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Fungal genome and mating system transitions facilitated by chromosomal translocations involving intercentromeric recombination

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Table S2. Pathways enriched in the genomes of *C. amyloletus* compared to those of pathogenic *Cryptococcus* species

Pathway	CRAM_CBS6039 ¹	CRAM_CBS6273 ¹	Pathogenic_H99 ²	Pathogenic_JEC21 ²	Pathogenic_R265 ²	Pathogenic_WM276 ²	log2(CRAM/ Pathogenic)	rawPvalue	Qvalue
PF13460.1 NAD_binding_10 [NADH(P)-binding]	56	54	20	23	14	16	2.43	3.20E-11	1.33E-07
PF00201.13 UDPGT [UDP-glucuronosyl_and_UDP-glucosyl_transferase]	14	14	2	2	1	2	3.78	1.12E-07	2.34E-04
PF04616.9 Glyco_hydro_43 [Glycosyl_hydrolases_family_43]	5	5	0	0	0	0	6.51	3.47E-05	3.24E-02
PF05368.8 NmrA [NmrA-like_family]	30	29	12	16	9	10	2.16	3.90E-05	3.24E-02

1: "CRAM" indicates *C. amyloletus*.

2: "Pathogenic" indicates species within the human pathogenic *Cryptococcus* species complex.