

Comprehensive analysis of long non-coding RNA-mRNA co-expression patterns in thyroid cancer

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Supplementary Table 3: GO enrichment analyses for 452 mRNAs

go_id	go_name	enrichment	pvalue	FDR
GO:0030198	extracellular matrix organization	11.57493404	9.81201E-16	1.46199E-12
GO:0007155	cell adhesion	7.138725838	3.07732E-15	2.2926E-12
GO:0006955	immune response	7.584714611	3.49447E-13	1.73559E-10
GO:0030168	platelet activation	8.51098091	1.53752E-09	5.16244E-07
GO:0006508	proteolysis	5.218207967	1.73236E-09	5.16244E-07
GO:0007165	signal transduction	3.596096011	2.5477E-09	6.3268E-07
GO:0060333	signaling pathway	16.02683174	2.03624E-08	4.33428E-06
GO:0007596	blood coagulation	4.978466252	2.40739E-08	4.48377E-06
GO:0030574	collagen catabolic process	14.46866755	5.14089E-08	8.51103E-06
GO:0019882	antigen processing and presentation	23.83074655	5.98354E-08	8.91547E-06
GO:0001525	angiogenesis	7.486275745	1.06644E-07	1.44455E-05
GO:0022617	extracellular matrix disassembly	13.18663371	1.17878E-07	1.46366E-05
GO:0050900	leukocyte migration	10.81769536	1.37518E-07	1.57617E-05
GO:0030199	collagen fibril organization	20.77552263	1.6484E-07	1.75437E-05
GO:0007411	axon guidance	5.477098125	5.74188E-07	5.7036E-05
GO:0001501	skeletal system development	9.114121289	7.02494E-07	6.54198E-05
GO:0006915	apoptotic process	3.716721938	1.41336E-06	0.000123877
GO:0030036	actin cytoskeleton organization	8.209173076	1.86396E-06	0.000154295
GO:0007612	learning	19.84274406	2.10002E-06	0.000159521
GO:0002576	platelet degranulation	11.43203362	2.14122E-06	0.000159521
GO:0002504	of peptide or polysaccharide antigen via MHC class II	46.29973615	4.42077E-06	0.000313664
GO:0035556	intracellular signal transduction	5.298385299	5.64561E-06	0.000382362
GO:0031295	T cell costimulation	11.91537327	8.37978E-06	0.000542864
GO:0010628	expression	7.952244758	9.13116E-06	0.000566893
GO:0016045	detection of bacterium	38.58311346	1.02786E-05	0.000612603
GO:0000278	mitotic cell cycle	4.464161888	1.65159E-05	0.00094649
GO:0045944	positive regulation of transcription from RNA polymerase II promoter	3.269755378	1.86088E-05	0.001026931
GO:0034097	response to cytokine stimulus	13.35569312	2.32741E-05	0.001238516
GO:0045087	innate immune response	3.551875065	3.34477E-05	0.001718519
GO:0043065	process	5.875601034	3.79006E-05	0.001882396
GO:0050890	cognition	27.23513891	4.77577E-05	0.002295449
GO:0032964	collagen biosynthetic process	57.87467018	5.02018E-05	0.002337522
GO:0044281	small molecule metabolic process	2.462751923	6.30557E-05	0.002847059
GO:0008285	proliferation	4.203188337	6.86041E-05	0.003006476
GO:0051591	response to cAMP	15.23017636	7.4444E-05	0.003169187
GO:0000187	activation of MAPK activity	8.528898764	7.8237E-05	0.003238142

GO:0002606	positive regulation of dendritic cell antigen processing and presentation	49.60686016	8.72891E-05	0.003422652
GO:0015693	magnesium ion transport	49.60686016	8.72891E-05	0.003422652
GO:0097190	apoptotic signaling pathway	8.102453826	0.000109233	0.004173244
GO:0035023	transduction	10.06516003	0.000121132	0.004512185
GO:0030325	adrenal gland development	21.04533461	0.000141853	0.005155154
GO:0005975	carbohydrate metabolic process	4.196350708	0.000146242	0.0051881
GO:0042127	regulation of cell proliferation	7.502272061	0.000179373	0.006215493
GO:0002480	of exogenous peptide antigen via MHC class I, TAP-independent	38.58311346	0.000206814	0.007003473
GO:0016042	lipid catabolic process	8.791089142	0.000261241	0.008474456
GO:0010976	projection development	11.81115718	0.000261628	0.008474456
GO:0030217	T cell differentiation	17.80759083	0.000282103	0.008770013
GO:0008284	proliferation	3.66117135	0.000282524	0.008770013
GO:0000272	polysaccharide catabolic process	115.7493404	0.000297773	0.009054732
GO:0051056	mediated signal transduction	5.680949221	0.000374312	0.011154487
GO:0043066	process	3.348121416	0.000387902	0.011332828
GO:0002063	chondrocyte development	31.56800192	0.000401049	0.011491606
GO:0016337	cell-cell adhesion	8.075535375	0.000420045	0.01159014
GO:0050852	T cell receptor signaling pathway	8.075535375	0.000420045	0.01159014
GO:0045893	DNA-dependent	3.300388524	0.000450575	0.012206496
GO:0019221	pathway	4.822889182	0.000484744	0.012897642
GO:0007162	negative regulation of cell adhesion	14.93539876	0.000573839	0.015000365
GO:0007268	synaptic transmission	3.617166887	0.000595663	0.015188196
GO:0019886	of exogenous peptide antigen via MHC class II	7.548870024	0.000610026	0.015188196
GO:0042493	response to drug	4.224428481	0.000611605	0.015188196
GO:0007568	aging	7.388255768	0.000686565	0.016770199
GO:0071526	pathway	24.80343008	0.000867849	0.019021426
GO:0009595	detection of biotic stimulus	77.16622691	0.000888201	0.019021426
GO:0014009	glial cell proliferation	77.16622691	0.000888201	0.019021426
GO:0033004	activation	77.16622691	0.000888201	0.019021426
GO:0035986	heterochromatin focus assembly	77.16622691	0.000888201	0.019021426
GO:0045058	T cell selection	77.16622691	0.000888201	0.019021426
GO:0055118	muscle contraction	77.16622691	0.000888201	0.019021426
GO:0086001	action potential	77.16622691	0.000888201	0.019021426
GO:0006629	lipid metabolic process	5.005376881	0.000893624	0.019021426
GO:0042060	wound healing	9.042917216	0.000940975	0.019747213
GO:0010951	endopeptidase activity	8.903795413	0.001012229	0.020660566
GO:0060337	pathway	8.903795413	0.001012229	0.020660566
GO:0030261	chromosome condensation	23.14986807	0.001077869	0.021605154
GO:0006952	defense response	8.768889422	0.001087508	0.021605154
GO:0055085	transmembrane transport	3.012064619	0.001146734	0.022291907
GO:0007584	response to nutrient	8.638010475	0.001166959	0.022291907
GO:0050731	tyrosine phosphorylation	8.638010475	0.001166959	0.022291907
GO:0008360	regulation of cell shape	6.551849455	0.001319124	0.024879673
GO:0001568	blood vessel development	11.87172722	0.001420565	0.026458016
GO:0000082	G1/S transition of mitotic cell cycle	5.365863461	0.001446422	0.026502226

GO:0030203	process	6.430518909	0.001458512	0.026502226
GO:0030178	signaling pathway	11.57493404	0.001567714	0.028143305
GO:0019048	virus-host interaction	3.745933345	0.001591937	0.028237931
GO:0046777	protein autophosphorylation	5.193880658	0.001759583	0.029905509
GO:0010815	bradykinin catabolic process	57.87467018	0.001766231	0.029905509
GO:2000774	senescence	57.87467018	0.001766231	0.029905509
	positive regulation of cysteine-type			
GO:2001056	endopeptidase activity	57.87467018	0.001766231	0.029905509
GO:0007166	pathway	5.160798615	0.001828257	0.030607899
GO:0007416	synapse assembly	11.0237467	0.001894149	0.030710434
GO:0032320	activity	19.29155673	0.001896215	0.030710434
GO:0042730	fibrinolysis	19.29155673	0.001896215	0.030710434
GO:0032496	response to lipopolysaccharide	6.092070546	0.001946738	0.031189678
GO:0042593	glucose homeostasis	7.716622691	0.001971302	0.031247239
GO:0045471	response to ethanol	7.516190933	0.002225149	0.034367847
	negative regulation of transcription			
GO:0000122	from RNA polymerase II promoter	2.95626999	0.002227957	0.034367847
GO:0031648	protein destabilization	18.27621164	0.00223737	0.034367847
GO:0042326	phosphorylation	17.36240106	0.002615392	0.039362964
GO:0070371	ERK1 and ERK2 cascade	17.36240106	0.002615392	0.039362964
GO:0001913	T cell mediated cytotoxicity	46.29973615	0.002926877	0.041141949
GO:0002830	immune response	46.29973615	0.002926877	0.041141949
GO:0019217	process	46.29973615	0.002926877	0.041141949
	positive regulation of mammary			
GO:0033601	gland epithelial cell proliferation	46.29973615	0.002926877	0.041141949
GO:0033619	membrane protein proteolysis	46.29973615	0.002926877	0.041141949
GO:0051983	segregation	46.29973615	0.002926877	0.041141949
	cell differentiation involved in			
GO:0060706	embryonic placenta development	46.29973615	0.002926877	0.041141949
GO:0006816	calcium ion transport	7.057886608	0.002966823	0.041313698
GO:0042220	response to cocaine	16.53562005	0.003031814	0.041519419
GO:0007264	transduction	3.444920844	0.003037327	0.041519419
GO:0045766	positive regulation of angiogenesis	6.889841689	0.003310005	0.044835525
GO:0016338	adhesion	15.78400096	0.003488124	0.046822559
GO:0051592	response to calcium ion	9.25994723	0.003691421	0.049109078
GO:0070374	ERK2 cascade	6.652260941	0.003879122	0.051149491
GO:0071300	cellular response to retinoic acid	9.078379637	0.00397854	0.051641584
GO:0043542	endothelial cell migration	15.09774005	0.00398576	0.051641584
GO:0030854	differentiation	38.58311346	0.004365214	0.055591192
GO:2000505	regulation of energy homeostasis	38.58311346	0.004365214	0.055591192
GO:0001958	endochondral ossification	14.46866755	0.004526116	0.056671538
GO:0045776	pressure	14.46866755	0.004526116	0.056671538
GO:0009611	response to wounding	8.735799273	0.004599217	0.057106947
GO:0006954	inflammatory response	3.531335808	0.004641852	0.05715999
GO:0007218	neuropeptide signaling pathway	6.29072502	0.004984927	0.060881483
GO:0006309	apoptotic DNA fragmentation	13.35569312	0.005740337	0.067347258
GO:0033209	signaling pathway	13.35569312	0.005740337	0.067347258
GO:0034446	spreading	13.35569312	0.005740337	0.067347258

GO:0042113	B cell activation	13.35569312	0.005740337	0.067347258
GO:0048013	ephrin receptor signaling pathway	13.35569312	0.005740337	0.067347258
GO:0006032	chitin catabolic process	33.07124011	0.006076385	0.068073782
GO:0032229	negative regulation of synaptic transmission, GABAergic	33.07124011	0.006076385	0.068073782
GO:0040036	regulation of fibroblast growth factor receptor signaling pathway	33.07124011	0.006076385	0.068073782
GO:0042304	process	33.07124011	0.006076385	0.068073782
GO:0043589	skin morphogenesis	33.07124011	0.006076385	0.068073782
GO:0051604	protein maturation	33.07124011	0.006076385	0.068073782
GO:0007507	heart development	4.85661568	0.006329296	0.070377996
GO:0007159	leukocyte cell-cell adhesion	12.86103782	0.006416765	0.070822069
GO:0000087	M phase of mitotic cell cycle	4.092148397	0.007074064	0.07710255
GO:0019370	leukotriene biosynthetic process	12.40171504	0.007141042	0.07710255
GO:0050690	virus by virus	12.40171504	0.007141042	0.07710255
GO:0000236	mitotic prometaphase	5.787467018	0.007215941	0.077350733
GO:0007190	activity	11.97406969	0.007914342	0.081100203
GO:0007631	feeding behavior	11.97406969	0.007914342	0.081100203
GO:0030219	megakaryocyte differentiation	28.93733509	0.008055591	0.081100203
GO:0032731	beta production	28.93733509	0.008055591	0.081100203
GO:0035458	cellular response to interferon-beta	28.93733509	0.008055591	0.081100203
GO:0042989	sequestering of actin monomers	28.93733509	0.008055591	0.081100203
GO:0045741	growth factor-activated receptor activity	28.93733509	0.008055591	0.081100203
GO:0050965	involved in sensory perception of pain	28.93733509	0.008055591	0.081100203
GO:0060997	dendritic spine morphogenesis	28.93733509	0.008055591	0.081100203
GO:0007204	concentration	5.564872133	0.008571051	0.085710512
GO:0006887	exocytosis	7.234333773	0.009264449	0.092026862
GO:0007257	activation of JUN kinase activity	11.20154907	0.009612512	0.094851935
GO:0010288	response to lead ion	25.72207564	0.010298098	0.097733544
GO:0014902	myotube differentiation	25.72207564	0.010298098	0.097733544
GO:0032863	activation of Rac GTPase activity	25.72207564	0.010298098	0.097733544
GO:0034063	stress granule assembly	25.72207564	0.010298098	0.097733544
GO:0042769	DNA damage	25.72207564	0.010298098	0.097733544
GO:0043583	ear development	25.72207564	0.010298098	0.097733544
GO:0051092	positive regulation of NF-kappaB transcription factor activity	5.309602769	0.010514847	0.099158999
GO:0008283	cell proliferation	3.10042876	0.011201826	0.104973084
GO:0006468	protein phosphorylation	3.082083028	0.011649537	0.108486311
GO:0050821	protein stabilization	6.710106688	0.012187471	0.112181525
GO:0030335	positive regulation of cell migration	5.076725455	0.012759673	0.112181525
GO:0002218	response	23.14986807	0.012799234	0.112181525
GO:0032495	response to muramyl dipeptide	23.14986807	0.012799234	0.112181525
GO:0033235	sumoylation	23.14986807	0.012799234	0.112181525
GO:0043623	cellular protein complex assembly	23.14986807	0.012799234	0.112181525
GO:0046888	secretion	23.14986807	0.012799234	0.112181525
GO:0060707	trophoblast giant cell differentiation	23.14986807	0.012799234	0.112181525

GO:0070208	protein heterotrimerization	23.14986807	0.012799234	0.112181525
GO:2000060	ubiquitination involved in ubiquitin-dependent protein catabolic process	23.14986807	0.012799234	0.112181525
GO:0006811	ion transport	4.209066923	0.012945751	0.112802156
GO:0001889	liver development	6.521089598	0.013514538	0.11617197
GO:0001890	placenta development	9.921372032	0.013644359	0.11617197
GO:0050830	bacterium	9.921372032	0.013644359	0.11617197
GO:0071230	stimulus	9.921372032	0.013644359	0.11617197
GO:0006024	process	9.645778364	0.014790362	0.124602344
GO:0007275	development	2.609103984	0.015131812	0.124602344
GO:0001678	cellular glucose homeostasis	21.04533461	0.015554387	0.124602344
GO:0010812	adhesion	21.04533461	0.015554387	0.124602344
GO:0010906	process	21.04533461	0.015554387	0.124602344
GO:0016064	response	21.04533461	0.015554387	0.124602344
GO:0019372	lipoxxygenase pathway	21.04533461	0.015554387	0.124602344
GO:0033628	by integrin	21.04533461	0.015554387	0.124602344
GO:0043518	response, signal transduction by p53 class mediator	21.04533461	0.015554387	0.124602344
GO:0050673	epithelial cell proliferation	21.04533461	0.015554387	0.124602344
GO:0060322	head development	21.04533461	0.015554387	0.124602344
GO:0007229	integrin-mediated signaling pathway	6.256721101	0.015684253	0.124970787
GO:0007160	cell-matrix adhesion	6.173298153	0.016456814	0.129738902
GO:0034329	cell junction assembly	6.173298153	0.016456814	0.129738902
GO:0007420	brain development	3.991356564	0.016777442	0.131570464
GO:0008544	epidermis development	6.092070546	0.017254673	0.134604521
GO:0032695	production	19.29155673	0.018559003	0.139069263
GO:0043113	receptor clustering	19.29155673	0.018559003	0.139069263
GO:0043922	transcription	19.29155673	0.018559003	0.139069263
GO:0048260	mediated endocytosis	19.29155673	0.018559003	0.139069263
GO:0000080	G1 phase of mitotic cell cycle	8.903795413	0.01857368	0.139069263
GO:0007188	protein coupled receptor signaling pathway	8.903795413	0.01857368	0.139069263
GO:0042542	response to hydrogen peroxide	8.903795413	0.01857368	0.139069263
GO:0045727	positive regulation of translation	8.903795413	0.01857368	0.139069263
GO:0006919	endopeptidase activity involved in apoptotic process	5.935863609	0.018927793	0.141012059
GO:0043434	stimulus	8.681200528	0.019952542	0.147174692
GO:0045860	activity	8.681200528	0.019952542	0.147174692
GO:0006917	induction of apoptosis	3.81591232	0.020835021	0.149248041
GO:0007067	mitosis	3.81591232	0.020835021	0.149248041
GO:0001706	endoderm formation	17.80759083	0.02180859	0.149248041
GO:0002087	exchange by neurological system process	17.80759083	0.02180859	0.149248041
GO:0007076	mitotic chromosome condensation	17.80759083	0.02180859	0.149248041
GO:0007413	axonal fasciculation	17.80759083	0.02180859	0.149248041
GO:0030534	adult behavior	17.80759083	0.02180859	0.149248041
GO:0030889	proliferation	17.80759083	0.02180859	0.149248041
GO:0045086	biosynthetic process	17.80759083	0.02180859	0.149248041

GO:0048268	clathrin coat assembly	17.80759083	0.02180859	0.149248041
GO:0051480	cytosolic calcium ion homeostasis	17.80759083	0.02180859	0.149248041
GO:0007173	signaling pathway	3.754032661	0.022527769	0.149248041
	rich repeat containing receptor			
GO:0035872	signaling pathway	8.267810026	0.022891322	0.149248041
GO:0042110	T cell activation	8.267810026	0.022891322	0.149248041
GO:0071363	stimulus	8.267810026	0.022891322	0.149248041
GO:0006355	dependent	1.864061463	0.023824146	0.149248041
GO:0033137	serine phosphorylation	16.53562005	0.025298713	0.149248041
GO:0042573	retinoic acid metabolic process	16.53562005	0.025298713	0.149248041
GO:0045332	phospholipid translocation	16.53562005	0.025298713	0.149248041
GO:0050995	catabolic process	16.53562005	0.025298713	0.149248041
GO:0006351	transcription, DNA-dependent	1.710581385	0.025751549	0.149248041
GO:0043406	activity	7.89200048	0.026075989	0.149248041
GO:0043647	process	7.89200048	0.026075989	0.149248041
GO:0006813	potassium ion transport	5.261333653	0.028935164	0.149248041
GO:0002230	response to virus by host	15.43324538	0.029024997	0.149248041
GO:0008637	apoptotic mitochondrial changes	15.43324538	0.029024997	0.149248041
GO:0030449	regulation of complement activation	15.43324538	0.029024997	0.149248041
GO:0035265	organ growth	15.43324538	0.029024997	0.149248041
GO:0043011	differentiation	15.43324538	0.029024997	0.149248041
GO:0048593	camera-type eye morphogenesis	15.43324538	0.029024997	0.149248041
GO:0060749	development	15.43324538	0.029024997	0.149248041
	negative regulation of G1/S			
GO:2000134	transition of mitotic cell cycle	15.43324538	0.029024997	0.149248041
GO:0006612	protein targeting to membrane	14.46866755	0.032983122	0.149248041
GO:0006750	glutathione biosynthetic process	14.46866755	0.032983122	0.149248041
GO:0030279	negative regulation of ossification	14.46866755	0.032983122	0.149248041
GO:0048546	digestive tract morphogenesis	14.46866755	0.032983122	0.149248041
GO:0048566	development	14.46866755	0.032983122	0.149248041
GO:0050870	activation	14.46866755	0.032983122	0.149248041
GO:0061098	tyrosine kinase activity	14.46866755	0.032983122	0.149248041
GO:0071158	arrest	14.46866755	0.032983122	0.149248041
	baroreceptor response to increased			
GO:0001984	systemic arterial blood pressure	115.7493404	0.034557432	0.149248041
GO:0002253	activation of immune response	115.7493404	0.034557432	0.149248041
GO:0002367	immune response	115.7493404	0.034557432	0.149248041
	immunoglobulin biosynthetic			
GO:0002642	process	115.7493404	0.034557432	0.149248041
GO:0002667	regulation of T cell anergy	115.7493404	0.034557432	0.149248041
GO:0002710	mediated immunity	115.7493404	0.034557432	0.149248041
GO:0002732	cytokine production	115.7493404	0.034557432	0.149248041
GO:0002764	signaling pathway	115.7493404	0.034557432	0.149248041
GO:0002792	secretion	115.7493404	0.034557432	0.149248041
GO:0002793	secretion	115.7493404	0.034557432	0.149248041
	inflammatory response to antigenic			
GO:0002866	stimulus	115.7493404	0.034557432	0.149248041
GO:0003062	signal	115.7493404	0.034557432	0.149248041

GO:0003131	signaling	115.7493404	0.034557432	0.149248041
GO:0006030	chitin metabolic process	115.7493404	0.034557432	0.149248041
GO:0006037	cell wall chitin metabolic process	115.7493404	0.034557432	0.149248041
GO:0006948	fusion	115.7493404	0.034557432	0.149248041
GO:0007063	cohesion	115.7493404	0.034557432	0.149248041
GO:0007387	formation	115.7493404	0.034557432	0.149248041
GO:0007388	posterior compartment specification	115.7493404	0.034557432	0.149248041
GO:0009181	catabolic process	115.7493404	0.034557432	0.149248041
GO:0010255	glucose mediated signaling pathway	115.7493404	0.034557432	0.149248041
GO:0010752	signaling	115.7493404	0.034557432	0.149248041
GO:0010758	chemotaxis	115.7493404	0.034557432	0.149248041
GO:0010813	neuropeptide catabolic process	115.7493404	0.034557432	0.149248041
GO:0010814	substance P catabolic process	115.7493404	0.034557432	0.149248041
GO:0010816	calcitonin catabolic process	115.7493404	0.034557432	0.149248041
GO:0010900	phosphatidylcholine catabolic process	115.7493404	0.034557432	0.149248041
GO:0014013	regulation of gliogenesis	115.7493404	0.034557432	0.149248041
GO:0014812	muscle cell migration	115.7493404	0.034557432	0.149248041
GO:0014856	skeletal muscle cell proliferation	115.7493404	0.034557432	0.149248041
GO:0019637	organophosphate metabolic process	115.7493404	0.034557432	0.149248041
GO:0019883	antigen processing and presentation of endogenous antigen	115.7493404	0.034557432	0.149248041
GO:0021629	organization	115.7493404	0.034557432	0.149248041
GO:0021692	morphogenesis	115.7493404	0.034557432	0.149248041
GO:0021793	axon	115.7493404	0.034557432	0.149248041
GO:0030322	stabilization of membrane potential	115.7493404	0.034557432	0.149248041
GO:0030421	defecation	115.7493404	0.034557432	0.149248041
GO:0030826	process	115.7493404	0.034557432	0.149248041
GO:0031052	chromosome breakage	115.7493404	0.034557432	0.149248041
GO:0031645	system process	115.7493404	0.034557432	0.149248041
GO:0032244	transport	115.7493404	0.034557432	0.149248041
GO:0032498	detection of muramyl dipeptide	115.7493404	0.034557432	0.149248041
GO:0032655	production	115.7493404	0.034557432	0.149248041
GO:0032701	production	115.7493404	0.034557432	0.149248041
GO:0032814	activation	115.7493404	0.034557432	0.149248041
GO:0032900	production	115.7493404	0.034557432	0.149248041
GO:0032960	biosynthetic process	115.7493404	0.034557432	0.149248041
GO:0034120	aggregation	115.7493404	0.034557432	0.149248041
GO:0034230	enkephalin processing	115.7493404	0.034557432	0.149248041
GO:0034231	islet amyloid polypeptide processing	115.7493404	0.034557432	0.149248041
GO:0034369	remodeling	115.7493404	0.034557432	0.149248041
GO:0034959	endothelin maturation	115.7493404	0.034557432	0.149248041
GO:0035476	angioblast cell migration	115.7493404	0.034557432	0.149248041
GO:0035691	macrophage migration inhibitory factor signaling pathway	115.7493404	0.034557432	0.149248041
GO:0035978	histone H2A-S139 phosphorylation	115.7493404	0.034557432	0.149248041
GO:0040040	thermosensory behavior	115.7493404	0.034557432	0.149248041
GO:0042228	interleukin-8 biosynthetic process	115.7493404	0.034557432	0.149248041

GO:0042976	activation of Janus kinase activity	115.7493404	0.034557432	0.149248041
GO:0045234	protein palmitoylation	115.7493404	0.034557432	0.149248041
GO:0045368	biosynthetic process	115.7493404	0.034557432	0.149248041
GO:0045605	differentiation	115.7493404	0.034557432	0.149248041
GO:0045622	differentiation	115.7493404	0.034557432	0.149248041
GO:0045624	differentiation	115.7493404	0.034557432	0.149248041
GO:0045769	cell division	115.7493404	0.034557432	0.149248041
GO:0045870	genome replication	115.7493404	0.034557432	0.149248041
GO:0046588	negative regulation of calcium-dependent cell-cell adhesion	115.7493404	0.034557432	0.149248041
GO:0046645	T cell activation	115.7493404	0.034557432	0.149248041
GO:0048242	epinephrine secretion	115.7493404	0.034557432	0.149248041
GO:0050923	regulation of negative chemotaxis	115.7493404	0.034557432	0.149248041
GO:0051153	differentiation	115.7493404	0.034557432	0.149248041
GO:0051494	organization	115.7493404	0.034557432	0.149248041
GO:0051939	gamma-aminobutyric acid import	115.7493404	0.034557432	0.149248041
GO:0060138	fetal process involved in parturition	115.7493404	0.034557432	0.149248041
GO:0060405	regulation of penile erection	115.7493404	0.034557432	0.149248041
GO:0060448	dichotomous subdivision of terminal units involved in lung branching	115.7493404	0.034557432	0.149248041
GO:0060721	cell proliferation	115.7493404	0.034557432	0.149248041
GO:0060739	signaling involved in prostate gland development	115.7493404	0.034557432	0.149248041
GO:0060809	mesodermal to mesenchymal transition involved in gastrulation	115.7493404	0.034557432	0.149248041
GO:0060857	barrier	115.7493404	0.034557432	0.149248041
GO:0061143	development	115.7493404	0.034557432	0.149248041
GO:0070092	regulation of glucagon secretion	115.7493404	0.034557432	0.149248041
GO:0070247	apoptotic process	115.7493404	0.034557432	0.149248041
GO:0070254	mucus secretion	115.7493404	0.034557432	0.149248041
GO:0070734	histone H3-K27 methylation	115.7493404	0.034557432	0.149248041
GO:0071105	response to interleukin-11	115.7493404	0.034557432	0.149248041
GO:0071107	stimulus	115.7493404	0.034557432	0.149248041
GO:0071336	proliferation	115.7493404	0.034557432	0.149248041
GO:0071608	alpha production	115.7493404	0.034557432	0.149248041
GO:0071939	vitamin A import	115.7493404	0.034557432	0.149248041
GO:0072675	osteoclast fusion	115.7493404	0.034557432	0.149248041
GO:0090287	growth factor stimulus	115.7493404	0.034557432	0.149248041
GO:1900275	phospholipase C activity	115.7493404	0.034557432	0.149248041
GO:1900276	receptor activity	115.7493404	0.034557432	0.149248041
GO:1900737	phospholipase C-activating G-protein coupled receptor signaling involved in ubiquitin-dependent	115.7493404	0.034557432	0.149248041
GO:2000058	protein catabolic process	115.7493404	0.034557432	0.149248041
GO:2000097	matrix adhesion	115.7493404	0.034557432	0.149248041
GO:2000169	nitrosylation	115.7493404	0.034557432	0.149248041
GO:2000193	transport	115.7493404	0.034557432	0.149248041
GO:2000363	E synthase activity	115.7493404	0.034557432	0.149248041

GO:2000685	response to X-ray	115.7493404	0.034557432	0.149248041
	positive regulation of N-terminal			
GO:2000761	peptidyl-lysine acetylation	115.7493404	0.034557432	0.149248041
GO:2000872	secretion	115.7493404	0.034557432	0.149248041
	break repair via nonhomologous end			
GO:2001033	joining	115.7493404	0.034557432	0.149248041
GO:0035335	peptidyl-tyrosine dephosphorylation	7.086694308	0.035144613	0.151345297
GO:0010923	activity	6.944960422	0.037152263	0.156896795
GO:0016486	peptide hormone processing	13.61756946	0.037168826	0.156896795
GO:0031290	retinal ganglion cell axon guidance	13.61756946	0.037168826	0.156896795
GO:0045777	positive regulation of blood pressure	13.61756946	0.037168826	0.156896795
GO:0048265	response to pain	13.61756946	0.037168826	0.156896795
GO:0050718	beta secretion	13.61756946	0.037168826	0.156896795
GO:0048011	signaling pathway	3.012064619	0.037170852	0.156896795
GO:0051289	protein homotetramerization	6.808784728	0.039225621	0.164637113
	positive regulation of canonical Wnt			
GO:0090263	receptor signaling pathway	6.808784728	0.039225621	0.164637113
GO:0007269	neurotransmitter secretion	6.67784656	0.041365088	0.172086316
GO:0006691	leukotriene metabolic process	12.86103782	0.041577902	0.172086316
GO:0007214	pathway	12.86103782	0.041577902	0.172086316
GO:0045926	negative regulation of growth	12.86103782	0.041577902	0.172086316
GO:0048863	stem cell differentiation	12.86103782	0.041577902	0.172086316
GO:0000902	cell morphogenesis	6.551849455	0.04357104	0.178845316
GO:0043627	response to estrogen stimulus	6.551849455	0.04357104	0.178845316
GO:0046330	positive regulation of JNK cascade	6.551849455	0.04357104	0.178845316
GO:0001666	response to hypoxia	3.733849689	0.045678024	0.186978726
GO:0051403	stress-activated MAPK cascade	6.430518909	0.045843828	0.187143297
GO:0070328	triglyceride homeostasis	12.18414109	0.0462062	0.188107207
GO:0006810	transport	2.645699208	0.0467989	0.190000985
GO:0042742	defense response to bacterium	4.539189818	0.048021019	0.194432929
