Table S1A. Quality control of proteomic data by protein identification probability, presented as average in patients with paracoccidioidomycosis, evaluated before treatment (at admission) - G1, G2, G3 patients groups and healthy individuals - G4 group.

Protein	Access code	Molecular mass (kDa)	Coverage rate (%)	[G1] *P. brasiliensis* with relapse AF (n=1) / CF (n=2) (%)	[G2] Patients with *P. lutzii* CF (n=4) (%)	[G3] *P. brasiliensis* without relapse AF (n=2) / CF (n=2) (%)	[G4] Control group (n=3) (%)	Main function
1. *Serum albumin*	P02768.2	69	79	100	100	100	100	Transport
2. *Transferrin*	P02787.3	77	34	100	100	100	100	Transport
3. *Apoliprotein A-I*	P02647.1	31	36	67	100	100	100	Transport
4. *Haptoglobin*	P00738.1	45	14	100	100	100	100	Immunomodulatory
5. *Ig kappa chain C region*	P01834.2	12	…	100	100	100	100	Immunomodulatory
6. *Ig gamma-1 chain C region*	P01857.1	36	...	100	100	100	100	Immunomodulatory
7. *Ig lambda-2 chain C region*	P0DOY2	11	75	100	100	100	100	Immunomodulatory
8. *Alpha-2-macroglobulin*	P01023.3	163	05	75	100	100	100	Activate/regulate the complement system
9. *Ig alpha-1 chain C region*	P01876.2	38	29	100	100	100	100	Immunomodulatory
10. *Alpha-1-antitrypsin*	P01009.3	47	08	66	92	100	100	Activate the coagulation/protease-inhibition pathway
11. *Hemopexin*	P02790.2	52	19	56	100	94	100	Transport
12. *Ig gamma-2 chain C region*	P01859.2	36	29	92	100	100	100	Immunomodulatory

AF - acute / subacute form; CF- chronic form; n- number of participants; … sequence not in database.

Table S1B. Quality control of proteomic data by protein identification probability, presented as average in patients with paracoccidioidomycosis, evaluated before treatment (at admission) - G1, G2, G3 patients groups and healthy individuals - G4 group.

Protein	Access code	Molecular mass (kDa)	Coverage rate (%)	[G1] *P. brasiliensis* with relapse AF (n=1) / CF (n=2) (%)	[G2] Patients with *P. lutzii* CF (n=4) (%)	[G3] *P. brasiliensis* without relapse AF (n=2) / CF (n=2) (%)	[G4] Control group (n=3) (%)	Main function
13. *Alpha-1-acid-glycoprotein*	P02763.1	24	19	66	74	100	99	Transport
14. *Complement C3*	P01024.2	187	05	25	78	68	89	Immunomodulatory
15. *Apolipoprotein A-II*	P02652.1	11	58	43	66	59	100	Transport/metabolize lipids
16. *Ig gamma-3 chain C region*	P01860.2	41	...	92	99	96	98	Immunomodulatory
17. *Ig gamma-4 chain C region*	P01861.1	36	23	84	85	92	89	Immunomodulatory
18. *Vitamin D-Binding Protein*	P02774.1	53	05	11	32	32	60	Immunomodulatory
19. *Ceruloplasmin*	P00450.1	122	01	0	55	57	11	Transport
20. *Complement C4-A*	P0C0L4.2	193	01	4	24	29	44	Immunomodulatory
21. *Alpha-1-antichymotrypsin*	P01011.2	48	02	11	25	42	0	protease-inhibition pathway/ metabolize lipids
22. *Kininogen*	P01042.2	72	02	11	34	11	11	protease-inhibition pathway

AF - acute / subacute form; CF- chronic form; n- number of participants; … sequence not in database.

Table S1C. Quality control of proteomic data by protein identification probability, presented as average in patients with paracoccidioidomycosis, evaluated before treatment (at admission) - G1, G2, G3 patients groups and healthy individuals - G4 group.

Protein	Access code	Molecular mass (kDa)	Coverage rate (%)	[G1] *P. brasiliensis* with relapse AF (n=1) / CF (n=2) (%)	[G2] Patients with *P. lutzii* FC (n=4) (%)	[G3] *P. brasiliensis* without relapse FA (n=2) / FC (n=2) (%)	[G4] Control group (n=3) (%)	Main function
23. *Ig alpha-2 chain C region*	P01877.3	37	08	0	0	0	0	Immunomodulatory
24. *Beta-globin*	P68871.2	16	09	26	66	24	31	Transport
25. *Ig kappa chain V-III*	P04433.1	13	08	11	56	24	21	Immunomodulatory
26. *Beta-2-glycoprotein 1*	P02749.3	38	15	11	39	16	75	Extracellular matrix
27. *Ig heavy chain V-III TIL*	P01764.2	12	26	22	0	33	11	Immunomodulatory
28. *Complement factor B*	P00751.2	86	01	0	29	32	32	Immunomodulatory
29. *Alpha-globin*	P69905.2	15	11	0	25	2	0	Transport

AF - acute / subacute form; CF- chronic form; n- number of participants; … sequence not in database.

DATABASE SEARCHING-- Tandem mass spectra were extracted by [unknown] version [unknown]. Charge state deconvolution and deisotoping were not performed. All MS/MS samples were analyzed using Mascot (Matrix Science, London, UK; version 2.3.02). Mascot was set up to search the Uniprot_Human_canonical_isoforms_release_17032016 database (unknown version, 92180 entries) assuming the digestion enzyme trypsin. Mascot was searched with a fragment ion mass tolerance of 0,100 Da and a parent ion tolerance of 0,100 Da. Carbamidomethyl of cysteine was specified in Mascot as a fixed modification. Oxidation of methionine was specified in Mascot as a variable modification.

CRITERIA FOR PROTEIN IDENTIFICATION-- Scaffold (version Scaffold_4.7.5, Proteome Software Inc., Portland, OR) was used to validate MS/MS based peptide and protein identifications. Peptide identifications were accepted if they could be established at greater than 24,0% probability to achieve an FDR less than 0,1% by the Scaffold Local FDR algorithm. Protein identifications were accepted if they could be established at greater than 99,0% probability to achieve an FDR less than 1,0% and contained at least 2 identified peptides. Protein probabilities were assigned by the Protein Prophet algorithm (Nesvizhskii, Al et al Anal. Chem. 2003;75(17):4646-58). Proteins that contained similar peptides and could not be differentiated based on MS/MS analysis alone were grouped to satisfy the principles of parsimony. Proteins sharing significant peptide evidence were grouped into clusters.