

Table S1. Gene ontology for *Leishmania* species.

Organism	DEG	Ontology	ID	Name	Conteo Bgd	Result Count	Pct of bgd	Fold Enrichment	Odds Ratio	Valor P	Benjamini	Bonferroni
		BIOLOGICAL PROCESS	GO:0008152	metabolic process	1486	38	26	176	2.59	4509367,194	3,66049E+11	1,26713E+11
			GO:0009987	cellular process	1524	32	21	145	1.8	9,69154E+11	2,3079E+11	10
			GO:0006807	nitrogen compound metabolic process	1077	27	25	173	2.17	1,6166E+11	5,45293E+11	4,54264E+11
			GO:0034641	cellular nitrogen compound metabolic process	626	21	34	231	2.89	1,42612E+11	8,7117E+11	4,00738E+11
			GO:1901360	organic cyclic compound metabolic process	486	19	39	27	3.37	4150054,294	3,66049E+11	1,16617E+11
			GO:0009058	biosynthetic process	452	15	33	229	2.67	1,75342E+11	5,58505E+11	4,92711E+11
			GO:0044249	cellular biosynthetic process	423	13	31	212	2.4	7,0611E+11	1,7405E+11	10
			GO:0065007	biological regulation	461	12	26	18	1.97	3,19753E+11	6,60667E+11	10
			GO:1901566	organonitrogen compound biosynthetic process	284	11	39	267	3.04	2,36431E+11	6,7793E+11	6,64372E+11
			GO:0044271	cellular nitrogen compound biosynthetic process	294	11	37	258	2.92	30997798979	8,37537E+11	8,71038E+11
			GO:1901135	carbohydrate derivative metabolic process	90	8	89	613	7.31	3986105,869	3,66049E+11	1,1201E+11
			GO:0009056	catabolic process	102	7	69	473	5.42	6,22772E+11	2,9835E+11	1,74999E+11
			GO:0034654	nucleobase-containing compound biosynthetic process	103	7	68	469	5.36	6,60516E+11	2,9835E+11	1,85605E+11
			GO:0019438	aromatic compound biosynthetic process	113	7	62	427	4.85	1,1472E+11	4,29818E+11	3,22363E+11
			GO:0018130	heterocycle biosynthetic process	121	7	58	399	4.5	1,71032E+11	5,55251E+11	4,806E+11
			GO:0006082	organic acid metabolic process	124	7	56	389	4.38	1,96974E+11	6,0387E+11	5,53498E+11
			GO:0072522	purine-containing compound biosynthetic process	35	7	200	138	18.64	49202,18866	6912907,507	1,38258E+11
			GO:0019637	organophosphate metabolic process	115	7	61	42	4.76	1,2718E+11	4,52375E+11	3,57376E+11
			GO:1901362	organic cyclic compound biosynthetic process	127	7	55	38	4.27	2,25878E+11	6,54348E+11	6,34717E+11
			GO:0046700	heterocycle catabolic process	34	6	176	1217	15.75	738721,25	1,72984E+11	2,07581E+11
			GO:0005975	carbohydrate metabolic process	70	6	86	591	6.84	4,76674E+11	2,3994E+11	13394542559
			GO:0050794	regulation of cellular process	178	6	34	233	2.49	4,331E+11	8,33569E+11	10
			GO:0019693	ribose phosphate metabolic process	45	6	133	92	11.28	3943208,046	3,66049E+11	11080414609
			GO:0046390	ribose phosphate biosynthetic process	29	5	172	1189	15.1	5064077,381	3,66049E+11	1,42301E+11
			GO:0017144	drug metabolic process	59	5	85	585	6.67	1,52243E+11	5,21711E+11	4,27803E+11
			GO:0044283	small molecule biosynthetic process	79	5	63	437	4.85	5,47715E+11	1,42507E+11	10
			GO:0006508	proteolysis	127	5	39	272	2.91	3,62435E+11	7,38002E+11	10
			GO:0006733	oxidoreduction coenzyme metabolic process	26	4	154	1061	13.0	4,78172E+11	2,3994E+11	1,34366E+11
			GO:0032787	monocarboxylic acid metabolic process	38	4	105	726	8.39	2,07027E+11	6,05985E+11	5,81745E+11
			GO:0042592	homeostatic process	52	4	77	531	5.93	6,51851E+11	1,68046E+11	10
			GO:0051186	cofactor metabolic process	63	4	63	438	4.81	1,27293E+11	3,00583E+11	10
			GO:0006006	glucose metabolic process	8	3	375	2587	42.45	1,55527E+11	9,29854E+11	4,37031E+11
			GO:0009132	nucleoside diphosphate metabolic process	13	3	231	1592	21.2	7,53837E+11	2,9835E+11	2,11828E+11
			GO:0046939	nucleotide phosphorylation	13	3	231	1592	21.2	7,53837E+11	2,9835E+11	2,11828E+11
			GO:0042866	pyruvate biosynthetic process	13	3	231	1592	21.			

