Supplementary figures 1-4

**Supplementary figure 1.** *Candida* DNA isolation and amplification. **A.** DNA quality and integrity from the extraction procedure implemented (see methods section) was analyzed on genetic material isolated from: Colony; CHROMagar plates, cytobrush; oral cytobrush scrapings and mouth rinse; oral rinse with PBS. Top panel depicts the images obtained after 0.8% agarose gel electrophoresis of 2.5µg genomic DNA/lane. Lambda HindIII is present to the left in each panel. Arrow indicates the integrity of the genomic DNA, smearing below hereof indicates degradation and/or presence of RNA. Lower panel depicts the results obtained after ITS1/2 PCR amplification of *Candida* DNA as described in the methods section. Products were analysed by 2% agarose gel electrophoresis. 50bp ladder is present in left lanes. The bracket depicts the variability in product sizes generated, indicating amplification of multiple species in certain samples. **B.** The diagnostic DNA amplification assay was validated on 60 reference strains. Representative results obtained from *Candida albicans/glabrata* amplification are shown. Arrows indicate the differing PCR product size obtained from the two strains after amplification and 2% agarose gel electrophoresis.

**Supplementary figure 2.** *Candida* internal transcribed spacer (ITS) target region. **A.** Relative position of the ITS1 and ITS2 regions, within the 5.8S ITS, tested for as target region for unbiased *Candida* amplification. Positions of the selected ITS1 and ITS2 regions, according to GanBank accession number L28817, are shown. **B.** Sequence results obtained from amplification and sequencing (see methods section) of the ITS1 or **C,** ITS2 target regions from *Candida parpsilosis* reference strains. Arrows indicate polymorphic positions obtained in both ITS regions in one particular *parpsilosis* reference strain species (D5 for ITS1 and D8 for ITS2). Sequences were aligned using ClustalW and
GenDoc (www.psc.edu/biomed/genedoc) software packages. Ref represents the \textit{parapsilosis} ITS sequence from GenBank accession number JF289157. Polymorphic positions are shown by arrows. Numbers indicate the nucleotide position relative to the sequence starting point of the amplified products.

\textbf{Supplementary figure 3.} Phenotypic \textit{albicans} species genetically identified as \textit{dubliniensis} species. Genetic material obtained from 7 patients was isolated, ITS1 amplified and sequenced (see methods section). Sequences were aligned against the sequence of one of the \textit{Candida albicans} reference strain sequences. Polymorphic positions discriminating the patients obtained sequences from \textit{albicans} are shaded in grey. Note the position of different mono- and di-nucleotide deletions within the reference \textit{albicans} and \textit{dubliniensis} sequences aligned. Sequences were aligned using ClustalW and GenDoc (www.psc.edu/biomed/genedoc) software packages. Ref represents the \textit{albicans} ITS sequence from GenBank accession number AY939786.1. Polymorphic insertions/deletions found among reference strain isolates are shown, substitutions are shown in grey shading. Numbers indicate the nucleotide position relative to the sequence starting point of the amplified products.

\textbf{Supplementary figure 4.} Polymorphisms identified in \textit{Candida} reference strains. Examples of polymorphic positions identified in the ITS1 amplified and sequenced products derived from \textit{tropicalis} and \textit{glabrata} reference strains. Single nucleotide substitutions and deletions were identified in multiple \textit{tropicalis} reference strains and single- to tetra–nucleotide insertions/deletions and polymorphic positions were identified in \textit{glabrata} reference strains. Sequences were aligned using ClustalW and GenDoc (www.psc.edu/biomed/genedoc) software packages. Numbers indicate the nucleotide position relative to the sequence starting point of the amplified products.
Supplementary figure 1

A

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<th>Colony</th>
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B

<table>
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Candida albicans internal transcribed spacer 1 (ITS1) nuc 197-729 and ITS2 nuc 970-1316; 5.8S ribosomal RNA; internal transcribed spacer. GenBank acc.: L28817

A

B

C

C. Parapsilosis reference strains
Supplementary figure 3

"albicans" colonies identified as dubliniensis
Supplementary figure 4

*C. tropicalis* reference strains

*C. glabrata* reference strains