

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

CELLO RESULTS

SeqID: li|LinJ_30_2820_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Mitochondrial	0.545
Di-peptide	Mitochondrial	0.821
part-Comp.	Mitochondrial	0.556
chemo-typy	Cytoplasmic	0.478
Neighboring	Cytoplasmic	0.322

Combined SVM classifier:

Extracellular	0.120
PlasmaMembrane	0.034
Cytoplasmic	1.319
Cytoskeletal	0.020
ER	0.031
Golgi	0.011
Lysosomal	0.019
Mitochondrial	2.287 *
Chloroplast	0.420
Peroxisomal	0.180
Vacuole	0.016
Nuclear	0.544

SeqID: li|LinJ_36_1160_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Nuclear	0.424
Di-peptide	Nuclear	0.471
part-Comp.	Nuclear	0.337
chemo-typy	Nuclear	0.693
Neighboring	Mitochondrial	0.377

Combined SVM classifier:

Extracellular	0.160
PlasmaMembrane	0.093
Cytoplasmic	0.587
Cytoskeletal	0.026
ER	0.017
Golgi	0.012
Lysosomal	0.014
Mitochondrial	1.442
Chloroplast	0.351
Peroxisomal	0.078
Vacuole	0.017
Nuclear	2.200 *

SeqID: li|LinJ_27_2320_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Mitochondrial	0.397

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

Di-peptide	Nuclear	0.526	
part-Comp.	Mitochondrial	0.595	
chemo-typy	Mitochondrial	0.471	
Neighboring	Nuclear	0.359	
Combined SVM classifier:			
	Extracellular	0.340	
	PlasmaMembrane	0.149	
	Cytoplasmic	0.500	
	Cytoskeletal	0.023	
	ER	0.060	
	Golgi	0.023	
	Lysosomal		0.023
	Mitochondrial	1.992	*
	Chloroplast	0.669	
	Peroxisomal	0.088	
	Vacuole	0.030	
	Nuclear	1.103	

SeqID: li LinJ_18_0650_mRNA			
CELLO prediction:			
(predictor	location	reliable-index)	
Composition	Cytoplasmic	0.337	
Di-peptide	Nuclear	0.389	
part-Comp.	Nuclear	0.375	
chemo-typy	Mitochondrial	0.368	
Neighboring	Cytoplasmic	0.350	
Combined SVM classifier:			
	Extracellular	0.095	
	PlasmaMembrane	0.121	
	Cytoplasmic	1.582	*
	Cytoskeletal	0.015	
	ER	0.020	
	Golgi	0.035	
	Lysosomal		0.018
	Mitochondrial	1.303	*
	Chloroplast	0.204	
	Peroxisomal	0.126	
	Vacuole	0.009	
	Nuclear	1.471	*

SeqID: li LinJ_35_4150_mRNA			
CELLO prediction:			
(predictor	location	reliable-index)	
Composition	Mitochondrial	0.292	
Di-peptide	Cytoplasmic	0.331	
part-Comp.	Cytoplasmic	0.339	
chemo-typy	Mitochondrial	0.604	
Neighboring	Cytoplasmic	0.378	
Combined SVM classifier:			
	Extracellular	0.680	
	PlasmaMembrane	0.031	
	Cytoplasmic	1.505	*

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

Cytoskeletal	0.027	
ER	0.025	
Golgi	0.028	
Lysosomal		0.012
Mitochondrial	1.374	*
Chloroplast	0.271	
Peroxisomal	0.030	
Vacuole	0.008	
Nuclear	1.009	*

SeqID: li|LinJ_07_0520_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Mitochondrial	0.457
Di-peptide	Cytoplasmic	0.351
part-Comp.	PlasmaMembrane	0.503
chemo-typy	Nuclear	0.315
Neighboring	PlasmaMembrane	0.682

Combined SVM classifier:

Extracellular	0.338	
PlasmaMembrane	1.694	*
Cytoplasmic	0.884	
Cytoskeletal	0.054	
ER	0.031	
Golgi	0.026	
Lysosomal		0.024
Mitochondrial	1.049	*
Chloroplast	0.300	
Peroxisomal	0.093	
Vacuole	0.013	
Nuclear	0.494	

SeqID: li|LinJ_09_0970_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Nuclear	0.679
Di-peptide	Cytoplasmic	0.897
part-Comp.	Cytoplasmic	0.600
chemo-typy	Cytoplasmic	0.754
Neighboring	Cytoplasmic	0.790

Combined SVM classifier:

Extracellular	0.033	
PlasmaMembrane	0.027	
Cytoplasmic	3.232	*
Cytoskeletal	0.012	
ER	0.101	
Golgi	0.043	
Lysosomal		0.004
Mitochondrial	0.065	
Chloroplast	0.163	
Peroxisomal	0.018	
Vacuole	0.021	
Nuclear	1.280	

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

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*****
*****
SeqID: li|LinJ_31_3320_mRNA|
      CELLO prediction:
              (predictor      location      reliable-index)
      Composition      Cytoplasmic      0.379
      Di-peptide       Nuclear         0.696
      part-Comp.       Nuclear         0.615
      chemo-typy       Nuclear         0.755
      Neighboring      Nuclear         0.503

      Combined SVM classifier:
                                Extracellular  0.128
                                PlasmaMembrane 0.035
                                Cytoplasmic     0.773
                                Cytoskeletal    0.013
                                ER               0.013
                                Golgi           0.007
                                Lysosomal              0.008
                                Mitochondrial  0.940
                                Chloroplast     0.274
                                Peroxisomal     0.034
                                Vacuole         0.016
                                Nuclear         2.760 *

*****
*****
SeqID: li|LinJ_03_0240_mRNA|
      CELLO prediction:
              (predictor      location      reliable-index)
      Composition      Cytoplasmic      0.341
      Di-peptide       Mitochondrial  0.610
      part-Comp.       Nuclear         0.778
      chemo-typy       Mitochondrial  0.589
      Neighboring      Nuclear         0.467

      Combined SVM classifier:
                                Extracellular  0.266
                                PlasmaMembrane 0.042
                                Cytoplasmic     0.778
                                Cytoskeletal    0.018
                                ER               0.021
                                Golgi           0.016
                                Lysosomal              0.010
                                Mitochondrial  1.639 *
                                Chloroplast     0.188
                                Peroxisomal     0.026
                                Vacuole         0.012
                                Nuclear         1.983 *

*****
*****
SeqID: li|LinJ_35_3840_mRNA|
      CELLO prediction:
              (predictor      location      reliable-index)
      Composition      Mitochondrial  0.385
      Di-peptide       Mitochondrial  0.624

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Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	part-Comp.	Cytoplasmic	0.340	
	chemo-typy	Mitochondrial	0.352	
	Neighboring	Mitochondrial	0.416	
Combined SVM classifier:				
		Extracellular	0.313	
		PlasmaMembrane	0.143	
		Cytoplasmic	1.111	
		Cytoskeletal	0.013	
		ER	0.023	
		Golgi	0.012	
		Lysosomal		0.020
		Mitochondrial	1.937	*
		Chloroplast	0.756	
		Peroxisomal	0.111	
		Vacuole	0.018	
		Nuclear	0.543	

SeqID: li LinJ_22_0720_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Nuclear	0.547	
	Di-peptide	Nuclear	0.860	
	part-Comp.	Nuclear	0.741	
	chemo-typy	Mitochondrial	0.425	
	Neighboring	Nuclear	0.692	
Combined SVM classifier:				
		Extracellular	0.070	
		PlasmaMembrane	0.011	
		Cytoplasmic	0.527	
		Cytoskeletal	0.032	
		ER	0.013	
		Golgi	0.016	
		Lysosomal		0.010
		Mitochondrial	0.797	
		Chloroplast	0.432	
		Peroxisomal	0.057	
		Vacuole	0.017	
		Nuclear	3.019	*

SeqID: li LinJ_35_0190_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Nuclear	0.564	
	Di-peptide	Cytoplasmic	0.349	
	part-Comp.	Cytoplasmic	0.314	
	chemo-typy	Chloroplast	0.478	
	Neighboring	Cytoplasmic	0.286	
Combined SVM classifier:				
		Extracellular	0.533	
		PlasmaMembrane	0.078	
		Cytoplasmic	1.441	*
		Cytoskeletal	0.021	

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	ER	0.129	
	Golgi	0.068	
	Lysosomal		0.081
	Mitochondrial	0.275	
	Chloroplast	0.811	
	Peroxisomal	0.188	
	Vacuole	0.047	
	Nuclear	1.328	*

SeqID: li LinJ_11_1180_mRNA			
CELLO prediction:			
	(predictor	location	reliable-index)
	Composition	Mitochondrial	0.520
	Di-peptide	Cytoplasmic	0.401
	part-Comp.	Mitochondrial	0.431
	chemo-typy	Extracellular	0.310
	Neighboring	Mitochondrial	0.433
Combined SVM classifier:			
	Extracellular	0.468	
	PlasmaMembrane	0.245	
	Cytoplasmic	1.045	
	Cytoskeletal	0.022	
	ER	0.032	
	Golgi	0.013	
	Lysosomal		0.014
	Mitochondrial	1.868	*
	Chloroplast	0.752	
	Peroxisomal	0.078	
	Vacuole	0.015	
	Nuclear	0.449	

SeqID: li LinJ_33_2710_mRNA			
CELLO prediction:			
	(predictor	location	reliable-index)
	Composition	Mitochondrial	0.644
	Di-peptide	Mitochondrial	0.421
	part-Comp.	Extracellular	0.341
	chemo-typy	Mitochondrial	0.427
	Neighboring	Mitochondrial	0.253
Combined SVM classifier:			
	Extracellular	0.811	
	PlasmaMembrane	0.306	
	Cytoplasmic	0.559	
	Cytoskeletal	0.015	
	ER	0.200	
	Golgi	0.019	
	Lysosomal		0.131
	Mitochondrial	1.984	*
	Chloroplast	0.680	
	Peroxisomal	0.085	
	Vacuole	0.026	
	Nuclear	0.183	

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

SeqID: li|LinJ_16_0950_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Cytoplasmic	0.698
Di-peptide	Cytoplasmic	0.749
part-Comp.	Cytoplasmic	0.429
chemo-typy	Nuclear	0.446
Neighboring	Cytoplasmic	0.750

Combined SVM classifier:

Extracellular	0.227
PlasmaMembrane	0.124
Cytoplasmic	3.034 *
Cytoskeletal	0.010
ER	0.027
Golgi	0.025
Lysosomal	0.022
Mitochondrial	0.565
Chloroplast	0.144
Peroxisomal	0.039
Vacuole	0.009
Nuclear	0.775

SeqID: li|LinJ_35_2250_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Nuclear	0.273
Di-peptide	Mitochondrial	0.401
part-Comp.	Nuclear	0.554
chemo-typy	Nuclear	0.406
Neighboring	Extracellular	0.302

Combined SVM classifier:

Extracellular	0.673
PlasmaMembrane	0.070
Cytoplasmic	1.243 *
Cytoskeletal	0.048
ER	0.029
Golgi	0.016
Lysosomal	0.012
Mitochondrial	0.827
Chloroplast	0.269
Peroxisomal	0.040
Vacuole	0.020
Nuclear	1.755 *

SeqID: li|LinJ_30_3060_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Chloroplast	0.379
Di-peptide	Cytoplasmic	0.325
part-Comp.	Cytoplasmic	0.473

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	chemo-typy	Cytoplasmic	0.500	
	Neighboring	Chloroplast	0.470	
Combined SVM classifier:				
		Extracellular	0.309	
		PlasmaMembrane	0.072	
		Cytoplasmic	1.650	*
		Cytoskeletal	0.016	
		ER	0.073	
		Golgi	0.042	
		Lysosomal		0.020
		Mitochondrial	0.739	
		Chloroplast	1.389	*
		Peroxisomal	0.152	
		Vacuole	0.070	
		Nuclear	0.468	

SeqID: li LinJ_35_1900_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Cytoplasmic	0.722	
	Di-peptide	Nuclear	0.581	
	part-Comp.	Nuclear	0.355	
	chemo-typy	Nuclear	0.917	
	Neighboring	Nuclear	0.318	
Combined SVM classifier:				
		Extracellular	0.072	
		PlasmaMembrane	0.026	
		Cytoplasmic	1.514	
		Cytoskeletal	0.020	
		ER	0.016	
		Golgi	0.009	
		Lysosomal		0.010
		Mitochondrial	0.829	
		Chloroplast	0.146	
		Peroxisomal	0.031	
		Vacuole	0.013	
		Nuclear	2.315	*

SeqID: li LinJ_22_1040_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Mitochondrial	0.706	
	Di-peptide	Nuclear	0.548	
	part-Comp.	Mitochondrial	0.903	
	chemo-typy	Mitochondrial	0.582	
	Neighboring	Mitochondrial	0.828	
Combined SVM classifier:				
		Extracellular	0.120	
		PlasmaMembrane	0.022	
		Cytoplasmic	0.279	
		Cytoskeletal	0.008	
		ER	0.009	

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Golgi	0.003	
	Lysosomal		0.014
	Mitochondrial	3.335	*
	Chloroplast	0.176	
	Peroxisomal	0.055	
	Vacuole	0.005	
	Nuclear	0.975	

SeqID: li LinJ_33_1560_mRNA			
CELLO prediction:			
	(predictor	location	reliable-index)
	Composition	Nuclear	0.551
	Di-peptide	Nuclear	0.439
	part-Comp.	Nuclear	0.344
	chemo-typy	Nuclear	0.694
	Neighboring	Nuclear	0.736
Combined SVM classifier:			
	Extracellular	0.251	
	PlasmaMembrane	0.207	
	Cytoplasmic	0.660	
	Cytoskeletal	0.043	
	ER	0.024	
	Golgi	0.017	
	Lysosomal		0.023
	Mitochondrial	0.749	
	Chloroplast	0.118	
	Peroxisomal	0.091	
	Vacuole	0.054	
	Nuclear	2.763	*

SeqID: li LinJ_36_0950_mRNA			
CELLO prediction:			
	(predictor	location	reliable-index)
	Composition	Nuclear	0.363
	Di-peptide	PlasmaMembrane	0.317
	part-Comp.	Extracellular	0.318
	chemo-typy	Cytoplasmic	0.309
	Neighboring	Cytoplasmic	0.260
Combined SVM classifier:			
	Extracellular	0.855	
	PlasmaMembrane	0.948	
	Cytoplasmic	0.985	*
	Cytoskeletal	0.022	
	ER	0.064	
	Golgi	0.144	
	Lysosomal		0.042
	Mitochondrial	0.312	
	Chloroplast	0.509	
	Peroxisomal	0.131	
	Vacuole	0.042	
	Nuclear	0.946	

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

SeqID: li|LinJ_26_0840_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Cytoplasmic	0.404
Di-peptide	Mitochondrial	0.743
part-Comp.	Mitochondrial	0.538
chemo-typy	Mitochondrial	0.383
Neighboring	Mitochondrial	0.670

Combined SVM classifier:

Extracellular	0.159
PlasmaMembrane	0.040
Cytoplasmic	1.402
Cytoskeletal	0.010
ER	0.012
Golgi	0.008
Lysosomal	0.015
Mitochondrial	2.698 *
Chloroplast	0.182
Peroxisomal	0.104
Vacuole	0.011
Nuclear	0.359

SeqID: li|LinJ_30_3650_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Cytoplasmic	0.360
Di-peptide	Chloroplast	0.354
part-Comp.	Cytoplasmic	0.877
chemo-typy	Cytoplasmic	0.772
Neighboring	Cytoplasmic	0.432

Combined SVM classifier:

Extracellular	0.085
PlasmaMembrane	0.024
Cytoplasmic	2.673 *
Cytoskeletal	0.014
ER	0.014
Golgi	0.009
Lysosomal	0.016
Mitochondrial	0.702
Chloroplast	0.713
Peroxisomal	0.054
Vacuole	0.023
Nuclear	0.674

SeqID: li|LinJ_30_3280_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Mitochondrial	0.456
Di-peptide	Mitochondrial	0.453
part-Comp.	Mitochondrial	0.605
chemo-typy	Mitochondrial	0.625

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Neighboring	Mitochondrial	0.484	
Combined SVM classifier:				
		Extracellular	0.132	
		PlasmaMembrane	0.037	
		Cytoplasmic	0.750	
		Cytoskeletal	0.018	
		ER	0.120	
		Golgi	0.020	
		Lysosomal		0.056
		Mitochondrial	2.623	*
		Chloroplast	0.469	
		Peroxisomal	0.044	
		Vacuole	0.029	
		Nuclear	0.702	

SeqID: li LinJ_17_1380_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Extracellular	0.333	
	Di-peptide	Mitochondrial	0.424	
	part-Comp.	Chloroplast	0.252	
	chemo-typy	Mitochondrial	0.427	
	Neighboring	Chloroplast	0.360	
Combined SVM classifier:				
		Extracellular	0.775	
		PlasmaMembrane	0.642	
		Cytoplasmic	0.481	
		Cytoskeletal	0.025	
		ER	0.043	
		Golgi	0.019	
		Lysosomal		0.050
		Mitochondrial	1.357	*
		Chloroplast	1.108	*
		Peroxisomal	0.207	
		Vacuole	0.041	
		Nuclear	0.252	

SeqID: li LinJ_34_2100_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	PlasmaMembrane	0.479	
	Di-peptide	Mitochondrial	0.233	
	part-Comp.	Cytoplasmic	0.423	
	chemo-typy	Mitochondrial	0.438	
	Neighboring	Nuclear	0.405	
Combined SVM classifier:				
		Extracellular	0.147	
		PlasmaMembrane	1.083	*
		Cytoplasmic	1.189	*
		Cytoskeletal	0.032	
		ER	0.031	
		Golgi	0.254	

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Lysosomal	0.015
	Mitochondrial	0.812
	Chloroplast	0.362
	Peroxisomal	0.063
	Vacuole	0.016
	Nuclear	0.996

SeqID: li LinJ_13_1410_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Cytoplasmic	0.647
Di-peptide	Nuclear	0.726
part-Comp.	Cytoplasmic	0.763
chemo-typy	Nuclear	0.844
Neighboring	Cytoplasmic	0.655
Combined SVM classifier:		
	Extracellular	0.145
	PlasmaMembrane	0.040
	Cytoplasmic	2.233 *
	Cytoskeletal	0.011
	ER	0.024
	Golgi	0.010
	Lysosomal	0.013
	Mitochondrial	0.550
	Chloroplast	0.061
	Peroxisomal	0.027
	Vacuole	0.018
	Nuclear	1.869 *

SeqID: li LinJ_36_0370_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Mitochondrial	0.367
Di-peptide	Nuclear	0.755
part-Comp.	Nuclear	0.573
chemo-typy	Nuclear	0.508
Neighboring	Mitochondrial	0.452
Combined SVM classifier:		
	Extracellular	0.156
	PlasmaMembrane	0.045
	Cytoplasmic	0.911
	Cytoskeletal	0.020
	ER	0.017
	Golgi	0.010
	Lysosomal	0.010
	Mitochondrial	1.306
	Chloroplast	0.318
	Peroxisomal	0.030
	Vacuole	0.010
	Nuclear	2.168 *

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

SeqID: li LinJ_36_1310_mRNA			
CELLO prediction:			
	(predictor	location	reliable-index)
	Composition	Nuclear	0.635
	Di-peptide	Nuclear	0.646
	part-Comp.	Nuclear	0.665
	chemo-typy	Nuclear	0.816
	Neighboring	Mitochondrial	0.511
Combined SVM classifier:			
		Extracellular	0.030
		PlasmaMembrane	0.032
		Cytoplasmic	0.461
		Cytoskeletal	0.014
		ER	0.004
		Golgi	0.005
		Lysosomal	0.003
		Mitochondrial	1.023
		Chloroplast	0.178
		Peroxisomal	0.036
		Vacuole	0.004
		Nuclear	3.209 *

SeqID: li LinJ_35_1320_mRNA			
CELLO prediction:			
	(predictor	location	reliable-index)
	Composition	Cytoplasmic	0.517
	Di-peptide	Nuclear	0.722
	part-Comp.	Nuclear	0.501
	chemo-typy	Nuclear	0.793
	Neighboring	Nuclear	0.455
Combined SVM classifier:			
		Extracellular	0.108
		PlasmaMembrane	0.036
		Cytoplasmic	1.013
		Cytoskeletal	0.013
		ER	0.013
		Golgi	0.007
		Lysosomal	0.008
		Mitochondrial	0.907
		Chloroplast	0.234
		Peroxisomal	0.032
		Vacuole	0.014
		Nuclear	2.615 *

SeqID: li LinJ_36_5350_mRNA			
CELLO prediction:			
	(predictor	location	reliable-index)
	Composition	Mitochondrial	0.638
	Di-peptide	Cytoplasmic	0.400
	part-Comp.	Mitochondrial	0.449
	chemo-typy	Cytoplasmic	0.545

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Neighboring	Cytoplasmic	0.527	
Combined SVM classifier:				
		Extracellular	0.078	
		PlasmaMembrane	0.083	
		Cytoplasmic	1.684	*
		Cytoskeletal	0.027	
		ER	0.024	
		Golgi	0.020	
		Lysosomal		0.008
		Mitochondrial	2.088	*
		Chloroplast	0.476	
		Peroxisomal	0.355	
		Vacuole	0.009	
		Nuclear	0.148	

SeqID: li LinJ_26_0540_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Extracellular	0.401	
	Di-peptide	Extracellular	0.806	
	part-Comp.	Extracellular	0.446	
	chemo-typy	Chloroplast	0.258	
	Neighboring	Cytoplasmic	0.269	
Combined SVM classifier:				
		Extracellular	2.103	*
		PlasmaMembrane	0.313	
		Cytoplasmic	0.726	
		Cytoskeletal	0.015	
		ER	0.111	
		Golgi	0.080	
		Lysosomal		0.075
		Mitochondrial	0.195	
		Chloroplast	0.570	
		Peroxisomal	0.038	
		Vacuole	0.165	
		Nuclear	0.609	

SeqID: li LinJ_20_0600_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Mitochondrial	0.848	
	Di-peptide	Mitochondrial	0.917	
	part-Comp.	Mitochondrial	0.863	
	chemo-typy	Mitochondrial	0.501	
	Neighboring	Mitochondrial	0.893	
Combined SVM classifier:				
		Extracellular	0.109	
		PlasmaMembrane	0.047	
		Cytoplasmic	0.334	
		Cytoskeletal	0.018	
		ER	0.010	
		Golgi	0.006	

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Lysosomal	0.008
	Mitochondrial	4.021 *
	Chloroplast	0.181
	Peroxisomal	0.050
	Vacuole	0.007
	Nuclear	0.209

SeqID: li LinJ_29_2480_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Nuclear	0.401
Di-peptide	Mitochondrial	0.502
part-Comp.	Nuclear	0.375
chemo-typy	Mitochondrial	0.570
Neighboring	Nuclear	0.311
Combined SVM classifier:		
	Extracellular	0.414
	PlasmaMembrane	0.109
	Cytoplasmic	0.593
	Cytoskeletal	0.015
	ER	0.019
	Golgi	0.011
	Lysosomal	0.013
	Mitochondrial	1.696 *
	Chloroplast	0.328
	Peroxisomal	0.026
	Vacuole	0.016
	Nuclear	1.760 *

SeqID: li LinJ_32_4050_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Mitochondrial	0.380
Di-peptide	Cytoplasmic	0.721
part-Comp.	Mitochondrial	0.419
chemo-typy	Nuclear	0.377
Neighboring	Mitochondrial	0.558
Combined SVM classifier:		
	Extracellular	0.045
	PlasmaMembrane	0.025
	Cytoplasmic	1.850 *
	Cytoskeletal	0.010
	ER	0.016
	Golgi	0.008
	Lysosomal	0.011
	Mitochondrial	1.666 *
	Chloroplast	0.134
	Peroxisomal	0.086
	Vacuole	0.006
	Nuclear	1.142

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

```

*****
*****
SeqID: li|LinJ_25_0260_mRNA|
      CELLO prediction:
              (predictor      location      reliable-index)
Composition      Extracellular  0.399
Di-peptide       Cytoplasmic   0.612
part-Comp.       Cytoplasmic   0.510
chemo-typy       Cytoplasmic   0.531
Neighboring      Cytoplasmic   0.507

      Combined SVM classifier:
                                Extracellular  0.479
                                PlasmaMembrane 0.045
                                Cytoplasmic     2.547 *
                                Cytoskeletal    0.023
                                ER               0.037
                                Golgi           0.016
                                Lysosomal              0.011
                                Mitochondrial    0.794
                                Chloroplast      0.197
                                Peroxisomal      0.213
                                Vacuole          0.006
                                Nuclear           0.632

*****
*****
SeqID: li|LinJ_34_0420_mRNA|
      CELLO prediction:
              (predictor      location      reliable-index)
Composition      Mitochondrial  0.247
Di-peptide       Mitochondrial  0.448
part-Comp.       Mitochondrial  0.499
chemo-typy       Extracellular  0.316
Neighboring      Mitochondrial  0.468

      Combined SVM classifier:
                                Extracellular  0.541
                                PlasmaMembrane 0.117
                                Cytoplasmic     0.712
                                Cytoskeletal    0.164
                                ER               0.065
                                Golgi           0.042
                                Lysosomal              0.029
                                Mitochondrial    1.943 *
                                Chloroplast      0.631
                                Peroxisomal      0.087
                                Vacuole          0.042
                                Nuclear           0.626

*****
*****
SeqID: li|LinJ_04_0680_mRNA|
      CELLO prediction:
              (predictor      location      reliable-index)
Composition      Nuclear        0.516
Di-peptide       Nuclear        0.288
part-Comp.       Nuclear        0.409
chemo-typy       Mitochondrial  0.467

```


Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Neighboring	Nuclear	0.781	
Combined SVM classifier:				
		Extracellular	0.333	
		PlasmaMembrane	0.088	
		Cytoplasmic	0.896	
		Cytoskeletal	0.022	
		ER	0.017	
		Golgi	0.013	
		Lysosomal		0.011
		Mitochondrial	1.165	
		Chloroplast	0.241	
		Peroxisomal	0.058	
		Vacuole	0.008	
		Nuclear	2.148	*

SeqID: li LinJ_28_0260_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Mitochondrial	0.832	
	Di-peptide	Mitochondrial	0.758	
	part-Comp.	Mitochondrial	0.364	
	chemo-typy	Cytoplasmic	0.440	
	Neighboring	Mitochondrial	0.876	
Combined SVM classifier:				
		Extracellular	0.215	
		PlasmaMembrane	0.048	
		Cytoplasmic	0.936	
		Cytoskeletal	0.015	
		ER	0.029	
		Golgi	0.014	
		Lysosomal		0.011
		Mitochondrial	2.932	*
		Chloroplast	0.386	
		Peroxisomal	0.243	
		Vacuole	0.021	
		Nuclear	0.148	

SeqID: li LinJ_06_1210_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Nuclear	0.490	
	Di-peptide	Cytoplasmic	0.333	
	part-Comp.	Nuclear	0.918	
	chemo-typy	Cytoplasmic	0.388	
	Neighboring	Nuclear	0.398	
Combined SVM classifier:				
		Extracellular	0.290	
		PlasmaMembrane	0.035	
		Cytoplasmic	1.176	
		Cytoskeletal	0.023	
		ER	0.053	
		Golgi	0.017	

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Lysosomal	0.036
	Mitochondrial	0.734
	Chloroplast	0.344
	Peroxisomal	0.179
	Vacuole	0.032
	Nuclear	2.082 *

SeqID: li LinJ_24_2300_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Mitochondrial	0.416
Di-peptide	Chloroplast	0.403
part-Comp.	Mitochondrial	0.448
chemo-typy	Extracellular	0.535
Neighboring	Cytoplasmic	0.448
Combined SVM classifier:		
	Extracellular	0.631
	PlasmaMembrane	0.027
	Cytoplasmic	1.379 *
	Cytoskeletal	0.014
	ER	0.023
	Golgi	0.014
	Lysosomal	0.013
	Mitochondrial	1.401 *
	Chloroplast	0.901
	Peroxisomal	0.122
	Vacuole	0.017
	Nuclear	0.457

SeqID: li LinJ_16_0150_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Nuclear	0.770
Di-peptide	Cytoplasmic	0.515
part-Comp.	Nuclear	0.620
chemo-typy	Chloroplast	0.388
Neighboring	Cytoplasmic	0.302
Combined SVM classifier:		
	Extracellular	0.060
	PlasmaMembrane	0.029
	Cytoplasmic	1.063
	Cytoskeletal	0.030
	ER	0.052
	Golgi	0.016
	Lysosomal	0.007
	Mitochondrial	0.367
	Chloroplast	0.847
	Peroxisomal	0.052
	Vacuole	0.051
	Nuclear	2.427 *

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

```

*****
*****
SeqID: li|LinJ_35_1030_mRNA|
      CELLO prediction:
              (predictor      location      reliable-index)
Composition      Cytoplasmic      0.423
Di-peptide       Cytoplasmic      0.562
part-Comp.       Cytoplasmic      0.559
chemo-typy       Cytoplasmic      0.493
Neighboring      Mitochondrial    0.504

      Combined SVM classifier:
                                Extracellular  0.056
                                PlasmaMembrane 0.083
                                Cytoplasmic     2.390 *
                                Cytoskeletal    0.014
                                ER               0.043
                                Golgi           0.008
                                Lysosomal       0.036
                                Mitochondrial   0.995
                                Chloroplast     0.091
                                Peroxisomal     0.078
                                Vacuole         0.045
                                Nuclear          1.160

*****
*****
SeqID: li|LinJ_25_0990_mRNA|
      CELLO prediction:
              (predictor      location      reliable-index)
Composition      Nuclear          0.420
Di-peptide       PlasmaMembrane 0.194
part-Comp.       Nuclear          0.414
chemo-typy       Cytoplasmic     0.469
Neighboring      Nuclear          0.313

      Combined SVM classifier:
                                Extracellular  0.305
                                PlasmaMembrane 0.550
                                Cytoplasmic     1.461 *
                                Cytoskeletal    0.014
                                ER               0.067
                                Golgi           0.037
                                Lysosomal       0.132
                                Mitochondrial   0.416
                                Chloroplast     0.235
                                Peroxisomal     0.105
                                Vacuole         0.094
                                Nuclear          1.583 *

*****
*****
SeqID: li|LinJ_36_3520_mRNA|
      CELLO prediction:
              (predictor      location      reliable-index)
Composition      Nuclear          0.857
Di-peptide       Nuclear          0.493
part-Comp.       Nuclear          0.610
chemo-typy       Cytoplasmic     0.383

```

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Neighboring	Cytoplasmic	0.506	
Combined SVM classifier:				
		Extracellular	0.147	
		PlasmaMembrane	0.049	
		Cytoplasmic	1.382	
		Cytoskeletal	0.041	
		ER	0.024	
		Golgi	0.049	
		Lysosomal		0.009
		Mitochondrial	0.251	
		Chloroplast	0.303	
		Peroxisomal	0.142	
		Vacuole	0.025	
		Nuclear	2.579	*

SeqID: li LinJ_01_0790_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Cytoplasmic	0.282	
	Di-peptide	Chloroplast	0.720	
	part-Comp.	Nuclear	0.426	
	chemo-typy	Cytoplasmic	0.818	
	Neighboring	Nuclear	0.288	
Combined SVM classifier:				
		Extracellular	0.030	
		PlasmaMembrane	0.192	
		Cytoplasmic	1.805	*
		Cytoskeletal	0.029	
		ER	0.054	
		Golgi	0.039	
		Lysosomal		0.010
		Mitochondrial	0.676	
		Chloroplast	1.031	
		Peroxisomal	0.110	
		Vacuole	0.023	
		Nuclear	1.003	

SeqID: li LinJ_22_0140_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Extracellular	0.697	
	Di-peptide	Mitochondrial	0.492	
	part-Comp.	Nuclear	0.817	
	chemo-typy	Nuclear	0.361	
	Neighboring	Nuclear	0.763	
Combined SVM classifier:				
		Extracellular	0.815	
		PlasmaMembrane	0.027	
		Cytoplasmic	0.757	
		Cytoskeletal	0.015	
		ER	0.015	
		Golgi	0.009	

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Lysosomal	0.012
	Mitochondrial	0.889
	Chloroplast	0.166
	Peroxisomal	0.011
	Vacuole	0.008
	Nuclear	2.275 *

SeqID: li LinJ_09_1190_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	PlasmaMembrane	0.386
Di-peptide	Mitochondrial	0.517
part-Comp.	PlasmaMembrane	0.561
chemo-typy	PlasmaMembrane	0.693
Neighboring	Mitochondrial	0.358
Combined SVM classifier:		
	Extracellular	0.142
	PlasmaMembrane	2.258 *
	Cytoplasmic	0.262
	Cytoskeletal	0.013
	ER	0.036
	Golgi	0.013
	Lysosomal	0.033
	Mitochondrial	1.386
	Chloroplast	0.565
	Peroxisomal	0.107
	Vacuole	0.051
	Nuclear	0.133

SeqID: li LinJ_34_4150_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Mitochondrial	0.319
Di-peptide	Mitochondrial	0.461
part-Comp.	Mitochondrial	0.445
chemo-typy	Mitochondrial	0.463
Neighboring	Mitochondrial	0.447
Combined SVM classifier:		
	Extracellular	0.269
	PlasmaMembrane	0.186
	Cytoplasmic	0.696
	Cytoskeletal	0.021
	ER	0.020
	Golgi	0.012
	Lysosomal	0.029
	Mitochondrial	2.135 *
	Chloroplast	0.651
	Peroxisomal	0.080
	Vacuole	0.021
	Nuclear	0.881

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

SeqID: li LinJ_21_0930_mRNA			
CELLO prediction:			
	(predictor	location	reliable-index)
	Composition	Nuclear	0.528
	Di-peptide	Mitochondrial	0.367
	part-Comp.	Nuclear	0.799
	chemo-typy	Nuclear	0.782
	Neighboring	Extracellular	0.353
Combined SVM classifier:			
		Extracellular	0.868
		PlasmaMembrane	0.012
		Cytoplasmic	0.352
		Cytoskeletal	0.011
		ER	0.013
		Golgi	0.006
		Lysosomal	0.038
		Mitochondrial	0.861
		Chloroplast	0.034
		Peroxisomal	0.054
		Vacuole	0.037
		Nuclear	2.713 *

SeqID: li LinJ_13_1120_mRNA			
CELLO prediction:			
	(predictor	location	reliable-index)
	Composition	Mitochondrial	0.611
	Di-peptide	Mitochondrial	0.540
	part-Comp.	Cytoplasmic	0.545
	chemo-typy	Mitochondrial	0.676
	Neighboring	Cytoplasmic	0.496
Combined SVM classifier:			
		Extracellular	0.039
		PlasmaMembrane	0.011
		Cytoplasmic	1.891 *
		Cytoskeletal	0.065
		ER	0.012
		Golgi	0.007
		Lysosomal	0.006
		Mitochondrial	2.489 *
		Chloroplast	0.130
		Peroxisomal	0.151
		Vacuole	0.007
		Nuclear	0.193

SeqID: li LinJ_36_1000_mRNA			
CELLO prediction:			
	(predictor	location	reliable-index)
	Composition	Nuclear	0.332
	Di-peptide	Mitochondrial	0.479
	part-Comp.	Cytoplasmic	0.485
	chemo-typy	Cytoplasmic	0.543

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Neighboring	Mitochondrial	0.400	
Combined SVM classifier:				
		Extracellular	0.086	
		PlasmaMembrane	0.020	
		Cytoplasmic	1.868	*
		Cytoskeletal	0.038	
		ER	0.016	
		Golgi	0.009	
		Lysosomal		0.008
		Mitochondrial	1.679	*
		Chloroplast	0.246	
		Peroxisomal	0.094	
		Vacuole	0.008	
		Nuclear	0.927	

SeqID: li LinJ_21_1320_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Cytoplasmic	0.434	
	Di-peptide	Cytoplasmic	0.455	
	part-Comp.	Nuclear	0.449	
	chemo-typy	Cytoplasmic	0.672	
	Neighboring	Mitochondrial	0.403	
Combined SVM classifier:				
		Extracellular	0.403	
		PlasmaMembrane	0.143	
		Cytoplasmic	2.199	*
		Cytoskeletal	0.010	
		ER	0.038	
		Golgi	0.028	
		Lysosomal		0.023
		Mitochondrial	0.779	
		Chloroplast	0.110	
		Peroxisomal	0.108	
		Vacuole	0.018	
		Nuclear	1.141	

SeqID: li LinJ_28_2280_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Cytoplasmic	0.300	
	Di-peptide	Mitochondrial	0.354	
	part-Comp.	Cytoplasmic	0.285	
	chemo-typy	Nuclear	0.279	
	Neighboring	Cytoplasmic	0.372	
Combined SVM classifier:				
		Extracellular	0.485	
		PlasmaMembrane	0.179	
		Cytoplasmic	1.390	*
		Cytoskeletal	0.017	
		ER	0.044	
		Golgi	0.021	

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Lysosomal	0.041
	Mitochondrial	1.290 *
	Chloroplast	0.788
	Peroxisomal	0.097
	Vacuole	0.038
	Nuclear	0.608

SeqID: li LinJ_21_2190_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Cytoplasmic	0.328
Di-peptide	Mitochondrial	0.514
part-Comp.	Nuclear	0.356
chemo-typy	Nuclear	0.533
Neighboring	Nuclear	0.285
Combined SVM classifier:		
	Extracellular	0.228
	PlasmaMembrane	0.075
	Cytoplasmic	0.717
	Cytoskeletal	0.014
	ER	0.014
	Golgi	0.008
	Lysosomal	0.019
	Mitochondrial	1.827 *
	Chloroplast	0.309
	Peroxisomal	0.065
	Vacuole	0.021
	Nuclear	1.703 *

SeqID: li LinJ_28_2940_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Extracellular	0.598
Di-peptide	Extracellular	0.640
part-Comp.	Cytoplasmic	0.347
chemo-typy	Chloroplast	0.524
Neighboring	Cytoplasmic	0.307
Combined SVM classifier:		
	Extracellular	1.645 *
	PlasmaMembrane	0.219
	Cytoplasmic	0.989
	Cytoskeletal	0.013
	ER	0.026
	Golgi	0.047
	Lysosomal	0.221
	Mitochondrial	0.414
	Chloroplast	0.877
	Peroxisomal	0.121
	Vacuole	0.079
	Nuclear	0.348

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

SeqID: li|LinJ_14_1350_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Cytoplasmic	0.662
Di-peptide	Cytoplasmic	0.472
part-Comp.	Nuclear	0.353
chemo-typy	Extracellular	0.363
Neighboring	Nuclear	0.440

Combined SVM classifier:

Extracellular	0.633
PlasmaMembrane	0.014
Cytoplasmic	1.534 *
Cytoskeletal	0.009
ER	0.042
Golgi	0.006
Lysosomal	0.009
Mitochondrial	0.756
Chloroplast	0.190
Peroxisomal	0.040
Vacuole	0.036
Nuclear	1.732 *

SeqID: li|LinJ_11_0960_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Nuclear	0.438
Di-peptide	Nuclear	0.599
part-Comp.	Mitochondrial	0.881
chemo-typy	Cytoplasmic	0.600
Neighboring	Mitochondrial	0.473

Combined SVM classifier:

Extracellular	0.024
PlasmaMembrane	0.011
Cytoplasmic	0.882
Cytoskeletal	0.015
ER	0.015
Golgi	0.007
Lysosomal	0.006
Mitochondrial	2.170 *
Chloroplast	0.413
Peroxisomal	0.052
Vacuole	0.007
Nuclear	1.397

SeqID: li|LinJ_28_2200_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Nuclear	0.577
Di-peptide	Nuclear	0.429
part-Comp.	Nuclear	0.877
chemo-typy	Cytoplasmic	0.682

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Neighboring	Cytoplasmic	0.446	
Combined SVM classifier:				
		Extracellular	0.225	
		PlasmaMembrane	0.027	
		Cytoplasmic	1.658	
		Cytoskeletal	0.030	
		ER	0.022	
		Golgi	0.144	
		Lysosomal		0.008
		Mitochondrial	0.156	
		Chloroplast	0.269	
		Peroxisomal	0.048	
		Vacuole	0.010	
		Nuclear	2.402	*

SeqID: li LinJ_34_4050_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Nuclear	0.688	
	Di-peptide	Cytoplasmic	0.521	
	part-Comp.	Mitochondrial	0.436	
	chemo-typy	Mitochondrial	0.516	
	Neighboring	Cytoplasmic	0.538	
Combined SVM classifier:				
		Extracellular	0.463	
		PlasmaMembrane	0.008	
		Cytoplasmic	1.363	*
		Cytoskeletal	0.022	
		ER	0.042	
		Golgi	0.007	
		Lysosomal		0.005
		Mitochondrial	1.449	*
		Chloroplast	0.024	
		Peroxisomal	0.043	
		Vacuole	0.005	
		Nuclear	1.568	*

SeqID: li LinJ_21_1990_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Nuclear	0.311	
	Di-peptide	Cytoplasmic	0.695	
	part-Comp.	Cytoplasmic	0.645	
	chemo-typy	Cytoplasmic	0.686	
	Neighboring	Cytoplasmic	0.437	
Combined SVM classifier:				
		Extracellular	0.168	
		PlasmaMembrane	0.191	
		Cytoplasmic	2.604	*
		Cytoskeletal	0.020	
		ER	0.058	
		Golgi	0.167	

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Lysosomal	0.011
	Mitochondrial	0.417
	Chloroplast	0.372
	Peroxisomal	0.102
	Vacuole	0.185
	Nuclear	0.705

SeqID: li LinJ_34_3620_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Extracellular	0.365
Di-peptide	Mitochondrial	0.510
part-Comp.	Mitochondrial	0.855
chemo-typy	Mitochondrial	0.495
Neighboring	Mitochondrial	0.673
Combined SVM classifier:		
	Extracellular	0.486
	PlasmaMembrane	0.075
	Cytoplasmic	0.205
	Cytoskeletal	0.008
	ER	0.009
	Golgi	0.005
	Lysosomal	0.013
	Mitochondrial	2.861 *
	Chloroplast	0.138
	Peroxisomal	0.087
	Vacuole	0.025
	Nuclear	1.088

SeqID: li LinJ_28_0730_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Cytoplasmic	0.372
Di-peptide	Cytoplasmic	0.597
part-Comp.	Cytoplasmic	0.862
chemo-typy	Cytoplasmic	0.564
Neighboring	Cytoplasmic	0.895
Combined SVM classifier:		
	Extracellular	0.345
	PlasmaMembrane	0.414
	Cytoplasmic	3.290 *
	Cytoskeletal	0.006
	ER	0.010
	Golgi	0.049
	Lysosomal	0.012
	Mitochondrial	0.113
	Chloroplast	0.063
	Peroxisomal	0.081
	Vacuole	0.011
	Nuclear	0.606

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

SeqID: li|LinJ_23_1470_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Extracellular	0.631
Di-peptide	Mitochondrial	0.753
part-Comp.	Nuclear	0.435
chemo-typy	Cytoplasmic	0.371
Neighboring	Mitochondrial	0.483

Combined SVM classifier:

Extracellular	0.748
PlasmaMembrane	0.046
Cytoplasmic	0.864
Cytoskeletal	0.026
ER	0.020
Golgi	0.024
Lysosomal	0.009
Mitochondrial	1.852 *
Chloroplast	0.387
Peroxisomal	0.031
Vacuole	0.024
Nuclear	0.968

SeqID: li|LinJ_35_0070_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Mitochondrial	0.816
Di-peptide	Mitochondrial	0.749
part-Comp.	Mitochondrial	0.505
chemo-typy	Chloroplast	0.913
Neighboring	Chloroplast	0.465

Combined SVM classifier:

Extracellular	0.028
PlasmaMembrane	0.191
Cytoplasmic	0.282
Cytoskeletal	0.020
ER	0.010
Golgi	0.022
Lysosomal	0.006
Mitochondrial	2.295 *
Chloroplast	1.701 *
Peroxisomal	0.358
Vacuole	0.028
Nuclear	0.057

SeqID: li|LinJ_19_0390_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Mitochondrial	0.584
Di-peptide	Nuclear	0.670
part-Comp.	Mitochondrial	0.932
chemo-typy	Nuclear	0.439

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Neighboring	Nuclear	0.823	
Combined SVM classifier:				
		Extracellular	0.152	
		PlasmaMembrane	0.036	
		Cytoplasmic	0.241	
		Cytoskeletal	0.013	
		ER	0.010	
		Golgi	0.010	
		Lysosomal		0.005
		Mitochondrial	2.068	*
		Chloroplast	0.231	
		Peroxisomal	0.022	
		Vacuole	0.006	
		Nuclear	2.206	*

SeqID: li LinJ_35_2270_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Nuclear	0.272	
	Di-peptide	Mitochondrial	0.515	
	part-Comp.	Nuclear	0.592	
	chemo-typy	Nuclear	0.406	
	Neighboring	Extracellular	0.301	
Combined SVM classifier:				
		Extracellular	0.680	
		PlasmaMembrane	0.068	
		Cytoplasmic	1.166	*
		Cytoskeletal	0.046	
		ER	0.029	
		Golgi	0.016	
		Lysosomal		0.011
		Mitochondrial	0.941	
		Chloroplast	0.263	
		Peroxisomal	0.041	
		Vacuole	0.019	
		Nuclear	1.721	*

SeqID: li LinJ_20_1020_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Nuclear	0.736	
	Di-peptide	Cytoplasmic	0.257	
	part-Comp.	Mitochondrial	0.560	
	chemo-typy	Cytoplasmic	0.354	
	Neighboring	Mitochondrial	0.396	
Combined SVM classifier:				
		Extracellular	0.315	
		PlasmaMembrane	0.198	
		Cytoplasmic	0.953	
		Cytoskeletal	0.019	
		ER	0.022	
		Golgi	0.024	

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Lysosomal	0.015
	Mitochondrial	1.623 *
	Chloroplast	0.267
	Peroxisomal	0.073
	Vacuole	0.012
	Nuclear	1.478 *

SeqID: li LinJ_32_2850_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Mitochondrial	0.693
Di-peptide	Mitochondrial	0.838
part-Comp.	Mitochondrial	0.299
chemo-typy	Mitochondrial	0.827
Neighboring	Mitochondrial	0.798
Combined SVM classifier:		
	Extracellular	0.095
	PlasmaMembrane	0.063
	Cytoplasmic	0.586
	Cytoskeletal	0.027
	ER	0.010
	Golgi	0.007
	Lysosomal	0.008
	Mitochondrial	3.454 *
	Chloroplast	0.117
	Peroxisomal	0.111
	Vacuole	0.012
	Nuclear	0.508

SeqID: li LinJ_34_3670_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Mitochondrial	0.749
Di-peptide	Mitochondrial	0.390
part-Comp.	Cytoplasmic	0.430
chemo-typy	Cytoplasmic	0.313
Neighboring	Cytoplasmic	0.311
Combined SVM classifier:		
	Extracellular	0.173
	PlasmaMembrane	0.072
	Cytoplasmic	1.263 *
	Cytoskeletal	0.015
	ER	0.070
	Golgi	0.020
	Lysosomal	0.006
	Mitochondrial	1.707 *
	Chloroplast	0.546
	Peroxisomal	0.045
	Vacuole	0.020
	Nuclear	1.062 *

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

SeqID: li|LinJ_33_0860_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Cytoplasmic	0.518
Di-peptide	Cytoplasmic	0.851
part-Comp.	Cytoplasmic	0.841
chemo-typy	Cytoplasmic	0.691
Neighboring	Cytoplasmic	0.814

Combined SVM classifier:

Extracellular	0.097	
PlasmaMembrane	0.180	
Cytoplasmic	3.714	*
Cytoskeletal	0.008	
ER	0.026	
Golgi	0.017	
Lysosomal		0.045
Mitochondrial	0.072	
Chloroplast	0.104	
Peroxisomal	0.031	
Vacuole	0.041	
Nuclear	0.664	

SeqID: li|LinJ_22_1280_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Cytoplasmic	0.363
Di-peptide	Cytoplasmic	0.616
part-Comp.	Chloroplast	0.628
chemo-typy	Cytoplasmic	0.499
Neighboring	Chloroplast	0.595

Combined SVM classifier:

Extracellular	0.086	
PlasmaMembrane	0.304	
Cytoplasmic	1.959	*
Cytoskeletal	0.009	
ER	0.038	
Golgi	0.022	
Lysosomal		0.040
Mitochondrial	0.310	
Chloroplast	1.809	*
Peroxisomal	0.056	
Vacuole	0.024	
Nuclear	0.343	

SeqID: li|LinJ_27_0180_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Nuclear	0.553
Di-peptide	Mitochondrial	0.507
part-Comp.	Nuclear	0.411
chemo-typy	Mitochondrial	0.515

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Neighboring	Mitochondrial	0.573	
Combined SVM classifier:				
		Extracellular	0.123	
		PlasmaMembrane	0.027	
		Cytoplasmic	0.555	
		Cytoskeletal	0.063	
		ER	0.022	
		Golgi	0.008	
		Lysosomal		0.011
		Mitochondrial	2.066	*
		Chloroplast	0.056	
		Peroxisomal	0.064	
		Vacuole	0.015	
		Nuclear	1.991	*

SeqID: li LinJ_03_0090_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Chloroplast	0.249	
	Di-peptide	Mitochondrial	0.375	
	part-Comp.	Nuclear	0.440	
	chemo-typy	Cytoplasmic	0.380	
	Neighboring	Mitochondrial	0.301	
Combined SVM classifier:				
		Extracellular	0.586	
		PlasmaMembrane	0.511	
		Cytoplasmic	0.826	
		Cytoskeletal	0.029	
		ER	0.070	
		Golgi	0.045	
		Lysosomal		0.038
		Mitochondrial	1.094	*
		Chloroplast	0.690	
		Peroxisomal	0.189	
		Vacuole	0.073	
		Nuclear	0.849	

SeqID: li LinJ_28_0680_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	PlasmaMembrane	0.975	
	Di-peptide	PlasmaMembrane	0.532	
	part-Comp.	PlasmaMembrane	0.393	
	chemo-typy	PlasmaMembrane	0.772	
	Neighboring	PlasmaMembrane	0.342	
Combined SVM classifier:				
		Extracellular	0.591	
		PlasmaMembrane	3.015	*
		Cytoplasmic	0.308	
		Cytoskeletal	0.010	
		ER	0.017	
		Golgi	0.014	

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Lysosomal	0.015
	Mitochondrial	0.342
	Chloroplast	0.369
	Peroxisomal	0.032
	Vacuole	0.008
	Nuclear	0.279

SeqID: li LinJ_26_1610_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Cytoplasmic	0.297
Di-peptide	Chloroplast	0.428
part-Comp.	Nuclear	0.938
chemo-typy	Nuclear	0.481
Neighboring	Nuclear	0.668
Combined SVM classifier:		
	Extracellular	0.061
	PlasmaMembrane	0.040
	Cytoplasmic	1.110
	Cytoskeletal	0.020
	ER	0.013
	Golgi	0.012
	Lysosomal	0.010
	Mitochondrial	0.489
	Chloroplast	0.688
	Peroxisomal	0.026
	Vacuole	0.018
	Nuclear	2.513 *

SeqID: li LinJ_36_3070_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Extracellular	0.945
Di-peptide	Extracellular	0.698
part-Comp.	Extracellular	0.343
chemo-typy	Nuclear	0.366
Neighboring	Extracellular	0.714
Combined SVM classifier:		
	Extracellular	2.728 *
	PlasmaMembrane	0.113
	Cytoplasmic	0.485
	Cytoskeletal	0.015
	ER	0.017
	Golgi	0.018
	Lysosomal	0.034
	Mitochondrial	0.404
	Chloroplast	0.253
	Peroxisomal	0.024
	Vacuole	0.015
	Nuclear	0.892

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

SeqID: li|LinJ_15_1010_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Mitochondrial	0.401
Di-peptide	Mitochondrial	0.599
part-Comp.	Mitochondrial	0.478
chemo-typy	Nuclear	0.432
Neighboring	Cytoplasmic	0.534

Combined SVM classifier:

Extracellular	0.032
PlasmaMembrane	0.089
Cytoplasmic	1.509 *
Cytoskeletal	0.014
ER	0.015
Golgi	0.014
Lysosomal	0.013
Mitochondrial	1.817 *
Chloroplast	0.352
Peroxisomal	0.154
Vacuole	0.014
Nuclear	0.977

SeqID: li|LinJ_30_0710_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Cytoplasmic	0.343
Di-peptide	Mitochondrial	0.441
part-Comp.	Nuclear	0.710
chemo-typy	Mitochondrial	0.432
Neighboring	Mitochondrial	0.396

Combined SVM classifier:

Extracellular	0.206
PlasmaMembrane	0.061
Cytoplasmic	0.980
Cytoskeletal	0.016
ER	0.017
Golgi	0.011
Lysosomal	0.011
Mitochondrial	1.504 *
Chloroplast	0.168
Peroxisomal	0.028
Vacuole	0.014
Nuclear	1.983 *

SeqID: li|LinJ_25_1050_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	PlasmaMembrane	0.643
Di-peptide	PlasmaMembrane	0.569
part-Comp.	PlasmaMembrane	0.402
chemo-typy	PlasmaMembrane	0.506

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Neighboring	Nuclear	0.243	
Combined SVM classifier:				
		Extracellular	0.517	
		PlasmaMembrane	2.210	*
		Cytoplasmic	0.426	
		Cytoskeletal	0.017	
		ER	0.024	
		Golgi	0.018	
		Lysosomal		0.023
		Mitochondrial	0.568	
		Chloroplast	0.360	
		Peroxisomal	0.040	
		Vacuole	0.023	
		Nuclear	0.776	

SeqID: li LinJ_05_0030_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Lysosomal		0.273
	Di-peptide	Extracellular	0.380	
	part-Comp.	Lysosomal		0.375
	chemo-typy	Cytoplasmic	0.362	
	Neighboring	Lysosomal		0.219
Combined SVM classifier:				
		Extracellular	0.911	
		PlasmaMembrane	0.095	
		Cytoplasmic	0.864	
		Cytoskeletal	0.013	
		ER	0.247	
		Golgi	0.040	
		Lysosomal		0.892
		Mitochondrial	0.942	*
		Chloroplast	0.595	
		Peroxisomal	0.121	
		Vacuole	0.072	
		Nuclear	0.208	

SeqID: li LinJ_18_1180_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Mitochondrial	0.296	
	Di-peptide	Extracellular	0.566	
	part-Comp.	PlasmaMembrane	0.465	
	chemo-typy	Extracellular	0.730	
	Neighboring	Mitochondrial	0.572	
Combined SVM classifier:				
		Extracellular	1.513	*
		PlasmaMembrane	0.660	
		Cytoplasmic	1.036	*
		Cytoskeletal	0.047	
		ER	0.051	
		Golgi	0.019	

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Lysosomal	0.055
	Mitochondrial	0.966
	Chloroplast	0.234
	Peroxisomal	0.114
	Vacuole	0.083
	Nuclear	0.222

SeqID: li LinJ_22_0340_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Mitochondrial	0.636
Di-peptide	Mitochondrial	0.711
part-Comp.	Cytoplasmic	0.428
chemo-typy	Nuclear	0.849
Neighboring	Mitochondrial	0.605
Combined SVM classifier:		
	Extracellular	0.058
	PlasmaMembrane	0.025
	Cytoplasmic	1.210
	Cytoskeletal	0.019
	ER	0.019
	Golgi	0.009
	Lysosomal	0.009
	Mitochondrial	2.167 *
	Chloroplast	0.115
	Peroxisomal	0.068
	Vacuole	0.007
	Nuclear	1.296

SeqID: li LinJ_13_1530_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Cytoplasmic	0.380
Di-peptide	Cytoplasmic	0.819
part-Comp.	Nuclear	0.643
chemo-typy	Cytoplasmic	0.691
Neighboring	Cytoplasmic	0.636
Combined SVM classifier:		
	Extracellular	0.193
	PlasmaMembrane	0.021
	Cytoplasmic	2.797 *
	Cytoskeletal	0.012
	ER	0.151
	Golgi	0.023
	Lysosomal	0.012
	Mitochondrial	0.404
	Chloroplast	0.179
	Peroxisomal	0.045
	Vacuole	0.036
	Nuclear	1.126

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

SeqID: li|LinJ_35_3810_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Mitochondrial	0.519
Di-peptide	Nuclear	0.820
part-Comp.	Mitochondrial	0.319
chemo-typy	Nuclear	0.991
Neighboring	Mitochondrial	0.757

Combined SVM classifier:

Extracellular	0.051
PlasmaMembrane	0.013
Cytoplasmic	0.755
Cytoskeletal	0.010
ER	0.013
Golgi	0.007
Lysosomal	0.016
Mitochondrial	1.691 *
Chloroplast	0.057
Peroxisomal	0.080
Vacuole	0.013
Nuclear	2.293 *

SeqID: li|LinJ_25_0670_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Mitochondrial	0.287
Di-peptide	Mitochondrial	0.617
part-Comp.	Mitochondrial	0.385
chemo-typy	Mitochondrial	0.571
Neighboring	Extracellular	0.844

Combined SVM classifier:

Extracellular	1.187
PlasmaMembrane	0.402
Cytoplasmic	0.126
Cytoskeletal	0.011
ER	0.054
Golgi	0.009
Lysosomal	0.079
Mitochondrial	1.921 *
Chloroplast	0.471
Peroxisomal	0.068
Vacuole	0.036
Nuclear	0.637

SeqID: li|LinJ_22_0004_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Cytoplasmic	0.578
Di-peptide	Cytoplasmic	0.851
part-Comp.	Cytoplasmic	0.668
chemo-typy	Nuclear	0.685

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Neighboring	Cytoplasmic	0.538	
Combined SVM classifier:				
		Extracellular	0.035	
		PlasmaMembrane	0.016	
		Cytoplasmic	2.909 *	
		Cytoskeletal	0.017	
		ER	0.023	
		Golgi	0.010	
		Lysosomal		0.006
		Mitochondrial	0.364	
		Chloroplast	0.126	
		Peroxisomal	0.037	
		Vacuole	0.007	
		Nuclear	1.452	

SeqID: li LinJ_30_2000_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Cytoplasmic	0.378	
	Di-peptide	Cytoplasmic	0.624	
	part-Comp.	Nuclear	0.407	
	chemo-typy	Cytoplasmic	0.479	
	Neighboring	Cytoplasmic	0.466	
Combined SVM classifier:				
		Extracellular	0.431	
		PlasmaMembrane	0.063	
		Cytoplasmic	2.150 *	
		Cytoskeletal	0.274	
		ER	0.020	
		Golgi	0.070	
		Lysosomal		0.010
		Mitochondrial	0.435	
		Chloroplast	0.378	
		Peroxisomal	0.038	
		Vacuole	0.020	
		Nuclear	1.111	

SeqID: li LinJ_22_0440_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Cytoplasmic	0.428	
	Di-peptide	Cytoplasmic	0.831	
	part-Comp.	Cytoplasmic	0.639	
	chemo-typy	Cytoplasmic	0.889	
	Neighboring	Cytoplasmic	0.536	
Combined SVM classifier:				
		Extracellular	0.015	
		PlasmaMembrane	0.011	
		Cytoplasmic	3.324 *	
		Cytoskeletal	0.020	
		ER	0.014	
		Golgi	0.012	

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Lysosomal	0.004
	Mitochondrial	0.626
	Chloroplast	0.176
	Peroxisomal	0.030
	Vacuole	0.005
	Nuclear	0.763

SeqID: li LinJ_34_2160_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Cytoplasmic	0.463
Di-peptide	Nuclear	0.937
part-Comp.	Nuclear	0.390
chemo-typy	Cytoplasmic	0.693
Neighboring	Nuclear	0.285
Combined SVM classifier:		
	Extracellular	0.142
	PlasmaMembrane	0.031
	Cytoplasmic	1.758 *
	Cytoskeletal	0.070
	ER	0.053
	Golgi	0.038
	Lysosomal	0.007
	Mitochondrial	0.449
	Chloroplast	0.377
	Peroxisomal	0.032
	Vacuole	0.052
	Nuclear	1.991 *

SeqID: li LinJ_06_0010_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Cytoplasmic	0.557
Di-peptide	Nuclear	0.808
part-Comp.	Nuclear	0.567
chemo-typy	Nuclear	0.793
Neighboring	Nuclear	0.511
Combined SVM classifier:		
	Extracellular	0.113
	PlasmaMembrane	0.036
	Cytoplasmic	0.889
	Cytoskeletal	0.013
	ER	0.013
	Golgi	0.008
	Lysosomal	0.008
	Mitochondrial	0.798
	Chloroplast	0.263
	Peroxisomal	0.032
	Vacuole	0.015
	Nuclear	2.811 *

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

SeqID: li|LinJ_21_1790_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Mitochondrial	0.545
Di-peptide	Mitochondrial	0.540
part-Comp.	Mitochondrial	0.613
chemo-typy	Mitochondrial	0.784
Neighboring	Mitochondrial	0.445

Combined SVM classifier:

Extracellular	0.084
PlasmaMembrane	0.032
Cytoplasmic	0.907
Cytoskeletal	0.010
ER	0.017
Golgi	0.008
Lysosomal	0.008
Mitochondrial	2.927 *
Chloroplast	0.128
Peroxisomal	0.056
Vacuole	0.008
Nuclear	0.814

SeqID: li|LinJ_35_3720_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Mitochondrial	0.588
Di-peptide	Mitochondrial	0.713
part-Comp.	Cytoplasmic	0.456
chemo-typy	Cytoplasmic	0.587
Neighboring	Mitochondrial	0.652

Combined SVM classifier:

Extracellular	0.281
PlasmaMembrane	0.157
Cytoplasmic	1.651 *
Cytoskeletal	0.018
ER	0.037
Golgi	0.010
Lysosomal	0.101
Mitochondrial	2.015 *
Chloroplast	0.147
Peroxisomal	0.075
Vacuole	0.009
Nuclear	0.498

SeqID: li|LinJ_16_1390_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Mitochondrial	0.537
Di-peptide	Mitochondrial	0.499
part-Comp.	Mitochondrial	0.827
chemo-typy	Mitochondrial	0.472

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Neighboring	Mitochondrial	0.737	
Combined SVM classifier:				
		Extracellular	0.121	
		PlasmaMembrane	0.021	
		Cytoplasmic	0.914	
		Cytoskeletal	0.008	
		ER	0.026	
		Golgi	0.011	
		Lysosomal		0.009
		Mitochondrial	3.072	*
		Chloroplast	0.329	
		Peroxisomal	0.094	
		Vacuole	0.019	
		Nuclear	0.377	

SeqID: li LinJ_10_0050_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Mitochondrial	0.337	
	Di-peptide	Nuclear	0.724	
	part-Comp.	Mitochondrial	0.576	
	chemo-typy	Nuclear	0.753	
	Neighboring	Mitochondrial	0.368	
Combined SVM classifier:				
		Extracellular	0.137	
		PlasmaMembrane	0.054	
		Cytoplasmic	0.303	
		Cytoskeletal	0.017	
		ER	0.013	
		Golgi	0.008	
		Lysosomal		0.010
		Mitochondrial	1.701	*
		Chloroplast	0.429	
		Peroxisomal	0.045	
		Vacuole	0.016	
		Nuclear	2.267	*

SeqID: li LinJ_28_1050_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Cytoplasmic	0.374	
	Di-peptide	Chloroplast	0.328	
	part-Comp.	Cytoplasmic	0.854	
	chemo-typy	Cytoplasmic	0.824	
	Neighboring	Cytoplasmic	0.468	
Combined SVM classifier:				
		Extracellular	0.084	
		PlasmaMembrane	0.025	
		Cytoplasmic	2.736	*
		Cytoskeletal	0.013	
		ER	0.013	
		Golgi	0.008	

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Lysosomal	0.015
	Mitochondrial	0.746
	Chloroplast	0.682
	Peroxisomal	0.049
	Vacuole	0.022
	Nuclear	0.606

SeqID: li LinJ_13_0330_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Cytoplasmic	0.739
Di-peptide	Cytoplasmic	0.775
part-Comp.	Cytoplasmic	0.914
chemo-typy	Chloroplast	0.354
Neighboring	Cytoplasmic	0.367
Combined SVM classifier:		
	Extracellular	0.271
	PlasmaMembrane	0.107
	Cytoplasmic	3.114 *
	Cytoskeletal	0.008
	ER	0.066
	Golgi	0.024
	Lysosomal	0.046
	Mitochondrial	0.187
	Chloroplast	0.507
	Peroxisomal	0.137
	Vacuole	0.119
	Nuclear	0.415

SeqID: li LinJ_35_0140_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Mitochondrial	0.864
Di-peptide	Mitochondrial	0.919
part-Comp.	Mitochondrial	0.554
chemo-typy	Mitochondrial	0.865
Neighboring	Mitochondrial	0.468
Combined SVM classifier:		
	Extracellular	0.199
	PlasmaMembrane	0.490
	Cytoplasmic	0.185
	Cytoskeletal	0.022
	ER	0.016
	Golgi	0.008
	Lysosomal	0.038
	Mitochondrial	3.669 *
	Chloroplast	0.059
	Peroxisomal	0.062
	Vacuole	0.009
	Nuclear	0.242

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

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*****
*****
SeqID: li|LinJ_31_2350_mRNA|
      CELLO prediction:
              (predictor      location      reliable-index)
Composition      Cytoplasmic      0.409
Di-peptide       Mitochondrial    0.287
part-Comp.       Chloroplast      0.310
chemo-typy       Extracellular    0.404
Neighboring      Chloroplast      0.324

      Combined SVM classifier:
                                Extracellular  1.064  *
                                PlasmaMembrane 0.539
                                Cytoplasmic     0.924
                                Cytoskeletal     0.018
                                ER               0.124
                                Golgi            0.050
                                Lysosomal        0.105
                                Mitochondrial    0.768
                                Chloroplast      1.076  *
                                Peroxisomal      0.090
                                Vacuole          0.070
                                Nuclear           0.170

*****
*****
SeqID: li|LinJ_30_3240_mRNA|
      CELLO prediction:
              (predictor      location      reliable-index)
Composition      Cytoplasmic      0.266
Di-peptide       Mitochondrial    0.459
part-Comp.       Nuclear          0.551
chemo-typy       Nuclear          0.467
Neighboring      Mitochondrial    0.374

      Combined SVM classifier:
                                Extracellular  0.110
                                PlasmaMembrane 0.055
                                Cytoplasmic     0.846
                                Cytoskeletal     0.022
                                ER               0.017
                                Golgi            0.013
                                Lysosomal        0.015
                                Mitochondrial    1.634  *
                                Chloroplast      0.196
                                Peroxisomal      0.048
                                Vacuole          0.018
                                Nuclear           2.026  *

*****
*****
SeqID: li|LinJ_13_0450_mRNA|
      CELLO prediction:
              (predictor      location      reliable-index)
Composition      Mitochondrial    0.507
Di-peptide       Mitochondrial    0.796
part-Comp.       Mitochondrial    0.381
chemo-typy       Nuclear          0.549

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Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Neighboring	Mitochondrial	0.490	
Combined SVM classifier:				
		Extracellular	0.068	
		PlasmaMembrane	0.152	
		Cytoplasmic	0.659	
		Cytoskeletal	0.023	
		ER	0.022	
		Golgi	0.016	
		Lysosomal		0.015
		Mitochondrial	2.409	*
		Chloroplast	0.357	
		Peroxisomal	0.092	
		Vacuole	0.018	
		Nuclear	1.170	

SeqID: li LinJ_34_0460_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Nuclear	0.588	
	Di-peptide	Mitochondrial	0.430	
	part-Comp.	Nuclear	0.738	
	chemo-typy	Nuclear	0.361	
	Neighboring	Nuclear	0.385	
Combined SVM classifier:				
		Extracellular	0.318	
		PlasmaMembrane	0.111	
		Cytoplasmic	0.646	
		Cytoskeletal	0.014	
		ER	0.009	
		Golgi	0.010	
		Lysosomal		0.007
		Mitochondrial	1.129	
		Chloroplast	0.223	
		Peroxisomal	0.030	
		Vacuole	0.008	
		Nuclear	2.494	*

SeqID: li LinJ_08_0830_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Cytoplasmic	0.603	
	Di-peptide	Cytoplasmic	0.732	
	part-Comp.	Mitochondrial	0.438	
	chemo-typy	Cytoplasmic	0.596	
	Neighboring	Cytoplasmic	0.583	
Combined SVM classifier:				
		Extracellular	0.006	
		PlasmaMembrane	0.007	
		Cytoplasmic	2.768	*
		Cytoskeletal	0.011	
		ER	0.016	
		Golqi	0.014	

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Lysosomal	0.002
	Mitochondrial	1.270
	Chloroplast	0.230
	Peroxisomal	0.213
	Vacuole	0.004
	Nuclear	0.458

SeqID: li LinJ_28_2360_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Extracellular	0.372
Di-peptide	Mitochondrial	0.747
part-Comp.	Nuclear	0.664
chemo-typy	Nuclear	0.441
Neighboring	Nuclear	0.506
Combined SVM classifier:		
	Extracellular	0.598
	PlasmaMembrane	0.083
	Cytoplasmic	0.465
	Cytoskeletal	0.020
	ER	0.011
	Golgi	0.009
	Lysosomal	0.010
	Mitochondrial	1.698 *
	Chloroplast	0.155
	Peroxisomal	0.033
	Vacuole	0.010
	Nuclear	1.909 *

SeqID: li LinJ_31_1420_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Extracellular	0.735
Di-peptide	Nuclear	0.358
part-Comp.	Extracellular	0.396
chemo-typy	Mitochondrial	0.412
Neighboring	Extracellular	0.788
Combined SVM classifier:		
	Extracellular	2.308 *
	PlasmaMembrane	0.266
	Cytoplasmic	0.440
	Cytoskeletal	0.017
	ER	0.026
	Golgi	0.021
	Lysosomal	0.040
	Mitochondrial	0.653
	Chloroplast	0.260
	Peroxisomal	0.028
	Vacuole	0.017
	Nuclear	0.923

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

SeqID: li|LinJ_36_3020_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Cytoplasmic	0.609
Di-peptide	Mitochondrial	0.453
part-Comp.	Cytoplasmic	0.512
chemo-typy	Nuclear	0.843
Neighboring	Mitochondrial	0.550

Combined SVM classifier:

Extracellular	0.102
PlasmaMembrane	0.043
Cytoplasmic	1.625 *
Cytoskeletal	0.012
ER	0.024
Golgi	0.009
Lysosomal	0.010
Mitochondrial	1.484 *
Chloroplast	0.098
Peroxisomal	0.093
Vacuole	0.014
Nuclear	1.486 *

SeqID: li|LinJ_25_0740_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Nuclear	0.737
Di-peptide	Cytoplasmic	0.459
part-Comp.	Cytoplasmic	0.481
chemo-typy	Cytoplasmic	0.527
Neighboring	Nuclear	0.937

Combined SVM classifier:

Extracellular	0.104
PlasmaMembrane	0.027
Cytoplasmic	1.681
Cytoskeletal	0.012
ER	0.038
Golgi	0.176
Lysosomal	0.017
Mitochondrial	0.155
Chloroplast	0.290
Peroxisomal	0.046
Vacuole	0.024
Nuclear	2.431 *

SeqID: li|LinJ_26_2020_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Cytoplasmic	0.340
Di-peptide	Nuclear	0.705
part-Comp.	Nuclear	0.602
chemo-typy	Nuclear	0.794

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Neighboring	Nuclear	0.405	
Combined SVM classifier:				
		Extracellular	0.154	
		PlasmaMembrane	0.067	
		Cytoplasmic	0.813	
		Cytoskeletal	0.014	
		ER	0.017	
		Golgi	0.010	
		Lysosomal		0.012
		Mitochondrial	0.966	
		Chloroplast	0.137	
		Peroxisomal	0.029	
		Vacuole	0.013	
		Nuclear	2.768	*

SeqID: li LinJ_35_4570_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Extracellular	0.511	
	Di-peptide	Extracellular	0.419	
	part-Comp.	Extracellular	0.335	
	chemo-typy	Mitochondrial	0.476	
	Neighboring	Extracellular	0.739	
Combined SVM classifier:				
		Extracellular	2.028	*
		PlasmaMembrane	0.101	
		Cytoplasmic	0.719	
		Cytoskeletal	0.014	
		ER	0.021	
		Golgi	0.014	
		Lysosomal		0.022
		Mitochondrial	0.974	
		Chloroplast	0.262	
		Peroxisomal	0.025	
		Vacuole	0.009	
		Nuclear	0.810	

SeqID: li LinJ_36_3940_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Extracellular	0.507	
	Di-peptide	Nuclear	0.683	
	part-Comp.	Nuclear	0.422	
	chemo-typy	Nuclear	0.773	
	Neighboring	Nuclear	0.556	
Combined SVM classifier:				
		Extracellular	1.256	
		PlasmaMembrane	0.042	
		Cytoplasmic	0.460	
		Cytoskeletal	0.011	
		ER	0.018	
		Golgi	0.008	

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Lysosomal	0.030
	Mitochondrial	0.335
	Chloroplast	0.169
	Peroxisomal	0.025
	Vacuole	0.016
	Nuclear	2.631 *

SeqID: li LinJ_25_1350_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Nuclear	0.441
Di-peptide	Nuclear	0.408
part-Comp.	Nuclear	0.566
chemo-typy	Nuclear	0.362
Neighboring	Nuclear	0.693
Combined SVM classifier:		
	Extracellular	0.649
	PlasmaMembrane	0.083
	Cytoplasmic	0.577
	Cytoskeletal	0.019
	ER	0.021
	Golgi	0.018
	Lysosomal	0.024
	Mitochondrial	0.909
	Chloroplast	0.201
	Peroxisomal	0.020
	Vacuole	0.010
	Nuclear	2.470 *

SeqID: li LinJ_28_0870_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Extracellular	0.516
Di-peptide	Nuclear	0.556
part-Comp.	Extracellular	0.351
chemo-typy	Extracellular	0.465
Neighboring	Extracellular	0.525
Combined SVM classifier:		
	Extracellular	1.986 *
	PlasmaMembrane	0.186
	Cytoplasmic	0.758
	Cytoskeletal	0.015
	ER	0.036
	Golgi	0.038
	Lysosomal	0.058
	Mitochondrial	0.263
	Chloroplast	0.317
	Peroxisomal	0.041
	Vacuole	0.043
	Nuclear	1.260

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

SeqID: li|LinJ_30_3270_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Mitochondrial	0.509
Di-peptide	Mitochondrial	0.739
part-Comp.	PlasmaMembrane	0.547
chemo-typy	Mitochondrial	0.721
Neighboring	Extracellular	0.329

Combined SVM classifier:

Extracellular	0.458
PlasmaMembrane	0.769
Cytoplasmic	0.603
Cytoskeletal	0.016
ER	0.035
Golgi	0.010
Lysosomal	0.037
Mitochondrial	2.236 *
Chloroplast	0.521
Peroxisomal	0.077
Vacuole	0.018
Nuclear	0.220

SeqID: li|LinJ_04_0950_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Nuclear	0.318
Di-peptide	Cytoplasmic	0.404
part-Comp.	Cytoplasmic	0.469
chemo-typy	Cytoplasmic	0.414
Neighboring	Mitochondrial	0.431

Combined SVM classifier:

Extracellular	0.045
PlasmaMembrane	0.025
Cytoplasmic	1.963 *
Cytoskeletal	0.037
ER	0.008
Golgi	0.008
Lysosomal	0.009
Mitochondrial	1.718 *
Chloroplast	0.126
Peroxisomal	0.066
Vacuole	0.008
Nuclear	0.989

SeqID: li|LinJ_34_3470_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Mitochondrial	0.899
Di-peptide	Mitochondrial	0.833
part-Comp.	Mitochondrial	0.759
chemo-typy	Mitochondrial	0.422

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Neighboring	Mitochondrial	0.893	
Combined SVM classifier:				
		Extracellular	0.151	
		PlasmaMembrane	0.015	
		Cytoplasmic	0.509	
		Cytoskeletal	0.007	
		ER	0.016	
		Golgi	0.004	
		Lysosomal		0.110
		Mitochondrial	3.806 *	
		Chloroplast	0.195	
		Peroxisomal	0.078	
		Vacuole	0.005	
		Nuclear	0.104	

SeqID: li LinJ_01_0150_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Mitochondrial	0.833	
	Di-peptide	Mitochondrial	0.710	
	part-Comp.	Mitochondrial	0.588	
	chemo-typy	Extracellular	0.300	
	Neighboring	Nuclear	0.655	
Combined SVM classifier:				
		Extracellular	0.593	
		PlasmaMembrane	0.102	
		Cytoplasmic	0.235	
		Cytoskeletal	0.045	
		ER	0.015	
		Golgi	0.023	
		Lysosomal		0.022
		Mitochondrial	2.539 *	
		Chloroplast	0.106	
		Peroxisomal	0.055	
		Vacuole	0.009	
		Nuclear	1.256	

SeqID: li LinJ_07_0160_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Extracellular	0.521	
	Di-peptide	Extracellular	0.512	
	part-Comp.	Extracellular	0.618	
	chemo-typy	Mitochondrial	0.429	
	Neighboring	Extracellular	0.395	
Combined SVM classifier:				
		Extracellular	2.157 *	
		PlasmaMembrane	0.083	
		Cytoplasmic	0.275	
		Cytoskeletal	0.010	
		ER	0.059	
		Golgi	0.007	

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Lysosomal	0.193
	Mitochondrial	1.607 *
	Chloroplast	0.054
	Peroxisomal	0.115
	Vacuole	0.018
	Nuclear	0.423

SeqID: li LinJ_11_1200_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Nuclear	0.853
Di-peptide	Extracellular	0.411
part-Comp.	Nuclear	0.564
chemo-typy	Cytoplasmic	0.711
Neighboring	Cytoplasmic	0.402
Combined SVM classifier:		
	Extracellular	0.631
	PlasmaMembrane	0.052
	Cytoplasmic	1.799 *
	Cytoskeletal	0.044
	ER	0.019
	Golgi	0.288
	Lysosomal	0.005
	Mitochondrial	0.068
	Chloroplast	0.138
	Peroxisomal	0.020
	Vacuole	0.005
	Nuclear	1.933 *

SeqID: li LinJ_35_1670_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Cytoplasmic	0.702
Di-peptide	Nuclear	0.801
part-Comp.	Mitochondrial	0.542
chemo-typy	Nuclear	0.481
Neighboring	Nuclear	0.641
Combined SVM classifier:		
	Extracellular	0.036
	PlasmaMembrane	0.023
	Cytoplasmic	1.045
	Cytoskeletal	0.013
	ER	0.009
	Golgi	0.007
	Lysosomal	0.005
	Mitochondrial	1.283
	Chloroplast	0.464
	Peroxisomal	0.022
	Vacuole	0.006
	Nuclear	2.087 *

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

SeqID: li|LinJ_28_2040_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Extracellular	0.277
Di-peptide	Nuclear	0.726
part-Comp.	Mitochondrial	0.428
chemo-typy	Cytoplasmic	0.331
Neighboring	Nuclear	0.408

Combined SVM classifier:

Extracellular	0.484
PlasmaMembrane	0.061
Cytoplasmic	0.996
Cytoskeletal	0.044
ER	0.015
Golgi	0.015
Lysosomal	0.011
Mitochondrial	1.025
Chloroplast	0.381
Peroxisomal	0.051
Vacuole	0.017
Nuclear	1.901 *

SeqID: li|LinJ_25_2590_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Chloroplast	0.473
Di-peptide	Cytoplasmic	0.414
part-Comp.	Cytoplasmic	0.694
chemo-typy	Chloroplast	0.621
Neighboring	Chloroplast	0.519

Combined SVM classifier:

Extracellular	0.301
PlasmaMembrane	0.057
Cytoplasmic	1.839 *
Cytoskeletal	0.020
ER	0.035
Golgi	0.115
Lysosomal	0.009
Mitochondrial	0.356
Chloroplast	1.841 *
Peroxisomal	0.224
Vacuole	0.037
Nuclear	0.165

SeqID: li|LinJ_27_0620_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	PlasmaMembrane	0.390
Di-peptide	Extracellular	0.176
part-Comp.	Golgi	0.832
chemo-typy	Cytoplasmic	0.419

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Neighboring	Golgi	0.230	
Combined SVM classifier:				
		Extracellular	0.410	
		PlasmaMembrane	0.601	
		Cytoplasmic	0.816	
		Cytoskeletal	0.020	
		ER	0.068	
		Golgi	1.494 *	
		Lysosomal		0.026
		Mitochondrial	0.404	
		Chloroplast	0.362	
		Peroxisomal	0.062	
		Vacuole	0.060	
		Nuclear	0.677	

SeqID: li LinJ_35_3990_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Mitochondrial	0.712	
	Di-peptide	Cytoplasmic	0.436	
	part-Comp.	Mitochondrial	0.509	
	chemo-typy	Mitochondrial	0.351	
	Neighboring	Cytoplasmic	0.517	
Combined SVM classifier:				
		Extracellular	0.047	
		PlasmaMembrane	0.020	
		Cytoplasmic	1.727 *	
		Cytoskeletal	0.034	
		ER	0.040	
		Golgi	0.010	
		Lysosomal		0.015
		Mitochondrial	2.160 *	
		Chloroplast	0.063	
		Peroxisomal	0.175	
		Vacuole	0.010	
		Nuclear	0.699	

SeqID: li LinJ_28_0210_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Cytoplasmic	0.546	
	Di-peptide	Nuclear	0.905	
	part-Comp.	Nuclear	0.860	
	chemo-typy	Nuclear	0.823	
	Neighboring	Mitochondrial	0.455	
Combined SVM classifier:				
		Extracellular	0.041	
		PlasmaMembrane	0.031	
		Cytoplasmic	0.682	
		Cytoskeletal	0.014	
		ER	0.010	
		Golgi	0.002	

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Lysosomal	0.003
	Mitochondrial	0.763
	Chloroplast	0.041
	Peroxisomal	0.047
	Vacuole	0.003
	Nuclear	3.363 *

SeqID: li LinJ_34_3720_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Nuclear	0.653
Di-peptide	Mitochondrial	0.331
part-Comp.	Nuclear	0.343
chemo-typy	Nuclear	0.491
Neighboring	Nuclear	0.691
Combined SVM classifier:		
	Extracellular	0.652
	PlasmaMembrane	0.059
	Cytoplasmic	0.562
	Cytoskeletal	0.046
	ER	0.022
	Golgi	0.016
	Lysosomal	0.012
	Mitochondrial	0.878
	Chloroplast	0.222
	Peroxisomal	0.029
	Vacuole	0.020
	Nuclear	2.481 *

SeqID: li LinJ_09_0030_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Mitochondrial	0.532
Di-peptide	Mitochondrial	0.786
part-Comp.	Mitochondrial	0.517
chemo-typy	Nuclear	0.384
Neighboring	Chloroplast	0.318
Combined SVM classifier:		
	Extracellular	0.310
	PlasmaMembrane	0.376
	Cytoplasmic	0.414
	Cytoskeletal	0.017
	ER	0.056
	Golgi	0.011
	Lysosomal	0.049
	Mitochondrial	2.366 *
	Chloroplast	0.626
	Peroxisomal	0.097
	Vacuole	0.019
	Nuclear	0.660

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

SeqID: li|LinJ_35_1540_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Chloroplast	0.596
Di-peptide	Nuclear	0.613
part-Comp.	Mitochondrial	0.530
chemo-typy	Cytoplasmic	0.608
Neighboring	Cytoplasmic	0.358

Combined SVM classifier:

Extracellular	0.087
PlasmaMembrane	0.099
Cytoplasmic	1.308 *
Cytoskeletal	0.013
ER	0.027
Golgi	0.015
Lysosomal	0.011
Mitochondrial	1.216 *
Chloroplast	1.157 *
Peroxisomal	0.180
Vacuole	0.019
Nuclear	0.867

SeqID: li|LinJ_08_1290_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Cytoplasmic	0.501
Di-peptide	Cytoplasmic	0.827
part-Comp.	Cytoplasmic	0.833
chemo-typy	Cytoplasmic	0.673
Neighboring	Cytoplasmic	0.808

Combined SVM classifier:

Extracellular	0.113
PlasmaMembrane	0.177
Cytoplasmic	3.642 *
Cytoskeletal	0.008
ER	0.024
Golgi	0.020
Lysosomal	0.050
Mitochondrial	0.074
Chloroplast	0.108
Peroxisomal	0.036
Vacuole	0.043
Nuclear	0.705

SeqID: li|LinJ_34_0900_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	PlasmaMembrane	0.943
Di-peptide	PlasmaMembrane	0.811
part-Comp.	PlasmaMembrane	0.390
chemo-typy	Extracellular	0.384

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Neighboring	Cytoplasmic	0.732	
Combined SVM classifier:				
		Extracellular	0.435	
		PlasmaMembrane	2.226	*
		Cytoplasmic	1.341	
		Cytoskeletal	0.005	
		ER	0.025	
		Golgi	0.019	
		Lysosomal		0.020
		Mitochondrial	0.125	
		Chloroplast	0.213	
		Peroxisomal	0.062	
		Vacuole	0.021	
		Nuclear	0.508	

SeqID: li LinJ_36_1690_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Nuclear	0.538	
	Di-peptide	Nuclear	0.499	
	part-Comp.	Extracellular	0.781	
	chemo-typy	Nuclear	0.658	
	Neighboring	Extracellular	0.623	
Combined SVM classifier:				
		Extracellular	2.009	*
		PlasmaMembrane	0.094	
		Cytoplasmic	0.263	
		Cytoskeletal	0.014	
		ER	0.016	
		Golgi	0.008	
		Lysosomal		0.041
		Mitochondrial	0.245	
		Chloroplast	0.076	
		Peroxisomal	0.014	
		Vacuole	0.012	
		Nuclear	2.207	*

SeqID: li LinJ_35_5420_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Nuclear	0.509	
	Di-peptide	Nuclear	0.863	
	part-Comp.	Nuclear	0.637	
	chemo-typy	Nuclear	0.840	
	Neighboring	Nuclear	0.487	
Combined SVM classifier:				
		Extracellular	0.440	
		PlasmaMembrane	0.087	
		Cytoplasmic	0.367	
		Cytoskeletal	0.013	
		ER	0.014	
		Golgi	0.008	

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Lysosomal	0.011
	Mitochondrial	0.517
	Chloroplast	0.170
	Peroxisomal	0.024
	Vacuole	0.013
	Nuclear	3.336 *

SeqID: li LinJ_35_3060_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Cytoplasmic	0.596
Di-peptide	Cytoplasmic	0.630
part-Comp.	Cytoplasmic	0.715
chemo-typy	Mitochondrial	0.411
Neighboring	Cytoplasmic	0.538
Combined SVM classifier:		
	Extracellular	0.313
	PlasmaMembrane	0.043
	Cytoplasmic	2.681 *
	Cytoskeletal	0.011
	ER	0.197
	Golgi	0.086
	Lysosomal	0.020
	Mitochondrial	0.785
	Chloroplast	0.508
	Peroxisomal	0.034
	Vacuole	0.026
	Nuclear	0.296

SeqID: li LinJ_25_1460_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Cytoplasmic	0.551
Di-peptide	Cytoplasmic	0.644
part-Comp.	Cytoplasmic	0.353
chemo-typy	Nuclear	0.537
Neighboring	Cytoplasmic	0.803
Combined SVM classifier:		
	Extracellular	0.171
	PlasmaMembrane	0.214
	Cytoplasmic	2.506 *
	Cytoskeletal	0.019
	ER	0.056
	Golgi	0.023
	Lysosomal	0.034
	Mitochondrial	0.259
	Chloroplast	0.715
	Peroxisomal	0.115
	Vacuole	0.028
	Nuclear	0.860

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

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*****
*****
SeqID: li|LinJ_31_1930_mRNA|
      CELLO prediction:
              (predictor      location      reliable-index)
Composition      Mitochondrial    0.496
Di-peptide       Nuclear          0.421
part-Comp.       Nuclear          0.591
chemo-typy       Nuclear          0.646
Neighboring      Extracellular    0.506

      Combined SVM classifier:
                                Extracellular    0.609
                                PlasmaMembrane    0.010
                                Cytoplasmic        0.958
                                Cytoskeletal       0.012
                                ER                  0.009
                                Golgi              0.005
                                Lysosomal          0.004
                                Mitochondrial      0.936
                                Chloroplast        0.152
                                Peroxisomal        0.040
                                Vacuole            0.004
                                Nuclear             2.262 *

*****
*****
SeqID: li|LinJ_30_3710_mRNA|
      CELLO prediction:
              (predictor      location      reliable-index)
Composition      Mitochondrial    0.400
Di-peptide       Mitochondrial    0.935
part-Comp.       Mitochondrial    0.814
chemo-typy       Nuclear          0.914
Neighboring      Mitochondrial    0.610

      Combined SVM classifier:
                                Extracellular    0.067
                                PlasmaMembrane    0.033
                                Cytoplasmic        0.532
                                Cytoskeletal       0.026
                                ER                  0.014
                                Golgi              0.010
                                Lysosomal          0.013
                                Mitochondrial      2.825 *
                                Chloroplast        0.077
                                Peroxisomal        0.075
                                Vacuole            0.015
                                Nuclear             1.312

*****
*****
SeqID: li|LinJ_14_0530_mRNA|
      CELLO prediction:
              (predictor      location      reliable-index)
Composition      Chloroplast      0.279
Di-peptide       Mitochondrial    0.384
part-Comp.       Cytoplasmic      0.414
chemo-typy       Nuclear          0.365

```

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

NeighboringMitochondrial0.390

Combined SVM classifier:

Extracellular0.443

PlasmaMembrane0.047

Cytoplasmic1.151 *

Cytoskeletal0.037

ER0.036

Golgi0.029

Lysosomal0.013

Mitochondrial1.219 *

Chloroplast0.733

Peroxisomal0.058

Vacuole0.105

Nuclear1.128 *

SeqID: li|LinJ_24_0730_mRNA|

CELLO prediction:

(predictorlocationreliable-index)

CompositionNuclear0.511

Di-peptideMitochondrial0.379

part-Comp.Nuclear0.504

chemo-typyMitochondrial0.463

NeighboringNuclear0.385

Combined SVM classifier:

Extracellular0.617

PlasmaMembrane0.123

Cytoplasmic0.785

Cytoskeletal0.041

ER0.027

Golgi0.020

Lysosomal0.027

Mitochondrial1.102 *

Chloroplast0.486

Peroxisomal0.071

Vacuole0.027

Nuclear1.675 *

SeqID: li|LinJ_20_1350_mRNA|

CELLO prediction:

(predictorlocationreliable-index)

CompositionCytoplasmic0.518

Di-peptideCytoplasmic0.291

part-Comp.Cytoplasmic0.550

chemo-typyNuclear0.604

NeighboringCytoplasmic0.602

Combined SVM classifier:

Extracellular0.288

PlasmaMembrane0.045

Cytoplasmic2.054 *

Cytoskeletal0.017

ER0.081

Golqi0.034

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Lysosomal	0.027
	Mitochondrial	0.273
	Chloroplast	0.525
	Peroxisomal	0.028
	Vacuole	0.038
	Nuclear	1.588 *

SeqID: li LinJ_15_1530_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Chloroplast	0.459
Di-peptide	Chloroplast	0.725
part-Comp.	Cytoplasmic	0.575
chemo-typy	Cytoplasmic	0.583
Neighboring	Nuclear	0.367
Combined SVM classifier:		
	Extracellular	0.493
	PlasmaMembrane	0.135
	Cytoplasmic	1.487 *
	Cytoskeletal	0.019
	ER	0.023
	Golgi	0.165
	Lysosomal	0.013
	Mitochondrial	0.346
	Chloroplast	1.564 *
	Peroxisomal	0.150
	Vacuole	0.013
	Nuclear	0.592

SeqID: li LinJ_34_0980_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Cytoplasmic	0.355
Di-peptide	Nuclear	0.312
part-Comp.	Mitochondrial	0.392
chemo-typy	Mitochondrial	0.520
Neighboring	Cytoplasmic	0.557
Combined SVM classifier:		
	Extracellular	0.349
	PlasmaMembrane	0.036
	Cytoplasmic	1.602 *
	Cytoskeletal	0.027
	ER	0.026
	Golgi	0.023
	Lysosomal	0.009
	Mitochondrial	1.633 *
	Chloroplast	0.236
	Peroxisomal	0.059
	Vacuole	0.023
	Nuclear	0.976

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

SeqID: li|LinJ_31_2650_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Extracellular	0.900
Di-peptide	Cytoplasmic	0.292
part-Comp.	Extracellular	0.780
chemo-typy	Cytoplasmic	0.421
Neighboring	Extracellular	0.520

Combined SVM classifier:

Extracellular	2.489	*
PlasmaMembrane	0.037	
Cytoplasmic	0.928	
Cytoskeletal	0.012	
ER	0.017	
Golgi	0.012	
Lysosomal		0.035
Mitochondrial	0.557	
Chloroplast	0.233	
Peroxisomal	0.028	
Vacuole	0.006	
Nuclear	0.646	

SeqID: li|LinJ_09_1130_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Cytoplasmic	0.691
Di-peptide	Mitochondrial	0.470
part-Comp.	Cytoplasmic	0.860
chemo-typy	Cytoplasmic	0.507
Neighboring	Nuclear	0.315

Combined SVM classifier:

Extracellular	0.078	
PlasmaMembrane	0.228	
Cytoplasmic	2.391	*
Cytoskeletal	0.009	
ER	0.019	
Golgi	0.065	
Lysosomal		0.027
Mitochondrial	0.835	
Chloroplast	0.471	
Peroxisomal	0.156	
Vacuole	0.016	
Nuclear	0.705	

SeqID: li|LinJ_04_0930_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Cytoplasmic	0.305
Di-peptide	Mitochondrial	0.445
part-Comp.	Nuclear	0.523
chemo-typy	Nuclear	0.558

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Neighboring	Nuclear	0.596	
Combined SVM classifier:				
		Extracellular	0.189	
		PlasmaMembrane	0.027	
		Cytoplasmic	1.243	
		Cytoskeletal	0.014	
		ER	0.010	
		Golgi	0.008	
		Lysosomal		0.007
		Mitochondrial	1.033	
		Chloroplast	0.388	
		Peroxisomal	0.019	
		Vacuole	0.006	
		Nuclear	2.056	*

SeqID: li LinJ_30_2760_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Nuclear	0.362	
	Di-peptide	Mitochondrial	0.380	
	part-Comp.	Nuclear	0.434	
	chemo-typy	Mitochondrial	0.457	
	Neighboring	Nuclear	0.372	
Combined SVM classifier:				
		Extracellular	0.482	
		PlasmaMembrane	0.115	
		Cytoplasmic	0.785	
		Cytoskeletal	0.022	
		ER	0.021	
		Golgi	0.012	
		Lysosomal		0.012
		Mitochondrial	1.284	*
		Chloroplast	0.378	
		Peroxisomal	0.028	
		Vacuole	0.015	
		Nuclear	1.845	*

SeqID: li LinJ_03_0940_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Mitochondrial	0.357	
	Di-peptide	Mitochondrial	0.351	
	part-Comp.	Extracellular	0.291	
	chemo-typy	Chloroplast	0.347	
	Neighboring	Extracellular	0.888	
Combined SVM classifier:				
		Extracellular	1.628	*
		PlasmaMembrane	0.401	
		Cytoplasmic	0.518	
		Cytoskeletal	0.018	
		ER	0.031	
		Golgi	0.032	

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Lysosomal	0.094
	Mitochondrial	1.155 *
	Chloroplast	0.666
	Peroxisomal	0.072
	Vacuole	0.015
	Nuclear	0.370

SeqID: li LinJ_05_0070_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	PlasmaMembrane	0.401
Di-peptide	Chloroplast	0.341
part-Comp.	Cytoplasmic	0.431
chemo-typy	Mitochondrial	0.370
Neighboring	Nuclear	0.510
Combined SVM classifier:		
	Extracellular	0.280
	PlasmaMembrane	0.559
	Cytoplasmic	1.395 *
	Cytoskeletal	0.015
	ER	0.028
	Golgi	0.042
	Lysosomal	0.038
	Mitochondrial	0.929
	Chloroplast	0.632
	Peroxisomal	0.047
	Vacuole	0.017
	Nuclear	1.018 *

SeqID: li LinJ_36_3530_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Mitochondrial	0.741
Di-peptide	Mitochondrial	0.450
part-Comp.	Mitochondrial	0.446
chemo-typy	Mitochondrial	0.645
Neighboring	Mitochondrial	0.458
Combined SVM classifier:		
	Extracellular	0.090
	PlasmaMembrane	0.015
	Cytoplasmic	0.439
	Cytoskeletal	0.040
	ER	0.008
	Golgi	0.022
	Lysosomal	0.006
	Mitochondrial	2.740 *
	Chloroplast	0.295
	Peroxisomal	0.030
	Vacuole	0.007
	Nuclear	1.307

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

SeqID: li|LinJ_27_1140_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Cytoplasmic	0.460
Di-peptide	Cytoplasmic	0.695
part-Comp.	Chloroplast	0.235
chemo-typy	Extracellular	0.314
Neighboring	Cytoplasmic	0.532

Combined SVM classifier:

Extracellular	0.956
PlasmaMembrane	0.260
Cytoplasmic	2.080 *
Cytoskeletal	0.019
ER	0.074
Golgi	0.045
Lysosomal	0.133
Mitochondrial	0.221
Chloroplast	0.558
Peroxisomal	0.307
Vacuole	0.076
Nuclear	0.269

SeqID: li|LinJ_21_2240_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Cytoplasmic	0.475
Di-peptide	Cytoplasmic	0.813
part-Comp.	Cytoplasmic	0.791
chemo-typy	Cytoplasmic	0.627
Neighboring	Cytoplasmic	0.785

Combined SVM classifier:

Extracellular	0.126
PlasmaMembrane	0.242
Cytoplasmic	3.491 *
Cytoskeletal	0.009
ER	0.028
Golgi	0.021
Lysosomal	0.054
Mitochondrial	0.082
Chloroplast	0.112
Peroxisomal	0.041
Vacuole	0.054
Nuclear	0.739

SeqID: li|LinJ_30_2860_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	PlasmaMembrane	0.444
Di-peptide	Extracellular	0.407
part-Comp.	Extracellular	0.471
chemo-typy	PlasmaMembrane	0.420

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

Neighboring	PlasmaMembrane	0.367	
Combined SVM classifier:			
	Extracellular	1.466	*
	PlasmaMembrane	1.621	*
	Cytoplasmic	0.098	
	Cytoskeletal	0.013	
	ER	0.036	
	Golgi	0.020	
	Lysosomal		0.068
	Mitochondrial	0.567	
	Chloroplast	0.667	
	Peroxisomal	0.042	
	Vacuole	0.017	
	Nuclear	0.384	

SeqID: li LinJ_11_0970_mRNA			
CELLO prediction:			
(predictor	location	reliable-index)	
Composition	Chloroplast	0.446	
Di-peptide	Nuclear	0.397	
part-Comp.	Mitochondrial	0.696	
chemo-typy	Mitochondrial	0.452	
Neighboring	Chloroplast	0.284	
Combined SVM classifier:			
	Extracellular	0.131	
	PlasmaMembrane	0.022	
	Cytoplasmic	0.852	
	Cytoskeletal	0.025	
	ER	0.035	
	Golgi	0.022	
	Lysosomal		0.019
	Mitochondrial	1.800	*
	Chloroplast	1.019	
	Peroxisomal	0.055	
	Vacuole	0.024	
	Nuclear	0.996	

SeqID: li LinJ_32_0930_mRNA			
CELLO prediction:			
(predictor	location	reliable-index)	
Composition	Mitochondrial	0.361	
Di-peptide	Mitochondrial	0.412	
part-Comp.	Nuclear	0.348	
chemo-typy	Cytoplasmic	0.362	
Neighboring	Nuclear	0.568	
Combined SVM classifier:			
	Extracellular	0.258	
	PlasmaMembrane	0.046	
	Cytoplasmic	0.947	
	Cytoskeletal	0.024	
	ER	0.034	
	Golgi	0.018	

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Lysosomal	0.027
	Mitochondrial	1.531 *
	Chloroplast	0.342
	Peroxisomal	0.163
	Vacuole	0.020
	Nuclear	1.591 *

SeqID: li LinJ_34_2080_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Nuclear	0.407
Di-peptide	Nuclear	0.441
part-Comp.	Extracellular	0.554
chemo-typy	Nuclear	0.463
Neighboring	Mitochondrial	0.333
Combined SVM classifier:		
	Extracellular	1.162 *
	PlasmaMembrane	0.042
	Cytoplasmic	0.405
	Cytoskeletal	0.012
	ER	0.016
	Golgi	0.007
	Lysosomal	0.011
	Mitochondrial	1.531 *
	Chloroplast	0.138
	Peroxisomal	0.036
	Vacuole	0.009
	Nuclear	1.630 *

SeqID: li LinJ_32_2860_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Extracellular	0.709
Di-peptide	Extracellular	0.390
part-Comp.	Extracellular	0.303
chemo-typy	Extracellular	0.483
Neighboring	Extracellular	0.323
Combined SVM classifier:		
	Extracellular	2.209 *
	PlasmaMembrane	0.410
	Cytoplasmic	0.770
	Cytoskeletal	0.015
	ER	0.040
	Golgi	0.140
	Lysosomal	0.051
	Mitochondrial	0.222
	Chloroplast	0.275
	Peroxisomal	0.106
	Vacuole	0.049
	Nuclear	0.713

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

SeqID: li|LinJ_35_1750_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	PlasmaMembrane	0.968
Di-peptide	Mitochondrial	0.666
part-Comp.	PlasmaMembrane	0.651
chemo-typy	PlasmaMembrane	0.408
Neighboring	PlasmaMembrane	0.463

Combined SVM classifier:

Extracellular	0.138	
PlasmaMembrane	2.545	*
Cytoplasmic	0.253	
Cytoskeletal	0.006	
ER	0.025	
Golgi	0.009	
Lysosomal		0.074
Mitochondrial	1.279	
Chloroplast	0.545	
Peroxisomal	0.026	
Vacuole	0.028	
Nuclear	0.071	

SeqID: li|LinJ_35_1380_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Extracellular	0.923
Di-peptide	Nuclear	0.386
part-Comp.	Mitochondrial	0.445
chemo-typy	Nuclear	0.424
Neighboring	Extracellular	0.927

Combined SVM classifier:

Extracellular	2.273	*
PlasmaMembrane	0.032	
Cytoplasmic	0.353	
Cytoskeletal	0.010	
ER	0.017	
Golgi	0.010	
Lysosomal		0.026
Mitochondrial	1.094	
Chloroplast	0.096	
Peroxisomal	0.040	
Vacuole	0.015	
Nuclear	1.032	

SeqID: li|LinJ_33_1430_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Mitochondrial	0.820
Di-peptide	Mitochondrial	0.610
part-Comp.	Nuclear	0.323
chemo-typy	Nuclear	0.422

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Neighboring	Mitochondrial	0.496	
Combined SVM classifier:				
		Extracellular	0.187	
		PlasmaMembrane	0.218	
		Cytoplasmic	0.917	
		Cytoskeletal	0.013	
		ER	0.031	
		Golgi	0.031	
		Lysosomal		0.027
		Mitochondrial	2.208	*
		Chloroplast	0.247	
		Peroxisomal	0.188	
		Vacuole	0.015	
		Nuclear	0.919	

SeqID: li LinJ_28_1120_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Mitochondrial	0.495	
	Di-peptide	Nuclear	0.604	
	part-Comp.	Mitochondrial	0.611	
	chemo-typy	Nuclear	0.361	
	Neighboring	Mitochondrial	0.521	
Combined SVM classifier:				
		Extracellular	0.164	
		PlasmaMembrane	0.049	
		Cytoplasmic	0.684	
		Cytoskeletal	0.013	
		ER	0.014	
		Golgi	0.014	
		Lysosomal		0.009
		Mitochondrial	1.952	*
		Chloroplast	0.469	
		Peroxisomal	0.069	
		Vacuole	0.007	
		Nuclear	1.556	*

SeqID: li LinJ_11_0570_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Extracellular	0.358	
	Di-peptide	Mitochondrial	0.687	
	part-Comp.	Mitochondrial	0.319	
	chemo-typy	Nuclear	0.643	
	Neighboring	Extracellular	0.639	
Combined SVM classifier:				
		Extracellular	1.123	*
		PlasmaMembrane	0.647	
		Cytoplasmic	0.276	
		Cytoskeletal	0.014	
		ER	0.144	
		Golgi	0.012	

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Lysosomal	0.152
	Mitochondrial	1.476 *
	Chloroplast	0.291
	Peroxisomal	0.061
	Vacuole	0.036
	Nuclear	0.769

SeqID: li LinJ_35_2230_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Mitochondrial	0.363
Di-peptide	Chloroplast	0.368
part-Comp.	Mitochondrial	0.434
chemo-typy	Extracellular	0.535
Neighboring	Cytoplasmic	0.426
Combined SVM classifier:		
	Extracellular	0.649
	PlasmaMembrane	0.028
	Cytoplasmic	1.343 *
	Cytoskeletal	0.015
	ER	0.026
	Golgi	0.015
	Lysosomal	0.015
	Mitochondrial	1.329 *
	Chloroplast	0.961
	Peroxisomal	0.129
	Vacuole	0.019
	Nuclear	0.473

SeqID: li LinJ_36_5660_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Nuclear	0.476
Di-peptide	Cytoplasmic	0.749
part-Comp.	Cytoplasmic	0.335
chemo-typy	Cytoplasmic	0.505
Neighboring	Cytoplasmic	0.526
Combined SVM classifier:		
	Extracellular	0.141
	PlasmaMembrane	0.032
	Cytoplasmic	2.366 *
	Cytoskeletal	0.162
	ER	0.050
	Golgi	0.055
	Lysosomal	0.009
	Mitochondrial	0.360
	Chloroplast	0.279
	Peroxisomal	0.099
	Vacuole	0.066
	Nuclear	1.382

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

SeqID: li|LinJ_27_2070_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Extracellular	0.332
Di-peptide	Mitochondrial	0.566
part-Comp.	Nuclear	0.339
chemo-typy	Chloroplast	0.344
Neighboring	Extracellular	0.654

Combined SVM classifier:

Extracellular	1.235	*
PlasmaMembrane	0.183	
Cytoplasmic	0.503	
Cytoskeletal	0.014	
ER	0.028	
Golgi	0.017	
Lysosomal		0.036
Mitochondrial	1.422	*
Chloroplast	0.687	
Peroxisomal	0.036	
Vacuole	0.023	
Nuclear	0.816	

SeqID: li|LinJ_31_0960_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Mitochondrial	0.273
Di-peptide	Extracellular	0.268
part-Comp.	Chloroplast	0.522
chemo-typy	PlasmaMembrane	0.477
Neighboring	Extracellular	0.299

Combined SVM classifier:

Extracellular	1.358	*
PlasmaMembrane	0.858	
Cytoplasmic	0.612	
Cytoskeletal	0.015	
ER	0.067	
Golgi	0.022	
Lysosomal		0.022
Mitochondrial	0.579	
Chloroplast	1.110	*
Peroxisomal	0.049	
Vacuole	0.032	
Nuclear	0.276	

SeqID: li|LinJ_32_3230_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	PlasmaMembrane	0.486
Di-peptide	Cytoplasmic	0.552
part-Comp.	Cytoplasmic	0.720
chemo-typy	Cytoplasmic	0.858

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Neighboring	Cytoplasmic	0.460	
Combined SVM classifier:				
		Extracellular	0.581	
		PlasmaMembrane	0.691	
		Cytoplasmic	2.807 *	
		Cytoskeletal	0.007	
		ER	0.022	
		Golgi	0.117	
		Lysosomal		0.040
		Mitochondrial	0.077	
		Chloroplast	0.115	
		Peroxisomal	0.078	
		Vacuole	0.015	
		Nuclear	0.448	

SeqID: li LinJ_24_2220_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Extracellular	0.301	
	Di-peptide	Extracellular	0.834	
	part-Comp.	Cytoplasmic	0.449	
	chemo-typy	Cytoplasmic	0.401	
	Neighboring	Cytoplasmic	0.321	
Combined SVM classifier:				
		Extracellular	1.330 *	
		PlasmaMembrane	0.359	
		Cytoplasmic	1.397 *	
		Cytoskeletal	0.027	
		ER	0.044	
		Golgi	0.055	
		Lysosomal		0.093
		Mitochondrial	0.310	
		Chloroplast	0.369	
		Peroxisomal	0.092	
		Vacuole	0.272	
		Nuclear	0.651	

SeqID: li LinJ_16_0470_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Cytoplasmic	0.725	
	Di-peptide	Mitochondrial	0.691	
	part-Comp.	Mitochondrial	0.501	
	chemo-typy	Nuclear	0.553	
	Neighboring	Mitochondrial	0.459	
Combined SVM classifier:				
		Extracellular	0.026	
		PlasmaMembrane	0.022	
		Cytoplasmic	1.466	
		Cytoskeletal	0.012	
		ER	0.010	
		Golgi	0.009	

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Lysosomal	0.008
	Mitochondrial	2.243 *
	Chloroplast	0.163
	Peroxisomal	0.108
	Vacuole	0.013
	Nuclear	0.919

SeqID: li LinJ_36_0660_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Cytoplasmic	0.692
Di-peptide	Nuclear	0.444
part-Comp.	Nuclear	0.347
chemo-typy	Extracellular	0.363
Neighboring	Nuclear	0.445
Combined SVM classifier:		
	Extracellular	0.612
	PlasmaMembrane	0.013
	Cytoplasmic	1.490 *
	Cytoskeletal	0.008
	ER	0.046
	Golgi	0.006
	Lysosomal	0.010
	Mitochondrial	0.748
	Chloroplast	0.202
	Peroxisomal	0.042
	Vacuole	0.037
	Nuclear	1.786 *

SeqID: li LinJ_35_2960_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Nuclear	0.811
Di-peptide	Cytoplasmic	0.376
part-Comp.	Mitochondrial	0.496
chemo-typy	Nuclear	0.584
Neighboring	Cytoplasmic	0.523
Combined SVM classifier:		
	Extracellular	0.164
	PlasmaMembrane	0.035
	Cytoplasmic	1.386 *
	Cytoskeletal	0.019
	ER	0.076
	Golgi	0.024
	Lysosomal	0.007
	Mitochondrial	0.935
	Chloroplast	0.266
	Peroxisomal	0.059
	Vacuole	0.018
	Nuclear	2.010 *

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

SeqID: li|LinJ_34_3280_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Cytoplasmic	0.691
Di-peptide	Cytoplasmic	0.783
part-Comp.	Cytoplasmic	0.854
chemo-typy	Cytoplasmic	0.704
Neighboring	Cytoplasmic	0.819

Combined SVM classifier:

Extracellular	0.013	
PlasmaMembrane	0.014	
Cytoplasmic	3.850	*
Cytoskeletal	0.005	
ER	0.063	
Golgi	0.029	
Lysosomal		0.002
Mitochondrial	0.536	
Chloroplast	0.357	
Peroxisomal	0.017	
Vacuole	0.005	
Nuclear	0.109	

SeqID: li|LinJ_21_1310_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Cytoplasmic	0.587
Di-peptide	Mitochondrial	0.769
part-Comp.	Mitochondrial	0.964
chemo-typy	Nuclear	0.571
Neighboring	Mitochondrial	0.855

Combined SVM classifier:

Extracellular	0.014	
PlasmaMembrane	0.011	
Cytoplasmic	0.934	
Cytoskeletal	0.009	
ER	0.005	
Golgi	0.006	
Lysosomal		0.004
Mitochondrial	3.159	*
Chloroplast	0.119	
Peroxisomal	0.052	
Vacuole	0.005	
Nuclear	0.682	

SeqID: li|LinJ_19_1500_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Nuclear	0.554
Di-peptide	Cytoplasmic	0.368
part-Comp.	Cytoplasmic	0.392
chemo-typy	Nuclear	0.264

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Neighboring	Extracellular	0.490	
Combined SVM classifier:				
		Extracellular	0.886	
		PlasmaMembrane	0.045	
		Cytoplasmic	1.225	*
		Cytoskeletal	0.035	
		ER	0.043	
		Golgi	0.021	
		Lysosomal		0.024
		Mitochondrial	0.804	
		Chloroplast	0.271	
		Peroxisomal	0.094	
		Vacuole	0.021	
		Nuclear	1.531	*

SeqID: li LinJ_36_3430_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Cytoplasmic	0.494	
	Di-peptide	Mitochondrial	0.569	
	part-Comp.	Mitochondrial	0.606	
	chemo-typy	Nuclear	0.811	
	Neighboring	Nuclear	0.413	
Combined SVM classifier:				
		Extracellular	0.163	
		PlasmaMembrane	0.065	
		Cytoplasmic	1.107	*
		Cytoskeletal	0.010	
		ER	0.034	
		Golgi	0.011	
		Lysosomal		0.016
		Mitochondrial	1.721	*
		Chloroplast	0.203	
		Peroxisomal	0.034	
		Vacuole	0.027	
		Nuclear	1.610	*

SeqID: li LinJ_32_3940_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Mitochondrial	0.776	
	Di-peptide	Mitochondrial	0.508	
	part-Comp.	Nuclear	0.447	
	chemo-typy	Nuclear	0.396	
	Neighboring	Mitochondrial	0.408	
Combined SVM classifier:				
		Extracellular	0.391	
		PlasmaMembrane	0.044	
		Cytoplasmic	0.702	
		Cytoskeletal	0.015	
		ER	0.020	
		Golgi	0.016	

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Lysosomal	0.013
	Mitochondrial	2.144 *
	Chloroplast	0.192
	Peroxisomal	0.070
	Vacuole	0.006
	Nuclear	1.388

SeqID: li LinJ_27_0590_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	PlasmaMembrane	0.739
Di-peptide	Mitochondrial	0.622
part-Comp.	Mitochondrial	0.657
chemo-typy	Mitochondrial	0.590
Neighboring	Mitochondrial	0.352
Combined SVM classifier:		
	Extracellular	0.288
	PlasmaMembrane	1.380
	Cytoplasmic	0.192
	Cytoskeletal	0.008
	ER	0.013
	Golgi	0.007
	Lysosomal	0.121
	Mitochondrial	2.334 *
	Chloroplast	0.254
	Peroxisomal	0.160
	Vacuole	0.014
	Nuclear	0.227

SeqID: li LinJ_36_6950_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Nuclear	0.516
Di-peptide	Extracellular	0.765
part-Comp.	Cytoplasmic	0.542
chemo-typy	Cytoplasmic	0.941
Neighboring	Cytoplasmic	0.717
Combined SVM classifier:		
	Extracellular	0.835
	PlasmaMembrane	0.347
	Cytoplasmic	2.606 *
	Cytoskeletal	0.029
	ER	0.007
	Golgi	0.048
	Lysosomal	0.007
	Mitochondrial	0.118
	Chloroplast	0.204
	Peroxisomal	0.037
	Vacuole	0.009
	Nuclear	0.754

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

SeqID: li|LinJ_25_0370_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Extracellular	0.309
Di-peptide	Mitochondrial	0.832
part-Comp.	Nuclear	0.340
chemo-typy	Nuclear	0.467
Neighboring	Mitochondrial	0.576

Combined SVM classifier:

Extracellular	0.395
PlasmaMembrane	0.032
Cytoplasmic	0.575
Cytoskeletal	0.022
ER	0.020
Golgi	0.010
Lysosomal	0.018
Mitochondrial	1.874 *
Chloroplast	0.478
Peroxisomal	0.053
Vacuole	0.024
Nuclear	1.499 *

SeqID: li|LinJ_32_0440_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Mitochondrial	0.382
Di-peptide	Nuclear	0.760
part-Comp.	Nuclear	0.558
chemo-typy	Mitochondrial	0.590
Neighboring	Mitochondrial	0.689

Combined SVM classifier:

Extracellular	0.044
PlasmaMembrane	0.021
Cytoplasmic	0.602
Cytoskeletal	0.036
ER	0.005
Golgi	0.005
Lysosomal	0.008
Mitochondrial	2.178 *
Chloroplast	0.087
Peroxisomal	0.027
Vacuole	0.006
Nuclear	1.979 *

SeqID: li|LinJ_22_1260_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Cytoplasmic	0.299
Di-peptide	Cytoplasmic	0.671
part-Comp.	Cytoplasmic	0.680
chemo-typy	Cytoplasmic	0.761

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Neighboring	Cytoplasmic	0.791	
Combined SVM classifier:				
		Extracellular	0.319	
		PlasmaMembrane	0.056	
		Cytoplasmic	3.203	*
		Cytoskeletal	0.019	
		ER	0.231	
		Golgi	0.043	
		Lysosomal		0.007
		Mitochondrial	0.173	
		Chloroplast	0.406	
		Peroxisomal	0.036	
		Vacuole	0.034	
		Nuclear	0.474	

SeqID: li LinJ_13_1020_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Extracellular	0.197	
	Di-peptide	Extracellular	0.774	
	part-Comp.	Extracellular	0.314	
	chemo-typy	Chloroplast	0.279	
	Neighboring	Extracellular	0.357	
Combined SVM classifier:				
		Extracellular	1.828	*
		PlasmaMembrane	0.389	
		Cytoplasmic	0.598	
		Cytoskeletal	0.023	
		ER	0.046	
		Golgi	0.059	
		Lysosomal		0.036
		Mitochondrial	0.587	
		Chloroplast	0.705	
		Peroxisomal	0.039	
		Vacuole	0.036	
		Nuclear	0.656	

SeqID: li LinJ_32_3260_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	PlasmaMembrane	0.397	
	Di-peptide	Extracellular	0.613	
	part-Comp.	PlasmaMembrane	0.743	
	chemo-typy	PlasmaMembrane	0.757	
	Neighboring	PlasmaMembrane	0.545	
Combined SVM classifier:				
		Extracellular	1.125	
		PlasmaMembrane	2.749	*
		Cytoplasmic	0.079	
		Cytoskeletal	0.011	
		ER	0.020	
		Golgi	0.013	

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Lysosomal	0.027
	Mitochondrial	0.365
	Chloroplast	0.373
	Peroxisomal	0.049
	Vacuole	0.030
	Nuclear	0.160

SeqID: li LinJ_26_1080_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Mitochondrial	0.689
Di-peptide	Mitochondrial	0.763
part-Comp.	Mitochondrial	0.602
chemo-typy	Mitochondrial	0.493
Neighboring	Mitochondrial	0.466
Combined SVM classifier:		
	Extracellular	0.090
	PlasmaMembrane	0.442
	Cytoplasmic	0.307
	Cytoskeletal	0.008
	ER	0.033
	Golgi	0.009
	Lysosomal	0.100
	Mitochondrial	3.013 *
	Chloroplast	0.607
	Peroxisomal	0.121
	Vacuole	0.018
	Nuclear	0.251

SeqID: li LinJ_36_3560_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Nuclear	0.424
Di-peptide	Mitochondrial	0.563
part-Comp.	Nuclear	0.497
chemo-typy	Nuclear	0.505
Neighboring	Nuclear	0.503
Combined SVM classifier:		
	Extracellular	0.265
	PlasmaMembrane	0.110
	Cytoplasmic	0.392
	Cytoskeletal	0.019
	ER	0.018
	Golgi	0.009
	Lysosomal	0.012
	Mitochondrial	1.556 *
	Chloroplast	0.319
	Peroxisomal	0.032
	Vacuole	0.014
	Nuclear	2.252 *

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

SeqID: li|LinJ_31_0070_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Mitochondrial	0.799
Di-peptide	Mitochondrial	0.794
part-Comp.	Mitochondrial	0.333
chemo-typy	Mitochondrial	0.509
Neighboring	Mitochondrial	0.396

Combined SVM classifier:

Extracellular	0.121
PlasmaMembrane	0.187
Cytoplasmic	0.576
Cytoskeletal	0.014
ER	0.016
Golgi	0.011
Lysosomal	0.022
Mitochondrial	2.831 *
Chloroplast	0.504
Peroxisomal	0.087
Vacuole	0.020
Nuclear	0.611

SeqID: li|LinJ_08_1280_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Cytoplasmic	0.524
Di-peptide	Cytoplasmic	0.857
part-Comp.	Cytoplasmic	0.816
chemo-typy	Cytoplasmic	0.648
Neighboring	Cytoplasmic	0.820

Combined SVM classifier:

Extracellular	0.100
PlasmaMembrane	0.191
Cytoplasmic	3.664 *
Cytoskeletal	0.008
ER	0.028
Golgi	0.018
Lysosomal	0.048
Mitochondrial	0.067
Chloroplast	0.104
Peroxisomal	0.027
Vacuole	0.047
Nuclear	0.698

SeqID: li|LinJ_33_3340_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Mitochondrial	0.558
Di-peptide	Extracellular	0.617
part-Comp.	Nuclear	0.556
chemo-typy	Nuclear	0.406

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Neighboring	Nuclear	0.362	
Combined SVM classifier:				
		Extracellular	0.852	
		PlasmaMembrane	0.041	
		Cytoplasmic	0.833	
		Cytoskeletal	0.018	
		ER	0.020	
		Golgi	0.032	
		Lysosomal		0.011
		Mitochondrial	1.389	*
		Chloroplast	0.158	
		Peroxisomal	0.053	
		Vacuole	0.009	
		Nuclear	1.584	*

SeqID: li LinJ_29_0910_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Cytoplasmic	0.446	
	Di-peptide	Mitochondrial	0.505	
	part-Comp.	Nuclear	0.468	
	chemo-typy	Nuclear	0.865	
	Neighboring	Mitochondrial	0.674	
Combined SVM classifier:				
		Extracellular	0.149	
		PlasmaMembrane	0.063	
		Cytoplasmic	0.740	
		Cytoskeletal	0.021	
		ER	0.019	
		Golgi	0.009	
		Lysosomal		0.011
		Mitochondrial	1.714	*
		Chloroplast	0.132	
		Peroxisomal	0.128	
		Vacuole	0.026	
		Nuclear	1.987	*

SeqID: li LinJ_07_0210_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Mitochondrial	0.355	
	Di-peptide	Cytoplasmic	0.539	
	part-Comp.	Mitochondrial	0.752	
	chemo-typy	Nuclear	0.414	
	Neighboring	Extracellular	0.365	
Combined SVM classifier:				
		Extracellular	0.511	
		PlasmaMembrane	0.054	
		Cytoplasmic	0.910	
		Cytoskeletal	0.010	
		ER	0.037	
		Golgi	0.011	

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Lysosomal	0.617
	Mitochondrial	1.472 *
	Chloroplast	0.438
	Peroxisomal	0.179
	Vacuole	0.083
	Nuclear	0.678

SeqID: li LinJ_36_3960_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Chloroplast	0.338
Di-peptide	Nuclear	0.663
part-Comp.	Mitochondrial	0.387
chemo-typy	Nuclear	0.681
Neighboring	Nuclear	0.300
Combined SVM classifier:		
	Extracellular	0.231
	PlasmaMembrane	0.033
	Cytoplasmic	0.918
	Cytoskeletal	0.013
	ER	0.021
	Golgi	0.011
	Lysosomal	0.010
	Mitochondrial	0.935
	Chloroplast	0.555
	Peroxisomal	0.117
	Vacuole	0.023
	Nuclear	2.133 *

SeqID: li LinJ_15_0090_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Cytoplasmic	0.713
Di-peptide	Cytoplasmic	0.916
part-Comp.	Mitochondrial	0.585
chemo-typy	Mitochondrial	0.433
Neighboring	Cytoplasmic	0.618
Combined SVM classifier:		
	Extracellular	0.012
	PlasmaMembrane	0.011
	Cytoplasmic	2.930 *
	Cytoskeletal	0.013
	ER	0.028
	Golgi	0.018
	Lysosomal	0.001
	Mitochondrial	1.435
	Chloroplast	0.220
	Peroxisomal	0.021
	Vacuole	0.002
	Nuclear	0.308

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

SeqID: li|LinJ_16_1330_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Mitochondrial	0.545
Di-peptide	Mitochondrial	0.626
part-Comp.	Cytoplasmic	0.408
chemo-typy	Extracellular	0.678
Neighboring	Cytoplasmic	0.361

Combined SVM classifier:

Extracellular	0.988
PlasmaMembrane	0.255
Cytoplasmic	1.092 *
Cytoskeletal	0.026
ER	0.043
Golgi	0.023
Lysosomal	0.045
Mitochondrial	1.576 *
Chloroplast	0.562
Peroxisomal	0.063
Vacuole	0.015
Nuclear	0.313

SeqID: li|LinJ_36_3550_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Nuclear	0.417
Di-peptide	Mitochondrial	0.462
part-Comp.	Nuclear	0.467
chemo-typy	Nuclear	0.535
Neighboring	Nuclear	0.475

Combined SVM classifier:

Extracellular	0.295
PlasmaMembrane	0.122
Cytoplasmic	0.431
Cytoskeletal	0.018
ER	0.019
Golgi	0.010
Lysosomal	0.014
Mitochondrial	1.393
Chloroplast	0.331
Peroxisomal	0.035
Vacuole	0.015
Nuclear	2.319 *

SeqID: li|LinJ_28_0780_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Mitochondrial	0.669
Di-peptide	Mitochondrial	0.708
part-Comp.	Mitochondrial	0.931
chemo-typy	Mitochondrial	0.723

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Neighboring	Mitochondrial	0.895	
Combined SVM classifier:				
		Extracellular	0.120	
		PlasmaMembrane	0.009	
		Cytoplasmic	0.114	
		Cytoskeletal	0.010	
		ER	0.011	
		Golgi	0.005	
		Lysosomal		0.007
		Mitochondrial	3.926 *	
		Chloroplast	0.127	
		Peroxisomal	0.048	
		Vacuole	0.004	
		Nuclear	0.619	

SeqID: li LinJ_01_0270_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Chloroplast	0.338	
	Di-peptide	Cytoplasmic	0.318	
	part-Comp.	Cytoplasmic	0.428	
	chemo-typy	Cytoplasmic	0.525	
	Neighboring	Extracellular	0.394	
Combined SVM classifier:				
		Extracellular	0.625	
		PlasmaMembrane	0.570	
		Cytoplasmic	1.705 *	
		Cytoskeletal	0.036	
		ER	0.039	
		Golgi	0.041	
		Lysosomal		0.025
		Mitochondrial	0.479	
		Chloroplast	0.795	
		Peroxisomal	0.166	
		Vacuole	0.018	
		Nuclear	0.502	

SeqID: li LinJ_35_3490_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Nuclear	0.326	
	Di-peptide	Cytoplasmic	0.541	
	part-Comp.	Nuclear	0.351	
	chemo-typy	Mitochondrial	0.332	
	Neighboring	Cytoplasmic	0.450	
Combined SVM classifier:				
		Extracellular	0.508	
		PlasmaMembrane	0.113	
		Cytoplasmic	1.457 *	
		Cytoskeletal	0.020	
		ER	0.041	
		Golgi	0.045	

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Lysosomal	0.045
	Mitochondrial	0.600
	Chloroplast	0.719
	Peroxisomal	0.076
	Vacuole	0.062
	Nuclear	1.313 *

SeqID: li LinJ_20_0250_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Nuclear	0.746
Di-peptide	Nuclear	0.590
part-Comp.	Mitochondrial	0.492
chemo-typy	Cytoplasmic	0.610
Neighboring	Extracellular	0.188
Combined SVM classifier:		
	Extracellular	0.283
	PlasmaMembrane	0.212
	Cytoplasmic	1.357 *
	Cytoskeletal	0.015
	ER	0.074
	Golgi	0.017
	Lysosomal	0.009
	Mitochondrial	0.631
	Chloroplast	0.445
	Peroxisomal	0.037
	Vacuole	0.029
	Nuclear	1.892 *

SeqID: li LinJ_20_0340_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Mitochondrial	0.712
Di-peptide	Extracellular	0.378
part-Comp.	Nuclear	0.465
chemo-typy	Mitochondrial	0.620
Neighboring	Mitochondrial	0.432
Combined SVM classifier:		
	Extracellular	0.837
	PlasmaMembrane	0.341
	Cytoplasmic	0.277
	Cytoskeletal	0.011
	ER	0.083
	Golgi	0.016
	Lysosomal	0.022
	Mitochondrial	2.428 *
	Chloroplast	0.097
	Peroxisomal	0.091
	Vacuole	0.013
	Nuclear	0.785

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

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*****
*****
SeqID: li|LinJ_24_0040_mRNA|
      CELLO prediction:
              (predictor      location      reliable-index)
Composition      Mitochondrial    0.429
Di-peptide       Nuclear          0.736
part-Comp.       Nuclear          0.540
chemo-typy       Mitochondrial    0.646
Neighboring      Mitochondrial    0.705

      Combined SVM classifier:
                                Extracellular    0.050
                                PlasmaMembrane    0.020
                                Cytoplasmic        0.539
                                Cytoskeletal        0.034
                                ER                  0.005
                                Golgi              0.006
                                Lysosomal          0.008
                                Mitochondrial      2.340 *
                                Chloroplast        0.087
                                Peroxisomal        0.030
                                Vacuole            0.007
                                Nuclear            1.875 *

*****
*****
SeqID: li|LinJ_03_0210_mRNA|
      CELLO prediction:
              (predictor      location      reliable-index)
Composition      Mitochondrial    0.651
Di-peptide       Mitochondrial    0.618
part-Comp.       Mitochondrial    0.464
chemo-typy       Nuclear          0.346
Neighboring      Mitochondrial    0.697

      Combined SVM classifier:
                                Extracellular    0.046
                                PlasmaMembrane    0.277
                                Cytoplasmic        0.528
                                Cytoskeletal        0.031
                                ER                  0.012
                                Golgi              0.010
                                Lysosomal          0.008
                                Mitochondrial      2.747 *
                                Chloroplast        0.210
                                Peroxisomal        0.155
                                Vacuole            0.009
                                Nuclear            0.967

*****
*****
SeqID: li|LinJ_14_1010_mRNA|
      CELLO prediction:
              (predictor      location      reliable-index)
Composition      Mitochondrial    0.918
Di-peptide       Mitochondrial    0.306
part-Comp.       Mitochondrial    0.718
chemo-typy       Mitochondrial    0.673

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Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Neighboring	Mitochondrial	0.797	
Combined SVM classifier:				
		Extracellular	0.067	
		PlasmaMembrane	0.446	
		Cytoplasmic	0.147	
		Cytoskeletal	0.013	
		ER	0.010	
		Golgi	0.008	
		Lysosomal		0.008
		Mitochondrial	3.413	*
		Chloroplast	0.450	
		Peroxisomal	0.165	
		Vacuole	0.025	
		Nuclear	0.248	

SeqID: li LinJ_35_0210_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	PlasmaMembrane	0.547	
	Di-peptide	PlasmaMembrane	0.424	
	part-Comp.	PlasmaMembrane	0.511	
	chemo-typy	Chloroplast	0.371	
	Neighboring	PlasmaMembrane	0.339	
Combined SVM classifier:				
		Extracellular	1.099	
		PlasmaMembrane	1.879	*
		Cytoplasmic	0.341	
		Cytoskeletal	0.012	
		ER	0.028	
		Golgi	0.024	
		Lysosomal		0.023
		Mitochondrial	0.421	
		Chloroplast	0.440	
		Peroxisomal	0.079	
		Vacuole	0.013	
		Nuclear	0.641	

SeqID: li LinJ_36_1680_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Nuclear	0.538	
	Di-peptide	Extracellular	0.515	
	part-Comp.	Extracellular	0.667	
	chemo-typy	Nuclear	0.658	
	Neighboring	Extracellular	0.563	
Combined SVM classifier:				
		Extracellular	1.882	*
		PlasmaMembrane	0.100	
		Cytoplasmic	0.263	
		Cytoskeletal	0.014	
		ER	0.016	
		Golgi	0.008	

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Lysosomal	0.041
	Mitochondrial	0.254
	Chloroplast	0.076
	Peroxisomal	0.013
	Vacuole	0.012
	Nuclear	2.320 *

SeqID: li LinJ_31_2890_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Chloroplast	0.280
Di-peptide	Mitochondrial	0.777
part-Comp.	Chloroplast	0.544
chemo-typy	Cytoplasmic	0.452
Neighboring	Mitochondrial	0.417
Combined SVM classifier:		
	Extracellular	0.491
	PlasmaMembrane	0.173
	Cytoplasmic	0.889
	Cytoskeletal	0.017
	ER	0.143
	Golgi	0.027
	Lysosomal	0.072
	Mitochondrial	1.587 *
	Chloroplast	1.152 *
	Peroxisomal	0.115
	Vacuole	0.032
	Nuclear	0.302

SeqID: li LinJ_04_1190_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Nuclear	0.597
Di-peptide	Nuclear	0.645
part-Comp.	Nuclear	0.955
chemo-typy	Extracellular	0.805
Neighboring	Nuclear	0.521
Combined SVM classifier:		
	Extracellular	1.162
	PlasmaMembrane	0.131
	Cytoplasmic	0.492
	Cytoskeletal	0.013
	ER	0.039
	Golgi	0.014
	Lysosomal	0.018
	Mitochondrial	0.174
	Chloroplast	0.106
	Peroxisomal	0.045
	Vacuole	0.045
	Nuclear	2.761 *

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

SeqID: li|LinJ_32_3370_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Cytoplasmic	0.419
Di-peptide	Extracellular	0.228
part-Comp.	PlasmaMembrane	0.256
chemo-typy	Chloroplast	0.355
Neighboring	Extracellular	0.366

Combined SVM classifier:

Extracellular	1.033	*
PlasmaMembrane	0.389	
Cytoplasmic	0.938	
Cytoskeletal	0.039	
ER	0.032	
Golgi	0.038	
Lysosomal		0.401
Mitochondrial	0.649	
Chloroplast	0.827	
Peroxisomal	0.092	
Vacuole	0.050	
Nuclear	0.512	

SeqID: li|LinJ_28_1620_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	PlasmaMembrane	0.822
Di-peptide	PlasmaMembrane	0.577
part-Comp.	PlasmaMembrane	0.833
chemo-typy	PlasmaMembrane	0.887
Neighboring	PlasmaMembrane	0.763

Combined SVM classifier:

Extracellular	0.291	
PlasmaMembrane	3.883	*
Cytoplasmic	0.038	
Cytoskeletal	0.004	
ER	0.015	
Golgi	0.006	
Lysosomal		0.029
Mitochondrial	0.426	
Chloroplast	0.198	
Peroxisomal	0.036	
Vacuole	0.005	
Nuclear	0.068	

SeqID: li|LinJ_36_5970_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Cytoplasmic	0.395
Di-peptide	Nuclear	0.707
part-Comp.	Nuclear	0.475
chemo-typy	Nuclear	0.907

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Neighboring	Nuclear	0.369	
Combined SVM classifier:				
		Extracellular	0.253	
		PlasmaMembrane	0.059	
		Cytoplasmic	0.900	
		Cytoskeletal	0.014	
		ER	0.020	
		Golgi	0.012	
		Lysosomal		0.013
		Mitochondrial	0.883	
		Chloroplast	0.215	
		Peroxisomal	0.024	
		Vacuole	0.015	
		Nuclear	2.592	*

SeqID: li LinJ_34_1880_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Chloroplast	0.331	
	Di-peptide	Cytoplasmic	0.517	
	part-Comp.	Chloroplast	0.862	
	chemo-typy	Chloroplast	0.425	
	Neighboring	Cytoplasmic	0.334	
Combined SVM classifier:				
		Extracellular	0.075	
		PlasmaMembrane	0.311	
		Cytoplasmic	1.158	
		Cytoskeletal	0.015	
		ER	0.020	
		Golgi	0.021	
		Lysosomal		0.006
		Mitochondrial	0.822	
		Chloroplast	2.081	*
		Peroxisomal	0.018	
		Vacuole	0.006	
		Nuclear	0.467	

SeqID: li LinJ_36_4570_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Mitochondrial	0.474	
	Di-peptide	Cytoplasmic	0.612	
	part-Comp.	Mitochondrial	0.652	
	chemo-typy	Cytoplasmic	0.795	
	Neighboring	Cytoplasmic	0.792	
Combined SVM classifier:				
		Extracellular	0.009	
		PlasmaMembrane	0.006	
		Cytoplasmic	2.623	*
		Cytoskeletal	0.010	
		ER	0.018	
		Golgi	0.020	

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Lysosomal	0.003
	Mitochondrial	1.519
	Chloroplast	0.449
	Peroxisomal	0.029
	Vacuole	0.004
	Nuclear	0.310

SeqID: li LinJ_32_0870_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	PlasmaMembrane	0.657
Di-peptide	Extracellular	0.277
part-Comp.	PlasmaMembrane	0.841
chemo-typy	PlasmaMembrane	0.289
Neighboring	PlasmaMembrane	0.519
Combined SVM classifier:		
	Extracellular	0.684
	PlasmaMembrane	2.486 *
	Cytoplasmic	0.149
	Cytoskeletal	0.012
	ER	0.023
	Golgi	0.128
	Lysosomal	0.042
	Mitochondrial	0.429
	Chloroplast	0.356
	Peroxisomal	0.052
	Vacuole	0.014
	Nuclear	0.624

SeqID: li LinJ_30_1650_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	PlasmaMembrane	0.715
Di-peptide	Mitochondrial	0.404
part-Comp.	Extracellular	0.329
chemo-typy	Mitochondrial	0.285
Neighboring	PlasmaMembrane	0.526
Combined SVM classifier:		
	Extracellular	1.144
	PlasmaMembrane	1.952 *
	Cytoplasmic	0.182
	Cytoskeletal	0.016
	ER	0.026
	Golgi	0.013
	Lysosomal	0.074
	Mitochondrial	0.891
	Chloroplast	0.464
	Peroxisomal	0.051
	Vacuole	0.088
	Nuclear	0.099

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

SeqID: li|LinJ_28_3220_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Mitochondrial	0.591
Di-peptide	Mitochondrial	0.732
part-Comp.	Mitochondrial	0.744
chemo-typy	Mitochondrial	0.569
Neighboring	Mitochondrial	0.751

Combined SVM classifier:

Extracellular	0.172
PlasmaMembrane	0.021
Cytoplasmic	0.361
Cytoskeletal	0.010
ER	0.016
Golgi	0.006
Lysosomal	0.012
Mitochondrial	3.386 *
Chloroplast	0.206
Peroxisomal	0.072
Vacuole	0.016
Nuclear	0.723

SeqID: li|LinJ_08_0340_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Extracellular	0.722
Di-peptide	Mitochondrial	0.265
part-Comp.	Cytoplasmic	0.303
chemo-typy	Nuclear	0.419
Neighboring	Extracellular	0.366

Combined SVM classifier:

Extracellular	1.580 *
PlasmaMembrane	0.045
Cytoplasmic	0.924
Cytoskeletal	0.017
ER	0.029
Golgi	0.028
Lysosomal	0.020
Mitochondrial	0.827
Chloroplast	0.321
Peroxisomal	0.033
Vacuole	0.012
Nuclear	1.163 *

SeqID: li|LinJ_36_6680_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Cytoplasmic	0.537
Di-peptide	Cytoplasmic	0.441
part-Comp.	Mitochondrial	0.639
chemo-typy	Nuclear	0.952

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Neighboring	Cytoplasmic	0.491	
Combined SVM classifier:				
		Extracellular	0.014	
		PlasmaMembrane	0.010	
		Cytoplasmic	1.508	*
		Cytoskeletal	0.024	
		ER	0.010	
		Golgi	0.007	
		Lysosomal		0.004
		Mitochondrial	1.479	*
		Chloroplast	0.070	
		Peroxisomal	0.035	
		Vacuole	0.006	
		Nuclear	1.831	*

SeqID: li LinJ_24_1240_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Nuclear	0.314	
	Di-peptide	Cytoplasmic	0.375	
	part-Comp.	Nuclear	0.431	
	chemo-typy	Nuclear	0.426	
	Neighboring	Nuclear	0.606	
Combined SVM classifier:				
		Extracellular	0.258	
		PlasmaMembrane	0.051	
		Cytoplasmic	1.353	
		Cytoskeletal	0.039	
		ER	0.032	
		Golgi	0.013	
		Lysosomal		0.013
		Mitochondrial	0.895	
		Chloroplast	0.211	
		Peroxisomal	0.061	
		Vacuole	0.009	
		Nuclear	2.064	*

SeqID: li LinJ_22_1300_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Extracellular	0.496	
	Di-peptide	Cytoplasmic	0.730	
	part-Comp.	Extracellular	0.791	
	chemo-typy	Extracellular	0.835	
	Neighboring	Cytoplasmic	0.330	
Combined SVM classifier:				
		Extracellular	2.281	*
		PlasmaMembrane	0.057	
		Cytoplasmic	1.334	
		Cytoskeletal	0.007	
		ER	0.084	
		Golgi	0.013	

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Lysosomal	0.080
	Mitochondrial	0.286
	Chloroplast	0.245
	Peroxisomal	0.072
	Vacuole	0.224
	Nuclear	0.317

SeqID: li LinJ_21_0440_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Nuclear	0.711
Di-peptide	Chloroplast	0.591
part-Comp.	PlasmaMembrane	0.265
chemo-typy	Nuclear	0.443
Neighboring	Nuclear	0.633
Combined SVM classifier:		
	Extracellular	0.191
	PlasmaMembrane	0.499
	Cytoplasmic	0.344
	Cytoskeletal	0.237
	ER	0.017
	Golgi	0.030
	Lysosomal	0.020
	Mitochondrial	0.596
	Chloroplast	0.920
	Peroxisomal	0.073
	Vacuole	0.015
	Nuclear	2.058 *

SeqID: li LinJ_36_2100_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Extracellular	0.503
Di-peptide	Extracellular	0.643
part-Comp.	Nuclear	0.473
chemo-typy	Chloroplast	0.360
Neighboring	Extracellular	0.690
Combined SVM classifier:		
	Extracellular	1.921 *
	PlasmaMembrane	0.059
	Cytoplasmic	0.811
	Cytoskeletal	0.019
	ER	0.018
	Golgi	0.057
	Lysosomal	0.016
	Mitochondrial	0.337
	Chloroplast	0.462
	Peroxisomal	0.036
	Vacuole	0.015
	Nuclear	1.250 *

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

SeqID: li|LinJ_35_5230_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Extracellular	0.488
Di-peptide	Nuclear	0.470
part-Comp.	Cytoplasmic	0.575
chemo-typy	Nuclear	0.483
Neighboring	Nuclear	0.299

Combined SVM classifier:

Extracellular	0.663
PlasmaMembrane	0.057
Cytoplasmic	1.404 *
Cytoskeletal	0.041
ER	0.034
Golgi	0.037
Lysosomal	0.009
Mitochondrial	0.825
Chloroplast	0.257
Peroxisomal	0.033
Vacuole	0.031
Nuclear	1.610 *

SeqID: li|LinJ_24_1870_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Cytoplasmic	0.321
Di-peptide	Extracellular	0.424
part-Comp.	Cytoplasmic	0.476
chemo-typy	Mitochondrial	0.346
Neighboring	Nuclear	0.377

Combined SVM classifier:

Extracellular	0.939
PlasmaMembrane	0.252
Cytoplasmic	1.178 *
Cytoskeletal	0.024
ER	0.032
Golgi	0.055
Lysosomal	0.026
Mitochondrial	0.870
Chloroplast	0.566
Peroxisomal	0.109
Vacuole	0.021
Nuclear	0.927

SeqID: li|LinJ_36_0510_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Cytoplasmic	0.354
Di-peptide	Cytoplasmic	0.590
part-Comp.	Mitochondrial	0.277
chemo-typy	Mitochondrial	0.280

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Neighboring	Nuclear	0.334
Combined SVM classifier:			
	Extracellular		0.646
	PlasmaMembrane		0.074
	Cytoplasmic		1.499 *
	Cytoskeletal		0.022
	ER		0.148
	Golgi		0.029
	Lysosomal		0.163
	Mitochondrial		0.983
	Chloroplast		0.376
	Peroxisomal		0.121
	Vacuole		0.066
	Nuclear		0.873

SeqID: li LinJ_34_0670_mRNA			
CELLO prediction:			
	(predictor	location	reliable-index)
	Composition	Mitochondrial	0.460
	Di-peptide	Chloroplast	0.383
	part-Comp.	Nuclear	0.546
	chemo-typy	Cytoplasmic	0.569
	Neighboring	Mitochondrial	0.600
Combined SVM classifier:			
	Extracellular		0.136
	PlasmaMembrane		0.058
	Cytoplasmic		1.235 *
	Cytoskeletal		0.014
	ER		0.026
	Golgi		0.019
	Lysosomal		0.018
	Mitochondrial		1.642 *
	Chloroplast		0.903
	Peroxisomal		0.112
	Vacuole		0.015
	Nuclear		0.822

SeqID: li LinJ_13_0460_mRNA			
CELLO prediction:			
	(predictor	location	reliable-index)
	Composition	Chloroplast	0.255
	Di-peptide	Chloroplast	0.402
	part-Comp.	Cytoplasmic	0.711
	chemo-typy	Cytoplasmic	0.871
	Neighboring	Cytoplasmic	0.459
Combined SVM classifier:			
	Extracellular		0.460
	PlasmaMembrane		0.072
	Cytoplasmic		2.619 *
	Cytoskeletal		0.019
	ER		0.044
	Golgi		0.052

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Lysosomal	0.013
	Mitochondrial	0.318
	Chloroplast	0.905
	Peroxisomal	0.089
	Vacuole	0.044
	Nuclear	0.366

SeqID: li LinJ_13_1080_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Cytoplasmic	0.290
Di-peptide	Mitochondrial	0.370
part-Comp.	Cytoplasmic	0.454
chemo-typy	Cytoplasmic	0.597
Neighboring	Nuclear	0.247
Combined SVM classifier:		
	Extracellular	0.354
	PlasmaMembrane	0.405
	Cytoplasmic	1.756 *
	Cytoskeletal	0.020
	ER	0.130
	Golgi	0.273
	Lysosomal	0.035
	Mitochondrial	0.506
	Chloroplast	0.264
	Peroxisomal	0.064
	Vacuole	0.107
	Nuclear	1.085 *

SeqID: li LinJ_22_0490_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Cytoplasmic	0.532
Di-peptide	Cytoplasmic	0.733
part-Comp.	Cytoplasmic	0.540
chemo-typy	Cytoplasmic	0.928
Neighboring	Cytoplasmic	0.752
Combined SVM classifier:		
	Extracellular	0.023
	PlasmaMembrane	0.009
	Cytoplasmic	3.485 *
	Cytoskeletal	0.024
	ER	0.040
	Golgi	0.035
	Lysosomal	0.002
	Mitochondrial	0.653
	Chloroplast	0.182
	Peroxisomal	0.036
	Vacuole	0.014
	Nuclear	0.496

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

SeqID: li|LinJ_34_3440_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Cytoplasmic	0.707
Di-peptide	Mitochondrial	0.687
part-Comp.	Mitochondrial	0.445
chemo-typy	Nuclear	0.553
Neighboring	Cytoplasmic	0.408

Combined SVM classifier:

Extracellular	0.033
PlasmaMembrane	0.026
Cytoplasmic	1.484 *
Cytoskeletal	0.013
ER	0.012
Golgi	0.012
Lysosomal	0.009
Mitochondrial	2.116 *
Chloroplast	0.190
Peroxisomal	0.115
Vacuole	0.015
Nuclear	0.975

SeqID: li|LinJ_31_0930_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Mitochondrial	0.244
Di-peptide	Cytoplasmic	0.308
part-Comp.	Chloroplast	0.500
chemo-typy	Extracellular	0.479
Neighboring	Extracellular	0.256

Combined SVM classifier:

Extracellular	1.288 *
PlasmaMembrane	0.714
Cytoplasmic	0.711
Cytoskeletal	0.014
ER	0.066
Golgi	0.022
Lysosomal	0.022
Mitochondrial	0.645
Chloroplast	1.096 *
Peroxisomal	0.044
Vacuole	0.034
Nuclear	0.344

SeqID: li|LinJ_27_1450_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Nuclear	0.368
Di-peptide	Nuclear	0.778
part-Comp.	Nuclear	0.729
chemo-typy	Cytoplasmic	0.674

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Neighboring	Nuclear	0.516	
Combined SVM classifier:				
		Extracellular	0.107	
		PlasmaMembrane	0.016	
		Cytoplasmic	1.238	
		Cytoskeletal	0.082	
		ER	0.012	
		Golgi	0.153	
		Lysosomal		0.007
		Mitochondrial	0.784	
		Chloroplast	0.086	
		Peroxisomal	0.022	
		Vacuole	0.007	
		Nuclear	2.484	*

SeqID: li LinJ_21_0800_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Cytoplasmic	0.742	
	Di-peptide	Nuclear	0.588	
	part-Comp.	Nuclear	0.464	
	chemo-typy	Nuclear	0.901	
	Neighboring	Nuclear	0.392	
Combined SVM classifier:				
		Extracellular	0.072	
		PlasmaMembrane	0.023	
		Cytoplasmic	1.346	
		Cytoskeletal	0.018	
		ER	0.015	
		Golgi	0.008	
		Lysosomal		0.008
		Mitochondrial	0.907	
		Chloroplast	0.103	
		Peroxisomal	0.024	
		Vacuole	0.011	
		Nuclear	2.464	*

SeqID: li LinJ_35_0240_mRNA				
CELLO prediction:				
	(predictor	location	reliable-index)	
	Composition	Extracellular	0.659	
	Di-peptide	Nuclear	0.297	
	part-Comp.	Mitochondrial	0.315	
	chemo-typy	Nuclear	0.694	
	Neighboring	Nuclear	0.466	
Combined SVM classifier:				
		Extracellular	1.447	*
		PlasmaMembrane	0.049	
		Cytoplasmic	0.428	
		Cytoskeletal	0.009	
		ER	0.013	
		Golgi	0.014	

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

	Lysosomal	0.016
	Mitochondrial	0.902
	Chloroplast	0.261
	Peroxisomal	0.050
	Vacuole	0.009
	Nuclear	1.802 *

SeqID: li LinJ_10_0830_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	Extracellular	0.449
Di-peptide	Extracellular	0.206
part-Comp.	Extracellular	0.912
chemo-typy	Nuclear	0.462
Neighboring	Cytoplasmic	0.390
Combined SVM classifier:		
	Extracellular	2.017 *
	PlasmaMembrane	0.584
	Cytoplasmic	0.833
	Cytoskeletal	0.014
	ER	0.161
	Golgi	0.066
	Lysosomal	0.102
	Mitochondrial	0.185
	Chloroplast	0.139
	Peroxisomal	0.099
	Vacuole	0.104
	Nuclear	0.695

SeqID: li LinJ_36_4070_mRNA		
CELLO prediction:		
(predictor	location	reliable-index)
Composition	PlasmaMembrane	0.359
Di-peptide	Extracellular	0.593
part-Comp.	Extracellular	0.609
chemo-typy	Chloroplast	0.230
Neighboring	Extracellular	0.606
Combined SVM classifier:		
	Extracellular	2.224 *
	PlasmaMembrane	0.546
	Cytoplasmic	0.484
	Cytoskeletal	0.010
	ER	0.101
	Golgi	0.041
	Lysosomal	0.251
	Mitochondrial	0.421
	Chloroplast	0.377
	Peroxisomal	0.125
	Vacuole	0.131
	Nuclear	0.287

Table S1. Subcellular localization of proteins retrieved for TriTypDB database showing >80% homology among *L. infantum*, *L. major* and *L. braziliensis*.

SeqID: li|LinJ_35_1310_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Mitochondrial	0.359
Di-peptide	Nuclear	0.288
part-Comp.	Nuclear	0.425
chemo-typy	Nuclear	0.323
Neighboring	Mitochondrial	0.342

Combined SVM classifier:

Extracellular	0.541
PlasmaMembrane	0.112
Cytoplasmic	0.899
Cytoskeletal	0.022
ER	0.029
Golgi	0.019
Lysosomal	0.061
Mitochondrial	1.263 *
Chloroplast	0.484
Peroxisomal	0.120
Vacuole	0.059
Nuclear	1.391 *

SeqID: li|LinJ_34_2720_mRNA|

CELLO prediction:

(predictor	location	reliable-index)
Composition	Cytoplasmic	0.804
Di-peptide	Mitochondrial	0.867
part-Comp.	Mitochondrial	0.806
chemo-typy	Mitochondrial	0.635
Neighboring	Mitochondrial	0.567

Combined SVM classifier:

Extracellular	0.043
PlasmaMembrane	0.023
Cytoplasmic	1.373
Cytoskeletal	0.012
ER	0.013
Golgi	0.007
Lysosomal	0.005
Mitochondrial	2.979 *
Chloroplast	0.175
Peroxisomal	0.039
Vacuole	0.004
Nuclear	0.325
