Supplemental Material

Table S1. Fungal isolates from breast milk.

For confirmation of fungal viability, 3-4 samples were selected from each country to obtain fungal isolates. Data show the tentative taxonomic classification as inferred by sequencing of the 18S rRNA gene, as well as the BLAST parameters against the closest relative in public databases. SA: South Africa, C: China, SP: Spain

| Isolate Code	Country	Species	Max score[a]	query cover[b]	BLAST e-value	Max Identity[c]	Accession Nº
IHMP29	CH	*Candida albicans*	527	99%	8e-146	98%	CP032012.1
IHMP110	CH	*Uncultured fungus clone YL_OTU04 18S ribosomal RNA gene, partial sequence*	551	96%	5e-153	99%	KT285760.1
IHMP111	CH	*Candida albicans strain SC5314-P0 chromosome RB*	538	97%	4e-149	97%	CP025165.1
IHMP58	SA	*Candida albicans strain TIMM 1768*	555	99%	4e-154	99%	CP032012.1
IHMP06R	SA	*Candida albicans strain SC5314-P0 chromosome RB*	569	96%	1e-158	99%	CP025165.1
IHMP60	SP	*Candida parapsilosis strain CDC317*	525	98%	6e-147	100%	HE605209.1
IHMP59	SP	*Uncultured fungus clone nco88e11c1 18S ribosomal RNA gene, partial sequence*	568	96%	5e-158	99%	KC674774.1
IHMP24	SP	*Candida orthopsilosis Co 90-125, chromosome 7 draft sequence*	571	96%	4e-159	99%	HE681725.1
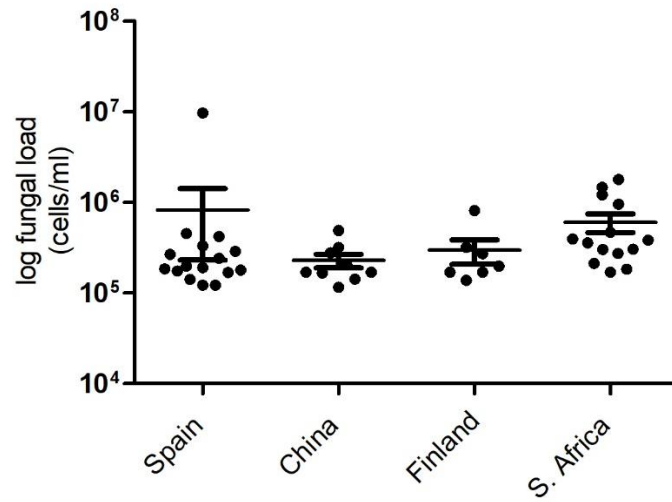
Figure S1. Fungal load in breast milk across geographic locations.
The plot shows median fungal loads with interquartile ranges in those samples that showed fungal presence by qPCR in each country. Spain, n=16; China, n=9; Finland, n=7 and South Africa, n= 14. Detection limit was 10^3 cells/ml, estimated as the lowest concentration at which 95% of the positive samples are detected.
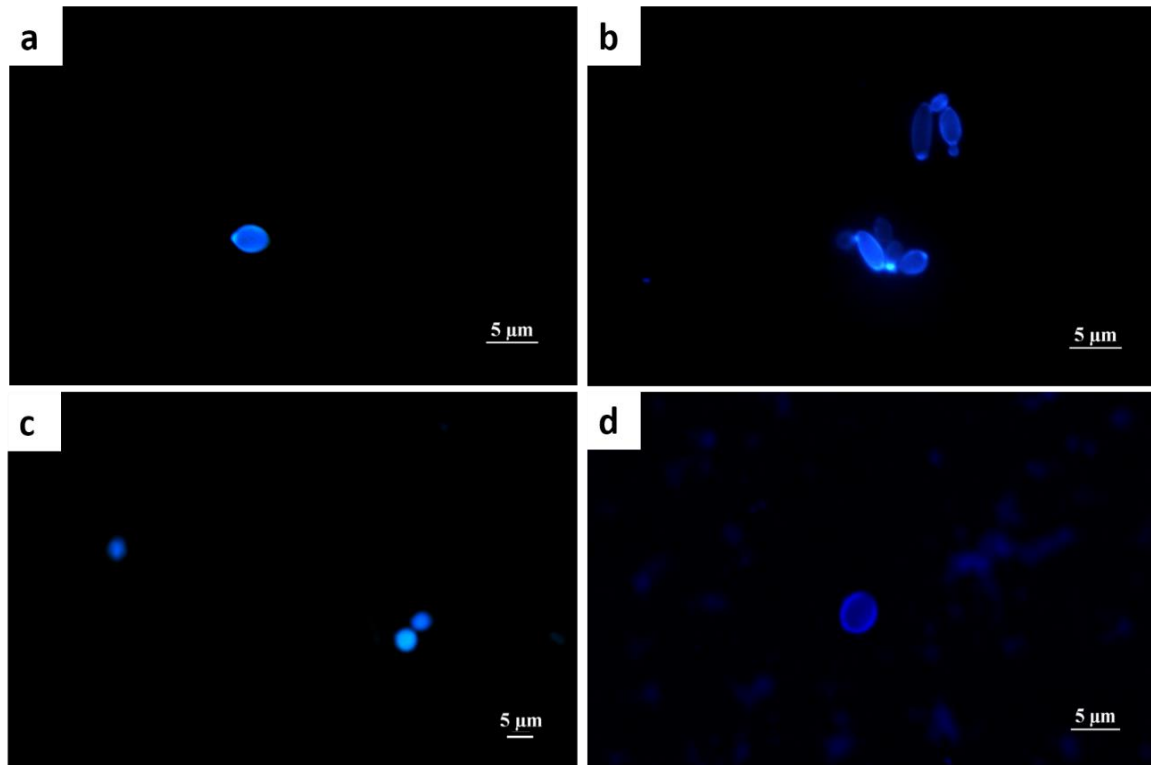
Figure S2. Fluorescence microscopy images of yeasts in human breast milk.
Panels are showing yeasts stained in blue with calcofluor-white from breast milk samples of different geographical origin (Panel a= Spain; b=South Africa; c= Finland; d= Spain.)
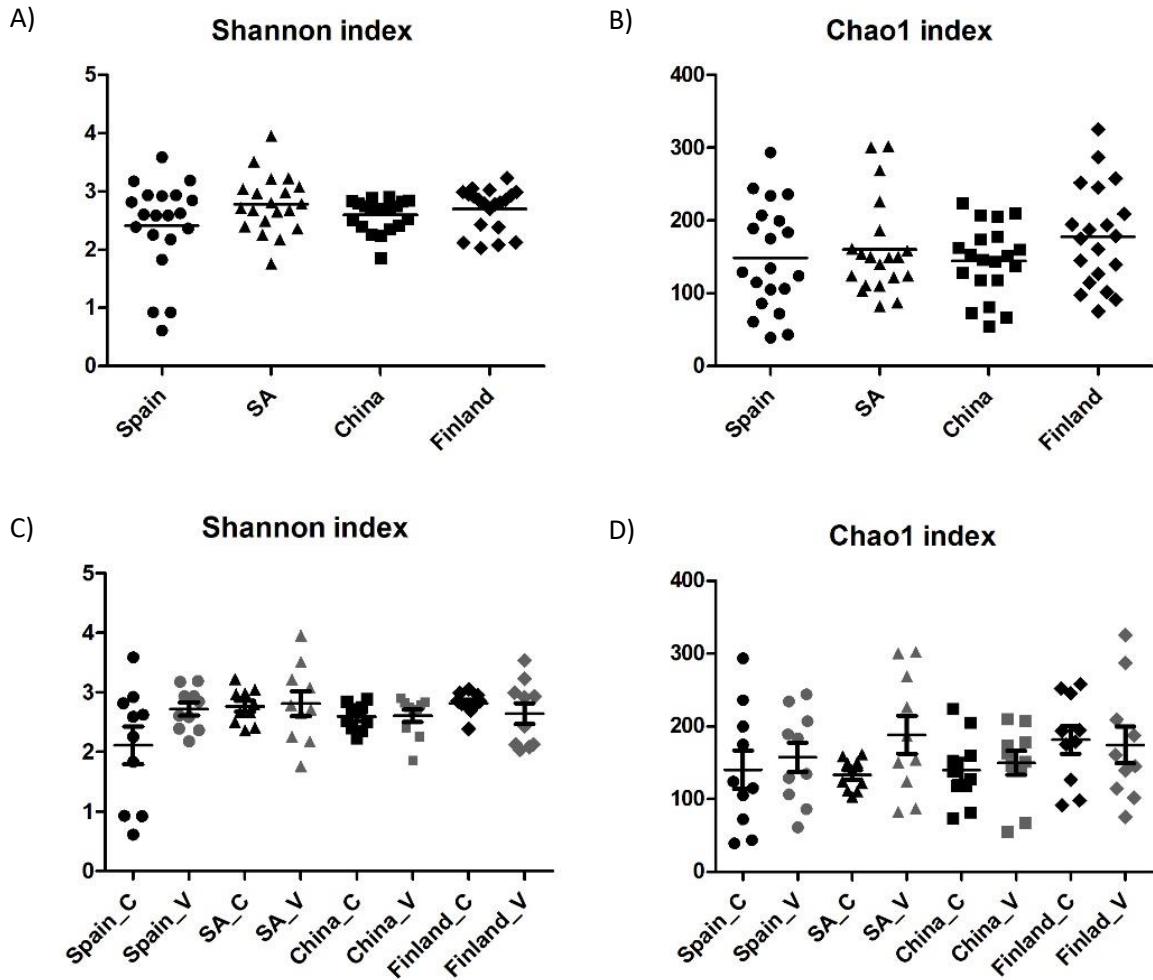V= vaginal delivery; C= C-section delivery.

Figure S3. Diversity and richness in breast milk samples.
Data show Shannon and Chao1 indices, respectively, per country (Panel A and B) and taking into account mode of delivery (Panel C and D). C=C-section, V=Vaginal
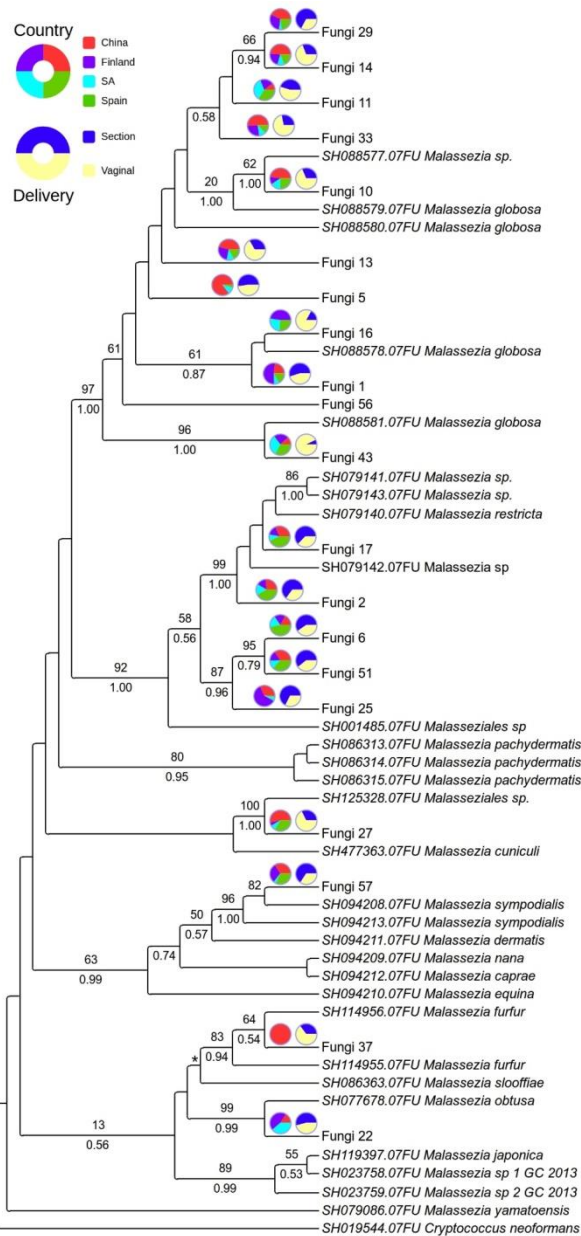
Figure S4. Molecular phylogenetic tree inferred from a maximum likelihood analysis of ITS sequences of the *Malassezia* OTUs obtained in this work and known members of the genus *Malassezia*. ML support values > 50% over 10,000 replicates are shown above the branches. For branches that were also supported by Bayesian inference, the posterior probability is shown below the branches. Brackets surrounding posterior probability values show a conflict between the Bayesian inference and maximum likelihood analysis, in which *M. nana* clustered in the *M. restricta* branch in maximum likelihood analysis, but outside it in bayesian inference. The tree is rooted with *Cryptococcus neoformans.* Pie charts indicate prevalence of each OTU per country and mode of delivery. The 20 most prevalent *Malassezia* OTUs found in this work are included in the tree.