

Table S2. Shared orthologous groups between *Leishmania* species.

Species	DEG	Orthologous group	Product Description	Gene ID	Log Fold Change	P Value	Chrom.
		OG6_100076	ATP-binding cassette protein subfamily G, member 5	LmxM.23.0380 LbrM.23.2.000420	9,63317E+14 7,71648E+13	8,60679E-25 6,58789E-27	23 23
		OG6_100158	organelle-type calcium ATPase	LmxM.04.0010 LbrM.04.2.201590	1,35957E+14 5,58673E+13	3,2418E-42 0,000528624	4 4
		OG6_100430	acetyl-CoA synthetase, putative	LmxM.23.0710 LbrM.23.2.000580	1,21531E+14 8,23969E+14	3,9012E-31 2,86297E-31	23 23
		OG6_100490	10 kDa heat shock protein, putative	LmxM.26.0640 LbrM.26.2.208230	1,31063E+14 7,33535E+14	9,17295E-21 1,32815E-23	26 26
		OG6_100528	peptidyl-prolyl cis-trans isomerase, putative	LmxM.23.0050 LbrM.25.2.000790	9,04472E+13 5,18666E+14	0,000128438 5,47042E-11	23 25
		OG6_100634	spermidine synthase, putative	LmxM.04.0580 LbrM.04.2.000630	1,00528E+14 5,06833E+14	3,65256E-07 0,000714964	4 4
		OG6_100682	metallo-peptidase, Clan MF, Family M17	LmxM.23.0950 LbrM.23.2.001030	1,75757E+14 8,47539E+14	6,98212E-50 4,34025E-10	23 23
		OG6_101014	leucyl-tRNA synthetase, putative	LmxM.13.1100 LbrM.13.2.000900	9,77825E+14 4,09948E+14	1,26303E-18 1,92255E-05	13 13
		OG6_101052	acetyl-CoA carboxylase	LmxM.30.2970 LbrM.31.2.003340	1,03878E+14 5,35404E+14	1,06046E-18 1,95284E-07	30 31
		OG6_101295	Proline dehydrogenase, mitochondrial	LmxM.26.1610 LbrM.26.2.001630	1,16539E+14 6,96592E+14	4,7836E-11 1,1942E-08	26 26
		OG6_102936	translation initiation factor SUI1, putative	LmxM.22.0790 LbrM.22.2.000730	1,3359E+14 6,1448E+14	3,67385E-36 5,39994E-06	22 22
		OG6_103862	mitogen-activated protein kinase kinase 2	LmxM.13.0440 LbrM.13.2.000260	1,03243E+14 7,77024E+14	1,32396E-15 3,59329E-08	13 13
		OG6_107645	ALBA-domain protein 1	LmxM.13.0450 LbrM.13.2.000270	1,49653E+14 1,01763E+14	1,75712E-31 1,0888E-51	13 13
		OG6_112956	permease-like protein	LmxM.23.0450 LbrM.23.2.000480	8,96833E+14 7,73511E+14	1,69962E-10 5,0652E-26	23 23
		OG6_120307	hypothetical protein, conserved	LmxM.30.0800 LbrM.31.2.209480	1,70692E+14 7,53881E+14	3,14027E-74 5,09896E-21	30 31
		OG6_138412	Protein of unknown function (DUF3250), putative	LmxM.23.1250 LbrM.23.2.001350	1,26513E+14 1,04409E+14	5,01613E-22 5,72607E-14	23 23
		OG6_139814	Heme Response-1 protein, putative	LmxM.24.2230 LbrM.24.2.002310	1,11204E+14 1,73972E+14	3,57055E-21 3,931E-135	24 24
		OG6_143027	Rapamycin-insensitive companion of TOR2	LmxM.23.1260 LbrM.23.2.001360	9,44993E+14 7,61222E+14	4,1969E-19 6,22258E-10	23 23
		OG6_146647	Sister chromatid cohesion C-terminus, putative	LmxM.13.0400 LbrM.13.2.000220	8,59234E+14 5,37062E+14	1,49234E-06 7,33194E-05	13 13
		OG6_146797	hypothetical protein, conserved	LmxM.35.2470 LbrM.11.2.000510	1,04151E+14 7,27148E+14	8,2587E-06 3,01561E-23	34 11
		OG6_147054	hypothetical protein, conserved	LmxM.04.1220 LbrM.04.2.001240	1,28334E+14 6,06971E+14	2,43521E-28 0,000410985	4 4
	UPREGULATED	OG6_147062	mRNA cap guanine-N7 methyltransferase, putative	LmxM.11.0480	1,48934E+14	2,78204E-26	11

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UPREGULATED	OG6_147002	HMMA Cap guanine-N7 methyltransferase, putative	LbrM.11.2.000180	9,78492E+14	7,96329E-13	11
	OG6_147144	protein kinase, putative	LmxM.26.1730	8,78426E+14	1,91291E-05	26
			LbrM.23.2.001950	5,98294E+14	0,000223437	26
	OG6_147287	kinesin-C	LmxM.23.0560	1,0788E+14	5,75831E-16	23
			LbrM.23.2.000710	9,4015E+14	4,80531E-15	23
	OG6_147365	PIF1 helicase-like protein, putative	LmxM.11.0330	1,085E+13	1,58713E-08	11
			LbrM.11.2.000020	9,45527E+14	1,42473E-29	11
	OG6_147390	mitochondrial RNA binding protein, putative	LmxM.23.0760	1,81922E+14	2,66198E-43	23
			LbrM.23.2.000850	9,05159E+14	1,2731E-05	23
	OG6_147392	mitochondrial DNA primase, putative	LmxM.23.0680	1,62931E+14	2,9298E-33	23
			LbrM.23.2.000780	9,48547E+14	1,97732E-06	23
	OG6_148298	hypothetical protein, conserved	LmxM.30.1500	8,88153E+14	0,00752474	30
			LbrM.31.2.001720	4,99187E+14	0,001245866	31
	OG6_158071	Kinetoplastid kinetochore protein 25, putative	LmxM.23.1610	1,00981E+14	1,04519E-06	23
			LbrM.23.2.000630	6,99517E+14	0,007052593	23
	OG6_158073	hypothetical protein, conserved	LmxM.23.0900	8,26408E+14	4,72576E-07	23
			LbrM.23.2.001010	6,40057E+14	4,37181E-11	23
	OG6_158274	hypothetical protein, conserved	LmxM.30.1510	7,81211E+14	6,90433E-06	30
			LbrM.31.2.001060	8,12554E+14	2,38289E-34	31
	OG6_170635	Iguana/Dzip1-like DAZ-interacting protein N-terminal, putative	LmxM.14.0420	9,00986E+14	0,006176921	14
			LbrM.14.2.000430	8,30513E+14	1,77931E-05	14
	OG6_172256	hypothetical protein	LmxM.04.0040	1,28625E+14	1,21021E-15	4
			LbrM.04.2.000080	7,91996E+14	8,50586E-06	4
	OG6_173634	hypothetical protein, conserved	LmxM.04.1180	9,36121E+13	5,68306E-09	4
			LbrM.04.2.001200	6,30746E+14	1,97392E-11	4
			LmxM.23.0480	1,23812E+14	7,11211E-34	23
	OG6_199889	hypothetical protein, conserved	LbrM.23.2.000510	8,72263E+14	5,45719E-16	23
			LmxM.23.1010	1,40485E+14	1,48575E-49	23
			LbrM.23.2.001090	8,64429E+14	2,69033E-26	23
	OG6_200105	PSP1 C-terminal conserved region, putative	LmxM.13.0690	1,9407E+14	1,57931E-39	13
			LbrM.13.2.000510	9,28234E+14	1,95999E-09	13
	OG6_478652	serine/threonine protein kinase-like protein	LmxM.04.0440	8,93599E+14	0,001812943	4
			LbrM.04.2.000480	4,70237E+14	3,66701E-06	4
	OG6_478669	kinetoplast-associated protein-like protein	LmxM.30.2760	1,31926E+14	2,90273E-27	30
			LbrM.31.2.003110	6,77578E+14	8,551E-09	31
	OG6_478685	hypothetical protein, conserved	LmxM.04.1090	1,34888E+14	6,29891E-29	4
			LbrM.04.2.001100	7,08572E+14	2,81691E-06	4
	OG6_478775	hypothetical protein	LmxM.04.0620	1,01027E+14	3,0192E-09	4
			LbrM.04.2.001290	5,93407E+14	5,31571E-07	4
	OG6_478895	hypothetical protein, conserved	LmxM.23.0990	1,42161E+14	1,83324E-61	23
			LbrM.23.2.001070	7,4121E+13	7,25628E-25	23
	OG6_479096	Nucleotidyltransferase domain containing protein, putative	LmxM.04.0500	9,42255E+14	2,5395E-18	4
			LbrM.04.2.000550	5,57692E+14	1,90896E-15	4
	OG6_102658	dihydroxyacetone kinase 1-like protein	LmxM.10.0420	-8,55121E+14	0,000299879	10
			LbrM.10.2.000420	-7,15137E+14	1,80614E-06	10
	OG6_103096	hypothetical protein, conserved	LmxM.34.5260	-1,17156E+14	1,31111E-07	34
			LbrM.34.2.005200	-8,95765E+14	0,00073441	34

	DOWNREGULATED	OG6_104518	amino acid permease, putative	LmxM.34.4410 LbrM.34.2.004390	-1,10768E+14 -1,08239E+13	3,17762E-07 3,45994E-09	34 34		
		OG6_145552	zinc-finger of a C2HC-type, putative	LmxM.31.3450 LbrM.32.2.003740	-1,0758E+14 -6,58248E+14	5,25219E-25 0,000152039	31 32		
		OG6_146939	hypothetical protein, conserved	LmxM.34.5080 LbrM.34.2.005020	-1,31501E+14 -9,0704E+14	1,24691E-25 3,18274E-07	34 34		
		OG6_200171	Arrestin (or S-antigen), N-terminal domain containing protein, putative	LmxM.34.0440 LbrM.34.2.000460	-1,27648E+14 -6,66653E+14	7,37647E-38 0,009436945	34 34		
		OG6_478627	hypothetical protein, conserved	LmxM.17.0260 LbrM.17.2.000240	-8,44686E+13 -6,2531E+14	3,39007E-08 1,76574E-05	17 17		
<i>L. amazonensis</i> y <i>L. donovani</i>	UPREGULATED	OG6_100228	phosphatidic acid phosphatase, putative	LmxM.18.0440 LdBPK_180430.1 LdBPK_180440.1	1,1069E+14 1,5542E+14 1,04936E+14	2,80604E-08 1,03108E-65 6,58771E-24	18 18 18		
		OG6_100262	serine hydroxymethyltransferase	LmxM.28.2370 LdBPK_141400.1	9,21905E+14 1,28287E+14	1,84864E-11 3,82427E-86	28 14		
		OG6_101988	universal minicircle sequence binding protein	LmxM.36.1620 LmxM.36.1640 LdBPK_361720.1	6,94026E+14 9,79236E+14 5,50788E+14	0,004151828 3,68235E-28 1,05317E-08	20 20 36		
		OG6_102008	arginase	LmxM.34.1480 LdBPK_351490.1	9,65465E+14 6,68634E+14	1,29512E-21 8,05693E-24	34 35		
		OG6_102076	gamma-glutamylcysteine synthetase, putative	LmxM.18.1660 LdBPK_181660.1	7,76959E+14 1,30184E+14	0,001224098 1,18325E-84	18 18		
		OG6_103178	hydrolase, alpha/beta fold family-like protein	LmxM.17.1010 LdBPK_171110.1	1,2165E+14 1,2488E+14	1,43129E-12 6,68054E-26	17 17		
		OG6_105154	chaperone DNAJ protein, putative	LmxM.18.1430 LdBPK_181410.1	7,55125E+14 9,52576E+14	0,001301615 2,93682E-24	18 18		
		OG6_111575	Protein Associated with Differentiation, putative	LmxM.13.1690 LdBPK_131430.1	1,66379E+13 4,11891E+14	4,37143E-33 0	13 13		
		OG6_132436	amino acid permease, putative	LmxM.27.0670 LdBPK_310350.1	1,55581E+13 1,23084E+14	6,15829E-32 8,20489E-64	27 31		
				LdBPK_310370.1	4,10904E+14	3,15137E-19	31		
		OG6_143838	amino acid transporter aATP11, putative	LmxM.30.3060	1,0406E+14	1,13379E-22	30		
				LmxM.30.3070 LdBPK_313190.1	1,08051E+14 1,13964E+13	9,39775E-17 2,05203E-31	30 31		
		OG6_147250	NLI interacting factor-like phosphatase, putative	LmxM.08_29.2400 LdBPK_292510.1	1,21632E+13 1,14847E+13	5,76579E-12 3,23737E-16	8 29		
		OG6_478849	histone h1-like protein	LmxM.09.0880 LdBPK_090930.1	9,71882E+14 4,47897E+13	1,24743E-14 0,000724188	9 9		
				OG6_100045	ABC1 transporter, putative	LmxM.02.0300	-1,23807E+14	2,75144E-17	2
						LmxM.11.1240	-8,5193E+13	2,6156E-07	11
						LmxM.11.1270	-1,05913E+13	1,31933E-05	11
LmxM.11.1290	-1,89978E+14					1,84281E-95	11		
LmxM.15.0760	-1,05272E+14					1,38873E-25	15		
LdBPK_111210.1	-5,34831E+14					2,87126E-36	11		
		OG6_102310	receptor-type adenylate cyclase, putative	LmxM.17.0190	-1,24739E+14	1,98666E-19	17		
				LmxM.17.0191	-1,03821E+14	7,32459E-05	17		

	DOWNREGULATED	OG6_102310	receptor-type adenylylase, putative	LmxM.17.0235 LdBPK_170140.1	-1,52914E+13 -6,92658E+14	5,30986E-25 6,67411E-15	17 17
		OG6_104369	NAD/FAD dependent dehydrogenase, putative	LmxM.15.0970 LdBPK_151030.1	-8,7133E+13 -5,27151E+14	2,93465E-06 2,46463E-06	15 15
		OG6_105866	hypothetical protein, conserved	LmxM.11.0810 LdBPK_110810.1	-1,36757E+14 -7,62239E+14	2,44803E-26 0,000607273	11 11
		OG6_139757	paraflagellar rod component par4, putative	LmxM.05.0040 LdBPK_050040.1	-1,20202E+14 -8,64456E+14	3,73098E-20 9,40113E-42	5 5
		OG6_199925	hypothetical protein, unknown function	LmxM.26.2680 LdBPK_262710.1	-3,38409E+14 -6,84178E+14	2,5096E-199 4,13028E-25	26 26
		OG6_200015	hypothetical protein, conserved	LmxM.08.0340 LdBPK_080350.1	-6,95936E+14 -6,32309E+14	8,04446E-05 4,02359E-05	8 8
<i>L. amazonensis</i> y <i>L. infantum</i>		UPREGULATED	OG6_100083	heat-shock protein hsp70, putative	LmxM.28.2770 LINF_280017800	1,04894E+14 3,17776E+14	2,89911E-17 6,28666E-58
	OG6_100417		5'-3' exoribonuclease A, putative	LmxM.06.0260 LINF_060007900	8,15341E+14 1,79063E+14	1,16635E-05 7,15618E-05	6 6
	OG6_100680		heat shock protein, putative	LmxM.18.1370 LINF_180019100	1,25452E+14 1,38888E+14	6,5057E-22 0,00149829	18 18
	OG6_106866		amino acid permease, putative	LmxM.22.0230 LINF_220007200	9,73351E+14 2,33447E+14	1,17775E-06 3,18143E-18	22 22
	OG6_129603		amino acid transporter, putative	LmxM.31.2660 LINF_320033600	9,41439E+14 1,52645E+13	3,0934E-23 1,11445E-05	31 32
	OG6_130239		WD domain, G-beta repeat, putative	LmxM.06.0030 LINF_060005200	8,10687E+14 1,66068E+14	3,02673E-08 0,000250359	6 6
	OG6_136931		hypothetical protein, conserved	LmxM.34.1830 LINF_350023200	9,69877E+14 1,7404E+14	1,21025E-13 6,38122E-05	34 35
	OG6_146725		ATP-dependent RNA helicase, putative	LmxM.34.3100 LINF_350036300	1,01918E+14 1,82367E+14	1,10657E-22 3,05744E-14	34 35
	OG6_147073		RNA recognition motif (a.k.a. RRM, RBD, or RNP domain), putative	LmxM.27.0350 LINF_270008600	1,77175E+12 2,54117E+14	2,59251E-33 0,000778832	27 27
	OG6_478818		hypothetical protein, conserved	LmxM.19.1150 LINF_190016900	1,22179E+14 2,23966E+14	3,36663E-28 0,000110191	19 19
	UPREGULATED	OG6_100014	cytochrome p450-like protein	LmxM.27.0090 LPMP_270090	9,42206E+14 3,11915E+14	5,17514E-15 0	27 27
		OG6_100085	pre-mRNA splicing factor ATP-dependent RNA helicase, putative	LmxM.34.1200 LPMP_341070	1,02116E+14 9,28181E+14	3,02685E-06 0,000253013	34 34
		OG6_100425	polyadenylate-binding protein 1, putative	LmxM.34.5040 LPMP_344870	1,52439E+14 8,76432E+14	4,12772E-78 8,71143E-42	34 34
		OG6_100595	RNA helicase, putative	LmxM.09.0070 LPMP_090090	1,02806E+14 8,211E+14	1,96E-09 1,01743E-07	9 9
		OG6_101289	nucleolar GTP-binding protein, putative	LmxM.32.1870 LPMP_331950	9,59976E+14 7,0844E+14	0,005703409 6,72251E-06	32 33
		OG6_103524	histone-lysine N-methyltransferase, putative	LmxM.07.0025 LmxM.20.0030 LPMP_204240	2,60513E+14 2,45857E+14 7,74591E+14	4,6387E-130 1,7853E-126 8,35698E-05	7 20 20
		OG6_146542	hypothetical protein, conserved	LmxM.25.1210	1,3455E+14	3,56261E-23	25

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	OG6_140342	hypothetical protein, conserved	LPMP_251230	1,0288E+14	4,26688E-07	25
	OG6_147197	Nucleolar protein 168, putative	LmxM.22.0210	1,09122E+14	2,44937E-22	22
			LPMP_220200	1,11939E+14	8,1598E-38	22
DOWNREGULATED	OG6_100101	myosin XXI, putative	LmxM.31.3870	-1,05462E+14	8,42493E-21	31
			LPMP_324000	-1,00236E+14	3,46188E-07	32
	OG6_100116	cathepsin L-like protease, putative	LmxM.08.1070	-1,26424E+14	2,50896E-10	8
			LmxM.08.1080	-2,33867E+14	1,5261E-106	8
			LPMP_191300	-1,04054E+14	1,29461E-59	19
	OG6_100137	beta tubulin	LmxM.21.1860	-1,8067E+14	1,88063E-90	21
			LmxM.32.0792	-1,14518E+13	2,81791E-14	32
			LPMP_330860	-8,76625E+14	2,52989E-67	33
	OG6_100163	aldehyde dehydrogenase, mitochondrial precursor	LmxM.25.1120	-7,91705E+14	1,3912E-09	25
			LPMP_251150	-1,12158E+14	2,35891E-89	25
	OG6_100194	n-ethylmaleimide reductase-like protein	LmxM.12.1140	-1,31322E+14	3,02121E-22	12
			LmxM.32.0830	-1,17437E+14	1,74871E-22	32
			LPMP_120820	-1,06136E+13	2,01085E-11	12
	OG6_100306	actin interacting protein-like protein	LmxM.08_29.0280	-1,27016E+14	6,30097E-12	8
			LPMP_230960	-9,75212E+14	8,06903E-05	23
	OG6_101088	transaldolase, putative	LmxM.16.0760	-1,03884E+14	3,03396E-24	16
			LPMP_160730	-1,07251E+14	2,77542E-12	16
	OG6_102689	Protein of unknown function (DUF667), putative	LmxM.21.0380	-1,29314E+14	9,51777E-15	21
			LPMP_210410	-9,4339E+14	2,91569E-13	21
	OG6_104102	adenylate kinase, putative	LmxM.21.1250	-1,2944E+13	2,59692E-21	21
			LPMP_211450	-9,57431E+14	1,63821E-21	21
	OG6_109033	flagellar calcium-binding protein, putative	LmxM.16.0920	-3,64908E+14	8,52947E-21	16
			LPMP_160880	-1,14141E+14	4,37043E-97	16
	OG6_109839	ATG8/AUT7/APG8/PAZ2, putative	LmxM.09.0180	-2,47093E+14	9,6016E-182	9
			LPMP_090170	-5,62204E+14	1,98978E-06	9
	OG6_112572	leucine-rich repeat protein, putative	LmxM.10.0180	-2,11794E+14	1,65086E-61	10
			LPMP_100150	-1,2039E+14	5,26421E-11	10
	OG6_134885	paraflagellar rod component, putative	LmxM.19.0520	-1,12639E+14	8,76637E-30	19
		LPMP_190500	-7,49831E+14	4,45576E-13	19	
OG6_139754	Mitochondrial outer membrane protein porin, putative	LmxM.02.0460	-2,01105E+12	7,70497E-46	2	
		LPMP_020340	-8,56789E+14	8,01831E-21	2	
OG6_144768	hypothetical protein, conserved	LmxM.24.1980	-1,22785E+14	5,39847E-19	24	
		LPMP_241960	-1,39596E+14	6,49163E-77	24	
OG6_145906	hypothetical protein, conserved	LmxM.36.4910	-8,37724E+14	0,001569288	20	
		LPMP_355030	-6,40392E+14	2,66999E-05	35	
OG6_146813	hypothetical protein, conserved	LmxM.24.1560	-1,7777E+14	8,96612E-83	24	
		LPMP_241530	-1,15977E+14	3,80041E-22	24	
OG6_147348	hypothetical protein, conserved	LmxM.29.2850	-1,30222E+14	2,35873E-28	29	
		LPMP_302800	-9,28527E+14	1,44067E-19	30	
OG6_147386	hypothetical protein, conserved	LmxM.08_29.1030	-2,18737E+14	1,61591E-81	8	
		LPMP_291080	-9,0163E+14	4,4206E-08	29	
OG6_147554	hypothetical protein, conserved	LmxM.24.0160	-1,59467E+14	2,21292E-27	24	
		LPMP_240150	-8,12679E+14	0,004986038	24	
OG6_148260	hypothetical protein, conserved	LmxM.31.0350	-1,11639E+14	5,36502E-29	31	

		OG6_148207	hypothetical protein, conserved	LPMP_320380	-9,12806E+14	4,60562E-29	32
		OG6_156861	Calpain-like protein 2	LmxM.30.0390	-1,00832E+14	3,95512E-16	30
				LPMP_310380	-7,38635E+14	1,77097E-18	31
		OG6_156915	hypothetical protein, conserved	LmxM.16.1260	-1,06929E+14	4,25058E-22	16
				LPMP_161220	-7,92184E+14	1,69607E-08	16
		OG6_157029	hypothetical protein, conserved	LmxM.18.1640	-1,35052E+13	1,75562E-20	18
				LPMP_181600	-1,16205E+14	2,72607E-44	18
		OG6_157030	paraflagellar rod component, putative	LmxM.32.0610	-2,2382E+14	9,37425E-72	32
				LPMP_330660	-9,45479E+14	2,44165E-19	33
		OG6_157990	hypothetical protein, unknown function	LmxM.10.0219	-1,73821E+14	5,39762E-53	10
				LPMP_100210	-1,02682E+14	5,18568E-23	10
		OG6_157996	Protein of unknown function (DUF2946), putative	LmxM.01.0010	-1,57238E+14	3,42027E-31	1
				LPMP_010010	-1,24682E+14	1,58236E-15	1
		OG6_158100	hypothetical protein, conserved	LmxM.31.0360	-1,06647E+14	1,45171E-14	31
				LPMP_320390	-1,04633E+14	2,39521E-34	32
		OG6_158154	hypothetical predicted multipass transmembrane protein	LmxM.24.1090	-9,91894E+13	2,99276E-09	24
				LPMP_241070	-8,57965E+14	8,80178E-21	24
		OG6_158332	Domain of unknown function (DUF1935), putative	LmxM.33.0190	-1,91209E+14	9,62835E-96	33
				LPMP_200140	-8,26786E+14	2,83899E-22	20
		OG6_173669	mitochondrial ornithine transporter 1-like protein	LmxM.16.0210	-8,03922E+14	0,002439925	16
				LPMP_160220	-1,17195E+14	3,65542E-27	16
		OG6_173691	hypothetical protein, unknown function	LmxM.02.0550	-1,34377E+14	2,48644E-39	2
				LPMP_020430	-8,87491E+14	2,4412E-18	2
		OG6_173698	protein kinase, putative	LmxM.26.2570	-3,55533E+14	0	26
				LPMP_262540	-1,59156E+13	1,7222E-206	26
		OG6_173761	hypothetical protein, unknown function	LmxM.30.1445	-2,86585E+13	2,56066E-36	30
				LPMP_311370	-2,24972E+13	1,7284E-173	31
		OG6_199847	hypothetical protein, conserved	LmxM.16.1100	-1,07215E+14	2,44802E-10	16
				LPMP_161060	-1,08943E+14	1,3617E-18	16
		OG6_199894	hypothetical protein, conserved	LmxM.23.0610	-1,2684E+13	2,01356E-40	23
				LPMP_230770	-1,82813E+14	1,25923E-32	23
		OG6_478668	hypothetical protein, unknown function	LmxM.26.1510	-1,62936E+14	1,57931E-39	26
				LPMP_261490	-7,6452E+14	3,1786E-10	26
		OG6_478956	hypothetical protein, unknown function	LmxM.13.1410	-1,39366E+14	2,30057E-24	13
				LPMP_131280	-8,27075E+13	2,91416E-09	13
<i>L. braziliensis</i> y <i>L. donovani</i>	UPREGULATED	OG6_100388	S-adenosylmethionine synthetase	LbrM.30.2.003550	4,66377E+14	9,24871E-19	30
				LdBPK_303560.1	9,6357E+14	8,2512E-131	30
		OG6_100418	Hexokinase, putative	LbrM.21.2.207050	5,10519E+14	0,000185285	21
				LdBPK_210300.1	4,18277E+14	6,647E-05	21
		OG6_100643	ABC transporter, putative	LbrM.19.2.000280	4,61491E+14	9,6308E-13	11
				LdBPK_291780.1	8,00239E+14	1,78842E-07	29
		OG6_101329	Thiolase, N-terminal domain/Beta-ketoacyl synthase, N-terminal domain/Thiolase, C-terminal domain containing protein, putative	LbrM.23.2.000840	5,42329E+14	0,000280955	23
		LdBPK_230860.1	5,2266E+13	6,27687E-20	23		
		OG6_103138	Cobalamin-independent synthase, N-terminal domain/Cobalamin-independent synthase, Catalytic domain containing protein, putative	LbrM.31.2.000010	6,28387E+14	3,42216E-24	31
				LdBPK_310010.1	2,28296E+12	0	31
		OG6_115676	Cytochrome b5-like Heme/Steroid binding domain containing protein, putative	LbrM.29.2.000920	7,55224E+14	7,39962E-26	29

		OG6_11070	Cytochrome b5-like hemep/steroid binding domain containing protein, putative	LdBPK_290930.1	2,26119E+14	6,4439E-138	29
		OG6_200033	hypothetical protein, conserved	LbrM.29.2.001700	6,0844E+12	4,15627E-06	29
				LdBPK_291720.1	8,60373E+14	1,45046E-26	29
	DOWNREGULATED	OG6_100398	thymine-7-hydroxylase, putative	LbrM.29.2.000510	-1,55988E+14	2,66003E-56	29
				LdBPK_290260.1	-4,62516E+14	2,48991E-08	29
		OG6_101599	Phosphorylase superfamily, putative	LbrM.05.2.000800	-8,3898E+14	6,22035E-07	5
				LdBPK_050830.1	-4,50898E+14	0,000235402	5
<i>L. braziliensis</i> y <i>L. infantum</i>	UPREGULATED	OG6_100305	ATP-dependent RNA helicase - putative	LbrM.13.2.000320	8,28593E+14	1,32431E-33	13
				LINF_130009900	1,57893E+14	0,000153622	13
		OG6_101511	Domain of unknown function (DUF3819)/CCR4-Not complex component - Not1 - putative	LbrM.21.2.000890	4,48395E+14	0,000250305	21
				LINF_210013800	1,96629E+13	8,74823E-20	21
		OG6_101713	Protein kinase domain/Protein tyrosine kinase, putative	LbrM.31.2.001740	7,34538E+14	4,40688E-27	31
				LINF_310022600	2,3431E+13	1,25426E-08	31
		OG6_111882	Tubulin-tyrosine ligase family, putative	LbrM.11.2.000080	5,1467E+14	9,24636E-08	11
				LINF_110008900	1,69642E+14	0,000589279	11
		OG6_111983	Protein of unknown function (DUF3638)/Protein of unknown function (DUF3645)/Zn-finger in Ran binding protein and others - putative	LbrM.31.2.001440	6,20986E+13	6,53129E-18	31
				LINF_310018600	2,71039E+14	1,63192E-32	31
		OG6_128926	RING-variant domain containing protein, putative	LbrM.31.2.002150	7,6725E+14	2,00072E-12	31
				LINF_310027000	2,58319E+14	3,28598E-22	31
		OG6_146743	Zn-finger in Ran binding protein and others/SPRY domain/HECT-domain (ubiquitin-transferase), putative	LbrM.26.2.002300	5,72615E+14	3,39601E-06	26
				LINF_260029200	2,21304E+14	3,10605E-17	26
		OG6_147035	Protein tyrosine kinase/Protein kinase domain containing protein, putative	LbrM.14.2.001060	8,70495E+14	1,68621E-16	14
				LINF_140016900	2,23866E+14	1,47016E-12	14
		OG6_154488	Fibronectin type III domain containing protein, putative	LbrM.26.2.002310	5,52827E+14	8,36497E-12	26
				LINF_260029300	2,56671E+14	3,49816E-29	26
		OG6_164267	hypothetical protein, conserved	LbrM.13.2.001290	9,81471E+14	6,4144E-11	20
				LINF_340011100	2,59303E+14	1,96513E-14	34
OG6_199822	GNS1/SUR4 family, putative	LbrM.14.2.000640	6,30778E+14	2,7574E-21	14		
		LINF_140012100	1,7555E+14	1,29534E-11	14		
OG6_200278	hypothetical protein, conserved	LbrM.31.2.001220	8,48531E+14	0,002670287	31		
		LINF_310016300	2,67561E+14	2,62334E-12	31		
OG6_478585	Protein of unknown function (DUF789), putative	LbrM.26.2.001750	6,1441E+14	4,68311E-12	26		
		LINF_260023500	1,7247E+14	9,7327E-05	26		
OG6_478848	hypothetical protein, conserved	LbrM.13.2.001590	7,52807E+14	1,44078E-30	13		
		LINF_130013000	1,9476E+14	1,00508E-07	13		
OG6_478896	Galactose oxidase, central domain containing protein, putative	LbrM.23.2.000660	6,32415E+14	1,2428E-13	23		
		LINF_230012700	2,60311E+14	2,06268E-27	23		
OG6_478901	hypothetical protein, conserved	LbrM.08.2.000390	4,94151E+14	3,84742E-14	8		
		LINF_080011400	2,64222E+14	0,005523957	8		
OG6_478916	FYVE zinc finger containing protein, putative	LbrM.26.2.001280	7,12937E+13	2,96553E-12	26		
		LINF_260017600	2,38643E+14	2,63581E-06	26		
OG6_479000	Protein kinase domain containing protein, putative	LbrM.26.2.002040	5,97758E+14	8,41062E-13	26		
		LINF_260026500	1,63021E+13	0,001816691	26		
		OG6_100723	Ribosomal S3Ae family, putative	LbrM.34.2.210540	-7,93031E+14	6,04431E-19	34
				LINF_350009300	-1,71419E+14	1,4442E-14	35
		OG6_100748	Ribosomal protein L18e/L15, putative	LbrM.34.2.211030	-7,44426E+14	1,21306E-24	34

	DOWNREGULATED	OG6_100748	ribosomal protein L18e/L19, putative	LINF_350043200	-1,46713E+14	0,000143768	35
		OG6_100789	Ribosomal L18p/L5e family/Ribosomal L18 C-terminal region containing protein, putative	LbrM.34.2.210700 LbrM.34.2.210710 LINF_350023700	-7,49971E+14 -9,42839E+14 -1,91662E+14	1,69913E-21 0,000509547 1,29978E-05	34 34 35
<i>L. braziliensis</i> y <i>L. panamensis</i>	UPREGULATED	OG6_101167	Sphingolipid Delta4-desaturase (DES)/Fatty acid desaturase, putative	LbrM.23.2.001980 LPMP_261660	8,29682E+14 8,85151E+14	1,46451E-13 2,39779E-07	26 26
	DOWNREGULATED	OG6_100337	aspartate aminotransferase, putative	LbrM.34.2.210580 LPMP_340750	-6,5943E+14 -7,6353E+14	1,21566E-06 1,80248E-06	34 34
		OG6_102311	Fatty acid desaturase, putative	LbrM.33.2.003550 LPMP_333400	-1,02141E+14 -1,07382E+14	6,18947E-20 2,10702E-23	33 33
		OG6_107314	generative cell specific 1 protein, putative	LbrM.34.2.000480 LPMP_340420	-7,57861E+14 -1,04228E+14	6,33046E-25 2,97855E-10	34 34
		OG6_108712	NLI interacting factor-like phosphatase/Zinc finger C-x8-C-x5-C-x3-H type (and similar), putative	LbrM.34.2.001420 LPMP_341360	-9,92411E+14 -7,07982E+14	6,90776E-70 3,04451E-07	34 34
		OG6_118579	Nucleoside 2-deoxyribosyltransferase, putative	LbrM.23.2.001820 LPMP_231860	-1,64398E+14 -1,5425E+13	1,4213E-230 9,2181E-58	23 23
		OG6_132802	Proteasome activator pa28 beta subunit, putative	LbrM.34.2.000740 LPMP_340680	-8,5198E+14 -7,85969E+14	6,80081E-08 1,24785E-05	34 34
<i>L. donovani</i> y <i>L. infantum</i>	UPREGULATED	OG6_100045	ATP-binding cassette protein subfamily A, member 10, putative	LdBPK_290640.1 LINF_020008000	7,6375E+14 2,74325E+14	2,68562E-37 6,67023E-18	29 2
		OG6_101028	aconitase, putative	LdBPK_180510.1 LINF_180010100	6,43794E+13 1,61199E+14	3,26909E-24 4,05978E-06	18 18
		OG6_101741	phosphatidylinositol-kinase domain protein, putative	LdBPK_291550.1 LINF_290020900	8,86785E+14 2,84255E+14	0,00324268 3,73416E-14	29 29
		OG6_206698	hypothetical protein, conserved	LdBPK_180850.1 LINF_180013700	8,08778E+14 2,00174E+14	2,05336E-15 1,54838E-05	18 18
		<i>L. donovani</i> y <i>L. panamensis</i>	DOWNREGULATED	OG6_100260	enolase	LdBPK_141240.1 LPMP_141140	-3,72135E+14 -6,14839E+14
OG6_100478	protein disulfide isomerase 2			LdBPK_367280.1 LPMP_357150	-4,58291E+14 -6,11209E+14	2,38505E-06 6,39578E-14	36 35
OG6_100643	ATP-binding cassette protein subfamily H, member 1, putative			LdBPK_110040.1 LPMP_110040	-7,04026E+14 -1,08398E+14	1,53665E-07 2,66929E-96	11 11
OG6_101151	cysteine peptidase C (CPC)			LdBPK_290860.1 LPMP_290820	-3,88965E+14 -1,16285E+14	4,70706E-06 1,37297E-87	29 29
OG6_101659	trypanothione reductase			LdBPK_050350.1 LPMP_050340	-5,60271E+14 -7,47266E+14	4,1638E-36 4,16381E-30	5 5
OG6_102030	glycosomal phosphoenolpyruvate carboxykinase, putative			LdBPK_072500.1 LPMP_271790	-5,45722E+14 -5,95053E+14	3,22931E-24 1,4401E-12	27 27
OG6_102275	delta-1-pyrroline-5-carboxylate dehydrogenase, putative			LdBPK_030190.1 LPMP_030190	-4,85808E+14 -5,42349E+14	1,59879E-06 0,0012961	3 3
OG6_113325	PAP2 superfamily, putative			LdBPK_230700.1 LPMP_230700	-8,73032E+14 -1,43326E+14	1,75074E-59 1,95995E-11	23 23
OG6_133635	EF-hand domain pair, putative			LdBPK_363780.1 LPMP_353700	-3,23241E+14 -1,02315E+12	8,94422E-05 1,27585E-38	36 35
OG6_136426	kinesin, putative (fragment)			LdBPK_161570.1 LPMP_161430	-7,80374E+14 -5,76475E+14	2,30466E-24 4,69505E-05	16 16

		OG6_152163	membrane-bound acid phosphatase 2, putative	LdBPK_362720.1 LPMP_352650	-3,85766E+14 -1,28419E+14	1,39472E-08 3,68329E-38	36 35	
		OG6_199942	calpain-like cysteine peptidase, putative	LdBPK_201320.1 LPMP_205470	-4,71361E+14 -1,34027E+14	7,80679E-15 2,53411E-81	20 20	
<i>L. infantum</i> y <i>L. panamensis</i>	UPREGULATED	OG6_103141	pteridine transporter (truncated) - putative	LINF_100009100 LINF_100009200 LPMP_100350	4,09611E+14 4,04737E+14 1,32143E+14	1,15424E-79 7,66817E-23 3,88487E-78	10 10 10	
		OG6_139700	hypothetical protein - conserved	LINF_350011300 LPMP_340600	2,04393E+14 8,5262E+14	3,38205E-10 2,79795E-09	35 34	
		OG6_200434	amastin-like protein	LINF_340016000 LPMP_203001	2,07208E+14 5,54756E+14	8,91843E-08 4,20263E-09	34 20	
	DOWNREGULATED	OG6_107645	Alba - putative	LINF_130009400 LPMP_130340	-1,30623E+14 -6,29403E+14	0,000437415 3,67752E-12	13 13	
<i>L. amazonensis</i> , <i>L. braziliensis</i> y <i>L. panamensis</i>	UPREGULATED	OG6_142640	DNA ligase k alpha, putative	LmxM.26.1340 LbrM.26.2.001360 LPMP_261320	2,72879E+14 8,39764E+14 5,62351E+14	1,6502E-223 3,00523E-73 2,38436E-12	26 26 26	
		DOWNREGULATED	OG6_100025	dynein heavy chain, point mutation	LmxM.27.2590 LmxM.33.3880 LbrM.22.2.001010 LPMP_231470	-8,79508E+14 -8,39766E+14 -4,9153E+14 -5,52262E+14	2,2173E-08 5,33188E-09 0,000261779 1,91091E-06	27 33 22 23
			OG6_156932	Dynein heavy chain and region D6 of dynein motor/Ankyrin repeat, putative	LmxM.34.5340 LbrM.34.2.005280 LPMP_345170	-1,88001E+14 -1,07145E+14 -9,54141E+14	4,87467E-54 2,05926E-17 4,77065E-13	34 34 34
	OG6_478666		hypothetical protein, unknown function	LmxM.34.0800 LbrM.34.2.000790 LPMP_340730	-9,40614E+14 -7,13589E+14 -1,02339E+14	1,61348E-07 5,08204E-21 5,24126E-10	34 34 34	
	UPREGULATED	OG6_101746	zinc transporter, putative	LmxM.28.1930 LdBPK_282050.1 LPMP_282040	1,6018E+14 2,50012E+14 7,34403E+14	2,0425E-26 2,5824E-245 4,03431E-31	28 28 28	
		OG6_157042	WW domain/Zinc finger C-x8-C-x5-C-x3-H type (and similar), putative	LmxM.27.0130 LdBPK_270130.1 LPMP_270130	1,1549E+14 4,77859E+14 3,46498E+14	1,58899E-23 2,15338E-27 0	27 27 27	
DOWNREGULATED		OG6_110995	paraflagellar rod protein 1D, putative	LmxM.08_29.1760 LmxM.16.1425partial LmxM.16.1430 LdBPK_161510.1 LPMP_161400 LPMP_291770	-1,88278E+13 -1,93147E+14 -1,18558E+14 -6,29583E+14 -1,39333E+14 -9,6322E+14	4,57361E-98 3,96235E-46 1,70407E-46 1,24398E-36 1,3104E-201 3,58904E-77	8 16 16 16 16 29	
		OG6_127587	calpain-like cysteine peptidase, putative	LmxM.04.0450 LmxM.20.1180 LmxM.20.1185 LdBPK_201210.1 LPMP_040400 LPMP_205350	-8,66115E+14 -1,58112E+14 -3,66155E+14 -8,71592E+14 -1,20213E+14 -8,79519E+14	2,12261E-09 2,01272E-57 1,64266E-92 0,009247193 2,41763E-51 0,003070022	4 20 20 20 4 20	
UPREGULATED	OG6_119258	nucleobase transporter	LbrM.13.2.204210 LdBPK_131110.1	9,17191E+14 5,34498E+14	1,14871E-73 1,17074E-28	13 13		

<i>L. infantum</i>				LINF_130017100	1,71549E+14	9,77057E-09	13
<i>L. amazonensis, L. braziliensis, L. donovani and L. panamensis</i>	UPREGULATED	OG6_152462	RNA-binding protein 5, putative	LmxM.09.0060	1,44495E+14	3,19927E-55	9
				LbrM.09.2.000080	1,66253E+13	1,02167E-49	9
				LdBPK_090080.1	3,51757E+14	0,008718418	9
				LPMP_090080	1,43071E+14	4,39878E-24	9
		OG6_200283	cytochrome b5-like Heme/Steroid binding domain containing protein, putative	LmxM.30.1190	1,0372E+14	9,25634E-08	30
				LbrM.31.2.001400	1,4451E+13	2,67415E-27	31
				LdBPK_311210.1	8,2207E+14	0,004470259	31
				LPMP_311110	1,93373E+14	1,13016E-65	31