

Supplementary Table 3. Biological processes represented by each species probe pair set. The top ranked biological processes are indicated in yellow, and those that are in common among the species are indicated in red text.

Index	Human	P-Value	AGM	P-Value	Cyno	P-Value	Rhesus	Corrected P-Value
1	immune response	8.52E-14	protein biosynthesis	1.47E-13	protein biosynthesis ubiquitin-dependent protein catabolism nuclear mRNA splicing, via spliceosome	3.79E-13	protein biosynthesis	1.53E-13
2	protein biosynthesis ATP synthesis coupled proton transport	1.28E-13	immune response ATP synthesis coupled proton transport	4.30E-10		2.52E-13	immune response ATP synthesis coupled proton transport	6.12E-13
3	antigen presentation, endogenous antigen	9.01E-12	ubiquitin-dependent protein catabolism	9.28E-09		3.79E-13		1.12E-11
4	antigen processing, endogenous antigen via MHC class I	2.65E-09		1.53E-07	RNA splicing	3.18E-12	proton transport	2.36E-09
5		1.78E-08	protein transport	3.20E-07	mRNA processing	7.57E-12	nuclear mRNA splicing, via spliceosome	2.18E-09
6	proton transport antigen presentation, exogenous antigen	2.73E-08	translational elongation	3.04E-07	protein transport	1.09E-11	antigen presentation, endogenous antigen regulation of translational initiation	3.18E-09
7		6.31E-07	proton transport antigen presentation, endogenous antigen antigen processing, endogenous antigen via MHC class I	1.93E-06	immune response	4.00E-10		8.19E-09
8	inflammatory response antigen processing, exogenous antigen via MHC class II	8.04E-07		9.04E-06	ubiquitin cycle	1.29E-09	RNA splicing antigen processing, endogenous antigen via MHC class I	7.86E-09
9		7.24E-07	regulation of translational initiation	3.53E-05	protein ubiquitination regulation of translational initiation	9.70E-09		2.47E-08
10	translational elongation positive regulation of I-kappaB kinase/NF-kappaB cascade	1.78E-06	response to oxidative stress antigen presentation, exogenous antigen	1.56E-04	protein folding	3.50E-08	translational elongation	4.60E-08
11		3.04E-06		1.55E-04		1.65E-07	protein transport antigen presentation, exogenous antigen	8.62E-08
12	cellular defense response	6.40E-06		1.49E-04	RNA processing ATP synthesis coupled proton transport	5.84E-07		4.32E-07
13	nucleosome assembly	6.93E-06	regulation of translation	1.49E-04		1.35E-06	mRNA processing antigen processing, exogenous antigen via MHC class II	5.64E-07
14	chemotaxis	1.38E-05	microtubule polymerization antigen processing, exogenous antigen via MHC class II	1.68E-04	regulation of translation	1.45E-06	mitochondrial electron transport, NADH to ubiquinone	5.50E-07
15	negative regulation of lymphocyte proliferation antimicrobial humoral response (sensu Vertebrata)	1.45E-05		1.63E-04	regulation of transcription, DNA-dependent	1.49E-06		3.08E-06
16	cell surface receptor linked signal transduction	1.47E-05	RNA splicing cotranslational membrane targeting	6.48E-04	small GTPase mediated signal transduction intracellular protein transport	2.09E-06	ubiquitin-dependent protein catabolism	1.41E-05
17		1.62E-05		6.50E-04	mitochondrial electron transport, NADH to ubiquinone	2.60E-06	microtubule polymerization	3.44E-05
18	cell motility mitochondrial electron transport, NADH to ubiquinone	1.53E-05	nuclear mRNA splicing, via spliceosome	7.32E-04	cotranslational membrane targeting	3.51E-06		6.84E-05
19	regulation of apoptosis	2.22E-05	electron transport	0.001145698	transcription	5.12E-06	nucleosome assembly	9.54E-05
20		3.57E-05	ubiquitin cycle	0.001186297	synaptic transmission protein-nucleus import, docking	8.16E-06	protein folding	1.67E-04
21	RNA splicing	4.21E-05	RNA processing	0.001562438	regulation of transcription from Pol II promoter	9.60E-06	RNA processing protein-nucleus import, docking	2.98E-04
22	dendrite morphogenesis	7.08E-05	energy pathways	0.00208299	protein amino acid phosphorylation	9.78E-06		5.77E-04
23	anti-apoptosis	2.18E-04	nucleosome assembly	0.002297439		1.02E-05	glycolysis	6.13E-04

24	protein transport	4.26E-04	dendrite morphogenesis mitochondrial electron transport, NADH to ubiquinone	0.00294977	cotranslational membrane targeting	4.24E-05	mRNA splice site selection	0.001071317
25	energy pathways mitochondrial electron transport, ubiquinol to cytochrome c	5.42E-04	cellular defense response (sensu Vertebrata) microtubule-based movement	0.003550205	apoptosis	4.27E-05	protein-nucleus import, translocation	0.001150072
26	cell proliferation	5.93E-04	antigen presentation, endogenous antigen	0.005116885	4.84E-05	regulation of cell cycle transcription from Pol III promoter	0.001143308	
27	regulation of actin filament polymerization	6.63E-04	nucleosome assembly	0.006033093	7.51E-05	mitochondrial electron transport, ubiquinol to cytochrome c	0.001258488	
28	regulation of translational initiation intracellular signaling cascade	0.001192353	protein-nucleus import, translocation negative regulation of transcription from Pol II promoter	0.006148958	proton transport	1.11E-04	0.001561506	
29	mRNA processing	0.001457896	signal transduction negative regulation of transcription	0.006538419	1.22E-04	small GTPase mediated signal transduction response to oxidative stress	0.001924091	
30	neutrophil chemotaxis	0.001580303	antigen processing, endogenous antigen via MHC class I	0.007717436	1.40E-04	regulation of translation microtubule-based movement	0.001923494	
31	protein folding aspartyl-tRNA aminoacylation intracellular iron ion storage	0.00163442	cell surface receptor linked signal transduction	0.007598477	2.15E-04	cell motility	0.001901321	
32	negative regulation of axon extension	0.001657432	DNA unwinding	0.008709177	5.79E-04	translational initiation regulation of actin filament polymerization	0.002388466	
33	negative regulation of anti- apoptosis	0.001799266	oxygen transport	0.008453025	7.77E-04	0.002666689		
34	0.001826791	mRNA processing neurotransmitter receptor biosynthesis	0.009843993	7.63E-04				
35	0.001877535	negative regulation of proteolysis and peptidolysis	0.01029218	potassium ion transport	7.55E-04			
36	0.001778717	transcription from Pol II promoter	0.010014013	8.74E-04	response to biotic stimulus	0.008203845		
37	superoxide metabolism	0.002458647	microtubule polymerization positive regulation of I- kappaB kinase/NF-kappaB cascade	9.41E-04	oxidative phosphorylation	0.007987954		
38	response to virus	0.002636446	protein-nucleus import, translocation	0.001389008	oxygen transport N-linked glycosylation via asparagine	0.009647584		
39	response to biotic stimulus	0.002609686	response to oxidative stress	0.00210331	natural killer cell mediated cytolysis	0.009495689		
40	oxidative phosphorylation response to oxidative stress	0.002673337	actin cytoskeleton organization and biogenesis	0.002748022	0.012028445			
41	response to pest/pathogen/parasite	0.002761128	glycolysis	0.002815047	0.012990152			
42	0.003452017	antigen presentation, exogenous antigen	0.003080958	viral genome replication	0.014273034			
43	microtubule polymerization	0.003409326	NLS-bearing substrate- nucleus import	0.003058925				
44	apoptotic nuclear changes	0.004685989	G-protein coupled receptor protein signaling pathway	0.003806245				
45	adenine salvage nuclear mRNA splicing, via spliceosome	0.004586287	anti-apoptosis	0.00399148				
46	hemocyte development	0.005447671	antigen processing, exogenous antigen via MHC class II	0.003987654				
47	defense response to fungi	0.005578146	regulation of cell cycle	0.003956367				
48	0.005691985	cell cycle	0.004384896					
49	mRNA splice site selection	0.004856594						

50	transcription from Pol III promoter	0.005585252	DNA replication	0.005533476
51	cation transport	0.005646594	translational elongation	0.00612315
52	rRNA transcription	0.006038812	negative regulation of lymphocyte proliferation	0.006190458
53	cell growth and/or maintenance	0.006764303	negative regulation of transcription from Pol II promoter	0.006210897
54	Golgi to secretory vesicle transport	0.007568328	response to stress	0.00719669
55	microtubule-based movement	0.00825348	cell proliferation	0.008965414
56	protein complex assembly	0.008146572	chromatin assembly/disassembly	0.009534971
57	cell homeostasis	0.0098879	polyamine biosynthesis	0.009674197
58	regulation of viral genome replication	0.009720309	cell surface receptor linked signal transduction	0.009895085
59	cellular morphogenesis	0.009982177	phosphate transport	0.01177921
	G-protein signaling, adenylate cyclase		chromosome organization and biogenesis (sensu Eukarya)	
60	activating pathway	0.00967738	tricarboxylic acid cycle	0.011819967
	cotranslational membrane targeting	0.009836025	mitochondrial electron transport, ubiquinol to cytochrome c	
62	monocyte differentiation	0.011015783	intracellular signaling cascade	0.013993397
63	regulation of peptidyl-tyrosine phosphorylation	0.011190637	transcription from Pol III promoter	0.014098666
64	lysyl-tRNA aminoacylation	0.010522539		0.014568711
	nascent polypeptide association	0.010681972		
66	clathrin cage assembly	0.01084631		
67	response to stress	0.010453268		
	detection of pest/pathogen/parasite			
68	cellular defense response (sensu Vertebrata)	0.013518881		
69	ubiquitin-dependent protein catabolism	0.013714806		
70		0.013531002		

