of blood vessel endothelial cell migration
GO:0008543      0.0022957669888139      12.7961194029851        0.265448757871428
3       137     fibroblast growth factor receptor signaling pathway
GO:0010595      0.0026982209398674      29.1194331983806        0.0775032869697599
2       40      positive regulation of endothelial cell migration
GO:0002040      0.00297130648490636     27.6596153846154        0.0813784513182479
2       42      sprouting angiogenesis
GO:0048041      0.00297130648490636     27.6596153846154        0.0813784513182479
2       42      focal adhesion assembly
GO:0044344      0.00308196496660673     11.4958389261745        0.294512490485088
3       152     cellular response to fibroblast growth factor stimulus
GO:0071774      0.00308196496660673     11.4958389261745        0.294512490485088
3       152     response to fibroblast growth factor stimulus
GO:0043281      0.00381707674728929     10.6300621118012        0.317763476576016
3       164     regulation of cysteine-type endopeptidase activity involved in
apoptotic process
GO:0010811      0.00402455770380558     23.5286415711948        0.0949415265379558
2       49      positive regulation of cell-substrate adhesion
GO:2000116      0.00415234104609564     10.306265060241 0.327451387447236       3
169     regulation of cysteine-type endopeptidase activity
GO:0002690      0.00418724208946625     23.036858974359 0.0968791087121998      2
50      positive regulation of leukocyte chemotaxis
GO:0043154      0.00522637642588173     20.468660968661 0.108504601757664       2
56      negative regulation of cysteine-type endopeptidase activity involved in
apoptotic process
GO:0001952      0.00540996391986441     20.0951048951049        0.110442183931908
2       57      regulation of cell-matrix adhesion
GO:0007044      0.00540996391986441     20.0951048951049        0.110442183931908
2       57      cell-substrate junction assembly
GO:0043534      0.00540996391986441     20.0951048951049        0.110442183931908
2       57      blood vessel endothelial cell migration
GO:0002688      0.00559649222465406     19.7348901098901        0.112379766106152
2       58      regulation of leukocyte chemotaxis
GO:2000117      0.00578595009340963     19.387314439946 0.114317348280396       2
59      negative regulation of cysteine-type endopeptidase activity
GO:0017014      0.00580189185011537     267.055555555556        0.00581274652273199
1       3       protein nitrosylation
GO:0018119      0.00580189185011537     267.055555555556        0.00581274652273199
1       3       peptidyl-cysteine S-nitrosylation
GO:0019682      0.00580189185011537     267.055555555556        0.00581274652273199
1       3       glyceraldehyde-3-phosphate metabolic process
GO:0038086      0.00580189185011537     267.055555555556        0.00581274652273199
1       3       VEGF-activated platelet-derived growth factor receptor signaling
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pathway
GO:0038091      0.00580189185011537     267.055555555556        0.00581274652273199
1       3       positive regulation of cell proliferation by VEGF-activated platelet
derived growth factor receptor signaling pathway
GO:2001028      0.00580189185011537     267.055555555556        0.00581274652273199
1       3       positive regulation of endothelial cell chemotaxis
GO:0002687      0.00597832630913533     19.051724137931 0.11625493045464        2
60      positive regulation of leukocyte migration
GO:0010594      0.00762106028238352     16.7331002331002        0.131755587848592
2       68      regulation of endothelial cell migration
GO:0006868      0.00772863236978594     178.024691358025        0.00775032869697599
1       4       glutamine transport
GO:0010748      0.00772863236978594     178.024691358025        0.00775032869697599
1       4       negative regulation of plasma membrane long-chain fatty acid
transport
GO:0010757      0.00772863236978594     178.024691358025        0.00775032869697599
1       4       negative regulation of plasminogen activation
GO:0032914      0.00772863236978594     178.024691358025        0.00775032869697599
1       4       positive regulation of transforming growth factor beta1 production
GO:0001936      0.00806015101635253     16.2386877828054        0.13563075219708
2       70      regulation of endothelial cell proliferation
GO:0050921      0.00828389719599944     16.0022296544036        0.137568334371324
2       71      positive regulation of chemotaxis
GO:0001666      0.00840043789092221     7.93004651162791        0.422392913985191
3       218     response to hypoxia
GO:0036293      0.00861263490302064     7.85585253456221        0.426268078333679
3       220     response to decreased oxygen levels
GO:0010746      0.00965177200387202     133.509259259259        0.00968791087121998
1       5       regulation of plasma membrane long-chain fatty acid transport
GO:0031077      0.00965177200387202     133.509259259259        0.00968791087121998
1       5       post-embryonic camera-type eye development
GO:0038083      0.00965177200387202     133.509259259259        0.00968791087121998
1       5       peptidyl-tyrosine autophosphorylation
GO:0043117      0.00965177200387202     133.509259259259        0.00968791087121998
1       5       positive regulation of vascular permeability
GO:0060753      0.00965177200387202     133.509259259259        0.00968791087121998
1       5       regulation of mast cell chemotaxis
GO:0060754      0.00965177200387202     133.509259259259        0.00968791087121998
1       5       positive regulation of mast cell chemotaxis
GO:2001026      0.00965177200387202     133.509259259259        0.00968791087121998
1       5       regulation of endothelial cell chemotaxis
GO:0045766      0.00992752501912228     14.5212550607287        0.151131409591032
2       78      positive regulation of angiogenesis
Tissue: Whole_Blood=>Skin_Sun_Exposed_Lower_leg Type:   asymmetric
SourceGene:     ENSG00000225196.1
TargetGeneSet:  AMY2A   KCNJ9   CENPF   BUB1    HNRNPA1P24      TACC3   OCLN
LMNB1   KIF20A  IMMP2L-IT1      RP11    CDK1    MKI67   DLGAP5  CTD     KIF23
TOP2A   RP1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0000087      9.48956711965608e-07    26.5197740112994        0.373676562175628
6       360     M phase of mitotic cell cycle
GO:0007017      1.58315647546335e-06    24.2015503875969        0.407930247041727
6       393     microtubule-based process
GO:0010564      2.14314006566758e-06    22.921568627451 0.429728046501972       6
414     regulation of cell cycle process
GO:0051301      3.5662306932291e-06     20.9118086696562        0.469171683620511
6       452     cell division
GO:0010389      3.61224493267115e-06    133.416666666667        0.0311397135146357
3       30      regulation of G2/M transition of mitotic cell cycle
GO:0000226      5.55086977687262e-06    26.8409090909091        0.279219431181233
5       269     microtubule cytoskeleton organization
GO:0007346      9.90879614328105e-06    23.7214765100671        0.31451110649782
5       303     regulation of mitotic cell cycle
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GO:0007093	1.0305623562036e-05	38.5212121212121	0.144280672617812	4	139	mitotic cell cycle checkpoint
GO:0007059	1.06022401963643e-05	38.2352941176471	0.1453186630683	4	140	chromosome segregation
GO:0030071	1.08913549185673e-05	89.975	0.0446335893709778	3	43	regulation of mitotic metaphase/anaphase transition
GO:0007091	1.25075550389255e-05	85.6785714285714	0.0467095702719535	3	45	mitotic metaphase/anaphase transition
GO:0000280	1.99136320865947e-05	20.4217391304348	0.363296657670749	5	350	nuclear division
GO:0007067	1.99136320865947e-05	20.4217391304348	0.363296657670749	5	350	mitosis
GO:0048285	2.60259821483528e-05	19.2753424657534	0.384056466680507	5	370	organelle fission
GO:0006921	5.38727986489396e-05	51.3071428571429	0.0757733028856135	3	73	cellular component disassembly involved in apoptotic process
GO:0071780	5.5013756314794e-05	246.615384615385	0.0114178949553664	2	11	mitotic cell cycle G2/M transition checkpoint
GO:0000075	9.05617880368276e-05	21.6928953399542	0.251193689018061	4	242	cell cycle checkpoint
GO:0007088	9.41657073479172e-05	42.2088235294118	0.0913431596429313	3	88	regulation of mitosis
GO:0051783	9.41657073479172e-05	42.2088235294118	0.0913431596429313	3	88	regulation of nuclear division
GO:0071156	0.000126805278921584	19.8265734265734	0.274029478928794	4	264	regulation of cell cycle arrest
GO:0050000	0.000208796395273854	116.736842105263	0.021797799460245	2	21	chromosome localization
GO:0051303	0.000208796395273854	116.736842105263	0.021797799460245	2	21	establishment of chromosome localization
GO:0001578	0.000347734809616318	88.6830769230769	0.0280257421631721	2	27	microtubule bundle formation
GO:0007018	0.000387608331108328	25.7140287769784	0.147394643969275	3	142	microtubule-based movement
GO:0000086	0.000403833428618816	25.3457446808511	0.149470624870251	3	144	G2/M transition of mitotic cell cycle
GO:2000602	0.000428983149259857	24.8125	0.152584596221715	3	147	regulation of interphase of mitotic cell cycle
GO:0030261	0.000430178861301616	79.1648351648352	0.0311397135146357	2	30	chromosome condensation
GO:0051640	0.000455122075835866	24.3010204081633	0.155698567573178	3	150	organelle localization
GO:0007050	0.000456665420313837	14.0184308841843	0.383018476230019	4	369	cell cycle arrest
GO:0007094	0.000521209766007249	71.4888337468983	0.0342536848660992	2	33	mitotic cell cycle spindle assembly checkpoint
GO:0071173	0.000553453451453472	69.25	0.0352916753165871	2	34	spindle assembly checkpoint
GO:0045841	0.000586644262671061	67.1468531468531	0.0363296657670749	2	35	negative regulation of mitotic metaphase/anaphase transition
GO:0071174	0.000620780463234249	65.1674208144796	0.0373676562175628	2	36	mitotic cell cycle spindle checkpoint
GO:0031576	0.000766744506681834	58.2914979757085	0.0415196180195142	2	40	G2/M transition checkpoint
GO:0045839	0.000766744506681834	58.2914979757085	0.0415196180195142	2	40	negative regulation of mitosis
GO:0051784	0.000766744506681834	58.2914979757085	0.0415196180195142	2	40	negative regulation of nuclear division
GO:0031577	0.000845353877431115	55.3692307692308	0.0435955989204899	2	42	spindle checkpoint
GO:0045786	0.000863583540872574	11.7598152424942	0.453601826863193	4	437	negative regulation of cell cycle
GO:0000819	0.0012941241237902	44.2646153846154	0.0539755034253685			

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2       52      sister chromatid segregation
GO:0031100      0.0012941241237902      44.2646153846154        0.0539755034253685
2       52      organ regeneration
GO:0006260      0.00243276797566254     13.3688679245283        0.278181440730745
3       268     DNA replication
GO:0071845      0.00286802235507748     12.5934163701068        0.294789287938551
3       284     cellular component disassembly at cellular level
GO:0022411      0.00298389037380053     12.4131578947368        0.298941249740502
3       288     cellular component disassembly
GO:0007051      0.00303273524619927     28.3195266272189        0.0830392360390284
2       80      spindle organization
GO:0014038      0.00311095525981198     515.5   0.00311397135146357     1       3
regulation of Schwann cell differentiation
GO:0030263      0.00311095525981198     515.5   0.00311397135146357     1       3
apoptotic chromosome condensation
GO:0030953      0.00311095525981198     515.5   0.00311397135146357     1       3
astral microtubule organization
GO:0035845      0.00311095525981198     515.5   0.00311397135146357     1       3
photoreceptor cell outer segment organization
GO:0051305      0.00311095525981198     515.5   0.00311397135146357     1       3
chromosome movement towards spindle pole
GO:0016202      0.00326008654118065     27.2649572649573        0.086153207390492
2       83      regulation of striated muscle tissue development
GO:0000236      0.00341597961863128     26.6042632066728        0.0882291882914677
2       85      mitotic prometaphase
GO:0048634      0.00341597961863128     26.6042632066728        0.0882291882914677
2       85      regulation of muscle organ development
GO:0070925      0.00407387402393737     24.2519019442096        0.0965331118953706
2       93      organelle assembly
GO:0051256      0.00414593142752384     343.642857142857        0.00415196180195142
1       4       spindle midzone assembly involved in mitosis
GO:0000910      0.00415994530842383     23.9866220735786        0.0975711023458584
2       94      cytokinesis
GO:0010948      0.00433462643898035     23.4729950900164        0.0996470832468341
2       96      negative regulation of cell cycle process
GO:0042493      0.00460505766649717     10.5878378378378        0.348764791363919
3       336     response to drug
GO:0051656      0.00478606257485682     22.2797202797203        0.104837035499273
2       101     establishment of organelle localization
GO:0045787      0.00487886269765889     22.0553846153846        0.105875025949761
2       102     positive regulation of cell cycle
GO:0044245      0.00517990464193407     257.714285714286        0.00518995225243928
1       5       polysaccharide digestion
GO:0051255      0.00517990464193407     257.714285714286        0.00518995225243928
1       5       spindle midzone assembly
GO:0000244      0.00621287580560359     206.157142857143        0.00622794270292713
1       6       assembly of spliceosomal tri-snRNP
GO:0034501      0.00621287580560359     206.157142857143        0.00622794270292713
1       6       protein localization to kinetochore
GO:0046498      0.00621287580560359     206.157142857143        0.00622794270292713
1       6       S-adenosylhomocysteine metabolic process
GO:0046548      0.00621287580560359     206.157142857143        0.00622794270292713
1       6       retinal rod cell development
GO:0042306      0.00626490232608711     19.3279352226721        0.120406892256591
2       116     regulation of protein import into nucleus
GO:1900180      0.00626490232608711     19.3279352226721        0.120406892256591
2       116     regulation of protein localization to nucleus
GO:0051329      0.00644008806096661     9.34840425531915        0.393398380734897
3       379     interphase of mitotic cell cycle
GO:0051325      0.00682344901783071     9.1484375       0.4017023043388 3       387
interphase
GO:0031099      0.0069078784347415      18.3538461538462        0.126634834959518
2       122     regeneration
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GO:0000712      0.00724484582034324     171.785714285714        0.00726593315341499
1       7       resolution of meiotic recombination intermediates
GO:0007095      0.00724484582034324     171.785714285714        0.00726593315341499
1       7       mitotic cell cycle G2/M transition DNA damage checkpoint
GO:0022027      0.00724484582034324     171.785714285714        0.00726593315341499
1       7       interkinetic nuclear migration
GO:0040016      0.00724484582034324     171.785714285714        0.00726593315341499
1       7       embryonic cleavage
GO:0045091      0.00724484582034324     171.785714285714        0.00726593315341499
1       7       regulation of retroviral genome replication
GO:0045842      0.00724484582034324     171.785714285714        0.00726593315341499
1       7       positive regulation of mitotic metaphase/anaphase transition
GO:0046500      0.00724484582034324     171.785714285714        0.00726593315341499
1       7       S-adenosylmethionine metabolic process
GO:0051307      0.00724484582034324     171.785714285714        0.00726593315341499
1       7       meiotic chromosome separation
GO:0071107      0.00724484582034324     171.785714285714        0.00726593315341499
1       7       response to parathyroid hormone stimulus
GO:0042670      0.00827581558721535     147.234693877551        0.00830392360390284
1       8       retinal cone cell differentiation
GO:0046549      0.00827581558721535     147.234693877551        0.00830392360390284
1       8       retinal cone cell development
GO:0046822      0.0086409709971007 4    16.2974358974359        0.142204691716836
2       137     regulation of nucleocytoplasmic transport
GO:0033157      0.00900879715509991     15.9397993311037        0.1453186630683 2
140     regulation of intracellular protein transport
GO:0006265      0.00930578600653176     128.821428571429        0.0093419140543907
1       9       DNA topological change
GO:0033160      0.00930578600653176     128.821428571429        0.0093419140543907
1       9       positive regulation of protein import into nucleus, translocation
GO:0035082      0.00930578600653176     128.821428571429        0.0093419140543907
1       9       axoneme assembly
GO:0045090      0.00930578600653176     128.821428571429        0.0093419140543907
1       9       retroviral genome replication
GO:0033043      0.0097705449191423      7.98972602739726        0.457753788665144
3       441     regulation of organelle organization
Tissue: Whole_Blood=>Skin_Sun_Exposed_Lower_leg Type:   asymmetric
SourceGene:     ENSG00000225231.1
TargetGeneSet:  ST7L    NCKAP1  CTNNB1  PCCB    SEPT11  RP11    RXRB    UNC5B
FRA10AC1        SCD     ZCCHC8  C14orf64        LMAN1L  RPL9P9  APOBR   HSD17B2
DBNDD1  ATP5A1  CTIF    ZNF44   ZNF418  PXMP4   CLDN14  COMT    SUN2    VGLL1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0051176      6.02870325080865e-06    1518.84210526316        0.00435955989204899
2       3       positive regulation of sulfur metabolic process
GO:0042762      1.20468370280895e-05    759.368421052632        0.00581274652273199
2       4       regulation of sulfur metabolic process
GO:0033002      0.000335926851389223    25.9746376811594        0.138052729914885
3       95      muscle cell proliferation
GO:0008210      0.000415403080031183    79.8393351800554        0.030516919244343
2       21      estrogen metabolic process
GO:0048660      0.00384061820742735     24.3938879456706        0.0930039443637119
2       64      regulation of smooth muscle cell proliferation
GO:0048659      0.00420107984164143     23.2631578947368        0.0973635042557608
2       67      smooth muscle cell proliferation
GO:0003136      0.00435352854395898     360.7   0.00435955989204899     1       3
negative regulation of heart induction by canonical Wnt receptor signaling pathway
GO:0009997      0.00435352854395898     360.7   0.00435955989204899     1       3
negative regulation of cardioblast cell fate specification
GO:0033239      0.00435352854395898     360.7   0.00435955989204899     1       3
negative regulation of cellular amine metabolic process
GO:0036022      0.00435352854395898     360.7   0.00435955989204899     1       3
limb joint morphogenesis
GO:0036023      0.00435352854395898     360.7   0.00435955989204899     1       3
```

						embryonic skeletal limb joint morphogenesis
GO:0042684	0.00435352854395898	360.7	0.00435955989204899	1	3	cardioblast cell fate commitment
GO:0042685	0.00435352854395898	360.7	0.00435955989204899	1	3	cardioblast cell fate specification
GO:0042686	0.00435352854395898	360.7	0.00435955989204899	1	3	regulation of cardioblast cell fate specification
GO:0043578	0.00435352854395898	360.7	0.00435955989204899	1	3	nuclear matrix organization
GO:0060066	0.00435352854395898	360.7	0.00435955989204899	1	3	oviduct development
GO:0060423	0.00435352854395898	360.7	0.00435955989204899	1	3	foregut regionalization
GO:0060424	0.00435352854395898	360.7	0.00435955989204899	1	3	lung field specification
GO:0060492	0.00435352854395898	360.7	0.00435955989204899	1	3	lung induction
GO:0061197	0.00435352854395898	360.7	0.00435955989204899	1	3	fungiform papilla morphogenesis
GO:0061198	0.00435352854395898	360.7	0.00435955989204899	1	3	fungiform papilla formation
GO:0070602	0.00435352854395898	360.7	0.00435955989204899	1	3	regulation of centromeric sister chromatid cohesion
GO:0090292	0.00435352854395898	360.7	0.00435955989204899	1	3	nuclear matrix anchoring at nuclear membrane
GO:1901099	0.00435352854395898	360.7	0.00435955989204899	1	3	negative regulation of signal transduction in absence of ligand
GO:1901320	0.00435352854395898	360.7	0.00435955989204899	1	3	negative regulation of heart induction
GO:2000017	0.00435352854395898	360.7	0.00435955989204899	1	3	positive regulation of determination of dorsal identity
GO:2000044	0.00435352854395898	360.7	0.00435955989204899	1	3	negative regulation of cardiac cell fate specification
GO:2001240	0.00435352854395898	360.7	0.00435955989204899	1	3	negative regulation of extrinsic apoptotic signaling pathway in absence of ligand
GO:0035051	0.00537282938892435	20.4210526315789	0.110442183931908	2	76	cardiac cell differentiation
GO:0006172	0.00580068911293552	240.45	0.00581274652273199	1	4	ADP biosynthetic process
GO:0009136	0.00580068911293552	240.45	0.00581274652273199	1	4	purine nucleoside diphosphate biosynthetic process
GO:0009180	0.00580068911293552	240.45	0.00581274652273199	1	4	purine ribonucleoside diphosphate biosynthetic process
GO:0009188	0.00580068911293552	240.45	0.00581274652273199	1	4	ribonucleoside diphosphate biosynthetic process
GO:0010457	0.00580068911293552	240.45	0.00581274652273199	1	4	centriole-centriole cohesion
GO:0014045	0.00580068911293552	240.45	0.00581274652273199	1	4	establishment of endothelial blood-brain barrier
GO:0022009	0.00580068911293552	240.45	0.00581274652273199	1	4	central nervous system vasculogenesis
GO:0042420	0.00580068911293552	240.45	0.00581274652273199	1	4	dopamine catabolic process
GO:0060789	0.00580068911293552	240.45	0.00581274652273199	1	4	hair follicle placode formation
GO:0060912	0.00580068911293552	240.45	0.00581274652273199	1	4	cardiac cell fate specification
GO:0060916	0.00580068911293552	240.45	0.00581274652273199	1	4	mesenchymal cell proliferation involved in lung development
GO:0061196	0.00580068911293552	240.45	0.00581274652273199	1	4	fungiform papilla development
GO:0061316	0.00580068911293552	240.45	0.00581274652273199	1	4	canonical Wnt receptor signaling pathway involved in heart development

GO:0061325	0.00580068911293552	240.45	0.00581274652273199	1	4	cell proliferation involved in outflow tract morphogenesis
GO:0070601	0.00580068911293552	240.45	0.00581274652273199	1	4	centromeric sister chromatid cohesion
GO:2000015	0.00580068911293552	240.45	0.00581274652273199	1	4	regulation of determination of dorsal identity
GO:2000043	0.00580068911293552	240.45	0.00581274652273199	1	4	regulation of cardiac cell fate specification
GO:2000136	0.00580068911293552	240.45	0.00581274652273199	1	4	regulation of cell proliferation involved in heart morphogenesis
GO:0008202	0.00696376315929654	8.70787207872079	0.398173136807141	3	274	steroid metabolic process
GO:0007097	0.00724584627557323	180.325	0.00726593315341499	1	5	nuclear migration
GO:0019614	0.00724584627557323	180.325	0.00726593315341499	1	5	catechol-containing compound catabolic process
GO:0019626	0.00724584627557323	180.325	0.00726593315341499	1	5	short-chain fatty acid catabolic process
GO:0034313	0.00724584627557323	180.325	0.00726593315341499	1	5	diol catabolic process
GO:0035117	0.00724584627557323	180.325	0.00726593315341499	1	5	embryonic arm morphogenesis
GO:0035140	0.00724584627557323	180.325	0.00726593315341499	1	5	arm morphogenesis
GO:0038034	0.00724584627557323	180.325	0.00726593315341499	1	5	signal transduction in absence of ligand
GO:0042424	0.00724584627557323	180.325	0.00726593315341499	1	5	catecholamine catabolic process
GO:0044340	0.00724584627557323	180.325	0.00726593315341499	1	5	canonical Wnt receptor signaling pathway involved in regulation of cell proliferation
GO:0045764	0.00724584627557323	180.325	0.00726593315341499	1	5	positive regulation of cellular amino acid metabolic process
GO:0060431	0.00724584627557323	180.325	0.00726593315341499	1	5	primary lung bud formation
GO:0060856	0.00724584627557323	180.325	0.00726593315341499	1	5	establishment of blood-brain barrier
GO:0061046	0.00724584627557323	180.325	0.00726593315341499	1	5	regulation of branching involved in lung morphogenesis
GO:0071680	0.00724584627557323	180.325	0.00726593315341499	1	5	response to indole-3-methanol
GO:0071681	0.00724584627557323	180.325	0.00726593315341499	1	5	cellular response to indole-3-methanol
GO:0090286	0.00724584627557323	180.325	0.00726593315341499	1	5	cytoskeletal anchoring at nuclear membrane
GO:0097192	0.00724584627557323	180.325	0.00726593315341499	1	5	extrinsic apoptotic signaling pathway in absence of ligand
GO:2001239	0.00724584627557323	180.325	0.00726593315341499	1	5	regulation of extrinsic apoptotic signaling pathway in absence of ligand
GO:0032526	0.00729915945075009	17.3539019963702	0.129333610130787	2	89	response to retinoic acid
GO:0032507	0.00827901156141599	16.2275042444822	0.138052729914885	2	95	maintenance of protein location in cell
GO:0000244	0.00868900266683825	144.25	0.00871911978409799	1	6	assembly of spliceosomal tri-snRNP
GO:0003159	0.00868900266683825	144.25	0.00871911978409799	1	6	morphogenesis of an endothelium
GO:0003263	0.00868900266683825	144.25	0.00871911978409799	1	6	cardioblast proliferation
GO:0009133	0.00868900266683825	144.25	0.00871911978409799	1	6	nucleoside diphosphate biosynthetic process
GO:0035315	0.00868900266683825	144.25	0.00871911978409799	1	6	hair cell differentiation

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GO:0046031      0.00868900266683825     144.25  0.00871911978409799     1       6
ADP metabolic process
GO:0060439      0.00868900266683825     144.25  0.00871911978409799     1       6
trachea morphogenesis
GO:0061154      0.00868900266683825     144.25  0.00871911978409799     1       6
endothelial tube morphogenesis
GO:0061323      0.00868900266683825     144.25  0.00871911978409799     1       6
cell proliferation involved in heart morphogenesis
GO:0090381      0.00868900266683825     144.25  0.00871911978409799     1       6
regulation of heart induction
GO:0034754      0.00913836677595833     15.3941997851772        0.1453186630683 2
100     cellular hormone metabolic process
GO:0033189      0.00949287242636354     15.0842105263158        0.148225036329666
2       102     response to vitamin A
Tissue: Skin_Sun_Exposed_Lower_leg=>Whole_Blood Type:   asymmetric
SourceGene:     IRF4(ENSG00000137265.9)
TargetGeneSet:  SLC2A5  CDCA8   CDC20   CTTNBP2NL       FCRL6   IGKJ5   IGKC
IGKJ4   IGKJ1   IGKV4-1 IGKV1-5 IGKV1-9 IGKV1-12        IGKV2-26        IGKV2-40
COBLL1  AGAP1   CMC1    WDR53   RP11    MYOM2   ESCO2   MRPL15  COPS5   WDR34
MMP21   CDCA5   POU2AF1 CD27    RFC3    DLGAP5  7SK     NUDT14  IGHG2   IGHA1
IGHV3-15        IGHV3-33        IGHV3-48        FBN1    SLC27A2 KIAA0101        CDT1
GNG8    TK1     TYMS    ALPK2   CCNE1   PLCB1   IGLV7-43        IGLV3-27
IGLV2-14        IGLV2-11        CENPM
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006958      7.01309979723971e-10    81.6875 0.103799045048786       6       50
complement activation, classical pathway
GO:0016064      2.29310278073255e-09    41.8975752508361        0.230433880008304
7       111     immunoglobulin mediated immune response
GO:0019724      2.7664437309013e-09     40.7143437626981        0.236661822711231
7       114     B cell mediated immunity
GO:0006956      2.94353652635558e-09    63      0.13078679676147        6       63
complement activation
GO:0002455      3.56814685279044e-09    60.8559322033898        0.134938758563421
6       65      humoral immune response mediated by circulating immunoglobulin
GO:0006959      4.45336909211651e-09    37.8608695652174        0.253269669919037
7       122     humoral immune response
GO:0072376      1.47636597233999e-08    47.1875 0.170230433880008       6       82
protein activation cascade
GO:0002449      3.94980493955782e-08    27.126902173913 0.346688810462944       7
167     lymphocyte mediated immunity
GO:0002460      6.87243232962086e-08    24.9197901049475        0.375752543076604
7       181     adaptive immune response based on somatic recombination of immune
receptors built from immunoglobulin superfamily domains
GO:0002250      1.27080174854711e-07    22.6747097655361        0.411044218393191
7       198     adaptive immune response
GO:0002443      1.9604963821117e-07     21.210358056266 0.438031970105875       7
211     leukocyte mediated immunity
GO:0002252      1.09965365066131e-05    11.27612710795  0.801328627776625       7
386     immune effector process
GO:0000083      1.21066813281208e-05    84.2222222222222        0.0456715798214656
3       22      regulation of transcription involved in G1/S phase of mitotic cell
cycle
GO:0006260      1.57117754284104e-05    13.5104961832061        0.556362881461491
6       268     DNA replication
GO:0046683      2.49334262054495e-05    514.964285714286        0.00830392360390284
2       4       response to organophosphorus
GO:0002253      2.91510381377966e-05    12.0546075085324        0.620718289391738
6       299     activation of immune response
GO:0050778      8.72085383437034e-05    9.82053072625698        0.755657047955159
6       364     positive regulation of immune response
GO:0051329      0.000108923006487434    9.41554959785523        0.786796761469794
6       379     interphase of mitotic cell cycle
GO:0051325      0.000122152905799682    9.21259842519685        0.8034046086776 6
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387     interphase
GO:0010564      0.000176542027190994    8.58639705882353        0.859456093003944
6       414     regulation of cell cycle process
GO:0017085      0.000490998754115649    73.5051020408163        0.0332156944156114
2       16      response to insecticide
GO:0046134      0.000490998754115649    73.5051020408163        0.0332156944156114
2       16      pyrimidine nucleoside biosynthetic process
GO:0000082      0.000560446262152684    12.0363482671175        0.386132447581482
4       186     G1/S transition of mitotic cell cycle
GO:0000280      0.00070096103904839     8.16    0.726593315341499       5       350
nuclear division
GO:0007067      0.00070096103904839     8.16    0.726593315341499       5       350
mitosis
GO:0000236      0.000710936159045463    19.429539295393 0.176458376582935       3
85      mitotic prometaphase
GO:0000087      0.000796001281507221    7.92450704225352        0.747353124351256
5       360     M phase of mitotic cell cycle
GO:0050000      0.000853721583027376    54.1428571428571        0.0435955989204899
2       21      chromosome localization
GO:0051303      0.000853721583027376    54.1428571428571        0.0435955989204899
2       21      establishment of chromosome localization
GO:0048285      0.000900405065550077    7.70191780821918        0.768112933361013
5       370     organelle fission
GO:0006261      0.000923656040316583    17.6925925925926        0.193066223790741
3       93      DNA-dependent DNA replication
GO:0006270      0.0015228893236490 2    39.5467032967033        0.0581274652273199
2       28      DNA-dependent DNA replication initiation
GO:0006206      0.0018661659196972      35.448275862069 0.064355407930247       2
31      pyrimidine nucleobase metabolic process
GO:0046328      0.00187949804348116     13.7021072796935        0.24704172721611
3       119     regulation of JNK cascade
GO:0006213      0.0022427532120335 3    32.1183035714286        0.0705833506331742
2       34      pyrimidine nucleoside metabolic process
GO:0009116      0.00244994736528106     6.08366013071895        0.96325513805273
5       464     nucleoside metabolic process
GO:0032872      0.00263552374485869     12.1204410517388        0.278181440730745
3       134     regulation of stress-activated MAPK cascade
GO:0072528      0.00265225176724534     29.3591836734694        0.0768112933361013
2       37      pyrimidine-containing compound biosynthetic process
GO:0070302      0.0026916646768698      12.0277777777778        0.280257421631721
3       135     regulation of stress-activated protein kinase signaling cascade
GO:0030071      0.003568401878669       25.0522648083624        0.0892671787419556
2       43      regulation of mitotic metaphase/anaphase transition
GO:0009163      0.00373351828160889     24.4540816326531        0.0913431596429313
2       44      nucleoside biosynthetic process
GO:0007091      0.00390214623434245     23.8837209302326        0.093419140543907
2       45      mitotic metaphase/anaphase transition
GO:0007254      0.00397341622746089     10.4305555555556        0.321777039651235
3       155     JNK cascade
GO:0046330      0.00407427144053518     23.3392857142857        0.0954951214448827
2       46      positive regulation of JNK cascade
GO:0000070      0.0046114882279282      21.8449848024316        0.10172306414781
2       49      mitotic sister chromatid segregation
GO:0000819      0.00517966953394121     20.53   0.107951006850737       2       52
sister chromatid segregation
GO:0031100      0.00517966953394121     20.53   0.107951006850737       2       52
organ regeneration
GO:0032874      0.00537587863173543     20.1260504201681        0.110026987751713
2       53      positive regulation of stress-activated MAPK cascade
GO:0070304      0.00557547207282642     19.7376373626374        0.11210296865268 8
2       54      positive regulation of stress-activated protein kinase signaling
cascade
GO:0006235      0.00621545179129268     248.603448275862        0.00622794270292713
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1       3       dTTP biosynthetic process
GO:0009176      0.00621545179129268     248.603448275862        0.00622794270292713
1       3       pyrimidine deoxyribonucleoside monophosphate metabolic process
GO:0009212      0.00621545179129268     248.603448275862        0.00622794270292713
1       3       pyrimidine deoxyribonucleoside triphosphate biosynthetic process
GO:0034421      0.00621545179129268     248.603448275862        0.00622794270292713
1       3       post-translational protein acetylation
GO:0035582      0.00621545179129268     248.603448275862        0.00622794270292713
1       3       sequestering of BMP in extracellular matrix
GO:0035583      0.00621545179129268     248.603448275862        0.00622794270292713
1       3       sequestering of TGFbeta in extracellular matrix
GO:0035722      0.00621545179129268     248.603448275862        0.00622794270292713
1       3       interleukin-12-mediated signaling pathway
GO:0035962      0.00621545179129268     248.603448275862        0.00622794270292713
1       3       response to interleukin-13
GO:0046075      0.00621545179129268     248.603448275862        0.00622794270292713
1       3       dTTP metabolic process
GO:0046078      0.00621545179129268     248.603448275862        0.00622794270292713
1       3       dUMP metabolic process
GO:0051305      0.00621545179129268     248.603448275862        0.00622794270292713
1       3       chromosome movement towards spindle pole
GO:0060574      0.00621545179129268     248.603448275862        0.00622794270292713
1       3       intestinal epithelial cell maturation
GO:0071349      0.00621545179129268     248.603448275862        0.00622794270292713
1       3       cellular response to interleukin-12
GO:0071921      0.00621545179129268     248.603448275862        0.00622794270292713
1       3       cohesin localization to chromatin
GO:0071922      0.00621545179129268     248.603448275862        0.00622794270292713
1       3       regulation of cohesin localization to chromatin
GO:0009112      0.00752182272701937     16.8149882903981        0.13078679676147
2       63      nucleobase metabolic process
GO:0051403      0.00761940766133823     8.19113413932067        0.406892256591239
3       196     stress-activated MAPK cascade
GO:0031098      0.00794330404242971     8.0640589569161 0.413120199294166       3
199     stress-activated protein kinase signaling cascade
GO:0002069      0.00827895791298872     165.724137931034        0.00830392360390284
1       4       columnar/cuboidal epithelial cell maturation
GO:0008588      0.00827895791298872     165.724137931034        0.00830392360390284
1       4       release of cytoplasmic sequestered NF-kappaB
GO:0009162      0.00827895791298872     165.724137931034        0.00830392360390284
1       4       deoxyribonucleoside monophosphate metabolic process
GO:0009202      0.00827895791298872     165.724137931034        0.00830392360390284
1       4       deoxyribonucleoside triphosphate biosynthetic process
GO:0009221      0.00827895791298872     165.724137931034        0.00830392360390284
1       4       pyrimidine deoxyribonucleotide biosynthetic process
GO:0019087      0.00827895791298872     165.724137931034        0.00830392360390284
1       4       transformation of host cell by virus
GO:0044539      0.00827895791298872     165.724137931034        0.00830392360390284
1       4       long-chain fatty acid import
GO:0070671      0.00827895791298872     165.724137931034        0.00830392360390284
1       4       response to interleukin-12
GO:0072527      0.00896611506890538     15.3027718550107        0.143242682167324
2       69      pyrimidine-containing compound metabolic process
Tissue: Whole_Blood=>Skin_Sun_Exposed_Lower_leg Type:   cluster
SourceGene:     RGS9BP(ENSG00000186326.3)
TargetGeneSet:  MTOR    SNORA44 YARS    FUBP1   CCT3    RP11    IL36G   SMARCC1
TBC1D23 GS1     NPHP3-AS1       ACTL6A  MAPK10  MCCC2   CETN3   WDR36   PCDHA3
UNC93B2 POLD2   IARS    SNORA65 NUP188  RP1     DDX21   EIF5AL1 SSRP1   SMARCD1 MARS
WARS    ERVK13-1        CIRH1A  RP13    GATAD2A RAB9A   HUWE1   EIF4A1P10
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006418      2.06875209418619e-06    54.4659090909091        0.0930039443637119
4       48      tRNA aminoacylation for protein translation
GO:0043038      2.64632817524487e-06    50.9787234042553        0.0988166908864438
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4       51      amino acid activation
GO:0043039      2.64632817524487e-06    50.9787234042553        0.0988166908864438
4       51      tRNA aminoacylation
GO:0006399      9.30078473704163e-05    19.6997245179063        0.2421977717805 4
125     tRNA metabolic process
GO:0006520      0.000158059955127382    8.8538283062645 0.846723410144627       6
437     cellular amino acid metabolic process
GO:0034660      0.000195112549181615    10.9805900621118        0.552210919659539
5       285     ncRNA metabolic process
GO:0006337      0.000427212296667532    79.1703296703297        0.031001314787904
2       16      nucleosome disassembly
GO:0031498      0.000427212296667532    79.1703296703297        0.031001314787904
2       16      chromatin disassembly
GO:0032986      0.000427212296667532    79.1703296703297        0.031001314787904
2       16      protein-DNA complex disassembly
GO:0006338      0.000728937332475213    19.3267415730337        0.178257560030448
3       92      chromatin remodeling
GO:0003407      0.00195462228590431     34.59375        0.0658777939242959      2
34      neural retina development
GO:0006284      0.00256637724351022     29.9085239085239        0.0755657047955159
2       39      base-excision repair
GO:0045727      0.00325684462408351     26.3388278388278        0.0852536156667359
2       44      positive regulation of translation
GO:0034623      0.00450506472400742     10.0014035087719        0.337139298318455
3       174     cellular macromolecular complex disassembly
GO:0032984      0.00487551796190549     9.71386363636364        0.346827209189675
3       179     macromolecular complex disassembly
GO:0006452      0.00580189185011537     267.055555555556        0.00581274652273199
1       3       translational frameshifting
GO:0031585      0.00580189185011537     267.055555555556        0.00581274652273199
1       3       regulation of inositol 1,4,5-trisphosphate-sensitive calcium-release
channel activity
GO:0031987      0.00580189185011537     267.055555555556        0.00581274652273199
1       3       locomotion involved in locomotory behavior
GO:0035845      0.00580189185011537     267.055555555556        0.00581274652273199
1       3       photoreceptor cell outer segment organization
GO:0045901      0.00580189185011537     267.055555555556        0.00581274652273199
1       3       positive regulation of translational elongation
GO:0045905      0.00580189185011537     267.055555555556        0.00581274652273199
1       3       positive regulation of translational termination
GO:0051643      0.00580189185011537     267.055555555556        0.00581274652273199
1       3       endoplasmic reticulum localization
GO:0006281      0.00601085130482567     6.17590149516271        0.742093972735451
4       383     DNA repair
GO:0007601      0.00700239291779578     8.49074626865672        0.395266763545775
3       204     visual perception
GO:0050953      0.0070972325754923      8.44811881188119        0.397204345720019
3       205     sensory perception of light stimulus
GO:0001842      0.00772863236978594     178.024691358025        0.00775032869697599
1       4       neural fold formation
GO:0007258      0.00772863236978594     178.024691358025        0.00775032869697599
1       4       JUN phosphorylation
GO:0042759      0.00772863236978594     178.024691358025        0.00775032869697599
1       4       long-chain fatty acid biosynthetic process
GO:0051534      0.00772863236978594     178.024691358025        0.00775032869697599
1       4       negative regulation of NFAT protein import into nucleus
GO:0016568      0.00821900438944382     5.62570281124498        0.811846931008235
4       419     chromatin modification
GO:0006552      0.00965177200387202     133.509259259259        0.00968791087121998
1       5       leucine catabolic process
GO:0008612      0.00965177200387202     133.509259259259        0.00968791087121998
1       5       peptidyl-lysine modification to hypusine
GO:0010172      0.00965177200387202     133.509259259259        0.00968791087121998
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1       5       embryonic body morphogenesis
GO:0010592      0.00965177200387202     133.509259259259        0.00968791087121998
1       5       positive regulation of lamellipodium assembly
GO:0046516      0.00965177200387202     133.509259259259        0.00968791087121998
1       5       hypusine metabolic process
Tissue: Skin_Sun_Exposed_Lower_leg=>Whole_Blood Type:   asymmetric
SourceGene:     RP11-30K9.1(ENSG00000242747.1)
TargetGeneSet:  IGKJ5   IGKC    IGKV3-20        IGKV1D-33       IGJ     RP11    OIT3
POU2AF1 CD27    IGHG4   IGHV6-1 IGHV3-48        IGHV3-66        PIN1    IGLV4-69
IGLV7-43        IGLV2-11        IGLL5   IGLC1   IGLC3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006958      2.99457525887675e-15    468.706976744186        0.0415196180195142
7       50      complement activation, classical pathway
GO:0016064      4.52579542866057e-15    278.368932038835        0.0921735520033216
8       111     immunoglobulin mediated immune response
GO:0019724      5.63696014075246e-15    270.433962264151        0.0946647290844924
8       114     B cell mediated immunity
GO:0006959      9.84305831228007e-15    251.315789473684        0.101307867967615
8       122     humoral immune response
GO:0006956      1.65219043065932e-14    359.575 0.0523147187045879      7       63
complement activation
GO:0002455      2.07771802599751e-14    347.127586206897        0.0539755034253685
7       65      humoral immune response mediated by circulating immunoglobulin
GO:0072376      1.12875009563322e-13    268.128 0.0680921735520033      7       82
protein activation cascade
GO:0002449      1.27933119593271e-13    179.622641509434        0.138675524185178
8       167     lymphocyte mediated immunity
GO:0002460      2.46018468357929e-13    164.924855491329        0.150301017230641
8       181     adaptive immune response based on somatic recombination of immune
receptors built from immunoglobulin superfamily domains
GO:0002250      5.09270648501912e-13    149.989473684211        0.164417687357276
8       198     adaptive immune response
GO:0002443      8.51842893630051e-13    140.256157635468        0.17521278804235
8       211     leukocyte mediated immunity
GO:0002252      1.08736784903e-10       74.3968253968254        0.32053145111065
8       386     immune effector process
GO:0002253      1.09725182564844e-09    67.8280821917808        0.248287315756695
7       299     activation of immune response
GO:0050778      4.31644181867618e-09    55.2235294117647        0.302262819182064
7       364     positive regulation of immune response
GO:0008588      0.00331777839570147     437.454545454545        0.00332156944156114
1       4       release of cytoplasmic sequestered NF-kappaB
GO:0010741      0.00386653165633848     25.5839285714286        0.0946647290844924
2       114     negative regulation of intracellular protein kinase cascade
GO:0000244      0.00497288091920933     262.436363636364        0.00498235416234171
1       6       assembly of spliceosomal tri-snRNP
GO:0045579      0.00745081118520774     163.988636363636        0.00747353124351256
1       9       positive regulation of B cell differentiation
GO:0007253      0.00827553007911286     145.757575757576        0.00830392360390284
1       10      cytoplasmic sequestering of NF-kappaB
Tissue: Whole_Blood=>Skin_Sun_Exposed_Lower_leg Type:   cluster
SourceGene:     RP11-793H13.3(ENSG00000257550.1)
TargetGeneSet:  RPL11   ENSA    RP11    SLC5A6  YPEL5   COX7A2L AMT     RPL24
PODXL2  NMNAT3  RPL35A  CAMLG   PCDHGA12        CNN2P9  IL20RA  FAM103A2P
PRKRIP1 RPS20   RPL30   C11orf54        ATP5L   PFDN5   RPL41   MYL6    C12orf47
COMMD6  ABCD4   MGRN1   PKD1P1  ZNF668  C16orf57        CXCL16  RPL17   RP1
TMEM241 ZNF554  PIN1    RAVER1  ZNF44   RRP1B   FIGF    GPR64   ALG13   RBMX2
SRRM1P3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006415      1.16140676328024e-09    45.9423076923077        0.207805688187669
7       91      translational termination
GO:0006414      3.1944222991207e-09     39.3406593406593        0.239775794062695
7       105     translational elongation
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GO:0006614      3.1944222991207e-09     39.3406593406593        0.239775794062695
7       105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      3.41488435085084e-09    38.9405594405594        0.242059373053768
7       106     cotranslational protein targeting to membrane
GO:0045047      3.41488435085084e-09    38.9405594405594        0.242059373053768
7       106     protein targeting to ER
GO:0072599      3.41488435085084e-09    38.9405594405594        0.242059373053768
7       106     establishment of protein localization to endoplasmic reticulum
GO:0070972      7.24882883816765e-09    34.7016632016632        0.269462320946647
7       118     protein localization to endoplasmic reticulum
GO:0000184      7.68970124063241e-09    34.3894230769231        0.271745899937721
7       119     nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0019080      4.02441630509631e-08    26.6875 0.344820427652066       7       151
viral genome expression
GO:0019083      4.02441630509631e-08    26.6875 0.344820427652066       7       151
viral transcription
GO:0006413      4.21201943469109e-08    26.5015915119363        0.347104006643139
7       152     translational initiation
GO:0006612      4.40697714283786e-08    26.31822971549  0.349387585634212       7
153     protein targeting to membrane
GO:0043624      4.40697714283786e-08    26.31822971549  0.349387585634212       7
153     cellular protein complex disassembly
GO:0043241      5.50047189202055e-08    25.437850229241 0.360805480589579       7
158     protein complex disassembly
GO:0000956      8.73563769337154e-08    23.6923076923077        0.385924849491385
7       169     nuclear-transcribed mRNA catabolic process
GO:0034623      1.0667937829241e-07     22.9748963611239        0.397342744446751
7       174     cellular macromolecular complex disassembly
GO:0006402      1.24631723310076e-07    22.4311740890688        0.406477060411044
7       178     mRNA catabolic process
GO:0032984      1.29498403200952e-07    22.2991949910555        0.408760639402117
7       179     macromolecular complex disassembly
GO:0072594      3.15403759765586e-07    19.4351815696993        0.46585011417895
7       204     establishment of protein localization to organelle
GO:0006401      3.26036440051995e-07    19.3356643356643        0.468133693170023
7       205     RNA catabolic process
GO:0019058      7.30213596072562e-07    17.0600961538462        0.527506746937928
7       231     viral infectious cycle
GO:0022415      1.61228593661965e-06    15.0737306172089        0.593730537679053
7       260     viral reproductive process
GO:0071845      2.89924998179782e-06    13.7443765620661        0.648536433464812
7       284     cellular component disassembly at cellular level
GO:0022411      3.18047733974922e-06    13.5448946071722        0.657670749429105
7       288     cellular component disassembly
GO:0016032      5.81527882048049e-05    8.47349272349272        1.02989412497405
7       451     viral reproduction
GO:0033365      7.8526277819052e-05     8.06074612083196        1.08013286277766
7       473     protein localization to organelle
GO:0006605      7.9575777695673e-05     8.04290891121726        1.08241644176874
7       474     protein targeting
GO:0042273      0.000329025405415394    92.9548387096774        0.0274029478928794
2       12      ribosomal large subunit biogenesis
GO:0022613      0.00164272199518457     8.86066469027929        0.513805272991488
4       225     ribonucleoprotein complex biogenesis
GO:0006364      0.00168869785645069     14.1752475247525        0.237492215071621
3       104     rRNA processing
GO:0016072      0.00198282663718325     13.3747663551402        0.251193689018061
3       110     rRNA metabolic process
GO:0071843      0.00204818652604451     8.32457813646368        0.545775378866514
4       239     cellular component biogenesis at cellular level
GO:0042254      0.00467287352945188     9.77534246575343        0.340253269669919
3       149     ribosome biogenesis
GO:0035845      0.00683557664080414     225.25  0.00685073697321985     1       3
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photoreceptor cell outer segment organization
GO:0006767      0.00933253719975094     14.9386056191467        0.14614905542869
2       64      water-soluble vitamin metabolic process
Tissue: Whole_Blood=>Skin_Sun_Exposed_Lower_leg Type:   asymmetric
SourceGene:     SEPT4(ENSG00000108387.9)
TargetGeneSet:  DNAJC11 MRTO4   TCEA3   CTPS    HPDL    SELRC1  CHD1L   TOMM40L
RNPEP   MTHFD2  TTC21B  NT5DC2  MYH15   LRRC58  SIAH2   SIAH2-AS1       MED12L
CLCN2   LSG1    RP11    MYO10   PAK1IP1 PPIL1   BYSL    XPO5    PLEKHG1 CYCS
BLVRA   ABCF2   RCL1    NGB     DDB2    NEU3    GLB1L2  CD9     ETV6    CPM     MVK
SYNE2   TMEM63C DIO2    SEMA7A  CHRNB4  EME2    TSR1    SHISA6  RPL17P43
SRCIN1  TRIM47  GAMT    KDELR1  MAFB    TOP1    C2CD2   BCRP8   PNPLA3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0022613      4.04205087004368e-06    12.6567278287462        0.669503840564667
7       225     ribonucleoprotein complex biogenesis
GO:0042254      4.83457333665675e-06    16.1765261765262        0.443360321085046
6       149     ribosome biogenesis
GO:0071843      6.01424224862718e-06    11.8812260536398        0.711161857310913
7       239     cellular component biogenesis at cellular level
GO:0009240      0.00890079624592366     171.5   0.00892671787419556     1       3
isopentenyl diphosphate biosynthetic process
GO:0019287      0.00890079624592366     171.5   0.00892671787419556     1       3
isopentenyl diphosphate biosynthetic process, mevalonate pathway
GO:0042396      0.00890079624592366     171.5   0.00892671787419556     1       3
phosphagen biosynthetic process
GO:0046490      0.00890079624592366     171.5   0.00892671787419556     1       3
isopentenyl diphosphate metabolic process
GO:0060084      0.00890079624592366     171.5   0.00892671787419556     1       3
synaptic transmission involved in micturition
GO:0060689      0.00890079624592366     171.5   0.00892671787419556     1       3
cell differentiation involved in salivary gland development
Tissue: Whole_Blood=>Skin_Sun_Exposed_Lower_leg Type:   asymmetric
SourceGene:     SMAD7(ENSG00000101665.3)
TargetGeneSet:  MTND1P23        RP4     POLN    FTH1P10 OGFRL1  MACC1   RP11
NIPSNAP3B       ZNF462  E2F1    C11orf2 USP28   RP1     RPL13AP25       PLEKHD1 FMN1
CTA     RPS2P45 RPSAP58 LMTK3   IGLON5
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0071482      2.14074345900805e-06    165.632183908046        0.0265725555324891
3       32      cellular response to light stimulus
GO:0071478      1.31565095878328e-05    87.1757575757576        0.0481627569026365
3       58      cellular response to radiation
GO:0007603      3.46231896661738e-05    320.666666666667        0.00913431596429313
2       11      phototransduction, visible light
GO:0009584      0.000119111662011372    160.233333333333        0.0166078472078057
2       20      detection of visible light
GO:0071214      0.000154307642306514    36.9767441860465        0.109611791571518
3       132     cellular response to abiotic stimulus
GO:0007602      0.000329025405415394    92.9548387096774        0.0274029478928794
2       33      phototransduction
GO:0009416      0.000417103363099922    26.1117216117216        0.153622586672203
3       185     response to light stimulus
GO:0009583      0.000484492897054804    75.7947368421053        0.0332156944156114
2       40      detection of light stimulus
GO:0009582      0.00143783917370817     42.9014925373134        0.0572970728669296
2       69      detection of abiotic stimulus
GO:0009314      0.00160013579753211     16.2061855670103        0.244135353954744
3       294     response to radiation
GO:0009581      0.00222261401593814     34.1785714285714        0.0714137429935645
2       86      detection of external stimulus
GO:0016056      0.0024892811208842      656.227272727273        0.00249117708117085
1       3       rhodopsin mediated signaling pathway
GO:0035845      0.0024892811208842      656.227272727273        0.00249117708117085
1       3       photoreceptor cell outer segment organization
GO:0060041      0.00264822548323841     31.1891304347826        0.0780568818766867
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2       94      retina development in camera-type eye
GO:0000244      0.00497288091920933     262.436363636364        0.00498235416234171
1       6       assembly of spliceosomal tri-snRNP
GO:0006657      0.00497288091920933     262.436363636364        0.00498235416234171
1       6       CDP-choline pathway
GO:0009586      0.00497288091920933     262.436363636364        0.00498235416234171
1       6       rhodopsin mediated phototransduction
GO:0046548      0.00497288091920933     262.436363636364        0.00498235416234171
1       6       retinal rod cell development
GO:0000077      0.00499651339916335     22.3609375      0.107951006850737       2
130     DNA damage checkpoint
GO:0031570      0.00545513075877989     21.3507462686567        0.112933361013079
2       136     DNA integrity checkpoint
GO:0042670      0.00662546365102634     187.428571428571        0.00664313888312228
1       8       retinal cone cell differentiation
GO:0046549      0.00662546365102634     187.428571428571        0.00664313888312228
1       8       retinal cone cell development
GO:0035082      0.00745081118520774     163.988636363636        0.00747353124351256
1       9       axoneme assembly
GO:0071398      0.00745081118520774     163.988636363636        0.00747353124351256
1       9       cellular response to fatty acid
GO:0000085      0.00909962076805748     131.172727272727        0.00913431596429313
1       11      G2 phase of mitotic cell cycle
GO:0050908      0.00909962076805748     131.172727272727        0.00913431596429313
1       11      detection of light stimulus involved in visual perception
GO:0050962      0.00909962076805748     131.172727272727        0.00913431596429313
1       11      detection of light stimulus involved in sensory perception
GO:0051319      0.00909962076805748     131.172727272727        0.00913431596429313
1       11      G2 phase
GO:0060219      0.00992308368708683     119.239669421488        0.00996470832468341
1       12      camera-type eye photoreceptor cell differentiation
GO:0051606      0.00999095106939415     15.4945652173913        0.154452979032593
2       186     detection of stimulus
Tissue: Whole_Blood=>Skin_Sun_Exposed_Lower_leg Type:   cluster
SourceGene:     ST6GALNAC5(ENSG00000117069.9)
TargetGeneSet:  RPL11   SYF2    NDUFS5  CCDC23  JAK1    NAP1L4P1        PARP1   RP11
RPS7    DPY30   DYNC2LI1        UBC     ASPRV1  RPL31   COQ10B  EEF1B2  RPL24
IL20RB-AS1      NMNAT3  WDR53   RPL35A  CHRNA9  LSM6    FRG1    RPL37   ZCCHC9
ATG12   TMEM14C TMEM14B CCDC28A TOMM7   PRKRIP1 DCTN6   TMEM68  RPS20   TCEB1
RPL30   RPS6    TXN     RPS24   RPS13   C11orf54        CWC15   ATP5L   HSPA8
PFDN5   SARNP   CCDC59  C12orf47        ARL6IP4 UFM1    GTF2F2  KLHDC2  NAA30
RSL24D1 RPS3AP6 CHD2    FAM192A CDH1    C17orf48        RPS7P1  RPL17   TLK2
CANT1   PIN1    ZNF350  LINC00493       LBP     C20orf111       DNTTIP1 ZNFX1-AS1
CYP2D6  MSN     COX7B   RP3
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0006414      1.19085887672311e-18    55.0230769230769        0.392360390284409
14      105     translational elongation
GO:0019080      5.80872877040334e-18    40.3308823529412        0.564251608885198
15      151     viral genome expression
GO:0019083      5.80872877040334e-18    40.3308823529412        0.564251608885198
15      151     viral transcription
GO:0006415      9.02877404166579e-18    58.2073170731707        0.340045671579821
13      91      translational termination
GO:0006614      6.3351830881119e-17     49.3014316012725        0.392360390284409
13      105     SRP-dependent cotranslational protein targeting to membrane
GO:0006613      7.20161658939872e-17    48.7678992918961        0.396097155906166
13      106     cotranslational protein targeting to membrane
GO:0045047      7.20161658939872e-17    48.7678992918961        0.396097155906166
13      106     protein targeting to ER
GO:0072599      7.20161658939872e-17    48.7678992918961        0.396097155906166
13      106     establishment of protein localization to endoplasmic reticulum
GO:0070972      3.04956531756217e-16    43.1581881533101        0.440938343367241
13      118     protein localization to endoplasmic reticulum
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GO:0000184	3.41449266051005e-16	42.748044178555	0.444675108988997	13	119	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0000956	1.12327767765401e-15	32.1593548387097	0.631513390076811	14	169	nuclear-transcribed mRNA catabolic process
GO:0006402	2.33465348657263e-15	30.3753048780488	0.665144280672618	14	178	mRNA catabolic process
GO:0019058	3.59021666478864e-15	25.2510683760684	0.863192858625701	15	231	viral infectious cycle
GO:0006413	8.77121072253619e-15	32.523951570451	0.567988374506954	13	152	translational initiation
GO:0006612	9.56022466007897e-15	32.2893728222997	0.571725140128711	13	153	protein targeting to membrane
GO:0043624	9.56022466007897e-15	32.2893728222997	0.571725140128711	13	153	cellular protein complex disassembly
GO:0043241	1.45764839761359e-14	31.1650126156434	0.590408968237492	13	158	protein complex disassembly
GO:0072594	1.57530292388641e-14	26.1707894736842	0.762300186838281	14	204	establishment of protein localization to organelle
GO:0006401	1.68635353020743e-14	26.0319371727749	0.766036952460037	14	205	RNA catabolic process
GO:0022415	2.07072879557206e-14	22.2166405023548	0.971559061656633	15	260	viral reproductive process
GO:0034623	5.134844663752e-14	28.0363581275564	0.650197218185593	13	174	cellular macromolecular complex disassembly
GO:0032984	7.42001189748255e-14	27.1823391125478	0.668881046294374	13	179	macromolecular complex disassembly
GO:0071845	1.495084767429e-12	18.3127777777778	1.06124143657878	14	284	cellular component disassembly at cellular level
GO:0022411	1.80774127218546e-12	18.0403284671533	1.07618849906581	14	288	cellular component disassembly
GO:0033365	9.0574114315115e-12	12.8434872739836	1.76749013909072	16	473	protein localization to organelle
GO:0006605	9.34999257885447e-12	12.8145253964606	1.77122690471248	16	474	protein targeting
GO:0016032	5.83936139457719e-11	12.3156316160903	1.68528129541208	15	451	viral reproduction
GO:0042254	7.36950037898148e-08	17.5837187789084	0.556778077641686	8	149	ribosome biogenesis
GO:0006364	1.09399988477819e-07	21.9565694231191	0.388623624662653	7	104	rRNA processing
GO:0022613	1.32623930740311e-07	13.1305555555556	0.840772264895163	9	225	ribonucleoprotein complex biogenesis
GO:0016072	1.61093682834633e-07	20.6688700681677	0.411044218393191	7	110	rRNA metabolic process
GO:0071843	2.21581441355786e-07	12.3191304347826	0.893086983599751	9	239	cellular component biogenesis at cellular level
GO:0034470	8.94038674369838e-06	10.9610847756587	0.747353124351256	7	200	ncRNA processing
GO:0008380	2.42786094698584e-05	7.77474120082816	1.20697529582728	8	323	RNA splicing
GO:0042274	3.86816589134669e-05	56.4	0.067261781191613	3	18	ribosomal small subunit biogenesis
GO:0034660	8.63683542749491e-05	7.56413592530231	1.06497820220054	7	285	ncRNA metabolic process
GO:0032480	0.000248580397639113	28.1705882352941	0.123313265517957	3	33	negative regulation of type I interferon production
GO:0042273	0.000883135281802382	55.3346153846154	0.0448411874610754	2	12	ribosomal large subunit biogenesis
GO:0000377	0.000962816076885864	7.28027894574915	0.762300186838281	5	204	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile
GO:0000398	0.000962816076885864	7.28027894574915	0.762300186838281	5	204	nuclear mRNA splicing, via spliceosome

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GO:0000375      0.00107282609640575     7.09933973589436        0.780984014947062
5       209     RNA splicing, via transesterification reactions
GO:0022900      0.00156140804356244     8.77969230769231        0.500726593315342
4       134     electron transport chain
GO:0032479      0.0017493014041062      13.824493731919 0.239152999792402       3
64      regulation of type I interferon production
GO:0032606      0.00217107408523695     12.7727272727273        0.257836827901183
3       69      type I interferon production
GO:0006397      0.00359947588662386     4.45419847328244        1.49096948308076
6       399     mRNA processing
GO:0022904      0.00551560640076413     9.04743833017078        0.358729499688603
3       96      respiratory electron transport chain
Tissue: Whole_Blood=>Skin_Sun_Exposed_Lower_leg Type:   asymmetric
SourceGene:     TMEM222(ENSG00000186501.8)
TargetGeneSet:  THRAP3  BCL9    KRCC1   TXNDC9  MTX2    HIGD1A  HESX1   THOC7
IL20RB-AS1      IL8     SH3D19  LMNB1   CAMLG   RP4     RP11    BRP44L  HNRNPA2B1
ZNF277  CTA     GANAB   TRPT1   SRPR    ESYT1   GAPDHP44        ARL6IP4 RBM23
TRAPPC6B        NAA30   ZNF689  PDXDC2P RP13    CORO6   STAT3   LMNB2   KHSRP
LIN7B   ITCH    C20orf111       RRP1B   SF3A1   FUNDC1  SMC1A   HUWE1   MSN
SNX12   PRPS1
GOBPID  Pvalue  OddsRatio       ExpCount        Count   Size    Term
GO:0008380      1.85087824769429e-07    13.0340045202383        0.894055774686873
9       323     RNA splicing
GO:0006397      1.11580166434056e-05    8.96419437340153        1.10442183931908
8       399     mRNA processing
GO:0000375      2.16916071209828e-05    12.3512025499855        0.578506677738565
6       209     RNA splicing, via transesterification reactions
GO:0000377      0.00023501262691921З    10.2024407753051        0.564666805065393
5       204     RNA splicing, via transesterification reactions with bulged
adenosine as nucleophile
GO:0000398      0.000235012626919213    10.2024407753051        0.564666805065393
5       204     nuclear mRNA splicing, via spliceosome
GO:0050657      0.0053958171239346      9.19240669240669        0.357068714967822
3       129     nucleic acid transport
GO:0050658      0.0053958171239346      9.19240669240669        0.357068714967822
3       129     RNA transport
GO:0051236      0.0053958171239346      9.19240669240669        0.357068714967822
3       129     establishment of RNA localization
GO:0006403      0.00624663134188405     8.70432838853892        0.376444536710262
3       136     RNA localization
GO:0015931      0.00817800154115776     7.86762272476558        0.415196180195142
3       150     nucleobase-containing compound transport
GO:0016056      0.00828153127754283     184.730769230769        0.00830392360390284
1       3       rhodopsin mediated signaling pathway
GO:0090085      0.00828153127754283     184.730769230769        0.00830392360390284
1       3       regulation of protein deubiquitination
GO:0019048      0.009077269810852       15.1168421052632        0.143934675800983
2       52      virus-host interaction
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