

Table S1A

"module"	"modSize"	"bkgrModSize"	"rank"	"enrichmentP"
"BonferoniP"	"nModGenesInTerm"	"fracOfBkgrModSize"		
"fracOfBkgrTermSize"	"bkgrTermSize"	"termID"	"termOntology"	
"termName"	"termDefinition"			
"black"	55	55	1	0.00102027033004189
10	0.181818181818182			0.0869565217391304
115	"G0:0003700"	"MF"	"DNA binding transcription factor activity"	"Interacting selectively and non-covalently with a specific DNA sequence (sometimes referred to as a motif) within the regulatory region of a gene in order to modulate transcription."
"black"	55	55	2	0.00228327036383225
2	0.0363636363636364			0.666666666666667
3	"G0:0030858"	"BP"	"positive regulation of epithelial cell differentiation"	"Any process that activates or increases the frequency, rate or extent of epithelial cell differentiation."
"black"	55	55	3	0.00228327036383225
2	0.0363636363636364			0.666666666666667
3	"G0:1902235"	"BP"	"regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway"	"Any process that modulates the frequency, rate or extent of an endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway."
"black"	55	55	4	0.0034724101754248
13	0.236363636363636			0.0631067961165049
206	"G0:0006366"	"BP"	"transcription by RNA polymerase II"	"The synthesis of RNA from a DNA template by RNA polymerase II, originating at an RNA polymerase II promoter. Includes transcription of messenger RNA (mRNA) and certain small nuclear RNAs (snRNAs)."
"black"	55	55	5	0.00385682654148793
3	0.0545454545454545			0.25
0002028"	"BP"	"regulation of sodium ion transport"	"Any process that modulates the frequency, rate or extent of the directed movement of sodium ions (Na+) into, out of or within a cell, or between cells, by means of some agent such as a transporter or pore."	
"black"	55	55	6	0.00422124135195175
7	0.127272727272727			0.0933333333333333
75	"G0:0000977"	"MF"	"RNA polymerase II regulatory region sequence-specific DNA binding"	"Interacting selectively and non-covalently with a specific sequence of DNA that is part of a regulatory region that controls the transcription of a gene or cistron by RNA polymerase II."
"black"	55	55	7	0.00454914803360826
7	0.127272727272727			0.0921052631578947
76	"G0:0001012"	"MF"	"RNA polymerase II regulatory region DNA binding"	"Interacting selectively and non-covalently with a DNA region that controls the transcription of a region of DNA by RNA polymerase II. Binding may occur as a sequence specific interaction or as an interaction observed only once a factor has been recruited to the DNA by other factors."
"black"	55	55	8	0.00478800741696137
8	0.145454545454545			0.0824742268041237

97 "GO:0044212" "MF" "transcription regulatory region DNA binding" "Interacting selectively and non-covalently with a DNA region that regulates the transcription of a region of DNA, which may be a gene, cistron, or operon. Binding may occur as a sequence specific interaction or as an interaction observed only once a factor has been recruited to the DNA by other factors."

"black" 55 55 9 0.00658913669227423 1
19 0.345454545454545 0.0490956072351421

387 "GO:0051252" "BP" "regulation of RNA metabolic process" "Any process that modulates the frequency, rate or extent of the chemical reactions and pathways involving RNA."

"black" 55 55 10 0.00681839673136198 1
12 0.218181818181818 0.0609137055837563

197 "GO:0006357" "BP" "regulation of transcription by RNA polymerase II" "Any process that modulates the frequency, rate or extent of transcription mediated by RNA polymerase II."

"blue" 517 516 1 3.59704861339132e-08
0.00063527475561104 267 0.517441860465116
0.328009828009828 814 "GO:
0016020" "CC" "membrane" "A lipid bilayer along with all the proteins and protein complexes embedded in it and attached to it."

"blue" 517 516 2 8.90002243191713e-08
0.00157183296170088 159 0.308139534883721
0.363844393592677 437 "GO:
0031224" "CC" "intrinsic component of membrane" "The component of a membrane consisting of the gene products having some covalently attached portion, for example part of a peptide sequence or some other covalently attached group such as a GPI anchor, which spans or is embedded in one or both leaflets of the membrane."

"blue" 517 516 3 9.22164233608937e-08
0.00162863425297674 153 0.296511627906977
0.366906474820144 417 "GO:
0016021" "CC" "integral component of membrane" "The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane."

"blue" 517 516 4 1.10328444081307e-06
0.0194851065091996 168 0.325581395348837
0.348547717842324 482 "GO:0005886" "CC" "plasma membrane" "The membrane surrounding a cell that separates the cell from its external environment. It consists of a phospholipid bilayer and associated proteins."

"blue" 517 516 5 1.3334439646557e-06
0.0235499538597843 172 0.333333333333333
0.346076458752515 497 "GO:0071944" "CC" "cell periphery" "The part of a cell encompassing the cell cortex, the plasma membrane, and any external encapsulating structures."

"blue" 517 516 6 1.44106247756729e-06
0.025450604416316 78 0.151162790697674
0.414893617021277 188 "GO:
0040011" "BP" "locomotion" "Self-propelled movement of a cell or organism from one location to another."

"blue" 517 516 7 1.61565774517377e-06

0.0285341314375139	129	0.25	0.366477272727273
352	"G0:0023051"	"BP"	"regulation of signaling"
process that modulates the frequency, rate or extent of a signaling process."			
"blue"	517	516	8
0.0297867324189008	193	0.374031007751938	1.68658243694586e-06
0.337412587412587	572	"G0:	
0023052"	"BP"	"signaling"	"The entirety of a process in which information is transmitted within a biological system. This process begins with an active signal and ends when a cellular response has been triggered."
"blue"	517	516	9
0.0320712449942192	95	0.184108527131783	1.81593596026381e-06
0.392561983471074	242	"G0:	
0009653"	"BP"	"anatomical structure morphogenesis"	"The process in which anatomical structures are generated and organized. Morphogenesis pertains to the creation of form."
"blue"	517	516	10
0.0339824739151808	99	0.191860465116279	1.92415344064214e-06
0.388235294117647	255	"G0:0006955"	"BP"
"immune response"			
"Any immune system process that functions in the calibrated response of an organism to a potential internal or invasive threat."			
"brown"	395	389	1
29	0.0745501285347044	0.391891891891892	7.26397695625327e-05
74	"G0:1903706"	"BP"	"regulation of hemopoiesis"
"Any process that modulates the frequency, rate or extent of hemopoiesis."			
"brown"	395	389	2
4	0.0102827763496144	1	4
0051591"	"BP"	"response to cAMP"	"Any process that results in a change in state or activity of a cell or an organism (in terms of movement, secretion, enzyme production, gene expression, etc.) as a result of a cAMP (cyclic AMP, adenosine 3',5'-cyclophosphate) stimulus."
"brown"	395	389	3
4	0.0102827763496144	1	4
0005507"	"MF"	"copper ion binding"	"Interacting selectively and non-covalently with copper (Cu) ions."
"brown"	395	389	4
50	0.12853470437018	0.290697674418605	0.00153872309165422
0002520"	"BP"	"immune system development"	"The process whose specific outcome is the progression of an organismal system whose objective is to provide calibrated responses by an organism to a potential internal or invasive threat, over time, from its formation to the mature structure. A system is a regularly interacting or interdependent group of organs or tissues that work together to carry out a given biological process."
"brown"	395	389	5
40	0.102827763496144	0.303030303030303	0.00202878256972319
132	"G0:0005730"	"CC"	"nucleolus"
"A small, dense body one or more of which are present in the nucleus of eukaryotic cells. It is rich in RNA and protein, is not bounded by a limiting membrane, and is not seen during mitosis. Its prime function is the			

transcription of the nucleolar DNA into 45S ribosomal-precursor RNA, the processing of this RNA into 5.8S, 18S, and 28S components of ribosomal RNA, and the association of these components with 5S RNA and proteins synthesized outside the nucleolus. This association results in the formation of ribonucleoprotein precursors; these pass into the cytoplasm and mature into the 40S and 60S subunits of the ribosome."

"brown" 395 389 6 0.00338550039299209 1

11 0.0282776349614396 0.458333333333333

24 "GO:0001935" "BP" "endothelial cell

proliferation" "The multiplication or reproduction of endothelial cells, resulting in the expansion of a cell population. Endothelial cells are thin flattened cells which line the inside surfaces of body cavities, blood vessels, and lymph vessels, making up the endothelium."

"brown" 395 389 7 0.00357282369479165 1

46 0.118251928020566 0.285714285714286

161 "GO:0048534" "BP" "hematopoietic or lymphoid organ development"

"The process whose specific outcome is the progression of any organ involved in hematopoiesis (also known as hemopoiesis) or lymphoid cell activation over time, from its formation to the mature structure. Such development includes differentiation of resident cell types (stromal cells) and of migratory cell types dependent on the unique microenvironment afforded by the organ for their proper differentiation."

"brown" 395 389 8 0.00368161376659798 1

10 0.025706940874036 0.476190476190476

21 "GO:0001936" "BP" "regulation of endothelial cell

proliferation" "Any process that modulates the frequency, rate, or extent of endothelial cell proliferation."

"brown" 395 389 9 0.00388694662242634 1

9 0.0231362467866324 0.5 18 "GO:

0007179" "BP" "transforming growth factor beta receptor signaling pathway" "A series of molecular signals initiated by the binding of an extracellular ligand to a transforming growth factor beta receptor on the surface of a target cell, and ending with regulation of a downstream cellular process, e.g. transcription."

"brown" 395 389 10 0.00445578440918749 1

5 0.012853470437018 0.714285714285714

7 "GO:0030512" "BP" "negative regulation of

transforming growth factor beta receptor signaling pathway" "Any process that stops, prevents, or reduces the frequency, rate or extent of any TGF-beta receptor signaling pathway."

"green" 103 100 1 0.000129446081022539 1

3 0.03 1 3 "GO:

0060441" "BP" "epithelial tube branching involved in lung

morphogenesis" "The process in which a highly ordered sequence of patterning events generates the branched epithelial tubes of the lung, consisting of reiterated combinations of bud outgrowth, elongation, and dichotomous subdivision of terminal units."

"green" 103 100 2 0.000498516390802402 1

3 0.03 0.75 4 "GO:0060425" "BP" "lung

morphogenesis" "The process in which the anatomical structures of the lung are generated and organized."

"green"	103	100	3	0.000662590827701156	1	
4	0.04	0.4444444444444444	9	"G0:		
0006367"	"BP"	"transcription initiation from RNA polymerase II promoter"				
"Any process involved in the assembly of the RNA polymerase II preinitiation complex (PIC) at an RNA polymerase II promoter region of a DNA template, resulting in the subsequent synthesis of RNA from that promoter. The initiation phase includes PIC assembly and the formation of the first few bonds in the RNA chain, including abortive initiation, which occurs when the first few nucleotides are repeatedly synthesized and then released. Promoter clearance, or release, is the transition between the initiation and elongation phases of transcription."						
"green"	103	100	4	0.000875944128420456	1	
5	0.05	0.3125	16	"G0:		
0035456"	"BP"	"response to interferon-beta"		"Any process that results in a change in state or activity of a cell or an organism (in terms of movement, secretion, enzyme production, gene expression, etc.) as a result of an interferon-beta stimulus. Interferon-beta is a type I interferon."		
"green"	103	100	5	0.00120001441051704	1	
3	0.03	0.6	5	"G0:0036041"	"MF"	"long-chain fatty acid binding"
"Interacting selectively and non-covalently with a long-chain fatty acid. A long-chain fatty acid is a fatty acid with a chain length between C13 and C22."						
"green"	103	100	6	0.00130783749389977	1	
10	0.1	0.153846153846154	65	"G0:		
0009615"	"BP"	"response to virus"		"Any process that results in a change in state or activity of a cell or an organism (in terms of movement, secretion, enzyme production, gene expression, etc.) as a result of a stimulus from a virus."		
"green"	103	100	7	0.00150446227638271	1	
24	0.24	0.0941176470588235	255	"G0:		
0006955"	"BP"	"immune response"		"Any immune system process that functions in the calibrated response of an organism to a potential internal or invasive threat."		
"green"	103	100	8	0.00158301461058731	1	
5	0.05	0.277777777777778	18	"G0:		
0060541"	"BP"	"respiratory system development"		"The progression of the respiratory system over time from its formation to its mature structure. The respiratory system carries out respiratory gaseous exchange."		
"green"	103	100	9	0.0016025792515915	1	
4	0.04	0.363636363636364	11	"G0:		
0035455"	"BP"	"response to interferon-alpha"		"Any process that results in a change in state or activity of a cell or an organism (in terms of movement, secretion, enzyme production, gene expression, etc.) as a result of an interferon-alpha stimulus. Interferon-alpha is a type I interferon."		
"green"	103	100	10	0.00193746081524262	1	
11	0.11	0.1375	80	"G0:0002764"	"BP"	"immune response-regulating signaling pathway"
"The cascade of processes by which a signal interacts with a receptor, causing a change in the level or activity of a second messenger or other downstream target, and ultimately leading to the activation, perpetuation, or						

inhibition of an immune response."

"grey" 12 12 1 0.00219730353393327 1

2 0.166666666666667 0.166666666666667

12 "GO:0004867" "MF" "serine-type endopeptidase

inhibitor activity" "Stops, prevents or reduces the activity of serine-type endopeptidases, enzymes that catalyze the hydrolysis of nonterminal peptide bonds in a polypeptide chain; a serine residue (and a histidine residue) are at the active center of the enzyme."

"grey" 12 12 2 0.00612870275791622 1

1 0.083333333333333 1 1 "GO:

0070054" "BP" "mRNA splicing, via endonucleolytic cleavage and ligation" "Splicing of mRNA substrates via recognition of the folded RNA structure that brings the 5' and 3' splice sites into proximity and cleavage of the RNA at both the 3' and 5' splice sites by an endonucleolytic mechanism, followed by ligation of the exons."

"grey" 12 12 3 0.00612870275791622 1

1 0.083333333333333 1 1 "GO:

0070055" "BP" "mRNA endonucleolytic cleavage involved in unfolded protein response" "The endonucleolytic cleavage of a mRNA containing an HAC1-type intron at the 5' and 3' splice sites. The cleavage step is part of unconventional mRNA splicing, and contributes to the endoplasmic reticulum unfolded protein response."

"grey" 12 12 4 0.00612870275791622 1

1 0.083333333333333 1 1 "GO:

1901142" "BP" "insulin metabolic process" "The chemical reactions and pathways involving insulin."

"grey" 12 12 5 0.00612870275791622 1

1 0.083333333333333 1 1 "GO:

1990579" "BP" "peptidyl-serine trans-autophosphorylation" "The phosphorylation of a peptidyl-serine to form peptidyl-O-phospho-L-serine on an identical protein. For example, phosphorylation by the other kinase within a homodimer."

"grey" 12 12 6 0.00612870275791622 1

1 0.083333333333333 1 1 "GO:

0005581" "CC" "collagen trimer" "A protein complex consisting of three collagen chains assembled into a left-handed triple helix. These trimers typically assemble into higher order structures."

"grey" 12 12 7 0.00612870275791622 1

1 0.083333333333333 1 1 "GO:

0031372" "CC" "UBC13-MMS2 complex" "A heterodimeric ubiquitin conjugating enzyme complex that catalyzes assembly of K63-linked polyubiquitin chains, which act as a signal to promote error-free DNA postreplication repair; in Saccharomyces the complex comprises Ubc13p and Mms2p."

"grey" 12 12 8 0.00612870275791622 1

1 0.083333333333333 1 1 "GO:

0035370" "CC" "UBC13-UEV1A complex" "A heterodimeric ubiquitin conjugating enzyme complex that catalyzes assembly of K63-linked polyubiquitin chains and is involved in NF-kappaB activation. In humans at least, the complex comprises the ubiquitin-conjugating enzyme UBC13 and ubiquitin-conjugating enzyme variant 1A (UEV1A)."

"grey"	12	12	9	0.00612870275791622	1
1	0.0833333333333333	1	1	"G0:	
1990597"	"CC"	"AIP1-IRE1 complex"	"A protein complex consisting of IRE1 (inositol-requiring enzyme-1) bound to AIP1 (ASK1-interacting protein 1/DAB2-interacting protein)."		
"grey"	12	12	10	0.00612870275791622	1
1	0.0833333333333333	1	1	"G0:	
1990604"	"CC"	"IRE1-TRAF2-ASK1 complex"	"A protein complex of the endoplasmic reticulum membrane that consists of IRE1 (Inositol-requiring enzyme-1), TRAF2 (TNF receptor-associated factor 2) and ASK1 (Apoptosis signal-regulating kinase 1, a MAP3K)."		
"red"	62	61	1	0.000236243073463681	1
6	0.0983606557377049	0.2	30	"G0:	
0045732"	"BP"	"positive regulation of protein catabolic process"	"Any process that activates or increases the frequency, rate or extent of the chemical reactions and pathways resulting in the breakdown of a protein by the destruction of the native, active configuration, with or without the hydrolysis of peptide bonds."		
"red"	62	61	2	0.000353830763853935	1
8	0.131147540983607	0.135593220338983			
59	"G0:0042176"	"BP"	"regulation of protein catabolic process"		
			"Any process that modulates the frequency, rate or extent of the chemical reactions and pathways resulting in the breakdown of a protein by the destruction of the native, active configuration, with or without the hydrolysis of peptide bonds."		
"red"	62	61	3	0.000676083034389494	1
4	0.0655737704918033	0.285714285714286			
14	"G0:1903052"	"BP"	"positive regulation of proteolysis involved in cellular protein catabolic process"		
			"Any process that activates or increases the frequency, rate or extent of proteolysis involved in cellular protein catabolic process."		
"red"	62	61	4	0.000955163178929205	1
2	0.0327868852459016	1	2	"G0:	
0060292"	"BP"	"long term synaptic depression"	"A process that modulates synaptic plasticity such that synapses are changed resulting in the decrease in the rate, or frequency of synaptic transmission at the synapse."		
"red"	62	61	5	0.00149825320565425	1
4	0.0655737704918033	0.235294117647059			
17	"G0:0043524"	"BP"	"negative regulation of neuron apoptotic process"		
			"Any process that stops, prevents, or reduces the frequency, rate or extent of cell death by apoptotic process in neurons."		
"red"	62	61	6	0.00149825320565425	1
4	0.0655737704918033	0.235294117647059			
17	"G0:1903364"	"BP"	"positive regulation of cellular protein catabolic process"		
			"Any process that activates or increases the frequency, rate or extent of cellular protein catabolic process."		
"red"	62	61	7	0.00172390875816899	1
11	0.180327868852459	0.0846153846153846			
130	"G0:0030163"	"BP"	"protein catabolic process"		
			"The chemical reactions and pathways resulting in the breakdown of a protein by the destruction of the native, active		

configuration, with or without the hydrolysis of peptide bonds."

"red"	62	61	8	0.00224893978687442	1
6	0.0983606557377049			0.1333333333333333	
45	"G0:0046390"	"BP"		"ribose phosphate biosynthetic process"	"The chemical reactions and pathways resulting in the formation of ribose phosphate, any phosphorylated ribose sugar."
"red"	62	61	9	0.00226446448323347	1
5	0.0819672131147541			0.161290322580645	
31	"G0:1903362"	"BP"		"regulation of cellular protein catabolic process"	"Any process that modulates the frequency, rate or extent of cellular protein catabolic process."
"red"	62	61	10	0.00233249153178043	1
9	0.147540983606557			0.09375	96
0051603	"BP"			"proteolysis involved in cellular protein catabolic process"	"The hydrolysis of a peptide bond or bonds within a protein as part of the chemical reactions and pathways resulting in the breakdown of a protein by individual cells."
"turquoise"	718	716	1	1.22363233871473e-16	
2.16105707340409e-12		70		0.0977653631284916	
0.786516853932584		89		"G0:0000280"	"BP"
division"				"The division of a cell nucleus into two nuclei, with DNA and other nuclear contents distributed between the daughter nuclei."	
"turquoise"	718	716	2	2.06928432447053e-16	
3.65456304544741e-12		72		0.100558659217877	
0.774193548387097		93		"G0:	
0048285	"BP"			"organelle fission"	"The creation of two or more organelles by division of one organelle."
"turquoise"	718	716	3	2.17231301665199e-16	
3.83652201870908e-12		115		0.160614525139665	
0.657142857142857		175		"G0:0000278"	"BP"
cell cycle"				"Progression through the phases of the mitotic cell cycle, the most common eukaryotic cell cycle, which canonically comprises four successive phases called G1, S, G2, and M and includes replication of the genome and the subsequent segregation of chromosomes into daughter cells. In some variant cell cycles nuclear replication or nuclear division may not be followed by cell division, or G1 and G2 phases may be absent."	
"turquoise"	718	716	4	7.28470232118828e-15	
1.28655127694506e-10		173		0.241620111731844	
0.565359477124183		306		"G0:0007049"	"BP"
cycle"				"The progression of biochemical and morphological phases and events that occur in a cell during successive cell replication or nuclear replication events. Canonically, the cell cycle comprises the replication and segregation of genetic material followed by the division of the cell, but in endocycles or syncytial cells nuclear replication or nuclear division may not be followed by cell division."	
"turquoise"	718	716	5	1.09740062203727e-13	
1.93811923858003e-09		59		0.0824022346368715	
0.776315789473684		76		"G0:	
0007059	"BP"			"chromosome segregation"	"The process in which genetic material, in the form of chromosomes, is organized into specific structures and then physically separated and apportioned to

two or more sets. In eukaryotes, chromosome segregation begins with the condensation of chromosomes, includes chromosome separation, and ends when chromosomes have completed movement to the spindle poles."

"turquoise"	718	716	6	1.3093518689316e-13
2.31244633572009e-09		127		0.177374301675978
0.601895734597156		211		"G0:
0005694"	"CC"	"chromosome"		"A structure composed of a very long molecule of DNA and associated proteins (e.g. histones) that carries hereditary information."
"turquoise"	718	716	7	3.26833620653413e-11
5.77220857435992e-07		41		0.0572625698324022
50	"G0:0000819"	"BP"		"sister chromatid segregation"
				"The cell cycle process in which sister chromatids are organized and then physically separated and apportioned to two or more sets."
"turquoise"	718	716	8	1.9425856731341e-10
3.43080055732214e-06		82		0.114525139664804
0.630769230769231		130		"G0:0051301"
			"BP"	"cell division"
				"The process resulting in division and partitioning of components of a cell to form more cells; may or may not be accompanied by the physical separation of a cell into distinct, individually membrane-bounded daughter cells."
"turquoise"	718	716	9	4.03367757081188e-10
7.12387795781086e-06		38		0.053072625698324
0.808510638297872		47		"G0:0000070"
			"BP"	"mitotic sister chromatid segregation"
				"The cell cycle process in which replicated homologous chromosomes are organized and then physically separated and apportioned to two sets during the mitotic cell cycle. Each replicated chromosome, composed of two sister chromatids, aligns at the cell equator, paired with its homologous partner. One homolog of each morphologic type goes into each of the resulting chromosome sets."
"turquoise"	718	716	10	7.75731067505495e-10
1.37001863832145e-05		62		0.0865921787709497
0.673913043478261		92		"G0:0006281"
			"BP"	"DNA repair"
				"The process of restoring DNA after damage. Genomes are subject to damage by chemical and physical agents in the environment (e.g. UV and ionizing radiations, chemical mutagens, fungal and bacterial toxins, etc.) and by free radicals or alkylating agents endogenously generated in metabolism. DNA is also damaged because of errors during its replication. A variety of different DNA repair pathways have been reported that include direct reversal, base excision repair, nucleotide excision repair, photoreactivation, bypass, double-strand break repair pathway, and mismatch repair pathway."
"yellow"	109	109	1	0.00028249302839376
5				1
0.0458715596330275				0.416666666666667
12	"G0:0008135"	"MF"		"translation factor activity, RNA binding"
				"Functions during translation by interacting selectively and non-covalently with RNA during polypeptide synthesis at the ribosome."
"yellow"	109	109	2	0.000922281647246977
4				1
0.036697247706422				0.444444444444444
9	"G0:0003743"	"MF"		"translation initiation factor"

activity" "Functions in the initiation of ribosome-mediated translation of mRNA into a polypeptide."

"yellow"	109	109	3	0.00159698293449057	1
13	0.119266055045872			0.138297872340426	
94	"G0:0043604"	"BP"		"amide biosynthetic process"	

"The chemical reactions and pathways resulting in the formation of an amide, any derivative of an oxoacid in which an acidic hydroxy group has been replaced by an amino or substituted amino group."

"yellow"	109	109	4	0.00176251899598819	1
5	0.0458715596330275			0.294117647058824	
17	"G0:0051087"	"MF"		"chaperone binding"	

"Interacting selectively and non-covalently with a chaperone protein, a class of proteins that bind to nascent or unfolded polypeptides and ensure correct folding or transport."

"yellow"	109	109	5	0.00183000872612569	1
12	0.110091743119266			0.142857142857143	
84	"G0:0043043"	"BP"		"peptide biosynthetic process"	

"The chemical reactions and pathways resulting in the formation of peptides, compounds of 2 or more (but usually less than 100) amino acids where the alpha carboxyl group of one is bound to the alpha amino group of another. This may include the translation of a precursor protein and its subsequent processing into a functional peptide."

"yellow"	109	109	6	0.00227958067996459	1
21	0.192660550458716			0.105527638190955	
199	"G0:0098772"	"MF"		"molecular function regulator"	

"A molecular function that modulates the activity of a gene product or complex. Examples include enzyme regulators and channel regulators."

"yellow"	109	109	7	0.00307218058534279	1
2	0.018348623853211		1	2	"G0:0033363"

"BP" "secretory granule organization" "A process that is carried out at the cellular level which results in the assembly, arrangement of constituent parts, or disassembly of a secretory granule. A secretory granule is a small subcellular vesicle, surrounded by a membrane, that is formed from the Golgi apparatus and contains a highly concentrated protein destined for secretion."

"yellow"	109	109	8	0.00307218058534279	1
2	0.018348623853211		1	2	"G0:0035162"

"BP" "embryonic hemopoiesis" "The stages of blood cell formation that take place within the embryo."

"yellow"	109	109	9	0.00307218058534279	1
2	0.018348623853211		1	2	"G0:0001405"

"CC" "presequence translocase-associated import motor" "Protein complex located on the matrix side of the mitochondrial inner membrane and associated with the presequence translocase complex; hydrolyzes ATP to provide the force to drive import of proteins into the mitochondrial matrix."

"yellow"	109	109	10	0.00307218058534279	1
2	0.018348623853211		1	2	"G0:0005851"

"CC" "eukaryotic translation initiation factor 2B complex" "A multisubunit guanine nucleotide exchange factor which catalyzes the exchange of GDP bound to initiation factor eIF2 for

GTP, generating active eIF2-GTP. In humans, it is composed of five subunits, alpha, beta, delta, gamma and epsilon."

Table S1B

"module"	"modSize"	"bkgrModSize"	"rank"	"enrichmentP"	
"BonferoniP"	"nModGenesInTerm"		"fracOfBkgrModSize"		
"fracOfBkgrTermSize"	"bkgrTermSize"		"termID"	"termOntology"	
"termName"	"termDefinition"				
"blue"	453	452	1	0.00288106655992114	1
8	0.0176991150442478			0.727272727272727	
11	"GO:0035282"	"BP"	"segmentation"	"The regionalization process that divides an organism or part of an organism into a series of semi-repetitive parts, or segments, often arranged along a longitudinal axis."	
"blue"	453	452	2	0.00288106655992114	1
8	0.0176991150442478			0.727272727272727	
11	"GO:2000779"	"BP"	"regulation of double-strand break repair"	"Any process that modulates the frequency, rate or extent of double-strand break repair."	
"blue"	453	452	3	0.00417208635173806	1
20	0.0442477876106195			0.48780487804878	41
0033218"	"MF"	"amide binding"	"Interacting selectively and non-covalently with an amide, any derivative of an oxoacid in which an acidic hydroxy group has been replaced by an amino or substituted amino group."		"GO:0033218"
"blue"	453	452	4	0.00532822279855509	1
14	0.0309734513274336			0.538461538461538	
26	"GO:0002224"	"BP"	"toll-like receptor signaling pathway"	"Any series of molecular signals generated as a consequence of binding to a toll-like receptor. Toll-like receptors directly bind pattern motifs from a variety of microbial sources to initiate innate immune response."	
"blue"	453	452	5	0.00533917707527118	1
83	0.183628318584071			0.357758620689655	
232	"GO:0006955"	"BP"	"immune response"	"Any immune system process that functions in the calibrated response of an organism to a potential internal or invasive threat."	
"blue"	453	452	6	0.0054652527882605	1
9	0.0199115044247788			0.642857142857143	
14	"GO:0032088"	"BP"	"negative regulation of NF-kappaB transcription factor activity"	"Any process that stops, prevents, or reduces the frequency, rate or extent of the activity of the transcription factor NF-kappaB."	
"blue"	453	452	7	0.00650150584143631	1
4	0.00884955752212389			1	4
0018027"	"BP"	"peptidyl-lysine dimethylation"	"The methylation of peptidyl-lysine to form peptidyl-N6,N6-dimethyl-L-lysine."		"GO:0018027"
"blue"	453	452	8	0.00650150584143631	1
4	0.00884955752212389			1	4
0036124"	"BP"	"histone H3-K9 trimethylation"	"The modification of histone H3 by addition of three methyl groups to lysine at position 9 of the histone."		"GO:0036124"
"blue"	453	452	9	0.00650150584143631	1
4	0.00884955752212389			1	4
0045953"	"BP"	"negative regulation of natural killer cell mediated cytotoxicity"	"Any process that stops, prevents, or reduces the rate of natural killer mediated cytotoxicity."		"GO:0045953"

"blue"	453	452	10	0.00650150584143631	1
4	0.00884955752212389	1	4	"G0:	
0051496"	"BP"	"positive regulation of stress fiber assembly"			
		"Any process that activates or increases the frequency, rate or extent of the assembly of a stress fiber, a bundle of microfilaments and other proteins found in fibroblasts."			
"brown"	202	202	1	0.00114784471337333	1
4	0.0198019801980198	0.8	5	"G0:	
0046654"	"BP"	"tetrahydrofolate biosynthetic process" "The chemical reactions and pathways resulting in the formation of tetrahydrofolate, 5,6,7,8-tetrahydrofolic acid, a folate derivative bearing additional hydrogens on the pterin group."			
"brown"	202	202	2	0.00114784471337333	1
4	0.0198019801980198	0.8	5	"G0:	
0071480"	"BP"	"cellular response to gamma radiation" "Any process that results in a change in state or activity of a cell (in terms of movement, secretion, enzyme production, gene expression, etc.) as a result of a gamma radiation stimulus. Gamma radiation is a form of electromagnetic radiation (EMR) or light emission of a specific frequency produced from sub-atomic particle interaction, such as electron-positron annihilation and radioactive decay. Gamma rays are generally characterized as EMR having the highest frequency and energy, and also the shortest wavelength, within the electromagnetic radiation spectrum."			
"brown"	202	202	3	0.00259780601442417	1
5	0.0247524752475248	0.555555555555556			
9	"G0:0030261"	"BP"	"chromosome condensation" "The progressive compaction of dispersed interphase chromatin into threadlike chromosomes prior to mitotic or meiotic nuclear division, or during apoptosis, in eukaryotic cells."		
"brown"	202	202	4	0.00278233163730142	1
11	0.0544554455445545	0.314285714285714			
35	"G0:0016607"	"CC"	"nuclear speck" "A discrete extra-nucleolar subnuclear domain, 20-50 in number, in which splicing factors are seen to be localized by immunofluorescence microscopy."		
"brown"	202	202	5	0.00310059871354082	1
4	0.0198019801980198	0.666666666666667			
6	"G0:0009396"	"BP"	"folic acid-containing compound biosynthetic process" "The chemical reactions and pathways resulting in the formation of folic acid and its derivatives."		
"brown"	202	202	6	0.00310059871354082	1
4	0.0198019801980198	0.666666666666667			
6	"G0:0042559"	"BP"	"pteridine-containing compound biosynthetic process" "The chemical reactions and pathways resulting in the formation of any compound containing pteridine (pyrazino(2,3-dipyrimidine)), e.g. pteric acid, xanthopterin and folic acid."		
"brown"	202	202	7	0.0058755113578508	1
18	0.0891089108910891	0.233766233766234			
77	"G0:0016604"	"CC"	"nuclear body" "Extra-nucleolar nuclear domains usually visualized by confocal microscopy and fluorescent antibodies to specific proteins."		
"brown"	202	202	8	0.00651730103494638	1

4 0.0198019801980198 0.571428571428571
7 "G0:0007076" "BP" "mitotic chromosome
condensation" "The cell cycle process in which chromatin
structure is compacted prior to and during mitosis in eukaryotic
cells."
"brown" 202 202 9 0.00729480443214277 1
6 0.0297029702970297 0.4 15 "G0:
0071479" "BP" "cellular response to ionizing radiation" "Any
process that results in a change in state or activity of a cell (in
terms of movement, secretion, enzyme production, gene expression,
etc.) as a result of a ionizing radiation stimulus. Ionizing
radiation is radiation with sufficient energy to remove electrons
from atoms and may arise from spontaneous decay of unstable
isotopes, resulting in alpha and beta particles and gamma rays.
Ionizing radiation also includes X-rays."
"brown" 202 202 10 0.00736133131089119 1
3 0.0148514851485149 0.75 4 "G0:
0003151" "BP" "outflow tract morphogenesis" "The process in
which the anatomical structures of the outflow tract are generated
and organized. The outflow tract is the portion of the heart through
which blood flows into the arteries."
"grey" 129 129 1 0.000549199072322138 1
4 0.0310077519379845 0.666666666666667
6 "G0:0051383" "BP" "kinetochore
organization" "A process that is carried out at the cellular
level which results in the assembly, arrangement of constituent
parts, or disassembly of the kinetochore, a multisubunit complex
that is located at the centromeric region of DNA and provides an
attachment point for the spindle microtubules."
"grey" 129 129 2 0.00120093830306354 1
4 0.0310077519379845 0.571428571428571
7 "G0:0032930" "BP" "positive regulation of superoxide
anion generation" "Any process that activates or increases
the frequency, rate or extent of enzymatic generation of superoxide
by a cell."
"grey" 129 129 3 0.00133952348435357 1
15 0.116279069767442 0.1875 80 "G0:
0055082" "BP" "cellular chemical homeostasis" "Any biological
process involved in the maintenance of an internal steady state of a
chemical at the level of the cell."
"grey" 129 129 4 0.00174458730862561 1
15 0.116279069767442 0.182926829268293
82 "G0:0046982" "MF" "protein heterodimerization
activity" "Interacting selectively and non-covalently with a
nonidentical protein to form a heterodimer."
"grey" 129 129 5 0.00197349258162666 1
3 0.0232558139534884 0.75 4 "G0:
0051382" "BP" "kinetochore assembly" "The aggregation,
arrangement and bonding together of a set of components to form the
kinetochore, a multisubunit complex that is located at the
centromeric region of DNA and provides an attachment point for the
spindle microtubules."
"grey" 129 129 6 0.00197349258162666 1
3 0.0232558139534884 0.75 4 "G0:

0005249" "MF" "voltage-gated potassium channel activity" "Enables the transmembrane transfer of a potassium ion by a voltage-gated channel. A voltage-gated channel is a channel whose open state is dependent on the voltage across the membrane in which it is embedded."

"grey" 129 129 7 0.00202061653626245 1
25 0.193798449612403 0.144508670520231
173 "GO:0051276" "BP" "chromosome organization" "A process that is carried out at the cellular level that results in the assembly, arrangement of constituent parts, or disassembly of chromosomes, structures composed of a very long molecule of DNA and associated proteins that carries hereditary information. This term covers covalent modifications at the molecular level as well as spatial relationships among the major components of a chromosome."

"grey" 129 129 8 0.00225130614615595 1
4 0.0310077519379845 0.5 8 "GO:
0032928" "BP" "regulation of superoxide anion generation" "Any process that modulates the frequency, rate or extent of enzymatic generation of superoxide by a cell."

"grey" 129 129 9 0.00225130614615595 1
4 0.0310077519379845 0.5 8 "GO:
0034508" "BP" "centromere complex assembly" "The aggregation, arrangement and bonding together of proteins and centromeric DNA molecules to form a centromeric protein-DNA complex. Includes the formation of the chromatin structures which form a platform for the kinetochore, and assembly of the kinetochore onto this specialized chromatin. In fission yeast and higher eukaryotes this process also includes the formation of heterochromatin at the outer repeat (pericentric) regions of the centromere."

"grey" 129 129 10 0.00225130614615595 1
4 0.0310077519379845 0.5 8 "GO:
2000027" "BP" "regulation of organ morphogenesis" "Any process that modulates the frequency, rate or extent of animal organ morphogenesis."

"turquoise" 656 654 1 0.00119598850717356
1 29 0.0443425076452599 0.6444444444444444
45 "GO:0001882" "MF" "nucleoside binding" "Interacting selectively and non-covalently with a nucleoside, a compound consisting of a purine or pyrimidine nitrogenous base linked either to ribose or deoxyribose."

"turquoise" 656 654 2 0.00186938264948625
1 27 0.0412844036697248 0.642857142857143
42 "GO:0005525" "MF" "GTP binding" "Interacting selectively and non-covalently with GTP, guanosine triphosphate."

"turquoise" 656 654 3 0.00208623827327965
1 9 0.0137614678899083 0.9 10 "GO:
0005164" "MF" "tumor necrosis factor receptor binding" "Interacting selectively and non-covalently with the tumor necrosis factor receptor."

"turquoise" 656 654 4 0.00309343548986666
1 27 0.0412844036697248 0.627906976744186
43 "GO:0001883" "MF" "purine nucleoside binding" "Interacting selectively and non-covalently with a purine nucleoside, a compound consisting of a purine base linked

either to ribose or deoxyribose."

"turquoise"	656	654	5	0.00309343548986666
1	27	0.0412844036697248	0.627906976744186	
43	"G0:0032549"	"MF"	"ribonucleoside binding"	"Interacting selectively and non-covalently with a ribonucleoside, a compound consisting of a purine or pyrimidine nitrogenous base linked to ribose."
"turquoise"	656	654	6	0.00352796220090091
1	10	0.0152905198776758	0.8333333333333333	
12	"G0:0032813"	"MF"	"tumor necrosis factor receptor superfamily binding"	"Interacting selectively and non-covalently with any member of the tumor necrosis factor receptor superfamily."
"turquoise"	656	654	7	0.00462285207280264
1	8	0.0122324159021407	0.8888888888888889	
9	"G0:0010765"	"BP"	"positive regulation of sodium ion transport"	"Any process that increases the frequency, rate or extent of the directed movement of sodium ions (Na+) into, out of or within a cell, or between cells, by means of some agent such as a transporter or pore."
"turquoise"	656	654	8	0.00760384761242237
1	27	0.0412844036697248	0.6	45 "G0:0019001" "MF" "guanyl nucleotide binding" "Interacting selectively and non-covalently with guanyl nucleotides, any compound consisting of guanosine esterified with (ortho)phosphate."
"turquoise"	656	654	9	0.00760384761242237
1	27	0.0412844036697248	0.6	45 "G0:0032561" "MF" "guanyl ribonucleotide binding" "Interacting selectively and non-covalently with a guanyl ribonucleotide, any compound consisting of guanosine esterified with (ortho)phosphate or an oligophosphate at any hydroxyl group on the ribose moiety."
"turquoise"	656	654	10	0.0101256007445482
1	7	0.0107033639143731	0.875	8 "G0:0030216" "BP" "keratinocyte differentiation" "The process in which a relatively unspecialized cell acquires specialized features of a keratinocyte."
"yellow"	151	151	1	0.000233024404374016 1
15	0.0993377483443709	0.254237288135593		
59	"G0:0071900"	"BP"	"regulation of protein serine/threonine kinase activity"	"Any process that modulates the rate, frequency, or extent of protein serine/threonine kinase activity."
"yellow"	151	151	2	0.00163473400425846 1
10	0.0662251655629139	0.27027027027027 37	"G0:0043405" "BP" "regulation of MAP kinase activity" "Any process that modulates the frequency, rate or extent of MAP kinase activity."	
"yellow"	151	151	3	0.00207215916107485 1
9	0.0596026490066225	0.28125 32	"G0:0000082" "BP" "G1/S transition of mitotic cell cycle" "The mitotic cell cycle transition by which a cell in G1 commits to S phase. The process begins with the build up of G1 cyclin-dependent kinase (G1 CDK), resulting in the activation of transcription of G1 cyclins. The process ends with the positive feedback of the G1	

cyclins on the G1 CDK which commits the cell to S phase, in which DNA replication is initiated."

"yellow" 151 151 4 0.00207215916107485 1
 9 0.0596026490066225 0.28125 32 "G0:
 0005743" "CC" "mitochondrial inner membrane" "The inner, i.e.
 lumen-facing, lipid bilayer of the mitochondrial envelope. It is
 highly folded to form cristae."

"yellow" 151 151 5 0.00226483868588603 1
 7 0.0463576158940397 0.3333333333333333
 21 "G0:0007281" "BP" "germ cell development" "The
 process whose specific outcome is the progression of an immature
 germ cell over time, from its formation to the mature structure
 (gamete). A germ cell is any reproductive cell in a multicellular
 organism."

"yellow" 151 151 6 0.00252256767850981 1
 10 0.0662251655629139 0.256410256410256
 39 "G0:0019866" "CC" "organelle inner
 membrane" "The inner, i.e. lumen-facing, lipid bilayer of an
 organelle envelope; usually highly selective to most ions and
 metabolites."

"yellow" 151 151 7 0.00327978936704289 1
 9 0.0596026490066225 0.264705882352941
 34 "G0:0044843" "BP" "cell cycle G1/S phase transition"
 "The cell cycle process by which a cell in G1 phase commits
 to S phase."

"yellow" 151 151 8 0.00332186158669777 1
 5 0.033112582781457 0.4166666666666667
 12 "G0:2000403" "BP" "positive regulation of lymphocyte
 migration" "Any process that activates or increases the
 frequency, rate or extent of lymphocyte migration."

"yellow" 151 151 9 0.00341669431456101 1
 6 0.0397350993377483 0.352941176470588
 17 "G0:0072678" "BP" "T cell migration" "The
 movement of a T cell within or between different tissues and organs
 of the body."

"yellow" 151 151 10 0.00405434524122959 1
 7 0.0463576158940397 0.304347826086957
 23 "G0:0043406" "BP" "positive regulation of MAP kinase
 activity" "Any process that activates or increases the
 frequency, rate or extent of MAP kinase activity."