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(54) 发明名称

用于检测酵母和真菌物种的核酸探针

(57) 摘要

本发明涉及 RPS7 基因的部分或其相应的 mRNA 在用于真菌和酵母物种的诊断测定法中的用途和用于此类测定法和方法的序列。

1. 用于酵母或其它真菌物种的诊断试剂盒,其包含能够结合 RPS7 基因或其相应 mRNA 的至少部分的寡核苷酸探针,其中 RPS7 基因的所述部分是曲霉属的 RPS7 基因的外显子 3 的部分或者其中 RPS7 基因的所述部分相当于白色假丝酵母的 RPS7 基因的碱基对位点 508 至碱基对位点 711 的这一部分。

2. 权利要求 1 中所述的试剂盒,其还包含用于扩增 RPS7 基因的至少部分的引物。

3. 权利要求 2 中所述的试剂盒,其包含用于 RPS7 基因的部分的正向和反向引物。

4. 权利要求 1 至 3 的任一项中所述的试剂盒,其包含针对曲霉属的 RPS7 基因的外显子 3 的部分的探针和针对相当于白假丝酵母的 RPS7 基因的位点 508 至 711 这一部分的探针。

5. 权利要求 1 至 3 的任一项中所述的诊断试剂盒,其中探针选自 SEQ ID NO 1 至 SEQ ID NO 7、SEQ ID No 176 至 SEQ ID NO 189 和 SEQ ID NO 378 至 SEQ ID NO 413 以及 SEQ ID NO 419 至 SEQ ID NO 448。

6. 权利要求 1 至 3 的任一项中所述的试剂盒,其包含至少一种正向体外扩增引物和至少一种反向体外扩增引物,正向扩增引物选自 SEQ ID NO 8 至 SEQ ID NO 40、SEQ ID NO 414、SEQ ID NO 417、SEQ ID NO 418,反向扩增引物选自 SEQ ID NO 3、SEQ ID NO 22 至 SEQ ID NO 49、SEQ ID NO 415 和 SEQ ID NO 416。

7. 权利要求 6 中所述的诊断试剂盒,其基于直接核酸检测技术。

8. 权利要求 6 中所述的诊断试剂盒,其基于信号扩增核酸检测技术。

9. 权利要求 6 中所述的诊断试剂盒,其基于核酸体外扩增技术。

10. 权利要求 9 中所述的诊断试剂盒,其中所述核酸体外扩增技术选自聚合酶链式反应 (PCR)、连接酶链式反应 (LCR)、基于核酸序列的扩增 (NASBA)、链置换扩增 (SDA)、转录介导的扩增 (TMA)、分支 DNA 技术 (bdNA) 和滚环扩增技术 (RCAT) 或其他基于酶促体外扩增的技术中的一种或多种。

11. 在适当的条件下能够结合 RPS7 基因或其相应 mRNA 的至少部分的至少一种寡核苷酸探针在制备用于检测测试样品中的靶生物体的试剂中的用途,其中 RPS7 基因的所述部分是曲霉属的 RPS7 基因的外显子 3 的部分或者其中 RPS7 基因的所述部分相当于白色假丝酵母的 RPS7 基因的碱基对位点 508 至碱基对位点 711 的这一部分,其中所述试剂用在检测测试样品中的靶生物体的方法,该方法包括步骤:

(i) 在适当的条件下将测试样品与至少一种能够结合 RPS7 基因或其相应 mRNA 的至少部分的寡核苷酸探针混合;

(ii) 在高严格度条件下将可能存在于测试样品中的任何核酸与所述寡核苷酸杂交从而形成探针:靶双链体;和

(iii) 确定探针:靶双链体是否存在;双链体的存在明确地确认了测试样品中所述靶生物体的存在。

12. 权利要求 11 中所述的用途,其中探针选自 SEQ ID NO 1 至 SEQ ID NO 49、SEQ ID NO 176 至 SEQ ID NO 189 和 SEQ ID NO 378 至 SEQ ID NO 448。

13. 在适当的条件下能够结合 RPS7 基因或其相应 mRNA 的至少部分的至少一种寡核苷酸探针在制备用于检测测试样品中的靶生物体的试剂中的用途,其中 RPS7 基因的所述部分是曲霉属的 RPS7 基因的外显子 3 的部分或者其中 RPS7 基因的所述部分相当于白色假丝酵母的 RPS7 基因的碱基对位点 508 至碱基对位点 711 的这一部分,其中所述试剂用在检测

一种或多种酵母和 / 或其它真菌物种的存在的诊断测定法中。

14. 在适当的条件下能够结合 RPS7 基因或其相应 mRNA 的至少部分的至少一种寡核苷酸探针在制备用于测量患者中酵母和 / 或其它真菌滴度的试剂中的用途, 其中 RPS7 基因的所述部分是曲霉属的 RPS7 基因的外显子 3 的部分或者其中 RPS7 基因的所述部分相当于白色假丝酵母的 RPS7 基因的碱基对位点 508 至碱基对位点 711 的这一部分, 其中所述试剂用在测量患者中酵母和 / 或其它真菌滴度的诊断测定法中。

15. 在适当的条件下能够结合 RPS7 基因或其相应 mRNA 的至少部分的至少一种寡核苷酸探针在制备用于测量患者中酵母和 / 或其它真菌滴度的试剂中的用途, 其中 RPS7 基因的所述部分是曲霉属的 RPS7 基因的外显子 3 的部分或者其中 RPS7 基因的所述部分相当于白色假丝酵母的 RPS7 基因的碱基对位点 508 至碱基对位点 711 的这一部分, 其中所述试剂用在评估经设计以减少患者中酵母和 / 或真菌滴度的治疗方案的功效的方法中的治疗方案的一种或多种关键阶段。

16. 权利要求 1 至 10 的任一项中所述的试剂盒或核酸分子在测量环境或测试样品中酵母和 / 或其它真菌污染的测定法中的用途, 其中所述核酸分子能够结合曲霉属的 RPS7 基因的外显子 3 的部分或者能够结合相当于白色假丝酵母的 RPS7 基因的碱基对位点 508 至碱基对位点 711 的这一部分的基因部分。

17. 权利要求 16 中所述的用途, 其中所述环境是医院, 并且所述测试样品选自需要生物体负载或质量评估的食物样品、环境样品、工业样品。

18. 权利要求 17 中所述的用途, 其中所述环境样品是水。

19. 权利要求 17 中所述的用途, 其中所述工业样品是半成品样品或成品。

20. 权利要求 1 至 10 的任一项中所述的试剂盒或核酸分子在鉴定和 / 或表征一种或多种能够用于破坏 RPS7 基因功能的破坏剂中的用途, 其中所述核酸分子能够结合曲霉属的 RPS7 基因的外显子 3 的部分或者能够结合相当于白色假丝酵母的 RPS7 基因的碱基对位点 508 至碱基对位点 711 的这一部分的基因部分。

21. 权利要求 20 中所述的用途, 其中所述破坏剂选自反义 RNA、PNA。

22. 权利要求 21 中所述的用途, 其中所述破坏剂选自 siRNA。

用于检测酵母和真菌物种的核酸探针

发明领域

[0001] 本发明涉及核糖体蛋白基因、相应的 mRNA 和与其相关的特异性探针、引物和寡核苷酸以及它们在检测和 / 或鉴别酵母和真菌物种的诊断测定法中的用途。具体地,本发明涉及相应于核糖体蛋白 RPS7 的基因和其相应的 mRNA。

[0002] 发明背景

[0003] 对作为感染的病因的酵母和真菌的检测和鉴定从未如此重要过。处于酵母和真菌感染风险中的免疫受损患者的数目持续增加,引发疾病的真菌因子 (fungal agent) 的群谱也同样在增加。真菌感染,特别地侵入性真菌感染的死亡率在某些处于风险中的患者群体中为 30%或更大 (“Stakeholder Insight: Invasive fungal infections”, Datamonitor, Jan 2004)。可获得的抗真菌剂的成员阵容在不断扩大;然而,对抗真菌药的固有和新出现抗性的识别也在不断增加。这些因素促成了对实验室试验中成本控制的不断增加的需要并且已导致在试验程序中实验室联合 (laboratory consolidation)。

[0004] 侵入性真菌感染正在增长。2003 年,据估计 900 万处于风险的患者中有 120 万发生感染。免疫受损患者 (包括移植和手术患者、新生儿、癌症患者、糖尿病患者和患有 HIV/AIDS 的患者) 处于发生侵入性真菌感染的高风险中 (Datamonitor report: Stakeholder opinion—Invasive fungal infections, options outweigh replacements 2004)。每年报导了大量的严重败血症 (sepsis)。尽管其医学管理取得了提高,但败血症仍然构成了重症监护医学 (intensive care medicine) 中的最大挑战之一。在医院实验室中,负责引发败血症病的微生物体 (细菌、真菌和酵母) 传统地借助于非常耗时 (通常花费 2 至 5 天的时间完成,对于真菌感染的诊断多达 8 天) 的灵敏度低 (25-82%) 的微生物体学培养方法来检测。最终的诊断通常基于从临床样品中回收和鉴定特异性因子或具有独特形态学特征的真菌的显微镜证实。然而,在许多情况下,这些方法不能提供关于感染因子的结论性证据。在这些情况中,可使用特异性宿主抗体反应的检测,虽然这再次可受到患者的免疫状态影响。在通常由细菌和真菌引起的血流感染的检测和鉴定中,时间是关键。有效的治疗取决于发现感染源以及快速和有效地对抗生素或抗真菌剂作出适当的决定。只有在正确鉴定病原体后,才可开始使用特异性抗生素的靶向疗法 (targeted therapy)。许多医生愿意看到用于酵母和真菌的早期诊断的更好的体外扩增和直接检测诊断技术的开发 (“Stakeholder Insight: Invasive fungal infections”, Datamonitor, Jan 2004)。最近 Roche™推出了用于在临床样品中检测细菌、真菌和酵母 DNA 的基于实时 PCR 的测定法 (Septifast™)。因此,存在对开发用于临床部门 (clinical sector) 中生物体分析应用的针对具有临床意义的细菌和真菌病原体的新型快速诊断试验的开发的明确需要。这已将我们引领至搜寻和鉴定用于核酸诊断 (NAD) 试验的新的真菌和酵母核酸靶。

[0005] 假丝酵母属物种 (*Candida* spp.) 和曲霉属物种 (*Aspergillus* spp.) 现列为感染免疫受损患者的最主要病原体。特别地,感染通常发生在尿道、呼吸系统和血流中,在支架、导管和矫形关节 (orthopaedic joint) 插入的位置。大约 10% 的已知的假丝酵母属物种牵涉人的感染。当假丝酵母进入血流时侵入性假丝酵母病发生,并且据估计其在美国以

8/100,000 人口的频率发生,死亡率为 40%。白色假丝酵母 (*Candida albicans*) 是血流感染的第 4 位常见病因。曲霉病通常开始为在一些患者中可发展成威胁生命的侵入性感染的肺部感染并且具有大于 90% 的死亡率。新出现的霉菌病致病因子 (mycoses agent) 包括镰刀菌属 (*Fusarium*)、足放线病菌属 (*Scedosporium*)、接合菌类 (*Zygomycetes*) 和毛孢子菌属物种 (*Trichosporon spp.*) (“Stakeholder Insight: Invasive fungal infections”, Datamonitor, Jan 2004)。

[0006] 基于真菌和酵母核酸的诊断大量集中在核糖体 RNA (rRNA) 基因、RNA 转录物和它们的相关 DNA/RNA 区域。rRNA 基因在所有真菌物种中高度保守并且它们还包含不同的和独特的基因间转录间隔体区域。核糖体 rRNA 包括 3 个基因: 大亚基基因 (28S)、小亚基基因 (18S) 和 5.8S 基因。28S 和 18S rRNA 基因被 5.8S rRNA 和两个内部转录的间隔体 (ITS1 和 ITS2) 分隔。因为 ITS 区域包含大量的序列多态性,因而许多研究者已将它们的努力集中将这些序列多态性作为靶标上 (Atkins 和 Clark, 2004)。rRNA 基因也是多拷贝基因,在真菌基因组中具有 10 个以上的拷贝。

[0007] 许多研究小组正在进行开发用于真菌和酵母感染的新型测定法。除其他方面以外, US2004044193 涉及白色假丝酵母的转录因子 CaTEC1; 其抑制剂和用于诊断和治疗与假丝酵母感染相关联的疾病的方法; 和此外包含核苷酸序列、蛋白质、宿主细胞和 / 或抗体的诊断和药物组合物。W00183824 涉及用于检测来自白色假丝酵母和 / 或都柏林假丝酵母 (*Candida dubliniensis*) 的核糖体核酸的杂交测定探针和 / 或辅助寡核苷酸 (accessory oligonucleotide)。US6017699 和 US5426026 涉及可用于扩增的 DNA 引物组和来自 5 个医学上重要的假丝酵母物种的物种形成 DNA。US 6747137 公开了用于假丝酵母感染的诊断的序列。EP 0422872 和 US 5658726 公开了基于 18S rRNA 基因的探针, 以及 US 5958693 公开了用于诊断一系列酵母和真菌物种的基于 28S rRNA 的探针。US 6017366 描述了用于针对一系列假丝酵母物种的基于核酸的、基于几丁质合成酶基因的序列。

[0008] 然而, 很清楚, 特别地鉴于由现代抗微生物体疗法引起的选择压力下, 需要开发更快、更精确的诊断方法, 所述抗微生物体疗法产生了增加的具有突变的基因组序列的抗性有毒菌株的群体。使得能够早期诊断感染的微生物体病因的方法使得能够选择特异性窄谱抗生素或抗真菌剂来治疗感染 (Datamonitor report: Stakeholder opinion—Invasive fungal infections, options outweigh replacements 2004; Datamonitor report: Stakeholder Opinion—Sepsis, under reaction to an overreaction, 2006)。

[0009] RPS7 是 70 多个核糖体蛋白中的一个。其发现于原核生物体和真核生物体中并且于小核糖亚单位中、在形成小核糖体亚单位的头部的 rRNA 的折叠中起作用。rps7 基因编码在核糖体内具有保守功能的必需蛋白质。在酵母例如酿酒酵母 (*Saccharomyces cerevisiae*) 中, RPS7 由在 14 个碱基对位点上相异的两个基因编码, 每一个基因具有 1 个内含子。Synetos 等人 (1992) 显示酵母属可在具有该基因的一个拷贝的情况下存活, 但两个基因的缺失是致命的。Delbrück 等人 (1997) 克隆和测序了白色假丝酵母中的 rps7 基因 (GenBank 目录号 U37009), 确定白色假丝酵母中的 rps7 缺少内含子并且在氨基酸水平上与酿酒酵母中的 RPS7 蛋白共有 83% 的同源性。该研究小组还显示在菌丝形成过程中 rps7 基因上调, 表达水平比 rRNA 高 3-6 倍。这表明该基因是临床相关的, 因为从酵母形状至菌丝形成的形态发生在假丝酵母属物种感染中是非常重要的。在曲霉菌属物种特别是烟曲霉

(*A. fumigatus*) 中, *rps7* 基因包含 3 个外显子和 2 个内含子, 从而该基因的结构与酵母中发现的基因结构不同。

[0010] 因此, 本发明的目的是提供可用于检测和鉴定一个或多个酵母或真菌物种的序列和 / 或诊断测定法。本发明人已探索了 *rps7* 基因的结构组织以设计假丝酵母和曲霉菌的基因特异性引物。这具有优于现有技术的优点, 因为如果想要在包含假丝酵母作为共生体 (commensal) 的样品中鉴定真菌病原体, 使用通用引物的方法可能是不成功的。假丝酵母将极可能在扩增过程中竞争过真菌病原体并且将优先扩增, 从而导致不能检测致病病原体。此外, Delbrück 等人 1997 已提出: 一个种中不同染色体上的 *rps7* 基因的不同等位基因之间的差异可能甚至比不同的相关无性种中的基因之间的差异大。这可导致本领域技术人员不选择该基因作为用于分子诊断的靶。同样, 对于一些物种例如白色假丝酵母存在不同的序列类型, 这也将导致人们不选择该基因作为用于分子诊断的靶基因。

[0011] 定义

[0012] 如本文中所使用的, 若非明确指出与之相反, 否则下列术语具有约定的意义。

[0013] “合成的寡核苷酸”是指非直接从基因组 DNA 或活生物体来源的 2 个或更多个核苷酸碱基的核酸聚合物的分子。术语合成的寡核苷酸意欲包括化学制造的或体外酶促合成的 DNA、RNA 和 DNA/RNA 杂种分子。

[0014] “寡核苷酸”是具有 2 个或更多个共价连接在一起的核苷酸亚单位的核苷酸聚合物。寡核苷酸通常为大约 10 至大约 100 个核苷酸。核苷酸亚单位的糖基可以是核糖、脱氧核糖或其经修饰的衍生物, 例如 OMe。核苷酸亚单位可通过不阻止寡核苷酸与其互补靶核苷酸序列杂交的键例如磷酸二酯键、经修饰的键或通过非核苷酸部分连接。经修饰的键包括其中用不同的键例如硫代磷酸酯键 (phosphorothioate linkage)、甲基磷酸酯键 (methylphosphonate linkage) 或中性肽键取代标准的磷酸二酯键的键。含氮碱基类似物也可以是根据本发明的寡核苷酸的组成部分。

[0015] “靶核酸”是包含靶核酸序列的核酸。“靶核酸序列”、“靶核苷酸序列”或“靶序列”是能够与互补寡核苷酸杂交的特定脱氧核糖核酸或核糖核苷酸序列。

[0016] “寡核苷酸探针”是具有与其靶核酸序列充分互补从而能够在高严格度杂交条件下形成可检测的杂交体探针: 靶双链体的核苷酸序列的寡核苷酸。寡核苷酸探针是分离的化学物类并且可包括靶向区域外的其他核苷酸, 只要这样的核苷酸不阻止在高严格度杂交条件下的杂交。非互补序列, 例如启动子序列、限制性内切核酸酶识别位点或赋予期望的二级或三级结构 (例如催化活性位) 的序列可用于帮助使用发明的探针进行的检测。寡核苷酸探针任选地被可用于检测或确认探针与其靶序列的杂交的可检测部分 (例如放射性同位素、荧光部分、化学发光部分、纳米颗粒部分、酶或配体) 来进行标记。寡核苷酸探针优选在长度为大约 10 至 500 个核苷酸的大小范围内, 虽然探针的长度可能多达或多于大约 500 个核苷酸, 或少于 10 个核苷酸。

[0017] “杂交体”或“双链体”是两个单链核酸序列之间通过互补碱基之间的 Watson-Crick 碱基配对或非常规碱基配对 (non-canonical base pairing) 形成的复合物。“杂交”是核酸的两个互补链通过其来结合形成双链结构 (“杂交体”或“双链体”) 的过程。

[0018] “真菌”或“酵母”是指真菌界的任何生物体, 并且优选, 是指子囊菌门 (phylum Ascomycota) 的任何生物体和最优选指半子囊菌纲 (class Hemiascomycete) 的任何生物

体。

[0019] “互补性”是由可通过各自链上 Watson-Crick 碱基对之间的氢键形成杂交体或双链 DNA:DNA 或 RNA:RNA 或 DNA:RNA 的 DNA 或 RNA 的单链的碱基序列赋予的性质。腺嘌呤 (A) 通常与胸腺嘧啶 (T) 或尿嘧啶 (U) 互补,而鸟嘌呤 (G) 通常与胞嘧啶 (C) 互补。

[0020] 术语“严格度”用于描述杂交和随后的处理步骤期间存在的温度、离子强度和溶剂组成。本领域技术人员将认识到,可通过个别地或一起地改变这些参数来改变“严格度”条件。在高严格度条件下,将只形成高度互补的核酸杂交体;无足够互补程度的杂交体将不形成。因此,测定条件的严格度决定形成杂交体的两个核酸链之间所需的互补性的量。选择严格度条件以使与靶和与非靶核酸形成的杂交体之间的稳定性的差异最大化。

[0021] 对于“高严格度”条件,核酸碱基配对将只在具有高频率的互补碱基序列的核酸片段之间发生(例如,在“高严格度”条件下的杂交可在具有大约 85-100% 的同一性,优选大约 70-100% 的同一性的同源物之间发生)。对于中等严格度条件,核酸碱基配对将在具有中等频率的互补序列的核酸之间发生(例如,在“中等严格度”条件下的杂交可在具有大约 50-70% 的同一性的同源物之间发生)。因此,对于来源于为遗传多样性的生物体的核酸,通常要求“弱”或“低”严格度的条件,因为互补序列的频率通常是较低的。

[0022] ‘高严格度’条件是相当于当使用长度为大约 500 个核苷酸的探针时,在 42°C 下于由 5xSSPE (43.8g/l NaCl, 6.9g/l $\text{NaH}_2\text{PO}_4\cdot\text{H}_2\text{O}$ 和 1.85g/l EDTA,用 NaOH 调节 pH 至 7.4)、0.5% SDS、5xDenhardt' s 试剂和 100 $\mu\text{g/ml}$ 变性鲑精 DNA 组成的溶液中结合或杂交,然后在 42°C 下于包含 0.1xSSPE、1.0% SDS 的溶液中清洗的条件。

[0023] “中等严格度”条件是相当于当使用长度为大约 500 个核苷酸探针时,在 42°C 下于由 5xSSPE (43.8g/l NaCl, 6.9g/l $\text{NaH}_2\text{PO}_4\cdot\text{H}_2\text{O}$ 和 1.85g/l EDTA,用 NaOH 调节 pH 至 7.4)、0.5% SDS、5xDenhardt' s 试剂和 100 $\mu\text{g/ml}$ 变性鲑精 DNA 组成的溶液中结合或杂交,然后在 42°C 下于包含 1.0xSSPE、1.0% SDS 的溶液中清洗的条件。

[0024] ‘低严格度’条件是相当于当使用长度为大约 500 个核苷酸探针时,在 42°C 下于由 5xSSPE (43.8g/l NaCl, 6.9g/l $\text{NaH}_2\text{PO}_4\cdot\text{H}_2\text{O}$ 和 1.85g/l EDTA,用 NaOH 调节 pH 至 7.4)、0.1% SDS、5xDenhardt' s 试剂 [每 500ml 的 50xDenhardt' s 包含:5g 菲可 (Ficoll) (Type 400, Pharmacia), 5g BSA (组分 V; Sigma)] 和 100 $\mu\text{g/ml}$ 变性鲑精 DNA 组成的溶液中结合或杂交,然后在 42°C 下于包含 5xSSPE、0.1% SDS 的溶液中清洗的条件。

[0025] 在基于核酸体外扩增的技术的情况中,“严格度”通过使用对于该体外扩增技术独有的温度条件和离子缓冲液条件来获得。例如,在 PCR 和实时 PCR 的情况中,“严格度”通过使用对于寡核苷酸引物和探针(对于实时 PCR 杂交)与靶核酸的杂交(以体外扩增靶核酸)的特定温度和离子缓冲强度来获得。

[0026] “高严格度”,当用于指基于体外扩增的检测系统(例如用于 PCR 和实时 PCR)时,包括在包含浓度为 1.5-8mM 的 MgCl_2 的缓冲液环境中范围是 55°C -65°C 的杂交(退火)温度的条件。

[0027] “中等严格度”,当用于基于体外扩增的检测系统例如用于 PCR 和实时 PCR 时,包括在包含浓度为 1.5-8mM 的 MgCl_2 的缓冲液环境中范围是 45°C -54°C 的杂交(退火)温度的条件。

[0028] “低严格度”,当用于基于体外扩增的检测系统例如用于 PCR 和实时 PCR 时,包括在

包含浓度为 1.5-8mM 的 $MgCl_2$ 的缓冲液环境中范围是 40°C -44°C 的杂交（退火）温度的条件。

[0029] 本领域技术人员将理解,本发明的大体上相应的探针可与所指 (referred-to) 的序列不同并且仍然能与相同的靶核酸序列杂交。来自核酸的该变异可以按照序列内相同碱基的百分数或探针与其靶序列之间完全互补的碱基的百分数来表示。本发明的探针大体上相应于核酸序列,如果这些百分数是大约 100% 至大约 80%, 或大约 10 个核苷酸的靶序列中存在 0 个错配的碱基至大约 10 个核苷酸的靶序列中存在大约 2 个错配的碱基。在优选实施方案中,百分数是大约 100% 至大约 85%。在更优选实施方案中,该百分数是大约 90% 至大约 100%; 在其他优选实施方案中,该百分数是大约 95% 至大约 100%。

[0030] “充分互补”或“大体上互补”是指具有足够量的、在高严格度杂交条件下形成对于检测是稳定的杂交体的连续互补核苷酸的核酸。“核酸杂交体”或“探针:靶双链体”是指作为双链的、氢键键合的结构,优选长度为大约 10 至大约 100 个核苷酸、更优选长度为 14 至 50 个核苷酸,尽管这将在一定程度上取决于寡核苷酸探针的总体长度的结构。所述结构对于通过例如化学发光或荧光检测、放射自显著影法、电化学分析或凝胶电泳的方法来检测是足够稳定的。这样的杂交体包括 RNA:RNA、RNA:DNA 或 DNA:DNA 双链体分子。

[0031] “RNA 和 DNA 等同物”是指具有相同互补碱基对杂交性质的 RNA 和 DNA 分子。RNA 和 DNA 等同物具有不同的糖基(即,核糖对脱氧核糖),并且不同在于在 RNA 中存在尿嘧啶而在 DNA 中存在胸腺嘧啶。RNA 和 DNA 等同物之间的差异不导致大体上相应的核酸序列中的差异,因为等同物具有与特定序列的相同程度的互补性。

[0032] “优先杂交”是指在高严格度杂交条件下寡核苷酸探针可以杂交它们的靶核酸,从而形成稳定的探针:靶杂交体(从而表明靶核酸的存在)而不形成稳定的探针:非靶杂交体(这可表明来自其他生物体的非靶核酸的存在)。因此,探针与靶核酸杂交的程度充分大于与非靶核酸杂交的程度,从而使得本领域技术人员能够准确地检测到(例如假丝酵母)的存在并将这些物种与其他生物体相区别。可使用本领域内已知的和本文中描述的技术测量优先杂交。

[0033] “治疗诊断学(theranostics)”是指使用诊断试验以诊断疾病、选择正确的治疗方案和监测患者对治疗的反应。本发明的治疗诊断学可基于本发明的 NAD 测定对从患者收集的样品、拭子(swab)或样本的应用。

[0034] 发明概述

[0035] 本发明提供了用于检测酵母和/或真菌物种的诊断试剂盒,该试剂盒包含能够结合 RPS7 基因或其相应的 mRNA 的至少部分的寡核苷酸探针。寡核苷酸探针可以具有与 RPS7 基因或其相应的 mRNA 的至少部分大体上同源或大体上互补的序列。因此其能够与互补 DNA 或 RNA 分子结合或杂交。RPS7 基因可以是真菌 RPS7 基因。RPS7 基因可以是酵母 RPS7 基因。核酸分子可以是合成的。试剂盒可以包含一个以上这样的探针。特别地,试剂盒可包含许多此类探针。此外试剂盒可包含针对其他生物体(例如细菌物种或病毒)的额外探针。

[0036] RPS7 基因编码作为酵母和真菌中的小核糖体亚基的蛋白质组分的核糖体蛋白 S7。其是核糖体生物体发生所必需的,从而是蛋白质合成所必需的。RPS7 参与 18S rRNA 装配的起始。本发明已鉴定了用于酵母和真菌诊断的高拷贝数目的 mRNA。鉴定的序列不仅适合于基于体外 DNA/RNA 扩增的检测系统,而且还适合于基于信号扩增的检测系统。

此外,鉴定为合适的靶的本发明的序列提供了在一些区域具有显著的基因内序列异质性 (heterogeneity) 的优点,这是有利的并且使得本发明的方面针对群体或物种特异性的靶,并且在一些区域内也具有显著的序列同质性 (homogeneity) 的优点,这使得本发明的方面能够针对用于属特异性酵母和真菌引物和探针,所述引物探针用于酵母和真菌诊断的直接核酸检测技术、信号扩增核酸检测技术和核酸体外扩增技术。RPS7 序列允许诊断测定的多次测试 (multi-test) 能力和自动化。

[0037] 本发明的序列的优点之一是密切相关的酵母和真菌物种之间的基因内 RPS7 核苷酸序列多样性使得能够设计用于检测酵母和真菌的诊断测定法的特异性引物和探针。RPS7 核苷酸序列 (DNA 和 RNA) 可以与直接检测、信号扩增检测和体外扩增技术结合用于诊断测定法。RPS7 序列允许诊断测定法的多决检测能力和自动化。

[0038] 高拷贝数的 RPS7 mRNA 为其与信号扩增检测技术结合用于诊断测定法提供了有利条件。此外, RPS7 转录物的易变性质允许该诊断靶用于存活力诊断测定法。

[0039] 试剂盒还可包含用于 RPS7 基因的至少部分的扩增的引物。适当地,试剂盒包含用于 RPS7 基因的的部分的正向或反向此物。RPS7 基因的部分可以是曲霉菌属 RPS7 基因的外显子 3 的部分。备选地, RPS7 基因的部分可以相当于来自白色假丝酵母 RPS7 基因的碱基对位点 508 至碱基对位点 711 的基因区域的部分。特别优选的是包含针对曲霉菌属 RPS7 基因的外显子 3 的部分的探针或针对相当于白色假丝酵母 RPS7 基因的碱基对位点 508 至碱基对位点 711 的基因区域的部分的探针的试剂盒。可在其他生物体 (例如酵母属物种和新型隐球酵母 (*Cryptococcus neoformans*)) 中发现碱基对位点 508 至碱基对位点 711 的等同区域 (但不必在位点 508 至 711 上)。试剂盒还可包含另外的探针。

[0040] 探针可具有选自如下的序列:SEQ ID NO 1 至 SEQ ID NO 7、SEQ ID NO 176 至 SEQ ID NO 189 和 SEQ ID NO 378 至 SEQ ID NO 413 和 SEQ ID NO 419 至 SEQ ID NO 448 或与这些序列大体上同源或大体上互补的、也可用作 RPS7 基因的探针的序列。

[0041] 试剂盒可包含至少一种正向体外扩增引物和至少一种反向体外扩增引物,正向扩增引物具有选自如下的序列:SEQ ID NO 8 至 SEQ 40、SEQ ID NO 414、SEQ ID NO 417、SEQ ID NO 418 或大体上与其同源或互补的、也可用作正向扩增引物的序列,并且反向扩增引物具有选自如下的序列:SEQ ID NO 3、SEQ ID NO 22 至 SEQ 49、SEQ ID NO 415 和 SEQ ID NO 416 或大体上与其同源或互补的、也可用作反向扩增引物的序列。诊断试剂盒可基于直接核酸检测技术,信号扩增核酸检测技术,以及核酸体外扩增技术,选自聚合酶链式反应 (PCR)、连接酶链式反应 (LCR)、基于核酸序列的扩增 (NASBA)、链置换扩增 (SDA)、转录介导的扩增 (TMA)、分支 DNA 技术 (bdDNA) 和滚环扩增技术 (RCAT) 或其他体外酶促扩增技术的一种或多种。

[0042] 本发明还提供了选自 SEQ ID NO 1 至 SEQ ID NO 466 和大体上与其同源或大体上与其部分互补且在基于 RPS7 基因的诊断中具有功能的序列的核酸分子。核酸分子可包括具有与 SEQ ID NO 1 至 SEQ ID NO 466 的核酸分子的部分大体上同源或大体上互补的序列的寡核苷酸。

[0043] 本发明还提供了检测测试样品中的靶生物体的方法,该方法包括步骤:

[0044] (i) 在适当的条件下将测试样品与至少一种上面定义的寡核苷酸探针混合;和

[0045] (ii) 在高严格度条件下将可存在于测试样品中的任何核酸与上述寡核苷酸杂交

从而形成探针 :靶双链体 ;和

[0046] (iii) 确定探针 :靶双链体是否存在 ;双链体的存在明确地确认了所述靶生物体在测试样品中的存在。

[0047] 探针可具有选自如下的序列 :SEQ ID NO 1至SEQ ID NO 49、SEQ ID NO 176至SEQ ID NO 189和SEQ ID NO 378至SEQ ID NO 448或与这些序列大体上同源或大体上互补的、也可用作 RPS7 基因的探针的序列。

[0048] 本发明的核酸分子和试剂盒可用于诊断测定法以检测一种或多种酵母和 / 或真菌物种的存在、测量患者中的酵母和 / 或真菌滴度或用于评估经设计以减少患者中的酵母和 / 或真菌滴度的治疗方案的功效的方法或测量环境中酵母和 / 或真菌污染。所述环境可以是医院,或其可以是要求生物体负载或质量评估的食物样品、环境样品例如水、工业样品例如半制品样品或成品。

[0049] 本发明的试剂盒和核酸分子可用于鉴定和 / 或表征一种或多种可用于破坏 RPS7 基因功能的破坏剂 (disruptive agent)。破坏剂可选自反义 RNA、PNA 和 siRNA。

[0050] 在一些实施方案中,RPS7 基因是 *E. gossypii* 的基因。在一些这样的实施方案中,RPS7 基因可选自 :SEQ ID NO 54、SEQ ID NO 194、SEQ ID NO 212 或它们各自的 mRNA 等同物、SEQ ID NO 55、SEQ ID NO 195、SEQ ID NO 213 或其部分、或大体上与其同源的序列或大体上与一个或多个序列的部分互补的序列。

[0051] 在一些实施方案中,RPS7 基因是乳酸克鲁维酵母 (*K. lactis*) 的基因。在一些这样的实施方案中,RPS7 基因可选自 :SEQ ID NO 56、SEQ ID NO 196、SEQ ID NO 210 或它们各自的 mRNA 等同物、SEQ ID NO 57、SEQ ID NO 197、SEQ ID NO 211 或其部分、或大体上与其同源的序列或大体上与一个或多个序列的部分互补的序列。

[0052] 在一些实施方案中,RPS7 基因是汉逊得巴利酵母 (*D. Hansenii*) 的基因。在一些这样的实施方案中,RPS7 基因可选自 :SEQ ID NO 60、SEQ ID NO 200、SEQ ID NO 214 或它们各自的 mRNA 等同物、SEQ ID NO 61、SEQ ID NO 201、SEQ ID NO 215 或其部分、或大体上与其同源的序列或大体上与一个或多个序列的部分互补的序列。

[0053] 在本发明的一些实施方案中,包含物种特异性探针的核酸分子可用于区别相同属的物种。

[0054] 例如,白色假丝酵母物种特异性探针可包含含有序列 SEQ ID NO 6、SEQ ID NO 7 和 SEQ ID NO 378 至 SEQ ID NO 385 或其部分、或大体上与其同源的序列或大体上与一个或多个序列的部分互补的序列的寡核苷酸。

[0055] 可在用于检测酵母和真菌靶生物体的核酸的组合物中提供本发明的寡核苷酸。视组合物的期望的用途而定,这样的组合物还可包含缓冲剂、酶、去垢剂、盐等。还可预期,本发明的组合物、试剂盒和方法虽然在本文中描述为包含至少一种合成的寡核苷酸,还可包含具有与合成的核苷酸片段基本上相同的序列的天然寡核苷酸,替代合成的寡核苷酸或在合成的寡核苷酸旁边。

[0056] 本发明还提供了用于靶酵母和 / 或真菌生物体的体外扩增诊断试剂盒,该试剂盒包含至少一种正向体外扩增引物和至少一种反向体外扩增引物,正向扩增引物选自 SEQ ID NO 8-40、SEQ ID NO 414、SEQ ID NO 417、SEQ ID NO 418 或与其大体上同源或互补的、也可用作正向扩增引物的序列中的一种或多种,反向扩增引物选自 SEQ ID NO 3、SEQ ID NO 22

至 SEQ ID NO 49、SEQ ID NO 415 和 SEQ ID NO 416 或与其大体上同源或互补的、也可用作反向扩增引物的序列中的一种或多种。

[0057] 本发明还提供了用于检测候选酵母和 / 或真菌物种的存在的诊断试剂盒,其包含一种或多种含有与候选酵母和 / 或真菌物种的 RPS7 基因的序列大体上互补或大体上同源的序列的 DNA 探针。本发明还提供了一种或多种合成的寡核苷酸,所述寡核苷酸具有与一种或多种选自 RPS7 基因或其 mRNA 转录物、酵母和 / 或真菌 RPS7 基因或其 mRNA 转录物、酵母 RPS7 基因或其 mRNA 转录物、SEQ ID NO 1 至 SEQ ID NO 466 中的一种或多种大体上同源或大体上互补的核苷酸序列。核苷酸可包括 DNA。核苷酸可包括 RNA。核苷酸可包括 DNA、RNA 和 PNA 的混合物。核苷酸可包括合成的核苷酸。本发明的序列(和与本发明的方法、试剂盒组合物和测定法相关的序列)可以经选择与 RPS7 基因的编码区的部分大体上同源。基因可以是来自靶酵母或真菌生物体的基因。本发明的序列优选足以能够与序列的部分形成探针:靶双链体。

[0058] 本发明还提供了用于靶酵母或真菌生物体的诊断试剂盒,其包含与本发明的寡核苷酸(其可以是合成的)大体上同源或大体上互补的寡核苷酸探针。将认识到,适合用作体外扩增引物的序列也可适合于用作寡核苷酸探针:虽然优选地扩增引物可具有大约 15 个核苷酸至大约 30 个核苷酸(更优选大约 15 至 23 个,最优选大约 20 至大约 23 个)的互补部分,但本发明的寡核苷酸探针可以是任何合适的长度。本领域技术人员将认识到,取决于选择的寡核苷酸探针的长度、性质及结构(例如用于 LightCycler 的杂交探针对、Taqman 5' 核酸外切酶探针、发夹环结构等)和序列,需要不同的杂交和 / 或退火条件。还可提供本发明的试剂盒和测定法,其中寡核苷酸探针被固定在表面上。这样的表面可以是珠粒、膜、柱、浸渍片(dipstick)、纳米颗粒、反应室(例如诊断平板的孔)的内表面或反应试管、毛细管或容器的内侧等。

[0059] 靶酵母或真菌生物体可选自白色假丝酵母、光滑假丝酵母(*C. glabrata*)、热带假丝酵母(*C. tropicalis*)、克柔假丝酵母(*C. krusei*)、近平滑假丝酵母(*C. parapsilosis*)、都柏林假丝酵母、高里假丝酵母(*C. guilliermondii*)、挪威假丝酵母(*C. norvegiensis*)、葡萄牙假丝酵母(*C. lusitaniae*)、解脂假丝酵母(*C. lipolytica*)、皱褶假丝酵母(*C. rugosa*)、链状假丝酵母(*C. catenulata*)、西弗假丝酵母(*C. cifferi*)、无名假丝酵母(*C. famata*)、黑马朗斯假丝酵母(*C. haemulonii*)、铁红假丝酵母(*C. pulcherrima*)、产朊假丝酵母(*C. utilis*)、乳酒假丝酵母(*C. kefir*)、维斯假丝酵母(*C. viswanthii*)、诞沫假丝酵母(*C. zealanoides*)、酿酒酵母、新型隐球菌、*E. gossypii*、乳酸克鲁维酵母(*K. Lactis*)、汉逊得巴利酵母、构巢曲霉(*Aspergillus nidulans*)、烟曲霉、土曲霉(*Aspergillus terreus*)、杂色曲霉(*A. versicolor*)、黄曲霉(*A. flavus*)、黑曲霉(*A. niger*)、白曲霉(*A. candidus*)、棒曲霉(*A. clavatus*)、灰绿曲霉(*A. glaucus*)、费氏曲霉(*Neosartorya fischeri*)和费氏曲霉(*A. fischeri*)。

[0060] 靶酵母生物体可以是给定的引物组已通过实验证明的假丝酵母物种,更优选,选自白色假丝酵母、光滑假丝酵母、热带假丝酵母、克柔假丝酵母、近平滑假丝酵母、都柏林假丝酵母、高里假丝酵母、挪威假丝酵母、葡萄牙假丝酵母、解脂假丝酵母、皱褶假丝酵母、链状假丝酵母、西弗假丝酵母、无名假丝酵母、黑马朗斯假丝酵母、铁红假丝酵母、产朊假丝酵母、乳酒假丝酵母、维斯假丝酵母、诞沫假丝酵母。在这些情况下,可针对基因特异性或属特

异性区域设计本发明的扩增引物和寡核苷酸探针,从而使其能够鉴定靶酵母生物体组群的一种或多种、或大部分或基本上所有期望的生物体。合适的正向扩增引物可选自:Can1F:5' -AGC TGG TTT CAT GGA TGT-3' (SEQ ID NO 40)、SEQ ID NO 36 和 SEQ ID NO 37,和/或,SEQ ID NO 38 和 39 的混合物。合适的反向扩增引物可选自 Can2R:5' -TCT GGG TAT CTGAT(A/G)GTT CT-3' (SEQ ID NO 3)、SEQ ID NO 2 和 / 或 SEQ ID NO 4 与 5 的混合物,或确实地,与 SEQ ID NO 41、SEQ ID NO 42、SEQ ID NO 46、SEQ ID NO 47 中的一种或多种大体上互补的寡核苷酸和 / 或 SEQ ID NO 43-45 的混合物和 / 或 SEQ ID NO 48-49 的混合物。合适的属特异性寡核苷酸探针是:CASP:5' -TAA CAT CGT AGG CTA ATC-3' (SEQ ID NO. 1)、SEQ ID NO 6 或 SEQ ID NO 7。假丝酵母物种特异性探针可选自 SEQ ID NO 378 至 SEQ ID NO 413。

[0061] 靶真菌生物体可以是给定的引物组已通过实验证明的曲霉物种,和更优选,选自构巢曲霉、烟曲霉土曲霉、杂色曲霉、黄曲霉、黑曲霉、白曲霉、棒曲霉、灰绿曲霉、费氏曲霉和费氏曲霉。适合的正向扩增引物可以是 SEQ ID NO 414、SEQ ID NO 417 和 SEQ ID NO 418,选择的反向引物可以是 SEQ ID NO 415 或 SEQ ID NO 416。曲霉属物种特异性探针可选自 SEQ ID NO 419 至 SEQ ID NO 448。

[0062] 测试样品可含靶酵母和 / 或真菌生物体的细胞。方法还可包括用于从可能存在于所述测试样品中的靶酵母或真菌生物体的任何细胞释放核酸的步骤。理想的情况是,测试样品是从患者获得的样品(例如拭子或血液、尿、唾液、支气管灌洗物、牙齿样本、皮肤样本、头皮样本、移植器官活检组织、粪便、粘液或排泄物样品)的裂解物。测试样品可以是食物样品、水样品和环境样品、成品、成品或半制品工业样品。

[0063] 本发明还提供了 SEQ ID NO :1-466 的任一种用于一种或多种酵母或真菌物种的存在的诊断测定的用途。所述物种可选自白色假丝酵母、光滑假丝酵母、热带假丝酵母、克柔假丝酵母、近平滑假丝酵母、都柏林假丝酵母、高里假丝酵母、挪威假丝酵母、葡萄牙假丝酵母、解脂假丝酵母、皱褶假丝酵母、链状假丝酵母、西弗假丝酵母、无名假丝酵母、黑马朗斯假丝酵母、铁红假丝酵母、产朊假丝酵母、乳酒假丝酵母、维斯假丝酵母、诞沫假丝酵母、酿酒酵母、新型隐球菌、E. gossypii、乳酸克鲁维酵母、汉逊得巴利酵母、构巢曲霉、烟曲霉土曲霉、杂色曲霉、黄曲霉、黑曲霉、白曲霉、棒曲霉、灰绿曲霉、费氏曲霉和费氏曲霉。

[0064] 本发明还提供了用于治疗诊断、食品安全诊断、工业微生物体诊断、环境监控、兽医诊断、生物体恐怖诊断的试剂盒,其包含一种或多种本发明的合成的寡核苷酸。试剂盒还可包含选自适当的样品收集装置、试剂容器、缓冲剂、标签部分、溶液、去垢剂和补充液的一种或多种物品。本发明还提供了本发明的序列、组合物、核苷酸片段、测定法和试剂盒在治疗诊断、食品安全诊断、工业微生物体诊断、环境监控、兽医诊断、生物体恐怖诊断中的用途。

[0065] 核酸分子、组合物、试剂盒或方法可用于针对检测酵母和 / 或真菌物种的基于诊断核苷酸的测定法。

[0066] 核酸分子、组合物、试剂盒或方法可用于测量患者中酵母和 / 或真菌滴度的诊断测定法。滴度可以体外测量。核酸分子、组合物、试剂盒或方法可用于评估经设计用于减少患者中的酵母和 / 或真菌滴度的治疗方案的功效的方法,其包括在治疗的一种或多种关键阶段评估患者中的酵母和 / 或真菌滴度(通过体内方法或体外方法)。合适的关键阶

段可包括治疗前、治疗期间和治疗后。治疗方案可包括抗真菌剂,例如药物。

[0067] 核酸分子、组合物、试剂盒或方法可用于测量例如医院内的潜在的酵母和 / 或真菌污染的诊断测定法。

[0068] 核酸分子、组合物、试剂盒或方法可用于鉴定和 / 或表征一种或多种可用于破坏 RPS7 基因功能的破坏剂。合适的破坏剂可选自反义 RNA、PNA、siRNA。

[0069] 附图概述

[0070] 图 1 :a :使用引物 Can1F 和 Can2R 扩增的假丝酵母物种 RT-PCR 部分 RPS7 序列的凝胶电泳 ;b :显示白色假丝酵母物种特异性探针 CASP. A 和 B 的特异性的放射自显影照片 ;泳道 1 :标记物 XIV ;2 :白色假丝酵母部分 RPS7 的 RT-PCR 产物 ;3 :热带假丝酵母的部分 RPS7 的 RT-PCR 产物 ;4 :近平滑假丝酵母的部分 RPS7 的 RT-PCR 产物 ;5 :光滑假丝酵母的部分 RPS7 的 RT-PCR 产物 ;6 :都柏林假丝酵母的部分 RPS7 的 RT-PCR 产物。使用假丝酵母属特异性引物 Can1F :5' -AGC TGGTTT CAT GGA TGT-3' ;SEQ ID NO :40 和 Can2R :5' -TCT GGG TAT CTGAT(A/G)GTT CT-3' ;SEQ ID NO :3 产生这些体外扩增的产物。

[0071] 图 2 :针对白色念球菌的基于 rps7 基因和整合引物 SEQ ID No 40 和 SEQ ID NO 3 以及 TaqMan 探针 SEQ ID NO 384 的实时 PCR 测定法的包含性 (Inclusivity) 试验 - 检测到所有 20 个白色假丝酵母株系。

[0072] 图 3 :针对白色念球菌的基于 rps7 基因和整合引物 SEQ ID No 40 和 SEQ ID NO 3 以及 TaqMan 探针 SEQ ID NO 384 的实时 PCR 测定法的特异性。与病理学相关的其他假丝酵母物种包括黑马朗斯假丝酵母、乳酒假丝酵母、铁红假丝酵母、产朊假丝酵母、维斯假丝酵母、涎沫假丝酵母和人 DNA 的交叉核对 - 未观察到交叉反应。

[0073] 图 4 :针对白色念球菌的基于 rps7 基因和整合引物 SEQ ID No 40 和 SEQ ID NO 3 以及 TaqMan 探针 SEQ ID NO 384 和包括白色假丝酵母基因组 DNA 的系列稀释 (10^6 -1 个细胞等同物) 的实时 PCR 测定法的检出限 (Limit of detection) - 检出限为 10 个细胞。

[0074] 图 5 :针对烟曲霉的基于 rps7 基因和整合引物 SEQ ID No 418 和 SEQ ID NO 415 以及 TaqMan 探针 SEQ ID NO 419 和包括烟曲霉基因组 DNA5062 的系列稀释 (10^6 -1 个细胞等同物) 的实时 PCR 测定法的检出限 - 检出限为 1 个细胞等同物。

[0075] 图 6 :针对烟曲霉 (烟曲霉的 20 个株系) 的基于 rps7 基因和整合引物 SEQ ID No 418 和 SEQ ID NO 415 以及 TaqMan 探针 SEQ ID NO419 的实时 PCR 测定法的包含性试验 - 检测到所有烟曲霉株系。

[0076] 图 7 :针对烟曲霉的基于 rps7 基因和整合引物 SEQ ID No 418 和 SEQ ID NO 415 以及 TaqMan 探针 SEQ ID NO 419 的实时 PCR 测定法的特异性试验。交叉反应性试验板包括一系列曲霉菌物种 - 未检测到交叉反应。

[0077] 发明详述

[0078] 材料和方法

[0079] 生物体和生长条件 :将假丝酵母物种 (CBS 562) 在 37°C 和 180rpm 下培养在 Sabouraud 琼脂 (4% wt/vol 葡萄糖、1% wt/vol 蛋白胨、1.5% 琼脂糖) 上过夜。单个菌落用于接种 10ml Sabouraud 肉汤 (Oxoid™) 并且在 37°C 下培养过夜。将 1ml 过夜培养物用于接种 100ml Sabouraud 肉汤 (Oxoid™) 并且让其生长至指数期和稳定期,分别为 8 小时和 16 小时。将黑曲霉在 30°C 下培养在 Sabouraud 琼脂上进行 48 小时。使用皮下注射针刺入

琼脂,然后转移至 100ml Sabouraud 肉汤中,并且让其生长 48 小时。还将来自倾斜培养的或干燥的储备物 (stock) 的曲霉菌物种于 25°C 下在 Sabouraud 琼脂中培养 1 至 7 天。

[0080] 总 RNA 分离:在培养至指数期后使用 RNeasy™ Mini 试剂盒™(Qiagen™) 从白色假丝酵母提取 RNA。以 10,000rpm 离心 1ml 培养物,将沉淀重悬浮于 100 μl YI 裂解缓冲液 (0.1M EDTA,1M 山梨醇,0.1% β-巯基乙醇手 1000U 裂解酶) 并且在 30°C 下温育 20 分钟。通过在 1.2% MOPS 变性凝胶上进行凝胶电泳来评估总 RNA 的量并且使用 TBS-380™迷你荧光计 (minifluorometer) (Turner Systems™) 来对其进行定量。

[0081] RPS7 真菌/酵母属特异性体外扩增引物的设计:使用 Ambion™酵母总 RNA 分离试剂盒从 5 个假丝酵母物种:白色假丝酵母、光滑假丝酵母、热带假丝酵母、近平滑假丝酵母和都柏林假丝酵母分离总 RNA 并且按照厂商说明书来进行该提取。然后对所有 5 种分离的总 RNA 进行体外 RT-PCR 扩增以证实 Can1F (SEQ ID NO. 40) 和 Can2R (SEQ ID NO. 3) 用于从未表征的酵母物种 (热带假丝酵母、近平滑假丝酵母和都柏林假丝酵母) 产生序列的用途。使用体外扩增引物 SEQ ID NO. 3 和 SEQ ID NO. 40,按照厂商说明书使用 Titan One Tube™ RT-PCR 系统 (Roche) 对检查的所有假丝酵母物种的分离的总 RNA 进行 RT-PCR 扩增。然后在 1.2% 的琼脂糖凝胶上对所得的 RT-PCR 体外扩增的产物进行电泳以确定体外扩增的成功并随后 Southern 印迹 (图 1A)。然后按照厂商说明书使用 Roche High Pure™ PCR 产物纯化试剂盒纯化来自未表征的假丝酵母 RPS7 序列的 RT-PCR 体外扩增产物的剩余物,随后使用 SEQ ID NO. 40 作为测序引物对其进行测序以产生这些生物体的新的 RPS 7 部分序列数据 (SEQ ID 64 和 65、66 和 67、68 和 69、70 和 71)。

[0082] Can1F :5' -AGC TGG TTT CAT GGA TGT-3' :SEQ ID NO :40。

[0083] Can2R :5' -TCT GGG TAT CTG AT(A/G)GTT CT-3' :SEQ ID NO :3。

[0084] 使用体外 PCR 扩增-引物 CanF1 (SEQ NO :40) 和 CanR2 (SEQ ID NO :3) 进行的假丝酵母、酿酒酵母和新型隐球菌物种的部分 RPS7 序列的确定:为了确定和扩大假丝酵母物种的部分 RPS7 序列的核苷酸序列数据库以及还为了进一步证明体外 PCR 扩增引物 CanF1 (SEQ ID NO 40) 和 Can2R (SEQ ID NO 3) 的广泛用途,对下列假丝酵母株系进行一系列 PCR 体外扩增,白色假丝酵母株系 178、180、320、369、765、16733、1560、9559、4154、2700、562、3822、3156、3345、3328,都柏林假丝酵母 3949、光滑假丝酵母株系 9087、4692、205444、10269、9556、5563、3959、138、3605、3897、8018、3863、3902、604、近平滑假丝酵母株系 3902、604、2194、2196、1001、1716、9557、5579、克柔假丝酵母株系 5579、9560、6055、17518、573、3165、3922、3847 和热带假丝酵母株系 3895、94、4225、5557、15902、4139、3873、3870、8157、2311。使用 Edge Biosystems Genomic DNA 纯化试剂盒从这些株系的每一个株系分离总基因组 DNA,然后通过 1.2% 琼脂糖凝胶上对每一种分离的 DNA 样品进行电泳来确定纯化的 DNA 的完整性。然后按照厂商说明书使用 Taq DNA 聚合酶 (Roche) 和 CanF1 及 CanR2 将各 DNA 样品经历体外 PCR 扩增。然后使用 Roche High Pure PCR 产物纯化试剂盒纯化从各假丝酵母株系的基因组 DNA 扩增的 PCR 产物。然后使用 CanF1 作为测序引物对纯化的 PCR 产物进行核苷酸测序列。这导致产生所有测试假丝酵母株系的新的部分 RPS7 核苷酸序列。由 SEQ ID 62 至 SEQ ID NO. 175 代表的序列代表了产生的测试的假丝酵母株系和上述的假丝酵母株系的部分 RPS7 核苷酸序列。此外,使用 PCR 扩增引物 SEQ ID NO 40 和 SEQ ID NO 3 扩增从假丝酵母物种 (n = 20 个物种 n = 120 个株系) 提取的 DNA。这些引物扩增相当

于白色假丝酵母中的 rps7 基因的位点 508 至 711(目录号 :U37009) 的 204bp 的 rps7 基因的区域。在用裂解酶预处理假丝酵母物种细胞后,使用 MagNA pure 酵母和细菌分离试剂盒 III 在 MagNA Pure 系统 (Roche MolecularSystems) 上提取 DNA。使用 EasyMag 系统 (BioMerieux) 获得一些 DNA 提取物。使用表 1 中概述的试剂和条件进行 PCR 扩增。使用 ExoSAP-IT 试剂盒 (USB) 或 High Pure PCR 纯化试剂盒 (Roche) 清除 PCR 产物以用于 DNA 测序。使用 SEQ ID NO 40 引物通过外界序列服务提供商,Sequiserve (Germany) 进行假丝酵母物种的 PCR 产物的 DNA 测序。此外,使用 PCR 引物 SEQ ID NO 40 和 SEQ ID NO 3 扩增来自新型隐球菌和酿酒酵母物种的 DNA。也使用 SEQ ID NO 40 引物,通过外界序列提供商,Sequiserve (Germany) 测定 PCR 产物的序列。序列 ID NO 222 至 SEQ ID NO 325 代表假丝酵母物质 rps 7 基因 (204bp) 的序列。SEQID NO 449 代表酿酒酵母 rps 7 基因 (204bp) 的序列,SEQ ID NO 451 代表新型隐球菌 rps 7 基因的序列。

[0085] 表 1 :用于扩增假丝酵母酿酒酵母和新型隐球菌中的 rps7 基因的 PCR 试剂和条件。

[0086]

PCR 条件:	反应条件	循环参数:
Icycler (50 μ L)	1 μ L 各引物@ 17 μ M	94 $^{\circ}$ C 1 分钟
	5 μ l 10 \times 缓冲液 (Roche) -	30 \times 45 $^{\circ}$ C 1 分钟
	[100mM Tris-HCL, 15mM MgCl ₂ , 500mM KCL, pH8.3]。	72 $^{\circ}$ C 1 分钟
		72 $^{\circ}$ C 7 分钟
	1 μ l (IU) Taq 聚合酶 (Roche)	

[0087]

1 μ l 储备 dNTP 混合物

(10mM 的各 dNTP)

2-5 μ l DNA 模板

LightCycler (20 μ l)	1 μ l 各引物@10 μ M	
	2 μ l FastStart Mix (HybProbe 试剂盒)	1 \times 40 $^{\circ}$ C 10 分钟 1 \times 95 $^{\circ}$ C 10 分钟
	2.4 μ l (4mM) MgCl ₂	

	0.5 μ l (1U) LightCycler UNG	95 $^{\circ}$ C-10 秒
	2 μ l DNA 模板	45 \times 55 $^{\circ}$ C-30 秒 72 $^{\circ}$ C-1 分钟 冷却 40 $^{\circ}$ C

[0088] 曲霉物种的 RPS7 基因外显子 3 的序列信息的产生。

[0089] PCR 引物 (正向引物 SEQ ID NO 414 和反向引物 SEQ ID NO 415) 经设计用于扩增来自于曲霉属物种中烟曲霉的 RPS7 (GenBank 目录号 :XM_749453 中) 的位点 664-980 的外显子 3 (317bp)。使用这些引物对来自 8 个物种 (n = 67 个株系 - 表 2) 的 DNA 进行 PCR 扩增, 并且成功地获得这些株系的外显子 3 片段的序列信息。设计独立的引物组 (正向引物 SEQ ID NO 417 和反向引物 SEQ ID NO 416) 并且将其用于扩增黑曲霉株系 (n = 10 - 表 2) 中的 RPS7 基因 (外显子 3-317bp)。使用表 3 中描述的条件, 在 iCycler (BioRad) 上使用这些引物进行曲霉属物种中的 RPS7 外显子 3 317bp 的 PCR 扩增。使用 High Pure PCR 纯化试剂盒 (Roche) 清除 PCR 产物以用于 DNA 测序。使用 SEQ ID NO 414 和 SEQ ID NO 417 (正向) 引物通过外界序列服务提供商, Sequiserve (Germany) 进行 DNA 测序。

[0090] 表 2 : 对其 RPS7 基因的外显子 3 进行测序的曲霉属物种和株系。

[0091]

种名	测序的株系的数目
烟曲霉	20
土曲霉	10
杂色曲霉	5
构巢曲霉	7
黄曲霉	10
黑曲霉	10
白曲霉	5
棒曲霉	5
灰绿曲霉	5

[0092] 表 3 :PCR 扩增用于 DNA 测序的曲霉属物种中的 RPS7 基因的外显子 3 的 317bp 区域的 PCR 试剂和 PCR 条件。

[0093]

PCR 条件:	反应条件	循环参数:
Icycler (50 μ L)	1 μ L 各引物@10 μ M	94 $^{\circ}$ C 1 分钟
	5 μ L 10 \times 缓冲液 (Roche) - [100mM Tris-HCL, 15mM MgCL ₂ , 500mM KCL, pH8.3].	30 \times 50/52 $^{\circ}$ C 1 分钟 72 $^{\circ}$ C 1 分钟
	1 μ L (IU) Taq 聚合酶	72 $^{\circ}$ C 7 分钟

[0094]

(Roche)

1 μ L 贮存的 dNTP 混合物

(10mM 的各 dNTP)

2-5 μ L DNA 模板

[0095] 基于 RPS7 基因序列的原型物种特异性白色假丝酵母核酸诊断 (NAD) 测定法的开发:然后检查新的和已存在的 RPS7 序列数据 (SEQ ID NO 62 至 SEQ ID NO 175),并且鉴定白色假丝酵母物种特异性寡核苷酸探针 (CASP, SEQ ID NO. 1),然后合成所述探针以用于与上述 Southern 印迹杂交。使用 T4 多核苷酸激酶 (Roche) 用 γ P³² 在 5' 末端对 CASP (SEQ ID NO. 1) 寡核苷酸探针进行放射性标记,然后将其在 55°C 下与 Southern 印迹杂交,进行 2 小时。移走杂交液,然后在室温下于 6XSSC, 0.1% SDS 中清洗 2 次 (每次 10 分钟),然后在 55°C 下于 6XSSC, 0.1% SDS 中进行高严格度清洗 1 分钟。将印迹暴露于 X 光片,在 -70°C 下进行放射自显影 2 小时。图 1B 显示 CASP 物种特异性寡核苷酸探针只与白色假丝酵母的 RT-PCR 体外扩增产物杂交,从而证明 RPS7 核酸序列作为用于检测目的酵母物种的靶的用途和潜能。

[0096] CASP :5' -TAA CAT CGT AGG CTA ATC-3' :SEQ ID NO. 1

[0097] 用于假丝酵母属物种的寡核苷酸探针的设计。

[0098] 使用生物体信息学工具 (包括 Clustal W 和 BLAST 程序) 对获得的假丝酵母属物种中的 rps7 基因 204bp 靶区域的序列信息 (其代表获得的各个物种的不同序列类型 (SEQ ID NO 222 至 SEQ ID NO 325)) 进行比对和分析,然后设计用于鉴定不同假丝酵母属物种的寡核苷酸探针。对于白色假丝酵母的鉴定,设计寡核苷酸探针 SEQ ID NO 378 至 SEQ ID NO 385。对于克柔假丝酵母的鉴定,设计寡核苷酸探针 SEQ ID NO 386 至 SEQ ID NO 389。对于近平滑假丝酵母的鉴定,设计寡核苷酸探针 SEQ ID NO 390 至 SEQ ID NO 393。对于热带假丝酵母的鉴定,设计寡核苷酸探针 SEQ ID NO 394 至 SEQ ID NO 405。对于光滑假丝酵母的鉴定,设计寡核苷酸探针 SEQ ID NO 406 至 SEQ ID NO 413。

[0099] 使用引物 SEQ ID NO 40 和 SEQ ID NO 3 以及寡核苷酸探针 SEQ NO 378-SEQ ID NO 413 设计针对假丝酵母属物种的核酸诊断测定法。开发的测定法的实例包括针对 5 个假丝酵母属物种 (包括白色假丝酵母、克柔假丝酵母、热带假丝酵母、光滑假丝酵母和近平滑假丝酵母) 的实时 PCR TaqMan 测定法。针对白色假丝酵母的测定法的实例包括引物 SEQ ID NO 40 和 SEQ ID NO 3 以及寡核苷酸探针 SEQ ID NO 384 (图 2)。针对克柔假丝酵母的测定法的实例包括引物 SEQ ID NO 40 和 SEQ ID NO 3 以及探针 SEQ ID NO 386。针对光滑假丝酵母的测定法的实例包括引物 SEQ ID NO 40 和 SEQ ID NO 3 以及探针 SEQ ID NO 412。针对热带假丝酵母的测定法的实例包括引物 SEQ ID NO 40 和 SEQ ID NO 3 以及探针 SEQ ID NO 400。针对近平滑假丝酵母的测定法的实例包括引物 SEQ ID NO 40 和 SEQ ID NO 3 以及探针 SEQ ID NO 392。在 LightCycler 实时 PCR 机器上设定在这些物种特异性测定法,使

用表 4 中描述的条件和试剂进行所述测定法。使用物种的 20 个株系试验每一个物种测定法的包含性,并且对于每一个物种测定法,检测相关株系 ($n = 20$)。就抗包括假丝酵母的 19 个种、其他酵母和皮肤癣菌 (dermatophytes) 的 24 个种、曲霉属的 9 个种、15 个细菌种和人 DNA (表 5) 的种的组群的交叉反应性试验每一个物种测定法。每一个种测定法只检测其设计用于检测的物种的株系,并且不存在与来自其他假丝酵母属物种、曲霉属物种、其他酵母、皮肤癣菌、细菌的 DNA 或人 DNA 的交叉反应。图 3 显示使用白色假丝酵母物种特异性测定法的特异性研究的实例。使用来自相关物种的基因组 DNA 的 10 倍系列稀释 (10^6-1 个细胞等同物) 来确定测定法的检出限 (LOD) 或灵敏度。对于每一个物种测定法确定了为 10 个细胞等同物的检出限。图 4 显示获得的白色假丝酵母测定法的检出限。

[0100] 表 4 :PCR 试剂和热循环条件 :

[0101]

PCR 试剂

反应混合物/20 μL 反应FastStart 混合物 2 μL (Roche LightCycler DNA

Master HybProbe 试剂盒 Cat no 12239272001)

 MgCl_2 3.2 μL 探针 2 μL (终浓度 0.2 μM)引物 1 μL (终浓度 0.5 μM)引物 1 μL UNG 0.5 μL (任选) H_2O 8.3 μL (8.8 μL , 如果未使用 UNG)DNA 模板 2 μL

热循环条件

40 $^{\circ}\text{C}$ 600 秒-1 个循环95 $^{\circ}\text{C}$ 600 秒-1 个循环95 $^{\circ}\text{C}$ 10 秒

45 个循环

62 $^{\circ}\text{C}$ 60 秒40 $^{\circ}\text{C}$ -10 秒-1 个循环

[0102] 用于假丝酵母属物种和烟曲霉测定法中交叉反应性试验中包括的物种的组群。

[0103] 烟曲霉 土曲霉 白曲霉

[0104] 杂色曲霉 构巢曲霉 黄曲霉

[0105] 灰绿曲霉 黑曲霉 棒曲霉

[0106] 白色假丝酵母 光滑假丝酵母 克柔假丝酵母

[0107] 近平滑假丝酵母 热带假丝酵母 都柏林假丝酵母

[0108] 吉勒莫地假丝酵母 解脂假丝酵母 葡萄牙假丝酵母

[0109] 挪威假丝酵母 皱褶假丝酵母 链状假丝酵母

- [0110] 西弗假丝酵母 无名假丝酵母 黑马朗斯假丝酵母
- [0111] 乳酒假丝酵母 铁红假丝酵母 产朊假丝酵母
- [0112] 维斯假丝酵母 诞沫假丝酵母 新型隐球菌
- [0113] 酿酒酵母 阿萨希毛孢子菌 (*T. asahii*) 粘质酵母 (*R. mucilaginosa*)
- [0114] 糠秕孢子菌 (*M. furfur*) 头状芽生裂殖酵母 (*B. capitatus*)
- [0115] 顶孢霉属物种 (*Acremonium* spp.)
- [0116] 澳大利亚离蠕孢 (*B. australiensis*) 夏威夷离蠕孢 (*B. hawiensis*) 新月弯孢菌 (*C. lunata*)
- [0117] 茄病镰孢 (*Fsolani*) 卷枝毛霉 (*Mcircillenoides*) 卷曲毛霉 (*Mramoissimus*)
- [0118] 多变拟青霉 (*P. variotti*) 淡紫拟青霉菌 (*Plilicinus*) 黄青霉 (*Penicillium chry*)
- [0119] 米根霉 (*R. oryzae*) 尖端赛多孢子菌 (*Sced. Apiosporum*)
- [0120] 多育赛多孢子菌 (*Sced, prolificans*)
- [0121] *Scop. Brevicaulis* 荚膜组织胞浆菌 (*H. capsulatum*) 犬小孢子菌 (*M. canis*)
- [0122] *T. quickeanum* 红色毛癣菌 (*T. rubrum*) 金黄色葡萄球菌 (*S. aureus*)
- [0123] 奇异变形杆菌 (*P. mirabilis*) 大肠杆菌 粘质沙雷氏菌 (*S. marcescens*)
- [0124] 铜绿假单胞菌 (*p. aeruginosa*) 阴沟肠杆菌 (*E. cloacae*)
- [0125] 弗氏柠檬酸杆菌 (*C. freundii*)
- [0126] 粪肠球菌 (*E. faecalis*) 肺炎链球菌 (*S. Pneumoniae*)
- [0127] 嗜麦寡养食单胞菌 (*S. maltophilia*)
- [0128] 肺炎克雷伯菌 (*K. pneumoniae*) 产气肠杆菌 (*E. aerogenes*) 鲍氏不动杆菌 (*A. baumani*)
- [0129] 产酸克雷伯菌 (*K. oxytoca*) 尿肠球菌 (*E. faecium*) 人 DNA
- [0130] 针对曲霉属物种的寡核苷酸引物和探针的设计
- [0131] 在 DNA 测序后,使用生物体信息学工具 (包括 Clustal W 和 BLAST 程序) 对外显子 3 RPS7 317bp,获得的从曲霉属物种扩增的 PCR 产物的序列信息 (代表获得的各个物种的不同序列类型 (SEQ ID NO 326 至 SEQ ID NO 377)) 进行比对和分析。然后设计用于扩增烟曲霉和其他曲霉属物种中的 RPS7 基因的 125bp 区域的 PCR 引物 SEQ ID NO 418 和 PCR 引物 SEQ ID NO 415。对于烟曲霉的鉴定,设计寡核苷酸探针 SEQ ID NO 419 至 SEQ ID NO 424。对于白曲霉的鉴定,设计寡核苷酸探针 SEQ ID NO 425 至 SEQ ID NO 428。对于土曲霉的鉴定,设计寡核苷酸探针 SEQ ID NO 429 至 SEQ ID NO 432。对于杂色曲霉的鉴定,设计寡核苷酸探针 SEQ ID NO 433 至 SEQ ID NO 436。对于构巢曲霉的鉴定,设计寡核苷酸探针 SEQ ID NO 437 至 SEQ ID NO 440。对于黄曲霉的鉴定,设计寡核苷酸探针 SEQ ID NO 441 至 SEQ ID NO 442。设计用于棒曲霉的鉴定的寡核苷酸探针 SEQ ID NO 443 至 SEQ ID NO448。
- [0132] 针对曲霉属物种,烟曲霉的基于核酸的诊断测定法:
- [0133] 使用引物 SEQ ID NO 414 至 SEQ ID NO 418 和寡核苷酸探针 SEQ ID NO 419 至 SEQ ID NO 448 设计针对曲霉属物种的核酸诊断测定法。开发的测定法的一个实例是针对烟曲霉的包括引物序列 SEQ ID NO 418 和 SEQ ID NO 415 以及 DNA 寡核苷酸探针 SEQ ID NO 419 的实时 PCRTaqMan 测定法。在 LightCycler 实时 PCR 机器上设定该测定法,使用表 4 中描述的条件和试剂进行所述测定法。使用来自烟曲霉株系编号 5062 的基因组 DNA 的 10 倍系列稀释 (10^6 -1 个细胞等同物) 来确定测定法的检出限 (LOD) 或灵敏度。图 5 显示烟曲霉

测定法的 LOD 为 1 个基因组等同物。通过使用烟曲霉的 20 个株系试验烟曲霉测定法的包含性来确认烟曲霉测定法的特异性。在测定法中检测所有 20 个株系 (图 6)。就抗包括念珠菌属的 20 个种、皮肤癣菌的 24 个种、曲霉属物种的 8 个种、15 个细菌种和人 DNA 的组群在检查烟曲霉测定法。在烟曲霉测定法中不存在这些株系 / 物种或人 DNA (表 5) 的交叉反应。图 7 显示使用曲霉属物种 DNA 组进行的交叉反应性研究的实例。

[0134] 在本文中公开的任何序列与 PatentIn3.3 软件中所附的列表中的其对应物 (counterpart) 不同的情况下, 该说明书中的序列被认为是正确的形式。

[0135] 单词“包含 / 含有”和单词“具有 / 包括”, 当在本文中参照本发明使用时, 用于明确说明所述特征、整体、步骤或组分的存在但不排除一种或多种其他特征、整体、步骤、组分或其组群的存在或添加。

[0136] 要认识到, 本发明的某些特征 (为了清楚起见在分开的实施方案的上下文中描述的) 也可以组合在单个实施方案中提供。相反, 本发明的不同特征 (为了简明起见, 在单个实施方案的上下文中描述的) 也可以分开地或以任何合适的亚组合提供。

[0137] SEQ ID

[0138] 以粗体和下划线显示探针、寡核苷酸等的位置。

[0139] N 或 x = 任何核苷酸 ; w = a/t, m = a/c, r = a/g, k = g/t, s = c/g, y = c/t, h = a/t/c, v = a/g/c, d = a/g/t, b = g/t/c。

[0140] 在一些情况下, 特定的简并选项标示于括号中 : 例如 : (a/g) 是 A 或 G。

- [0141] **SEQ ID NO 1** TAACATCGTAGGCTAATC CASP
- [0142] **SEQ ID NO 2** TCTGGGTATCTGATGTTCT Can2R-n15
- [0143] **SEQ ID NO 3** TCTGGGTATCTGAT (a/g) GTTCT Can2R-d15 :
- [0144] **SEQ ID NO 4** TCTGGGTATCTGATAGTTCT Can2R-A15 :
- [0145] **SEQ ID NO 5** TCTGGGTATCTGATGGTTCT Can2R-G15 :
- [0146] **SEQ ID NO 6** TAACATCGTAGGCTAATC C. albicans antisense probe
- [0147] **SEQ ID NO 7** GATTAGCCTACGATGTTA C. albicans specific probe
- [0148] **RPS7 primer (i)**
- [0149] **SEQ ID NO 8** ATGGnTAGAGGnCCAAAGAA nCA
- [0150] **SEQ ID NO 9** ATGG (c/g) TAGAGG (a/t) CCAAAGAA (g/a) CA
- [0151] **SEQ ID NO 10** ATGGCTAGAGGnCCAAAGAAGCA
- [0152] **SEQ ID NO 11** ATGGCTAGAGGnCCAAAGAAACA
- [0153] **SEQ ID NO 12** ATGGGTAGAGGnCCAAAGAAGCA
- [0154] **SEQ ID NO 13** ATGGGTAGAGGnCCAAAGAAACA
- [0155] **SEQ ID NO 14** ATGGCTAGAGGACCAAAGAAGCA
- [0156] **SEQ ID NO 15** ATGGCTAGAGGACCAAAGAAACA
- [0157] **SEQ ID NO 16** ATGGCTAGAGGTCCAAAGAAGCA
- [0158] **SEQ ID NO 17** ATGGCTAGAGGTCCAAAGAAACA
- [0159] **SEQ ID NO 18** ATGGGTAGAGGACCAAAGAAGCA
- [0160] **SEQ ID NO 19** ATGGGTAGAGGACCAAAGAAACA
- [0161] **SEQ ID NO 20** ATGGGTAGAGGTCCAAAGAAGCA

- [0162] SEQ ID NO 21 ATGGGTAGAGGTCCAAAGAAACA
- [0163] RPS7 primer (ii)
- [0164] SEQ ID NO 22 GCnCCAAGACCATCnGCTGGTCCnCACACA
- [0165] SEQ ID NO 23 GC (c/t/a) CCAAGACCATC (t/c) GCTGGTCC (a/t) CACA
- [0166] SEQ ID NO 24 GCCCCAAGACCATCTGCTGGTCCACACA
- [0167] SEQ ID NO 25 GCTCCAAGACCATCTGCTGGTCCACACA
- [0168] SEQ ID NO 26 GCACCAAGACCATCTGCTGGTCCACACA
- [0169] SEQ ID NO 27 GCCCCAAGACCATCCGCTGGTCCACACA
- [0170] SEQ ID NO 28 GCTCCAAGACCATCCGCTGGTCCACACA
- [0171] SEQ ID NO 29 GCACCAAGACCATCCGCTGGTCCACACA
- [0172] SEQ ID NO 30 GCCCCAAGACCATCTGCTGGTCCCTCACA
- [0173] SEQ ID NO 31 GCTCCAAGACCATCTGCTGGTCCCTCACA
- [0174] SEQ ID NO 32 GCACCAAGACCATCTGCTGGTCCCTCACA
- [0175] SEQ ID NO 33 GCCCCAAGACCATCCGCTGGTCCCTCACA
- [0176] SEQ ID NO 34 GCTCCAAGACCATCCGCTGGTCCCTCACA
- [0177] SEQ ID NO 35 GCACCAAGACCATCCGCTGGTCCCTCACA
- [0178] RPS7 primer (iii)
- [0179] SEQ ID NO 36 CCAGCTGGTTTCATGGATGTnATCA
- [0180] SEQ ID NO 37 CCCAGCTGGTTTCATGGATGT (c/t) ATCA
- [0181] SEQ ID NO 38 CCCAGCTGGTTTCATGGATGTCATCA
- [0182] SEQ ID NO 39 CCCAGCTGGTTTCATGGATGTTATCA
- [0183] SEQ ID NO 40 **AGCTGGTTTCATGGATGT** CanIF genus specific primer
- [0184] RPS7 primer (iv)
- [0185] SEQ ID NO 41 AGAACHnATCAGATACCCAGAnCCA
- [0186] SEQ ID NO 42 AGAAC (c/t) ATCAGATACCCAGA (c/t) CCA
- [0187] SEQ ID NO 43 AGAACTATCAGATACCCAGACCCA
- [0188] SEQ ID NO 44 AGAACTATCAGATACCCAGATCCA
- [0189] SEQ ID NO 45 AGAACCATCAGATACCCAGACCCA
- [0190] SEQ ID NO 46 AGAACHnATCAGATACCCAGA
- [0191] SEQ ID NO 47 AGAAC (c/t) ATCAGATACCCAGA degen. 3' -5' genus spec. primer
- [0192] SEQ ID NO 48 AGAACCATCAGATACCCAGA
- [0193] SEQ ID NO 49 AGAACTATCAGATACCCAGA
- [0194] SEQ ID NO :50 :S. cerevisiae
- [0195] AGCTGGTTTC ATGGATGTCT AGATGCCACC AATGAAAAC T CAGATTGGT CTACGATGTC
AAGGGTAGAT
- [0196] TCGCTGTCCA CCGTATCACC GATGAAGAAG CTTCTTACAA GTTGGGTAAG GTCAAGAAGG
TTCAATTAGG
- [0197] TAAGAAGGGT GTTCCATACG TTGTTACCCA CGATGGTAGA ACTATCAGAT ACCCAGA
- [0198] SEQ ID NO :51 :

- [0199] AGCUGGUUUC AUGGAUGUCU AGAUGCCACC AAUGAAAACU UCAGAUUGGU CUACGAUGUC
AAGGGUAGAU
- [0200] UCGCUGUCCA CCGUAUCACC GAUGAAGAAG CUUCUUACAA GUUGGGUAAG GUCAAGAAGG
UUCAAUUAGG
- [0201] UAAGAAGGGU GUUCCAUCAG UUGUUACCCA CGAUGGUAGA ACUAUCAGAU ACCCAGA
- [0202] SEQ ID NO :52 ;C. glabrata
- [0203] AGCTGGTTTC ATGGATGTTT GGAAGCTACC AACGAAAAC T CAGATTGGT CTACGACGTC
AAGGGTAGAT
- [0204] TCGCTGTCCA CCGTATCACT GACGAAGAAG CTCCTACAA GTTGGGTAAG GTCAAGAAGG
TCCAATTGGG
- [0205] TAAGAAGGGT GTCCATACG TTGTCCTGA CGATGGTAGA ACTATCAGAT ACCCAGA
- [0206] SEQID NO :53 ;C. glabrata
- [0207] AGCUGGUUUC AUGGAUGUUU GGAAGCUACC AACGAAAACU UCAGAUUGGU CUACGACGUC
AAGGGUAGAU
- [0208] UCGCUGUCCA CCGUAUCACU GACGAAGAAG CUUCCUACAA GUUGGGUAAG GUCAAGAAGG
UCCAAUUGGG
- [0209] UAAGAAGGGU GUUCCAUCAG UUGUCACUGA CGAUGGUAGA ACUAUCAGAU ACCCAGA
- [0210] SEQ ID NO :54 ;E. gossypii
- [0211] AGCTGGTTTC ATGGATGTCT AGAGGCTACC AACGAGAACT TCAGATTGGT ATACGATGTC
AAGGGCAGAT
- [0212] TTGCTGTCCA CCGTATCACC GATGAGGAGG CTA CTTACAA GTTGGGTAAG GTTAAGCGCG
TTCAGCTAGG
- [0213] TAAGAAGGGT GTCCATACG TGGTCACTCA CGACGGCAGA ACCATCAGAT ACCCAGA
- [0214] SEQ ID NO :55 ;E. gossypii
- [0215] AGCUGGUUUC AUGGAUGUCU AGAGGCUACC AACGAGAACU UCAGAUUGGU AUACGAUGUC
AAGGGCAGAU
- [0216] UUGCUGUCCA CCGUAUCACC GAUGAGGAGG CUACUUACAA GUUGGGUAAG GUUAAGCGCG
UUCAGCUAGG
- [0217] UAAGAAGGGU GUCCAUACG UGGUCACUCA CGACGGCAGA ACCAUCAGAU ACCCAGA
- [0218] SEQ ID NO :56 ;K. lactis
- [0219] AGCTGGTTTC ATGGATGTTT GGAAGCTACC AACGAAAAC T CAGATTGGT CTACGATGTT
AAGGGTAGAT
- [0220] TCGCTGTCCA CCGTATCACT GATGAAGAAG CTCCTACAA GTTGGCTAAG GTCAAGAAGG
TTCAACTAGG
- [0221] TAAGAAGGGT ATTCCATACG TCGTTACCCA CGACGGTAGA ACCATCAGAT ACCCAGA
- [0222] SEQ ID NO :57 ;K. lactis
- [0223] AGCUGGUUUC AUGGAUGUUU GGAAGCUACC AACGAAAACU UCAGAUUGGU CUACGAUGUU
AAGGGUAGAU
- [0224] UCGCUGUCCA CCGUAUCACU GAUGAAGAAG CUUCCUACAA GUUGGCUAAG GUCAAGAAGG

UUCAACUAGG

[0225] UAAGAAGGGU AUUCCAUACG UCGUUACCCA CGACGGUAGA ACCAUCAGAU ACCCAGA

[0226] SEQ ID NO :58 ;C.albicansRPS7

[0227] AGCTGGTTTC ATGGATGTCT GGAAGCTACC AACGAACATT TCAGATTAGC CTACGATGTT
AAAGGTAAAT

[0228] TCGCCGTTCA CAGAATTTCT GCTGAAGAAG CTGTCTACAA ATTGGGTAAA GTCAAGAAAG
TCCAATTAGG

[0229] TAAGAAAGGT GTTCCATACG TTGTTACCCA CGACGGTAGA ACTATCAGAT ACCCAGA

[0230] SEQ ID NO :59 ;C.albicansRPS7

[0231] AGCUGGUUUC AUGGAUGUCU GGAAGCUACC AACGAACAUU UCAGAUUAGC CUACGAUGUU
AAAGGUAAA

[0232] UCGCCGUUCA CAGAAUUUCU GCUGAAGAAG CUGUCUACAA AUUGGGUAAA GUCAAGAAAG
UCCAAUUAGG

[0233] UAAGAAAGGU GUUCCAUACG UUGUUACCCA CGACGGUAGA ACUAUCAGAU ACCCAGA

[0234] SEQ ID NO :60 ;D.hansenii

[0235] AGCTGGTTTC ATGGATGTCT AGAAGCTACC AACGAACACT TCAGATTAAT CTATGATGTC
AAGGGTAGAT

[0236] TCACTGTCCA CAGAATCACT GCTGAAGAAG CTTCTTACAA GTTAGCTAAG GTCAAGAAGG
TCCAATTAGG

[0237] TAAGAGAGGT ATTCCATACG TTGTCACCCA CGACGGTAGA ACTATCAGAT ACCCAGA

[0238] SEQ ID NO :61 ;D.hansenii

[0239] AGCUGGUUUC AUGGAUGUCU AGAAGCUACC AACGAACACU UCAGAUUAAU CUAUGAUGUC
AAGGGUAGAU

[0240] UCACUGUCCA CAGAAUCACU GCUGAAGAAG CUUCUUACAA GUUAGCUAAG GUCAAGAAGG
UCCAAUUAGG

[0241] UAAGAGAGGU AUUCCAUACG UUGUCACCCA CGACGGUAGA ACUAUCAGAU ACCCAGA

[0242] SEQ ID NO :62 ;C.albicans

[0243] ACCTACCCAGCTGGTTTCATGGATGTCATCACCTTGAAGCTACCAACGAACATTTCA GA 300

[0244] TTAGCCTACGATGTTA AAGGTAAATTCGCCGTTACAGAATTTCTGCTGAAGAAGCTGTC 360

[0245] TACAAATTGGGTAAAGTCAAGAAAGTCCAATTAGGTAAGAAAGGTGTTCCATACGTTGTT 420

[0246] ACCCACGACGGTAGAACTATCAGATACCCAGATCCATTGATCAGAGCTAACGATACCGTT 480

[0247] SEQ ID NO :63 ;C.albicans

[0248] ACCUACCCAGCUGGUUUCUUGGAUGUCAUACCUUGGAAGCUACCAACGAACAUUUCA GA 300

[0249] UUAGCCUACGAUGUUA AAGGUAAAUUCGCCGUUCACAGAAUUUCUGCUGAAGAAGCUGUC 360

[0250] UACAAAUUGGGUAAAGUCAAGAAAGUCCAAUUAGGUAAAGAAAGGUGUCCAUACGUUGU 420

[0251] ACCCACGACGGUAGAACUAUCAGAUACCCAGAUCCAUUGAUCAGAGCUAACGAUACCGUU 480

[0252] SEQ ID NO :64 ;C.glabrata

[0253] ACCTACCCAGCTGGTTTCATGGATGTTATCACCTTGAAGCTACCAACGAAAACTTCAGA 300

[0254] TTGGTCTACGACGTCAAGGGTAGATTTCGCTGTCCACCGTATCACTGACGAAGAAGCTTCC 360

[0255]	TACAAGTTGGGTAAGGTCAAGAAGGTCCAATTGGGTAAGAAGGGTGTTCACATACGTTGTC	420
[0256]	ACTGACGATGGTAGAACTATCAGATACCCAGACCCAAACATCAAGGTCAATGACACCGTC	480
[0257]	SEQ ID NO :65 ;C. glabrata	
[0258]	ACCUACCCAGCUGGUUUCAUGGAUGUUAUCACCUUGGAAGCUACCAACGAAAACUUCAGA	300
[0259]	UUGGUCUACGACGUCAAGGGUAGAUUCGUGUCCACCGUAUCACUGACGAAGAAGCUUCC	360
[0260]	UACAAGUUGGGUAAAGGUCAAGAAGGUCCAAUUGGGUAAAGAAGGGUGUCCAUACGUUGUC	420
[0261]	ACUGACGAUGGUAGAACUAUCAGAUACCCAGACCCAAACAUCAAGGUCAAUGACACCGUC	480
[0262]	SEQ ID NO :66 ;C. tropicalis	
[0263]	-----GGAAGCTACCAACGAACACTTCA GA	25
[0264]	TTGATTACGATGTT AAAGGTAAATTCGCTGTTCACAGAATTTCTGCTGAAGAAGCTTCT	85
[0265]	TACAAATTAGGTAAAGTCAAGAAGGTTCAATTAGGTAAAAAAGGTGTTCACATACGTTGTC	145
[0266]	ACCCACGATGGT AGAACCATCAGATACCCAGA -----	177
[0267]	SEQ ID NO :67 ;C. Tropicalis	
[0268]	-----GGAAGCUACCAACGAACACUUCAGA	25
[0269]	UUGAUUUACGAUGUAAAAGGUAAAUUCGUGUUCACAGAAUUUCUGCUGAAGAAGCUUCU	85
[0270]	UACAAUUUAGGUAAAAGUCAAGAAGGUCAAUUAGGUAAAAAAGGUGUCCAUACGUUGUC	145
[0271]	ACCCACGAUGGUAGAACCAUCAGAUACCCAGA -----	177
[0272]	SEQ ID NO :68 ;C. parapsilosis	
[0273]	-----GGAAGCCACCAATGAAAACCTTTA GA	25
[0274]	TTGATTACGATGTC AAAGGTAGATTTGCTGTCCACAGAATCTCAGCTGAAGAAGCCACT	85
[0275]	TACAAATTGGGTAAAGTCAAGAGAGTCCAATTGGGTAAGAAGGGAATCCCACATACGTTGTC	145
[0276]	ACCCACGATGGT AGAACCATCAGATACCCAGA -----	177
[0277]	SEQ ID NO :69 ;C. parapsilosis	
[0278]	-----GGAAGCCACCAAUGAAAACUUUAGA	25
[0279]	UUGAUUUACGAUGUCAAAAGGUAGAUUUCGUGUCCACAGAAUCUCAGCUGAAGAAGCCACU	85
[0280]	UACAAUUUGGGUAAAAGUCAAGAGAGUCCAAUUGGGUAAAGAAGGGAAUCCCAUACGUUGUC	145
[0281]	ACCCACGAUGGUAGAACCAUCAGAUACCCAGA -----	177
[0282]	SEQ ID NO :70 ;C. dubliniensis	
[0283]	-----GGAAGCTACCAACGAAAACCTTCA GA	25
[0284]	TTGGTCTACGACGTCA AGGGTAGATTCGCTGTCCACCGTATCACTGACGAAGAAGCTTCC	85
[0285]	TACAAGTTGGGTAAGGTCAAGAAGGTCCAATTGGGTAAGAAGGGTGTTCACATACGTTGTC	145
[0286]	ACTGACGATGGT AGAACYATCAGATACCCAGA -----	177
[0287]	SEQ ID NO :71 ;C. dubliniensis	
[0288]	-----GGAAGCUACCAACGAAAACUUCAGA	25
[0289]	UUGGUCUACGACGUCAAGGGUAGAUUCGUGUCCACCGUAUCACUGACGAAGAAGCUUCC	85
[0290]	UACAAGUUGGGUAAAGGUCAAGAAGGUCCAAUUGGGUAAAGAAGGGUGUCCAUACGUUGUC	145
[0291]	ACUGACGAUGGUAGAACYAUCAGAUACCCAGA -----	177
[0292]	SEQ ID NO :72 ;> C. albicans369	
[0293]	CATCACCTTGAAGCTACCAACGAACATTTTCAGATTAGTCTACGATGTTAAAGGTAAATTCGCTGTTCA	

CAGAATTTCTG

[0294] CTGAAGAAGCTGCCTACAAATTGGGTAAAGTCAAGAAAGTCCAATTAGGTAAGAAAGGTGTTCCATACG
TTGTTACCCAC

[0295] GACGGTAGAACYATCAGATACCCAG

[0296] SEQ ID NO :73 ;> C. albicans369

[0297] CAUCACCUUGGAAGCUACCAACGAACAUUUCAGAUUAGUCUACGAUGUUAAAGGUAAAUCGCUGUUCA
CAGAAUUUCUG

[0298] CUGAAGAAGCUGCCUACAAAUUGGGUAAAAGUCAAGAAAGUCCAAUUAGGUAAGAAAGGUGUCCAUACG
UUGUUACCCAC

[0299] GACGGUAGAACYAUCAGAUACCCAG

[0300] SEQ ID NO :74 ;> C. albicans178

[0301] CATCACCTTGGAAGCTACCAACGAACATTTTCAGATTAGTCTACGATGTTAAAGGTAAATTCGCTGTTCA
CAGAATTTCTG

[0302] CTGAAGAAGCTGCCTACAAATTGGGTAAAGTCAAGAAAGTCCAATTAGGTAAGAAAGGTGTTCCATACG
TTGTTACCCAC

[0303] GACGGTAGAACYATCAGATACCCAG

[0304] SEQ ID NO :75 ;> C. albicans178

[0305] CAUCACCUUGGAAGCUACCAACGAACAUUUCAGAUUAGUCUACGAUGUUAAAGGUAAAUCGCUGUUCA
CAGAAUUUCUG

[0306] CUGAAGAAGCUGCCUACAAAUUGGGUAAAAGUCAAGAAAGUCCAAUUAGGUAAGAAAGGUGUCCAUACG
UUGUUACCCAC

[0307] GACGGUAGAACYAUCAGAUACCCAG

[0308] SEQ ID NO :76 ;> C. albicans180

[0309] CATCACCTTGGAAGCTACCAACGAACATTTTCAGATTAGTCTACGATGTTAAAGGTAAATTCGCTGTTCA
CAGAATTTCTG

[0310] CTGAAGAAGCTGCCTACAAATTGGGTAAAGTCAAGAAAGTCCAATTAGGTAAGAAAGGTGTTCCATACG
TTGTTACCCAC

[0311] GACGGTAGAACYATCAGATACCCAG

[0312] SEQ ID NO :77 ;> C. albicans180

[0313] CAUCACCUUGGAAGCUACCAACGAACAUUUCAGAUUAGUCUACGAUGUUAAAGGUAAAUCGCUGUUCA
CAGAAUUUCUG

[0314] CUGAAGAAGCUGCCUACAAAUUGGGUAAAAGUCAAGAAAGUCCAAUUAGGUAAGAAAGGUGUCCAUACG
UUGUUACCCAC

[0315] GACGGUAGAACYAUCAGAUACCCAG

[0316] SEQ ID NO :78 ;> C. albicans320

[0317] CATCACCTTGGAAGCTACCAACGAACATTTTCAGATTAGTCTACGATGTTAAAGGTAAATTCGCTGTTCA
CAGAATTTCTG

[0318] CTGAAGAAGCTGCCTACAAATTGGGTAAAGTCAAGAAAGTCCAATTAGGTAAGAAAGGTGTTCCATACG
TTGTTACCCAC

- [0319] GACGGTAGAACYATCAGATACCCAG
- [0320] SEQ ID NO :79 ;> *C. albicans*320
- [0321] CAUCACCUUGGAAGCUACCAACGAACAUUUCAGAUUAGUCUACGAUGUUAAGGUAAAUCGCUGUUCA
CAGAAUUUCUG
- [0322] CUGAAGAAGCUGCCUACAAAUUGGGUAAAAGUCAAGAAAGUCCAUUAGGUAAGAAAGGUGUCCAUCG
UUGUUACCCAC
- [0323] GACGGUAGAACYAUCAGAUACCCAG
- [0324] SEQ ID NO :80 ;> *C. albicans*765
- [0325] CATCACCTTGAAGCTACCAACGAACATTTTCAGATTAGTCTACGATGTTAAAGGTAAATTCGCTGTTCA
CAGAATTTCTG
- [0326] CTGAAGAAGCTGCCTACAAATTGGGTAAAGTCAAGAAAGTCCAATTAGGTAAGAAAGGTGTTCCATACG
TTGTTACCCAC
- [0327] GACGGTAGAACYATCAGATACCCAG
- [0328] SEQ ID NO :81 ;> *C. albicans*765
- [0329] CAUCACCUUGGAAGCUACCAACGAACAUUUCAGAUUAGUCUACGAUGUUAAGGUAAAUCGCUGUUCA
CAGAAUUUCUG
- [0330] CUGAAGAAGCUGCCUACAAAUUGGGUAAAAGUCAAGAAAGUCCAUUAGGUAAGAAAGGUGUCCAUCG
UUGUUACCCAC
- [0331] GACGGUAGAACYAUCAGAUACCCAG
- [0332] SEQ ID NO :82 ;> *C. albicans*16733
- [0333] CATCACCTTGAAGCTACCAACGAACATTTTCAGATTAGTCTACGATGTTAAAGGTAAATTCGCTGTTCA
CAGAATTTCTG
- [0334] CTGAAGAAGCTGCCTACAAATTGGGTAAAGTCAAGAAAGTCCAATTAGGTAAGAAAGGTGTTCCATACG
TTGTTACCCAC
- [0335] GACGGTAGAACYATCAGATACCCAG
- [0336] SEQ ID NO :83 ;> *C. albicans*16733
- [0337] CAUCACCUUGGAAGCUACCAACGAACAUUUCAGAUUAGUCUACGAUGUUAAGGUAAAUCGCUGUUCA
CAGAAUUUCUG
- [0338] CUGAAGAAGCUGCCUACAAAUUGGGUAAAAGUCAAGAAAGUCCAUUAGGUAAGAAAGGUGUCCAUCG
UUGUUACCCAC
- [0339] GACGGUAGAACYAUCAGAUACCCAG
- [0340] SEQ ID NO :84 ;> *C. albicans*15640
- [0341] CATCACCTTGAAGCTACCAACGAACATTTTCAGATTAGTCTACGATGTTAAAGGTAAATTCGCTGTTCA
CAGAATTTCTG
- [0342] CTGAAGAAGCTGCCTACAAATTGGGTAAAGTCAAGAAAGTCCAATTAGGTAAGAAAGGTGTTCCATACG
TTGTTACCCAC
- [0343] GACGGTAGAACYATCAGATACCCAG
- [0344] SEQ ID NO :85 ;> *C. albicans*15640
- [0345] CAUCACCUUGGAAGCUACCAACGAACAUUUCAGAUUAGUCUACGAUGUUAAGGUAAAUCGCUGUUCA

CAGAAUUUCUG

[0346] CUGAAGAAGCUGCCUACAAAUUGGGUAAAAGUCAAGAAAGUCCAAUUAGGUAAGAAAGGUGUCCAUACG
UUGUUACCCAC

[0347] GACGGUAGAACYAUCAGAUACCCAG

[0348] SEQ ID NO :86 ;> C. albicans9559

[0349] CATCACCTTGGAAGCTACCAACGAACATTTTCAGATTAGTCTACGATGTTAAAGGTAAATTCGCTGTTCA
CAGAATTTCTG

[0350] CTGAAGAAGCTGCCTACAAATTGGGTAAAGTCAAGAAAGTCCAATTAGGTAAGAAAGGTGTTCCATACG
TTGTTACCCAC

[0351] GACGGTAGAACYATCAGATACCCAG

[0352] SEQ ID NO :87 ;> C. albicans9559

[0353] CAUCACCUUGGAAGCUACCAACGAACAUUUCAGAUUAGUCUACGAUGUUAAAGGUAAAUCGCUGUUCA
CAGAAUUUCUG

[0354] CUGAAGAAGCUGCCUACAAAUUGGGUAAAAGUCAAGAAAGUCCAAUUAGGUAAGAAAGGUGUCCAUACG
UUGUUACCCAC

[0355] GACGGUAGAACYAUCAGAUACCCAG

[0356] SEQ ID NO :88 ;> C. albicans4154

[0357] CATCACCTTGGAAGCTACCAACGAACATTTTCAGATTAGTCTACGATGTTAAAGGTAAATTCGCTGTTCA
CAGAATTTCTG

[0358] CTGAAGAAGCTGCCTACAAATTGGGTAAAGTCAAGAAAGTCCAATTAGGTAAGAAAGGTGTTCCATACG
TTGTTACCCAC

[0359] GACGGTAGAACYATCAGATACCCAG

[0360] SEQ ID NO :89 ;> C. albicans4154

[0361] CAUCACCUUGGAAGCUACCAACGAACAUUUCAGAUUAGUCUACGAUGUUAAAGGUAAAUCGCUGUUCA
CAGAAUUUCUG

[0362] CUGAAGAAGCUGCCUACAAAUUGGGUAAAAGUCAAGAAAGUCCAAUUAGGUAAGAAAGGUGUCCAUACG
UUGUUACCCAC

[0363] GACGGUAGAACYAUCAGAUACCCAG

[0364] SEQ ID NO :90 ;> C. albicans2700

[0365] CATCACCTTGGAAGCTACCAACGAACATTTTCAGATTAGTCTACGATGTTAAAGGTAAATTCGCTGTTCA
CAGAATTTCTG

[0366] CTGAAGAAGCTGCCTACAAATTGGGTAAAGTCAAGAAAGTCCAATTAGGTAAGAAAGGTGTTCCATACG
TTGTTACCCAC

[0367] GACGGTAGAACYATCAGATACCCAG

[0368] SEQ ID NO :91 ;> C. albicans2700

[0369] CAUCACCUUGGAAGCUACCAACGAACAUUUCAGAUUAGUCUACGAUGUUAAAGGUAAAUCGCUGUUCA
CAGAAUUUCUG

[0370] CUGAAGAAGCUGCCUACAAAUUGGGUAAAAGUCAAGAAAGUCCAAUUAGGUAAGAAAGGUGUCCAUACG
UUGUUACCCAC

- [0371] GACGGUAGAACYAUCAGAUACCCAG
- [0372] SEQ ID NO :92 ;> C. albicans562
- [0373] CATCACCTTGGAAGCTACCAACGAACATTTTCAGATTAGTCTACGATGTTAAAGGTAAATTCGCTGTTCA
CAGAATTTCTG
- [0374] CTGAAGAAGCTGCCTACAAATTGGGTAAAGTCAAGAAAGTCCAATTAGGTAAGAAAGGTGTTCCATACG
TTGTTACCCAC
- [0375] GACGGTAGAACYATCAGATACCCAG
- [0376] SEQID NO :93 ;> C. albicans562
- [0377] CAUCACCUUGGAAGCUACCAACGAACAUUUCAGAUUAGUCUACGAUGUUAAAGGUAAAAUUCGUGUUCA
CAGAAUUUCUG
- [0378] CUGAAGAAGCUGCCUACAAAUUGGGUAAAGUCAAGAAAGUCCAAUUAGGUAAGAAAGGUGUCCAUACG
UUGUUACCCAC
- [0379] GACGGUAGAACYAUCAGAUACCCAG
- [0380] SEQ ID NO :94 ;> C. albicans3822
- [0381] CATCACCTTGGAAGCTACCAACGAACATTTTCAGATTAGTCTACGATGTTAAAGGTAAATTCGCTGTTCA
CAGAATTTCTG
- [0382] CTGAAGAAGCTGCCTACAAATTGGGTAAAGTCAAGAAAGTCCAATTAGGTAAGAAAGGTGTTCCATACG
TTGTTACCCAC
- [0383] GACGGTAGAACYATCAGATACCCAG
- [0384] SEQ ID NO :95 ;> C. albicans3822
- [0385] CAUCACCUUGGAAGCUACCAACGAACAUUUCAGAUUAGUCUACGAUGUUAAAGGUAAAAUUCGUGUUCA
CAGAAUUUCUG
- [0386] CUGAAGAAGCUGCCUACAAAUUGGGUAAAGUCAAGAAAGUCCAAUUAGGUAAGAAAGGUGUCCAUACG
UUGUUACCCAC
- [0387] GACGGUAGAACYAUCAGAUACCCAG
- [0388] SEQ ID NO :96 ;> C. albicans3156
- [0389] CATCACCTTGGAAGCTACCAACGAACATTTTCAGATTAGTCTACGATGTTAAAGGTAAATTCGCTGTTCA
CAGAATTTCTG
- [0390] CTGAAGAAGCTGCCTACAAATTGGGTAAAGTCAAGAAAGTCCAATTAGGTAAGAAAGGTGTTCCATACG
TTGTTACCCAC
- [0391] GACGGTAGAACYATCAGATACCCAG
- [0392] SEQ ID NO :97 ;> C. albicans3156
- [0393] CAUCACCUUGGAAGCUACCAACGAACAUUUCAGAUUAGUCUACGAUGUUAAAGGUAAAAUUCGUGUUCA
CAGAAUUUCUG
- [0394] CUGAAGAAGCUGCCUACAAAUUGGGUAAAGUCAAGAAAGUCCAAUUAGGUAAGAAAGGUGUCCAUACG
UUGUUACCCAC
- [0395] GACGGUAGAACYAUCAGAUACCCAG
- [0396] SEQ ID NO :98 ;> C. albicans3345
- [0397] CATCACCTTGGAAGCTACCAACGAACATTTTCAGATTAGTCTACGATGTTAAAGGTAAATTCGCTGTTCA

CAGAATTTCTG

[0398] CTGAAGAAGCTGCCTACAAATTGGGTAAAGTCAAGAAAGTCCAATTAGGTAAGAAAGGTGTTCCATACG
TTGTTACCCAC

[0399] GACGGTAGAACYATCAGATACCCAG

[0400] SEQ ID NO :99 ;> C. albicans3345

[0401] CAUCACCUUGGAAGCUACCAACGAACAUUUCAGAUUAGUCUACGAUGUUAAAGGUAAAUCGCUGUUCA
CAGAAUUUCUG

[0402] CUGAAGAAGCUGCCUACAAAUUGGGUAAAAGUCAAGAAAGUCCAAUUAGGUAAGAAAGGUGUCCAUACG
UUGUUACCCAC

[0403] GACGGUAGAACYAUCAGAUACCCAG

[0404] SEQ ID NO :100 ;> C. albicans3328

[0405] CATCACCTTGAAGCTACCAACGAACATTTTCAGATTAGTCTACGATGTTAAAGGTAAATTCGCTGTTC
CAGAATTTCTG

[0406] CTGAAGAAGCTGCCTACAAATTGGGTAAAGTCAAGAAAGTCCAATTAGGTAAGAAAGGTGTTCCATACG
TTGTTACCCAC

[0407] GACGGTAGAACYATCAGATACCCAG

[0408] SEQ ID NO :101 ;> C. albicans3328

[0409] CAUCACCUUGGAAGCUACCAACGAACAUUUCAGAUUAGUCUACGAUGUUAAAGGUAAAUCGCUGUUCA
CAGAAUUUCUG

[0410] CUGAAGAAGCUGCCUACAAAUUGGGUAAAAGUCAAGAAAGUCCAAUUAGGUAAGAAAGGUGUCCAUACG
UUGUUACCCAC

[0411] GACGGUAGAACYAUCAGAUACCCAG

[0412] SEQ ID NO :102 ;> C. glabrata90876

[0413] CATCACCTTGAAGCTACCAACGAAAACCTTCAGATTGGTCTACGACGTCAAGGGTAGATTCGCTGTCCA
CCGTATCACTG

[0414] ACGAAGAAGCTTCTACAAGTTGGGTAAAGTCAAGAAGTCCAATTGGGTAAGAAGGGTGTTCATACG
TTGTCACTGAC

[0415] GATGGTAGAACYATCAGATACCCAG

[0416] SEQ ID NO :103 ;> C. glabrata90876

[0417] CAUCACCUUGGAAGCUACCAACGAAAACUUCAGAUUGGUCUACGACGUCAAGGGUAGAUUCGCUGUCCA
CCGUAUCACUG

[0418] ACGAAGAAGCUUCCUACAAGUUGGGUAAAGUCAAGAAGGUCCAAUUGGGUAGAAGGGUGUCCAUACG
UUGUCACUGAC

[0419] GAUGGUAGAACYAUCAGAUACCCAG

[0420] SEQ ID NO :104 ;> C. glabrata4692

[0421] CATCACCTTGAAGCTACCAACGAAAACCTTCAGATTGGTCTACGACGTCAAGGGTAGATTCGCTGTCCA
CCGTATCACTG

[0422] ACGAAGAAGCTTCTACAAGTTGGGTAAAGTCAAGAAGTCCAATTGGGTAAGAAGGGTGTTCATACG
TTGTCACTGAC

- [0423] GATGGTAGAACYATCAGATACCCAG
- [0424] SEQ ID NO :105 ;> C. glabrata4692
- [0425] CAUCACCUUGGAAGCUACCAACGAAAACUUCAGAUUGGUCUACGACGUCAAGGGUAGAUUCGCUGUCCA
CCGUAUCACUG
- [0426] ACGAAGAAGCUUCCUACAAGUUGGGUAAGGUCAAGAAGGUCCA AUUGGGUAAGAAGGGUGUCCA UACG
UUGUCACUGAC
- [0427] GAUGGUAGAACYAUCAGAUACCCAG
- [0428] SEQ ID NO :106 ;> C. glabrata205444
- [0429] CATCACCTTGAAGCTACCAACGAAAACCTCAGATTGGTCTACGACGTCAAGGGTAGATTCGCTGTCCA
CCGTATCACTG
- [0430] ACGAAGAAGCTTCCTACAAGTTGGGTAAGGTCAAGAAGGTCCAATTGGGTAAGAAGGGTGTTCATACG
TTGTCACTGAC
- [0431] GATGGTAGAACYATCAGATACCCAG
- [0432] SEQ ID NO :107 ;> C. glabrata205444
- [0433] CAUCACCUUGGAAGCUACCAACGAAAACUUCAGAUUGGUCUACGACGUCAAGGGUAGAUUCGCUGUCCA
CCGUAUCACUG
- [0434] ACGAAGAAGCUUCCUACAAGUUGGGUAAGGUCAAGAAGGUCCA AUUGGGUAAGAAGGGUGUCCA UACG
UUGUCACUGAC
- [0435] GAUGGUAGAACYAUCAGAUACCCAG
- [0436] SEQ ID NO :108 ;> C. glabrata10269
- [0437] CATCACCTTGAAGCTACCAACGAAAACCTCAGATTGGTCTACGACGTCAAGGGTAGATTCGCTGTCCA
CCGTATCACTG
- [0438] ACGAAGAAGCTTCCTACAAGTTGGGTAAGGTCAAGAAGGTCCAATTGGGTAAGAAGGGTGTTCATACG
TTGTCACTGAC
- [0439] GATGGTAGAACYATCAGATACCCAG
- [0440] SEQ ID NO :109 ;> C. glabrata10269
- [0441] CAUCACCUUGGAAGCUACCAACGAAAACUUCAGAUUGGUCUACGACGUCAAGGGUAGAUUCGCUGUCCA
CCGUAUCACUG
- [0442] ACGAAGAAGCUUCCUACAAGUUGGGUAAGGUCAAGAAGGUCCA AUUGGGUAAGAAGGGUGUCCA UACG
UUGUCACUGAC
- [0443] GAUGGUAGAACYAUCAGAUACCCAG
- [0444] SEQ ID NO :110 ;> C. glabrata9556
- [0445] CATCACCTTGAAGCTACCAACGAAAACCTCAGATTGGTCTACGACGTCAAGGGTAGATTCGCTGTCCA
CCGTATCACTG
- [0446] ACGAAGAAGCTTCCTACAAGTTGGGTAAGGTCAAGAAGGTCCAATTGGGTAAGAAGGGTGTTCATACG
TTGTCACTGAC
- [0447] GATGGTAGAACYATCAGATACCCAG
- [0448] SEQ ID NO :111 ;> C. glabrata9556
- [0449] CAUCACCUUGGAAGCUACCAACGAAAACUUCAGAUUGGUCUACGACGUCAAGGGUAGAUUCGCUGUCCA

CCGUAUCACUG

[0450] ACGAAGAAGCUUCCUACAAGUUGGGUAAGGUCAAGAAGGUCCA AUUGGGUAAGAAGGGUGUCCAUACG
UUGUCACUGAC

[0451] GAUGGUAGAACYAUCAGAUACCCAG

[0452] SEQ ID NO :112 ;> C. glabrata5563

[0453] CATCACCTTGGAAGCTACCAACGAAAACCTCAGATTGGTCTACGACGTCAAGGGTAGATTCGCTGTCCA
CCGTATCACTG

[0454] ACGAAGAAGCTTCTACAAGTTGGGTAAGGTCAAGAAGGTCCAATTGGGTAAGAAGGGTGTTCATACG
TTGTCACTGAC

[0455] GATGGTAGAACYATCAGATACCCAG

[0456] SEQ ID NO :113 ;> C. glabrata5563

[0457] CAUCACCUUGGAAGCUACCAACGAAAACUUCAGAUUGGUCUACGACGUCAAGGGUAGAUUCGCUGUCCA
CCGUAUCACUG

[0458] ACGAAGAAGCUUCCUACAAGUUGGGUAAGGUCAAGAAGGUCCA AUUGGGUAAGAAGGGUGUCCAUACG
UUGUCACUGAC

[0459] GAUGGUAGAACYAUCAGAUACCCAG

[0460] SEQ ID NO :114 ;> C. glabrata3959

[0461] CATCACCTTGGAAGCTACCAACGAAAACCTCAGATTGGTCTACGACGTCAAGGGTAGATTCGCTGTCCA
CCGTATCACTG

[0462] ACGAAGAAGCTTCTACAAGTTGGGTAAGGTCAAGAAGGTCCAATTGGGTAAGAAGGGTGTTCATACG
TTGTCACTGAC

[0463] GATGGTAGAACYATCAGATACCCAG

[0464] SEQ ID NO :115 ;> C. glabrata3959

[0465] CAUCACCUUGGAAGCUACCAACGAAAACUUCAGAUUGGUCUACGACGUCAAGGGUAGAUUCGCUGUCCA
CCGUAUCACUG

[0466] ACGAAGAAGCUUCCUACAAGUUGGGUAAGGUCAAGAAGGUCCA AUUGGGUAAGAAGGGUGUCCAUACG
UUGUCACUGAC

[0467] GAUGGUAGAACYAUCAGAUACCCAG

[0468] SEQ ID NO :116 ;> C. glabrata138

[0469] CATCACCTTGGAAGCTACCAACGAAAACCTCAGATTGGTCTACGACGTCAAGGGTAGATTCGCTGTCCA
CCGTATCACTG

[0470] ACGAAGAAGCTTCTACAAGTTGGGTAAGGTCAAGAAGGTCCAATTGGGTAAGAAGGGTGTTCATACG
TTGTCACTGAC

[0471] GATGGTAGAACYATCAGATACCCAG

[0472] SEQ ID NO :117 ;> C. glabrata138

[0473] CAUCACCUUGGAAGCUACCAACGAAAACUUCAGAUUGGUCUACGACGUCAAGGGUAGAUUCGCUGUCCA
CCGUAUCACUG

[0474] ACGAAGAAGCUUCCUACAAGUUGGGUAAGGUCAAGAAGGUCCA AUUGGGUAAGAAGGGUGUCCAUACG
UUGUCACUGAC

- [0475] GAUGGUAGAACYAUCAGAUACCCAG
[0476] SEQ ID NO :118 ;> C. glabrata3605
[0477] TATCACCTTGGAAGCTACCAACGAAAACCTCAGATTGGTCTACGACGTCAAGGGTAGATTCGCTGTCCA
CCGTATCACTG
[0478] ACGAAGAAGCTTCCTACAAGTTGGGTAAGGTCAAGAAGGTCCAATTGGGTAAGAAGGGTGTTCATACG
TTGTCACTGAC
[0479] GATGGTAGAACYATCAGATACCCAG
[0480] SEQ ID NO :119 ;> C. glabrata3605
[0481] UAUCACCUUGGAAGCUACCAACGAAAACUUCAGAUUGGUCUACGACGUAAGGGUAGAUUCGCUGUCCA
CCGUAUCACUG
[0482] ACGAAGAAGCUUCCUACAAGUUGGGUAAGGUCAAGAAGGUCCAUUGGGUAAGAAGGGUGUCCAUACG
UUGUCACUGAC
[0483] GAUGGUAGAACYAUCAGAUACCCAG
[0484] SEQ ID NO :120 ;> C. glabrata3897
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CCGTATCACTG
[0486] ACGAAGAAGCTTCCTACAAGTTGGGTAAGGTCAAGAAGGTCCAATTGGGTAAGAAGGGTGTTCATACG
TTGTCACTGAC
[0487] GATGGTAGAACYATCAGATACCCAG
[0488] SEQ ID NO :121 ;> C. glabrata3897
[0489] UAUCACCUUGGAAGCUACCAACGAAAACUUCAGAUUGGUCUACGACGUAAGGGUAGAUUCGCUGUCCA
CCGUAUCACUG
[0490] ACGAAGAAGCUUCCUACAAGUUGGGUAAGGUCAAGAAGGUCCAUUGGGUAAGAAGGGUGUCCAUACG
UUGUCACUGAC
[0491] GAUGGUAGAACYAUCAGAUACCCAG
[0492] SEQ ID NO :122 ;> C. glabrata8018
[0493] TATCACCTTGGAAGCTACCAACGAAAACCTCAGATTGGTCTACGACGTCAAGGGTAGATTCGCTGTCCA
CCGTATCACTG
[0494] ACGAAGAAGCTTCCTACAAGTTGGGTAAGGTCAAGAAGGTCCAATTGGGTAAGAAGGGTGTTCATACG
TTGTCACTGAC
[0495] GATGGTAGAACYATCAGATACCCAG
[0496] SEQ ID NO :123 ;> C. glabrata8018
[0497] UAUCACCUUGGAAGCUACCAACGAAAACUUCAGAUUGGUCUACGACGUAAGGGUAGAUUCGCUGUCCA
CCGUAUCACUG
[0498] ACGAAGAAGCUUCCUACAAGUUGGGUAAGGUCAAGAAGGUCCAUUGGGUAAGAAGGGUGUCCAUACG
UUGUCACUGAC
[0499] GAUGGUAGAACYAUCAGAUACCCAG
[0500] SEQ ID NO :124 ;> C. glabrata3863
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CCGTATCACTG

[0502] ACGAAGAAGCTTCCTACAAGTTGGGTAAGGTCAAGAAGGTCCAATTGGGTAAGAAGGGTGTTCATACG
TTGTCACTGAC

[0503] GATGGTAGAACYATCAGATACCCAG

[0504] SEQ ID NO :125 ;> C. glabrata3863

[0505] UAUCACCUUGGAAGCUACCAACGAAAACUUCAGAUUGGUCUACGACGUCAAGGGUAGAUUCGCUGUCCA
CCGUAUCACUG

[0506] ACGAAGAAGCUUCCUACAAGUUGGGUAAGGUCAAGAAGGUCCA AUUGGGUAAGAAGGGUGUCCA UACG
UUGUCACUGAC

[0507] GAUGGUAGAACYAUCAGAUACCCAG

[0508] SEQ ID NO :126 ;> C. parapsilosis3902

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CAGAATCTCAG

[0510] CTGAAGAAGCCACTTACAAATTGGGTAAAGTCAAGAGAGTCCAATTGGGTAAGAAGGGAATCCCATACG
TTGTCACCCAC

[0511] GATGGTAGAACYATCAGATACCCAG

[0512] SEQ ID NO :127 ;> C. parapsilosis3902

[0513] CAUUACUUUGGAAGCCACYAAUGAAAACUUUAGAUUGAUUUACGAUGUCAAGGUAGAUUUGCUGUCCA
CAGAAUCUCAG

[0514] CUGAAGAAGCCACUUACAAAUUGGGUAAAAGUCAAGAGAGUCCA AUUGGGUAAGAAGGGAAUCCCAUACG
UUGUCACCCAC

[0515] GAUGGUAGAACYAUCAGAUACCCAG

[0516] SEQ ID NO :128 ;> C. parapsilosis604

[0517] CATTACTTTGGAAGCCACYAATGAAAACCTTTAGATTGATTTACGATGTCAAAGGTAGATTTGCTGTCCA
CAGAATCTCAG

[0518] CTGAAGAAGCCACTTACAAATTGGGTAAAGTCAAGAGAGTCCAATTGGGTAAGAAGGGAATCCCATACG
TTGTCACCCAC

[0519] GATGGTAGAACYATCAGATACCCAG

[0520] SEQ ID NO :129 ;> C. parapsilosis604

[0521] CAUUACUUUGGAAGCCACYAAUGAAAACUUUAGAUUGAUUUACGAUGUCAAGGUAGAUUUGCUGUCCA
CAGAAUCUCAG

[0522] CUGAAGAAGCCACUUACAAAUUGGGUAAAAGUCAAGAGAGUCCA AUUGGGUAAGAAGGGAAUCCCAUACG
UUGUCACCCAC

[0523] GAUGGUAGAACYAUCAGAUACCCAG

[0524] SEQ ID NO :130 ;> C. parapsilosis2194

[0525] CATTACTTTGGAAGCCACYAATGAAAACCTTTAGATTGATTTACGATGTCAAAGGTAGATTTGCTGTCCA
CAGAATCTCAG

[0526] CTGAAGAAGCCACTTACAAATTGGGTAAAGTCAAGAGAGTCCAATTGGGTAAGAAGGGAATCCCATACG
TTGTCACCCAC

- [0527] GATGGTAGAACYATCAGATACCCAG
- [0528] SEQ ID NO :131 ;> C. parapsilosis2194
- [0529] CAUUACUUUGGAAGCCACYAAUGAAAACUUUAGAUUGAUUUACGAUGUCAAGGUAGAUUUGCUGUCCA
CAGAAUCUCAG
- [0530] CUGAAGAAGCCACUUACAAAUUGGGUAAAAGUCAAGAGAGUCCAAUUGGGUAAGAAGGGAUCCCAUACG
UUGUCACCCAC
- [0531] GAUGGUAGAACYAUCAGAUACCCAG
- [0532] SEQ ID NO :132 ;> C. parapsilosis2196
- [0533] CATTACTTTGGAAGCCACYAATGAAAACCTTTAGATTGATTTACGATGTCAAAGGTAGATTTGCTGTCCA
CAGAATCTCAG
- [0534] CTGAAGAAGCCACTTACAAATTGGGTAAAGTCAAGAGAGTCCAATTGGGTAAAGAAGGGAATCCCATACG
TTGTCACCCAC
- [0535] GATGGTAGAACYATCAGATACCCAG
- [0536] SEQ ID NO :133 ;> C. parapsilosis2196
- [0537] CAUUACUUUGGAAGCCACYAAUGAAAACUUUAGAUUGAUUUACGAUGUCAAGGUAGAUUUGCUGUCCA
CAGAAUCUCAG
- [0538] CUGAAGAAGCCACUUACAAAUUGGGUAAAAGUCAAGAGAGUCCAAUUGGGUAAGAAGGGAUCCCAUACG
UUGUCACCCAC
- [0539] GAUGGUAGAACYAUCAGAUACCCAG
- [0540] SEQ ID NO :134 ;> C. parapsilosis1001
- [0541] CATTACTTTGGAAGCCACYAATGAAAACCTTTAGATTGATTTACGATGTCAAAGGTAGATTTGCTGTCCA
CAGAATCTCAG
- [0542] CTGAAGAAGCCACTTACAAATTGGGTAAAGTCAAGAGAGTCCAATTGGGTAAAGAAGGGAATCCCATACG
TTGTCACCCAC
- [0543] GATGGTAGAACYATCAGATACCCAG
- [0544] SEQ ID NO :135 ;> C. parapsilosis1001
- [0545] CAUUACUUUGGAAGCCACYAAUGAAAACUUUAGAUUGAUUUACGAUGUCAAGGUAGAUUUGCUGUCCA
CAGAAUCUCAG
- [0546] CUGAAGAAGCCACUUACAAAUUGGGUAAAAGUCAAGAGAGUCCAAUUGGGUAAGAAGGGAUCCCAUACG
UUGUCACCCAC
- [0547] GAUGGUAGAACYAUCAGAUACCCAG
- [0548] SEQ ID NO :136 ;
- [0549] > C. parapsilosis1716
- [0550] CATTACTTTGGAAGCCACYAATGAAAACCTTTAGATTGATTTACGATGTCAAAGGTAGATTTGCTGTCCA
CAGAATCTCAG
- [0551] CTGAAGAAGCCACTTACAAATTGGGTAAAGTCAAGAGAGTCCAATTGGGTAAAGAAGGGAATCCCATACG
TTGTCACCCAC
- [0552] GATGGTAGAACYATCAGATACCCAG
- [0553] SEQ ID NO :137 ;

- [0554] > C. parapsilosis1716
[0555] CAUUACUUUGGAAGCCACYAAUGAAAACUUUAGAUUGAUUUACGAUGUCAAGGUAGAUUUUGCUGUCCA
CAGAAUCUCAG
[0556] CUGAAGAAGCCACUUACAAAUUGGGUAAAAGUCAAGAGAGUCCA AUUGGGUAAGAAGGGAAUCCCAUACG
UUGUCACCCAC
[0557] GAUGGUAGAACYAUCAGAUACCCAG
[0558] SEQ ID NO :138 ;> C. parapsilosis9557
[0559] CATTACTTTGGAAGCCACYAATGAAAACCTTTAGATTGATTTACGATGTCAAAGGTAGATTTGCTGTCCA
CAGAATCTCAG
[0560] CTGAAGAAGCCACTTACAAATTGGGTAAAGTCAAGAGAGTCCAATTGGGTAAGAAGGGAATCCCATACG
TTGTCACCCAC
[0561] GATGGTAGAACYATCAGATACCCAG
[0562] SEQ ID NO :139 ;> C. parapsilosis9557
[0563] CAUUACUUUGGAAGCCACYAAUGAAAACUUUAGAUUGAUUUACGAUGUCAAGGUAGAUUUUGCUGUCCA
CAGAAUCUCAG
[0564] CUGAAGAAGCCACUUACAAAUUGGGUAAAAGUCAAGAGAGUCCA AUUGGGUAAGAAGGGAAUCCCAUACG
UUGUCACCCAC
[0565] GAUGGUAGAACYAUCAGAUACCCAG
[0566] SEQ ID NO :140 ;> C. krusei5579
[0567] CATCACTTTAGATGCAACCAACGAACACTTCAGATTAATCTATGACATCAAGGGTAGATTCGCAATCCA
CAGAATCACCC
[0568] CAGAAGAAGCTGCATACAAGTTATGTAAGGTCAAGAAGGTCCAATTAGGTAAGAAGGGTATTCCTTATG
TTGTTACCCAC
[0569] GATGGTAGAACYATCAGATACCCAG
[0570] SEQ ID NO :141 ;
[0571] > C. krusei5579
[0572] CAUCACUUUAGAUGCAACCAACGAACACUUCAGAUUAAUCUAUGACAUCAAGGGUAGAUUCGCAAUCCA
CAGAAUCACCC
[0573] CAGAAGAAGCUGCAUACAAGUUAUGUAAGGUCAAGAAGGUCCA AUUAGGUAAGAAGGGUAUUCUUAUG
UUGUUACCCAC
[0574] GAUGGUAGAACYAUCAGAUACCCAG
[0575] SEQ ID NO :142 ;> C. krusei9560
[0576] CATCACTTTAGATGCAACCAACGAACACTTCAGATTAATCTATGACATCAAGGGTAGATTCGCAATCCA
CAGAATCACCC
[0577] CAGAAGAAGCTGCATACAAGTTATGTAAGGTCAAGAAGGTCCAATTAGGTAAGAAGGGTATTCCTTATG
TTGTTACCCAC
[0578] GATGGTAGAACYATCAGATACCCAG
[0579] SEQ ID NO :143 ;> C. krusei9560
[0580] CAUCACUUUAGAUGCAACCAACGAACACUUCAGAUUAAUCUAUGACAUCAAGGGUAGAUUCGCAAUCCA

CAGAAUCACCC

[0581] CAGAAGAAGCUGCAUACAAGUUAUGUAAGGUCAAGAAGGUCCAUUAGGUAAGAAGGGUAUUCUUUAUG
UUGUUACCCAC

[0582] GAUGGUAGAACYAUCAGAUACCCAG

[0583] SEQ ID NO :144 ;> C. krusei6055

[0584] CATCACTTTAGATGCAACCAACGAACACTTCAGATTAATCTATGACATCAAGGGTAGATTCGCAATCCA
CAGAATCACCC

[0585] CAGAAGAAGCTGCATACAAGTTATGTAAGGTCAAGAAGGTCCAATTAGGTAAGAAGGGTATTCCTTATG
TTGTTACCCAC

[0586] GATGGTAGAACYATCAGATACCCAG

[0587] SEQ ID NO :145 ;> C. krusei6055

[0588] CAUCACUUUAGAUGCAACCAACGAACACUUCAGAUUAAUCUAUGACAUCAAGGGUAGAUUCGCAAUCCA
CAGAAUCACCC

[0589] CAGAAGAAGCUGCAUACAAGUUAUGUAAGGUCAAGAAGGUCCAUUAGGUAAGAAGGGUAUUCUUUAUG
UUGUUACCCAC

[0590] GAUGGUAGAACYAUCAGAUACCCAG

[0591] SEQ ID NO :146 ;> C. krusei17518

[0592] CATCACTTTAGATGCAACCAACGAACACTTCAGATTAATCTATGACATCAAGGGTAGATTCGCAATCCA
CAGAATCACCC

[0593] CAGAAGAAGCTGCATACAAGTTATGTAAGGTCAAGAAGGTCCAATTAGGTAAGAAGGGTATTCCTTATG
TTGTTACCCAC

[0594] GATGGTAGAACYATCAGATACCCAG

[0595] SEQ ID NO :147 ;> C. krusei17518

[0596] CAUCACUUUAGAUGCAACCAACGAACACUUCAGAUUAAUCUAUGACAUCAAGGGUAGAUUCGCAAUCCA
CAGAAUCACCC

[0597] CAGAAGAAGCUGCAUACAAGUUAUGUAAGGUCAAGAAGGUCCAUUAGGUAAGAAGGGUAUUCUUUAUG
UUGUUACCCAC

[0598] GAUGGUAGAACYAUCAGAUACCCAG

[0599] SEQ ID NO :148 ;> C. krusei573

[0600] CATCACTTTAGATGCAACCAACGAACACTTCAGATTAATCTATGACATCAAGGGTAGATTCGCAATCCA
CAGAATCACCC

[0601] CAGAAGAAGCTGCATACAAGTTATGTAAGGTCAAGAAGGTCCAATTAGGTAAGAAGGGTATTCCTTATG
TTGTTACCCAC

[0602] GATGGTAGAACYATCAGATACCCAG

[0603] SEQ ID NO :149 ;> C. krusei573

[0604] CAUCACUUUAGAUGCAACCAACGAACACUUCAGAUUAAUCUAUGACAUCAAGGGUAGAUUCGCAAUCCA
CAGAAUCACCC

[0605] CAGAAGAAGCUGCAUACAAGUUAUGUAAGGUCAAGAAGGUCCAUUAGGUAAGAAGGGUAUUCUUUAUG
UUGUUACCCAC

- [0606] GAUGGUAGAACYAUCAGAUACCCAG
[0607] SEQ ID NO :150 ;> C. krusei3165
[0608] CATCACTTTAGATGCAACCAACGAACACTTCAGATTAATCTATGACATCAAGGGTAGATTCGCAATCCA
CAGAATCACCC
[0609] CAGAAGAAGCTGCATACAAGTTATGTAAGGTCAAGAAGGTCCAATTAGGTAAGAAGGGTATTCCTTATG
TTGTTACCCAC
[0610] GATGGTAGAACYATCAGATACCCAG
[0611] SEQ ID NO :151 ;> C. krusei3165
[0612] CAUCACUUUAGAUGCAACCAACGAACACUUCAGAUUAAUCUAUGACAUCAAGGGUAGAUUCGCAAUCCA
CAGAAUCACCC
[0613] CAGAAGAAGCUGCAUACAAGUUUGUAAGGUCAAGAAGGUCCAUUAGGUAAGAAGGGUAAUCCUUAUG
UUGUUACCCAC
[0614] GAUGGUAGAACYAUCAGAUACCCAG
[0615] SEQ ID NO :152 ;> C. krusei3922
[0616] CATCACTTTAGATGCAACCAACGAACACTTCAGATTAATCTATGACATCAAGGGTAGATTCGCAATCCA
CAGAATCACCC
[0617] CAGAAGAAGCTGCATACAAGTTATGTAAGGTCAAGAAGGTCCAATTAGGTAAGAAGGGTATTCCTTATG
TTGTTACCCAC
[0618] GATGGTAGAACYATCAGATACCCAG
[0619] SEQ ID NO :153 ;> C. krusei3922
[0620] CAUCACUUUAGAUGCAACCAACGAACACUUCAGAUUAAUCUAUGACAUCAAGGGUAGAUUCGCAAUCCA
CAGAAUCACCC
[0621] CAGAAGAAGCUGCAUACAAGUUUGUAAGGUCAAGAAGGUCCAUUAGGUAAGAAGGGUAAUCCUUAUG
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[0622] GAUGGUAGAACYAUCAGAUACCCAG
[0623] SEQ ID NO :154 ;> C. krusei3847
[0624] CATCACTTTAGATGCAACCAACGAACACTTCAGATTAATCTATGACATCAAGGGTAGATTCGCAATCCA
CAGAATCACCC
[0625] CAGAAGAAGCTGCATACAAGTTATGTAAGGTCAAGAAGGTCCAATTAGGTAAGAAGGGTATTCCTTATG
TTGTTACCCAC
[0626] GATGGTAGAACYATCAGATACCCAG
[0627] SEQ ID NO :155 ;> C. krusei3847
[0628] CAUCACUUUAGAUGCAACCAACGAACACUUCAGAUUAAUCUAUGACAUCAAGGGUAGAUUCGCAAUCCA
CAGAAUCACCC
[0629] CAGAAGAAGCUGCAUACAAGUUUGUAAGGUCAAGAAGGUCCAUUAGGUAAGAAGGGUAAUCCUUAUG
UUGUUACCCAC
[0630] GAUGGUAGAACYAUCAGAUACCCAG
[0631] SEQ ID NO :156 ;> C. tropicalis3895
[0632] CATTACCTTGAAGCTACCAACGAACACTTCAGATTGATTTACGATGTTAAAGGTAAATTCGCTGTTCA

CAGAATTTCTG

[0633] CTGAAGAAGCTTCTTACAAATTAGGTAAAGTCAAGAAGGTTCAATTAGGTAAAAAGGTGTTCCATACG
TTGTCACCCAC

[0634] GATGGTAGAACYATCAGATACCCAG

[0635] SEQ ID NO :157 ;> C. tropicalis3895

[0636] CAUUACCUUGGAAGCUACCAACGAACACUUCAGAUUGAUUUACGAUGUUAAAGGUAAAAUUCGCUGUUCA
CAGAAUUUCUG

[0637] CUGAAGAAGCUUCUUACAAAUUAGGUAAAAGUCAAGAAGGUUCAUUAGGUAAAAAGGUGUCCAUACG
UUGUCACCCAC

[0638] GAUGGUAGAACYAUCAGAUACCCAG

[0639] SEQ ID NO :158 ;> C. tropicalis94

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CAGAATTTCTG

[0641] CTGAAGAAGCTTCTTACAAATTAGGTAAAGTCAAGAAGGTTCAATTAGGTAAAAAGGTGTTCCATACG
TTGTCACCCAC

[0642] GATGGTAGAACYATCAGATACCCAG

[0643] SEQ ID NO :159 ;> C. tropicalis94

[0644] CAUUACCUUGGAAGCUACCAACGAACACUUCAGAUUGAUUUACGAUGUUAAAGGUAAAAUUCGCUGUUCA
CAGAAUUUCUG

[0645] CUGAAGAAGCUUCUUACAAAUUAGGUAAAAGUCAAGAAGGUUCAUUAGGUAAAAAGGUGUCCAUACG
UUGUCACCCAC

[0646] GAUGGUAGAACYAUCAGAUACCCAG

[0647] SEQ ID NO :160 ;> C. tropicalis4225

[0648] CATTACCTTGGAAGCTACCAACGAACACTTCAGATTGATTTACGATGTTAAAGGTAAATTCGCTGTTCA
CAGAATTTCTG

[0649] CTGAAGAAGCTTCTTACAAATTAGGTAAAGTCAAGAAGGTTCAATTAGGTAAAAAGGTGTTCCATACG
TTGTCACCCAC

[0650] GATGGTAGAACYATCAGATACCCAG

[0651] SEQ ID NO :161 ;> C. tropicalis4225

[0652] CAUUACCUUGGAAGCUACCAACGAACACUUCAGAUUGAUUUACGAUGUUAAAGGUAAAAUUCGCUGUUCA
CAGAAUUUCUG

[0653] CUGAAGAAGCUUCUUACAAAUUAGGUAAAAGUCAAGAAGGUUCAUUAGGUAAAAAGGUGUCCAUACG
UUGUCACCCAC

[0654] GAUGGUAGAACYAUCAGAUACCCAG

[0655] SEQ ID NO :162 ;> C. tropicalis5557

[0656] CATTACCTTGGAAGCTACCAACGAACACTTCAGATTGATTTACGATGTTAAAGGTAAATTCGCTGTTCA
CAGAATTTCTG

[0657] CTGAAGAAGCTTCTTACAAATTAGGTAAAGTCAAGAAGGTTCAATTAGGTAAAAAGGTGTTCCATACG
TTGTCACCCAC

- [0658] GATGGTAGAACYATCAGATACCCAG
- [0659] SEQ ID NO:163 ;> *C. tropicalis*5557
- [0660] CAUUACCUUGGAAGCUACCAACGAACACUUCAGAUUGAUUUACGAUGUUAAGGUAAAAUUCGCUGUUCA
CAGAAUUUCUG
- [0661] CUGAAGAAGCUUCUUACAAAUUAGGUAAAAGUCAAGAAGGUCAAUUAGGUAAAAAAGGUGUCCAUACG
UUGUCACCCAC
- [0662] GAUGGUAGAACYAUCAGAUACCCAG
- [0663] SEQ ID NO:164 ;> *C. tropicalis*15902
- [0664] CATTACCTTGAAGCTACCAACGAACACTTCAGATTGATTTACGATGTTAAAGGTAAATTCGCTGTTCA
CAGAATTTCTG
- [0665] CTGAAGAAGCTTCTTACAAATTAGGTAAAGTCAAGAAGGTTCAATTAGGTAAAAAAGGTGTTCCATACG
TTGTCACCCAC
- [0666] GATGGTAGAACYATCAGATACCCAG
- [0667] SEQ ID NO:165 ;> *C. tropicalis*15902
- [0668] CAUUACCUUGGAAGCUACCAACGAACACUUCAGAUUGAUUUACGAUGUUAAGGUAAAAUUCGCUGUUCA
CAGAAUUUCUG
- [0669] CUGAAGAAGCUUCUUACAAAUUAGGUAAAAGUCAAGAAGGUCAAUUAGGUAAAAAAGGUGUCCAUACG
UUGUCACCCAC
- [0670] GAUGGUAGAACYAUCAGAUACCCAG
- [0671] SEQ ID NO:166 ;> *C. tropicalis*4139
- [0672] CATTACCTTGAAGCTACCAACGAACACTTCAGATTGATTTACGATGTTAAAGGTAAATTCGCTGTTCA
CAGAATTTCTG
- [0673] CTGAAGAAGCTTCTTACAAATTAGGTAAAGTCAAGAAGGTTCAATTAGGTAAAAAAGGTGTTCCATACG
TTGTCACCCAC
- [0674] GATGGTAGAACYATCAGATACCCAG
- [0675] SEQ ID NO:167 ;> *C. tropicalis*4139
- [0676] CAUUACCUUGGAAGCUACCAACGAACACUUCAGAUUGAUUUACGAUGUUAAGGUAAAAUUCGCUGUUCA
CAGAAUUUCUG
- [0677] CUGAAGAAGCUUCUUACAAAUUAGGUAAAAGUCAAGAAGGUCAAUUAGGUAAAAAAGGUGUCCAUACG
UUGUCACCCAC
- [0678] GAUGGUAGAACYAUCAGAUACCCAG
- [0679] SEQ ID NO:168 ;> *C. tropicalis*3873
- [0680] CATTACCTTGAAGCTACCAACGAACACTTCAGATTGATTTACGATGTTAAAGGTAAATTCGCTGTTCA
CAGAATTTCTG
- [0681] CTGAAGAAGCTTCTTACAAATTAGGTAAAGTCAAGAAGGTTCAATTAGGTAAAAAAGGTGTTCCATACG
TTGTCACCCAC
- [0682] GATGGTAGAACYATCAGATACCCAG
- [0683] SEQ ID NO:169 ;> *C. tropicalis*3873
- [0684] CAUUACCUUGGAAGCUACCAACGAACACUUCAGAUUGAUUUACGAUGUUAAGGUAAAAUUCGCUGUUCA

CAGAAUUUCUG

[0685] CUGAAGAAGCUUCUUACAAAUUAGGUAAAAGUCAAGAAGGUUCAUUUAGGUAAAAAAGGUGUCCAUACG
UUGUCACCCAC

[0686] GAUGGUAGAACYAUCAGAUACCCAG

[0687] SEQ ID NO :170 ;> *C. tropicalis*3870

[0688] CATTACCTTGGAAGCTACCAACGAACACTTCAGATTGATTTACGATGTTAAAGGTAAATTCGCTGTTCA
CAGAATTTCTG

[0689] CTGAAGAAGCTTCTTACAAATTAGGTAAAGTCAAGAAGGTTCAATTAGGTAAAAAAGGTGTTCCATACG
TTGTCACCCAC

[0690] GATGGTAGAACYATCAGATACCCAG

[0691] SEQ ID NO :171 ;> *C. tropicalis*3870

[0692] CAUUACCUUGGAAGCUACCAACGAACACUUCAGAUUGAUUUACGAUGUUAAAGGUAAAAUUCGUGUUCA
CAGAAUUUCUG

[0693] CUGAAGAAGCUUCUUACAAAUUAGGUAAAAGUCAAGAAGGUUCAUUUAGGUAAAAAAGGUGUCCAUACG
UUGUCACCCAC

[0694] GAUGGUAGAACYAUCAGAUACCCAG

[0695] SEQ ID NO :172 ;> *C. tropicalis*8157

[0696] CATTACCTTGGAAGCTACCAACGAACACTTCAGATTGATTTACGATGTTAAAGGTAAATTCGCTGTTCA
CAGAATTTCTG

[0697] CTGAAGAAGCTTCTTACAAATTAGGTAAAGTCAAGAAGGTTCAATTAGGTAAAAAAGGTGTTCCATACG
TTGTCACCCAC

[0698] GATGGTAGAACYATCAGATACCCAG

[0699] SEQ ID NO :173 ;> *C. tropicalis*8157

[0700] CAUUACCUUGGAAGCUACCAACGAACACUUCAGAUUGAUUUACGAUGUUAAAGGUAAAAUUCGUGUUCA
CAGAAUUUCUG

[0701] CUGAAGAAGCUUCUUACAAAUUAGGUAAAAGUCAAGAAGGUUCAUUUAGGUAAAAAAGGUGUCCAUACG
UUGUCACCCAC

[0702] GAUGGUAGAACYAUCAGAUACCCAG

[0703] SEQ ID NO :174 ;> *C. tropicalis*2311

[0704] CATCACCTTGGAAGCTACCAACGAACACTTCAGATTGATTTACGATGTTAAAGGTAAATTCGCTGTTCA
CAGAATTTCTG

[0705] CTGAAGAAGCTTCTTACAAATTAGGTAAAGTCAAGAAGGTTCAATTAGGTAAAAAAGGTGTTCCATACG
TTGTCACCCAC

[0706] GATGGTAGAACYATCAGATACCCAG

[0707] SEQ ID NO :175 ;> *C. tropicalis*2311

[0708] CAUCACCUUGGAAGCUACCAACGAACACUUCAGAUUGAUUUACGAUGUUAAAGGUAAAAUUCGUGUUCA
CAGAAUUUCUG

[0709] CUGAAGAAGCUUCUUACAAAUUAGGUAAAAGUCAAGAAGGUUCAUUUAGGUAAAAAAGGUGUCCAUACG
UUGUCACCCAC

- [0710] GAUGGUAGAACYAUCAGAUACCCAG
[0711] SEQ ID NO :176 ;*Saccharomyces cerevisiae*
[0712] *Saccharomyces cerevisiae* probe 1
[0713] GATTGGTCTACGATGTCA
[0714] SEQ ID NO 177 ;*Saccharomyces cerevisiae*
[0715] *Saccharomyces cerevisiae* probe 2
[0716] TGACATCGTAGACCAATC
[0717] SEQ ID NO :178 ;*Eremothecium gossypii*
[0718] *Eremothecium gossypii* probe 1
[0719] GATTGGTATAACGATGTCA
[0720] SEQ ID NO :179 ;*Eremothecium gossypii*
[0721] *Eremothecium gossypii* probe 2
[0722] TGACATCGTATAACCAATC
[0723] SEQ ID NO 180 ;*Kluyveromyces lactis*
[0724] *Kluyveromyces lactis* probe 1
[0725] GATTGGTCTACGATGTTA
[0726] SEQ ID NO :181 ;*Kluyveromyces lactis*
[0727] *Kluyveromyces lactis* probe 2
[0728] TAACATCGTAGACCAATC
[0729] SEQ ID NO 182 ;*C. dubliniensis* and *Candida glabrata*
[0730] *C. dubliniensis* and *Candida glabrata* probe 1
[0731] GATTGGTCTACGACGTCA
[0732] SEQ ID NO 183 ;*C. dubliniensis* and *Candida glabrata*
[0733] *C. dubliniensis* and *Candida glabrata* probe 2
[0734] TGACGTCGTAGACCAATC
[0735] SEQ ID NO 184 ;*Debaryomyces hansenii*
[0736] *Debaryomyces hansenii* probe 1
[0737] GATTGATCTATGACGTCA
[0738] SEQ ID NO :185 ;*Debaryomyces hansenii*
[0739] *Debaryomyces hansenii* probe 2
[0740] TGACGTCATAGATCAATC
[0741] SEQ ID NO 186 ;*C. tropicalis*
[0742] *C. tropicalis* probe 1
[0743] GATTGATTTACGATGTTA
[0744] SEQ ID NO 187 ;*C. tropicalis*
[0745] *C. tropicalis* probe 2
[0746] TAACATCGTAAATCAATC
[0747] SEQ ID NO 188 ;*C. parapsilosis*
[0748] *C. parapsilosis* probe 1

[0749]	GATTGATTTACGATGTCA	
[0750]	SEQ ID NO 189 ;C.parapsilosis probe 2	
[0751]	C.parapsilosis	
[0752]	TGACATCGTAAATCAATC	
[0753]	SEQ ID NO 190 ;Saccharomyces cerevisiae	
[0754]	<u>ATGGCTAGAG GACCAAAGAA GCATCTAAAA</u> AGATTAGCAG CTCCACACCA CTGGTTATTG	60
[0755]	GACAAGTTGT CCGGTTGTTA <u>CGCCCCAAGA CCATCTGCTG</u> GTCCACACAA ATTGCGTGAA	120
[0756]	TCCTTGCCAT TGATTGTCTT TCTAAGAAAC AGATTAAAGT ATGCTTTGAA CGGCCGTGAA	180
[0757]	GTCAAGGCTA TCTTGATGCA ACGTCACGTT AAAGTGGACG GTAAGGTTAG AACCGACACT	240
[0758]	ACCTACCC <u>AG CTGGTTTCAT GGATGT</u> CATC ACTCTAGATG CCACCAATGA AAACTTCA GA	300
[0759]	TTGGTCTACG ATGTCA AGGG TAGATTGCT GTCCACCGTA TCACCGATGA AGAAGCTTCT	360
[0760]	TACAAGTTGG GTAAGGTCAA GAAGGTTCAA TTAGGTAAGA AGGGTGTTC ATACGTTGTT	420
[0761]	ACCCACGATG GT <u>AGAACTAT CAGATACCCA GA</u> CCCAAACA TCAAGGTCAA TGACTGTT	480
[0762]	AAGATCGACT TGGCCTCTGG TAAGTACT GATTCATCA AGTTCGATGC CGGTAAGTTG	540
[0763]	GTTTACGTTA CTGGTGGTCG TAACTTGGGT CGTATCGGTA CTATCGTTCA CAAGGAAAGA	600
[0764]	CACGATGGTG GTTTCGATTT AGTTCACATC AAGGACTCCT TGGACAACAC TTTGTCACT	660
[0765]	AGATTGAACA ATGTCTTCGT CATCGGTGAA CAAGGTAAGC CTTACATTTT TTTGCCAGGT	720
[0766]	AAGGGTAAGG GTATCAAGTT GTCTATTGCT GAAGAACGTG ACAGAAGAAG AGCTCAACAA	780
[0767]	TTATAA---	786
[0768]	SEQ ID NO 191 ;RNA ;Saccharomyces cerevisiae	
[0769]	<u>AUGGCUAGAG GACCAAAGAA GCAUCUAAAA</u> AGAUUAGCAG CUCCACACCA CUGGUUAUUG	60
[0770]	GACAAGUUGU CCGGUUGUUA <u>CGCCCCAAGA CCAUCUGCUG</u> GUCCACACAA AUUGCGUGAA	120
[0771]	UCCUUGCCAU UGAUUGUCUU UCUAAGAAAC AGAUUAAAGU AUGCUUUGAA CGGCCGUGAA	180
[0772]	GUCAAGGCUA UCUUGAUGCA ACGUCACGUU AAAGUGGACG GUAAGGUUAG AACCGACACU	240
[0773]	ACCUACCC <u>AG CUGGUUUCAU GGAUGU</u> CAUC ACUCUAGAUG CCACCAUGA AAACUUCA GA	300
[0774]	UUGGUCUACG AUGUCA AGGG UAGAUUCGCU GUCCACCGUA UCACCGAUGA AGAAGCUUCU	360
[0775]	UACAAGUUGG GUAAGGUCAA GAAGGUUCAA UUAGGUAAGA AGGGUGUUC AUACGUUGUU	420
[0776]	ACCCACGAUG GU <u>AGAACUAI CAGAUACCCA GA</u> CCCAAACA UCAAGGUCAA UGACACUGUU	480
[0777]	AAGAUCGACU UGGCCUCUGG UAAGAUUACU GAUUUCAUCA AGUUCGAUGC CGGUAAGUUG	540
[0778]	GUUUACGUUA CUGGUGGUCG UAACUUGGU CGUAUCGGUA CUAUCGUUCA CAAGGAAAGA	600
[0779]	CACGAUGGUG GUUUCGAUUU AGUUCACAUC AAGGACUCCU UGGACAACAC UUUCGUCACU	660
[0780]	AGAUUGAACA AUGUCUUCGU CAUCGGUGAA CAAGGUAAGC CUUACAUUUC UUUGCCAGGU	720
[0781]	AAGGGUAAGG GUAUCAAGUU GUCUAUUGCU GAAGAACGUG ACAGAAGAAG AGCUCAACAA	780
[0782]	UUAUAA---	786
[0783]	SEQ ID NO 192 ;Candida glabrata	
[0784]	<u>ATGGCTAGAG GACCAAAGAA GCATCTAAAG</u> AGATTAGCAG CTCCACACCA CTGGTTGTTG	60
[0785]	GACAAGTTGT CCGGCTGTTA <u>CGCCCCAAGA CCATCCGCTG</u> GTCCACACAA GTTGCCTGAA	120
[0786]	TCCCTACCAT TGATCGTTTT CTTGAGAAAC AGATTAAAGT ACGCTTTGAA CGGTCGTGAA	180
[0787]	GTAAAGGCTA TCATGATGCA ACGTCATGTT AAGGTTGACG GTAAGGTCAG AACTGACGCT	240

[0788]	ACCTACCC AG CTGGTTTCAT GGATGT TATC ACCTTGAAG CTACCAACGA AACTTCA GA	300
[0789]	TTGGTCTACG ACGTCA AGGG TAGATTCGCT GTCCACCGTA TCACTGACGA AGAAGCTTCC	360
[0790]	TACAAGTTGG GTAAGGTCAA GAAGGTCCAA TTGGGTAAGA AGGGTGTTC ATACGTTGTC	420
[0791]	ACTGACGATG GT AGAACTAT CAGATACCCA GA CCCAAACA TCAAGGTCAA TGACACCGTC	480
[0792]	AAGGTCGACT TGGCTTCCGG TAAGATCACT GACTACATCA AGTTCGACAT TGGTAAGTTG	540
[0793]	GTCTACATCA CCGGTGGTCG TAACTGGGT CGTATCGGTA CCATCGTTCA CAAGGAAAGA	600
[0794]	CACGATGGTG GTTTCGACTT GGTTACGTC AAGGACTCCT TGGACAACAC TTTCGTCACC	660
[0795]	AGATTGAACA ACGTTTTTCGT TATCGGTGAA CAAGGTAAGC CATACTCTC CTTGCCAAAG	720
[0796]	GGTAAGGGTA TCAAGTTGAC CATTGCTGAA GAACGTGACA GAAGAAGAGC TCAACAAGGT	780
[0797]	TTATAA---	786
[0798]	SEQ ID NO 193 ;RNA ;Candida glabrata	
[0799]	<u>AUGGCUAGAG GACCAAAGAA GCAUCUAAAG</u> AGAUUAGCAG CUCCACACCA CUGGUUGUUG	60
[0800]	GACAAGUUGU CCGGCUGUUA <u>CGCCCCAAGA CCAUCCGCUG</u> GUCCACACAA GUUGCUGUGAA	120
[0801]	UCCCUACCAU UGAUCGUUUU CUUGAGAAAC AGAUUAAAGU ACGCUUUGAA CGGUCGUGAA	180
[0802]	GUUAAGGCUA UCAUGAUGCA ACGUCAUGUU AAGGUUGACG GUAAGGUCAG AACUGACGCU	240
[0803]	ACCUACCC AG CUGGUUUCAU GGAUGU UAUC ACCUUGGAAG CUACCAACGA AAACUUCA GA	300
[0804]	UUGGUCUACG ACGUCA AGGG UAGAUUCGCU GUCCACCGUA UCACUGACGA AGAAGCUUCC	360
[0805]	UACAAGUUGG GUAAGGUCAA GAAGGUCCAA UUGGGUAGA AGGGUGUUC AUACGUUGUC	420
[0806]	ACUGACGAUG GU AGAACUAV CAGAUACCCA GA CCCAAACA UCAAGGUCAA UGACACCGUC	480
[0807]	AAGGUCGACU UGGCUUCCGG UAAGAUCACU GACUACAUCU AGUUCGACAU UGGUAAGUUG	540
[0808]	GUCUACAUCU CCGGUGGUCG UAACUUGGGU CGUAUCGGUA CCAUCGUUCA CAAGGAAAGA	600
[0809]	CACGAUGGUG GUUUCGACUU GGUUCACGUC AAGGACUCCU UGGACAACAC UUUCGUCACC	660
[0810]	AGAUUGAACA ACGUUUUCGU UAUCGGUGAA CAAGGUAAGC CAUACAUCUC CUUGCCAAAG	720
[0811]	GGUAAGGGUA UCAAGUUGAC CAUUGCUGAA GAACGUGACA GAAGAAGAGC UCAACAAGGU	780
[0812]	UUUAAA---	786
[0813]	SEQ ID NO 194 ;Eremothecium gossypii	
[0814]	<u>ATGGCTAGAG GACCAAAGAA GCACCTGAAG</u> AGATTGGCAG CTCCACACCA CTGGTTGTTG	60
[0815]	GACAAGCTAT CCGGCTGTTA <u>CGCTCCAAGA CCATCCGCTG</u> GTCCACACAA GTTGC GCGAG	120
[0816]	TCTTTGCCAT TGATCGTCTT CTTGAGAAAC AGATTAAAGT ATGCTTTGAA CGGTCGCGAG	180
[0817]	GTCAAGGCCA TCCTAATGCA GCGTCATGTT AAGGTTGACG GTAAGGTCAG AACTGACT	240
[0818]	ACCTACCC AG CTGGTTTCAT GGATGT CATC ACTCTAGAGG CTACCAACGA GAACTTCA GA	300
[0819]	TTGGTATACG ATGTCA AGGG CAGATTTGCT GTCCACCGTA TCACCGATGA GGAGGCTACT	360
[0820]	TACAAGTTGG GTAAGGTAA GCGCGTTCAG CTAGGTAAGA AGGGTGTCCC ATACGTGGTC	420
[0821]	ACTCACGACG GC AGAACCAT CAGATACCCA GA CCCAAACA TCAAGGTAA CGACACCGTC	480
[0822]	AAGGTTGACC TTGCTACTGG TAAGATTACC GACTTCATCA AGTTCGACAC TGGTAAGTTG	540
[0823]	GTGTACGTCA CCGGTGGCCG TAACTGGGC CGTATTGGTG TCATCACCCA CAGAGAGAGA	600
[0824]	CACGAGGGTG GCTTTGACTT GGTTACATC AAGGACTCCT TGGAGAACAC TTTCGTCACC	660
[0825]	AGATTGAACA ACGTTTTTCGT CATCGGTGAG CAAGGTAGAC CATGGATCTC CTTGCCAAGG	720
[0826]	GGTAAGGGTA TTAAGTTGTC CATTGCTGAG GAGCGTGACC GTAGAAGAGC TCAACAAGGT	780

[0827]	TTGTAA---	786
[0828]	SEQ ID NO 195 ;RNA ;Eremothecium gossypii	
[0829]	<u>AUGGCUAGAG GACCAAAGAA GCACCUGAAG</u> AGAUUGGCAG CUCCACACCA CUGGUUGUUG	60
[0830]	GACAAGCUAU CCGGCUGUUA <u>CGCUCCAAGA CCAUCCGCUG GUCCACACAA</u> GUUGC GCGAG	120
[0831]	UCUUUGCCAU UGAUCGUCUU CUUGAGAAAC AGAUAAAAGU AUGCUUUGAA CGGUCGCGAG	180
[0832]	GUCAAGGCCA UCCUAAUGCA GCGUCAUGUU AAGGUUGACG GUAAGGUCAG AACUGACACU	240
[0833]	ACCUACCC AG CUGGUUUCAU GGAUGU CAUC ACUCUAGAGG CUACCAACGA GAACUUCA GA	300
[0834]	UUGGUUACG AUGUCA AGGG CAGAUUUGCU GUCCACCGUA UCACCGAUGA GGAGGCUACU	360
[0835]	UACAAGUUGG GUAAGGUUAA GCGCGUUCAG CUAGGUAAGA AGGGUGUCCC AUACGUGGUC	420
[0836]	ACUCACGACG GC <u>AGAACCAU CAGAUACCCA GA</u> CCCAAACA UCAAGGUUAA CGACACCGUC	480
[0837]	AAGGUUGACC UUGCUCUGG UAAGAUUACC GACUUCAUCA AGUUCGACAC UGGUAAGUUG	540
[0838]	GUGUACGUCA CCGGUGGCCG UAACUUGGGC CGUAUUGGUG UCAUCACCCA CAGAGAGAGA	600
[0839]	CACGAGGGUG GCUUUGACUU GGUUCACAUC AAGGACUCCU UGGAGAACAC UUUCGUCACC	660
[0840]	AGAUUGAACA ACGUUUUCGU CAUCGGUGAG CAAGGUAGAC CAUGGAUCUC CUUGCCAAGG	720
[0841]	GGUAAGGGUA UUAAGUUGUC CAUUGCUGAG GAGCGUGACC GUAGAAGAGC UCAACAAGGU	780
[0842]	UUGUAA---	786
[0843]	SEQ ID NO 196 ;Kluyveromyces lactis	
[0844]	<u>ATGGCTAGAG GACCAAAGAA GCATCTAAAG</u> AGATTAGCAG CTCCACATCA TTGGATGTTG	60
[0845]	GACAAGTTGT CCGGTTGTTA <u>CGCACCAAGA CCATCTGCTG GTCCACACAA</u> GTTGC GTGAA	120
[0846]	TCCTTGCCAT TGATCGTTTT CTTGAGAAAC AGATTAAAGT ATGCTTTGAA CGGTCGTGAA	180
[0847]	GTCAAGGCCA TCTTGATGCA ACGTCATGTC AAGGTTGACG GTAAGGTCAG AACCGACACT	240
[0848]	ACTTTCCC AG CTGGTTTCAT GGATGT TATC ACCTTGAAG CTACCAACGA AAATTCA GA	300
[0849]	TTGGTCTACG ATGTTA AGGG TAGATTCGCT GTCCACCGTA TCACTGATGA AGAAGCTTCC	360
[0850]	TACAAGTTGG CTAAGGTCAA GAAGGTTCAA CTAGGTAAGA AGGGTATTCC ATACGTCGTT	420
[0851]	ACCCACGACG GT <u>AGAACCAT CAGATACCCA GA</u> CCCAAACA TCAAGGTAA CGACACCGTT	480
[0852]	AAGGTTGATT TGGCTACTGG TACTATCACC GATTTTCATCA AATTCGACAC TGGAAGTTG	540
[0853]	GTTTATGTTA CCGGTGGTCG TAACCTGGGT AGAGTTGGTA CCATCGTCCA CAGAGAAAGA	600
[0854]	CACGAAGGTG GTTTCGATTT GGTTCACATC AAGGATTCTT TGGAAAACAC TTTCGTCACC	660
[0855]	AGATTGAACA ACGTTTTTCGT CATCGGTGAA CCAGGTAGAC CATGGATCTC CTTGCCAAAG	717
[0856]	GGTAAGGGTA TCAAGTTGAC CATCTCTGAA GAACGTGACC GTAGAAGAGC TCAACATGGT	777
[0857]	TTGTAA---	786
[0858]	SEQ ID NO 197 ;RNA ;Kluyveromyces lactis	
[0859]	<u>AUGGCUAGAG GACCAAAGAA GCAUCUAAAG</u> AGAUUAGCAG CUCCACAUCA UUGGAUGUUG	60
[0860]	GACAAGUUGU CCGGUUGUUA <u>CGCACCAAGA CCAUCUGCUG GUCCACACAA</u> GUUGC GUGAA	120
[0861]	UCCUUGCCAU UGAUCGUUUU CUUGAGAAAC AGAUAAAAGU AUGCUUUGAA CGGUCGUGAA	180
[0862]	GUCAAGGCCA UCUUGAUGCA ACGUCAUGUC AAGGUUGACG GUAAGGUCAG AACCGACACU	240
[0863]	ACUUUCCC AG CUGGUUUCAU GGAUGU UAUC ACCUUGGAAG CUACCAACGA AAACUUCA GA	300
[0864]	UUGGUCUACG AUGUUA AGGG UAGAUUCGCU GUCCACCGUA UCACUGAUGA AGAAGCUUCC	360
[0865]	UACAAGUUGG CUAAGGUCAA GAAGGUUCAA CUAGGUAAGA AGGGUAUUCC AUACGUCGUU	420

[0866]	ACCCACGACG GU <u>AGAACCAU CAGAUACCCA GA</u> CCCAAACA UCAAGGUUAA CGACACCGUU	480
[0867]	AAGGUUGAUU UGGCUACUGG UACUAUCACC GAUUUCAUCA AAUUCGACAC UGGUAAGUUG	540
[0868]	GUUUUAUGUUA CCGGUGGUCG UAACUUGGGU AGAGUUGGUA CCAUCGUCCA CAGAGAAAGA	600
[0869]	CACGAAGGUG GUUUCGAUUU GGUUCACAUC AAGGAUUCUU UGGAAAACAC UUUCGUCACC	660
[0870]	AGAUUGAACA ACGUUUUCGU CAUCGGUGAA CCAGGUAGAC CAUGGAUCUC CUUGCCAAAG	717
[0871]	GGUAAGGGUA UCAAGUUGAC CAUCUCUGAA GAACGUGACC GUAGAAGAGC UCAACAUGGU	777
[0872]	UUGUAA---	786
[0873]	SEQ ID NO 198 ;Candida albicans	
[0874]	<u>ATGGGTAGAG GTCCAAAGAA ACACTTGAAA</u> AGATTAGCAG CTCCATCTCA CTGGATGTTG	60
[0875]	GNCAAATTGT CCGGTACTTA <u>TGCTCCAAGA</u> CCATCTGCTG <u>GTCCACACAN</u> ATTGAGAGAA	120
[0876]	TCATTACCAT TGGNTGTCTT TTTAAGAAAC AGATTGNAGT ATGCTTTGTG CGGTAGAGAA	180
[0877]	GTCAAAGCCA TCATGATGCA ACAACACGTT CAAGTTGTCG GTAAAGTCAG AACTGATACC	240
[0878]	ACCTACCC <u>AG CTGGTTTCAT GGATGT</u> CATC ACCTTGAAG CTACCAACGA ACATTTCA <u>GA</u>	300
[0879]	<u>TTAGCCTACG ATGTTA</u> AAGG TAAATTCGCC GTTCACAGAA TTTCTGCTGA AGAAGCTGTC	360
[0880]	TACAAATTGG GTAAAGTCAA GAAAGTCCAA TTAGGTAAGA AAGGTGTTCC ATACGTTGTT	420
[0881]	ACCCACGACG GT <u>AGAACTAT CAGATACCCA GA</u> TCCATTGA TCAGAGCTAA CGATACCGTT	480
[0882]	AAAATCGATT TGGCTACCGG TAAGATCGRT AGTTTCATCA AATTCGACAC TGGTAGATTA	540
[0883]	GTTATGGTTA CTGGTGGTAG AAATTTGGGT AGAGTTGGTG TTATTGTCCA CAGAGAAAAA	600
[0884]	CTCGAAGGAG GTTTCGATTT GGTCCACATC AAAGATGCTT TGGAAAACAC TTTGTTACC	660
[0885]	AGATTGTCTA ACGTTTTTGT TATTGGTACT GAAGCCGGTA AACCATGGGT CTCATTACCA	720
[0886]	AAGGGTAAAG GTATCAAATT GTCTATTTCT GAAGAAAGAG ACAGAAGAAN AGCTCAACAA	780
[0887]	GGTTTGTA---	789
[0888]	SEQ ID NO 199 ;RNA ;Candida albicans	
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[0890]	GNCAAAUUGU CCGGUACUUA <u>UGCUCCAAGA</u> CCAUCUGCUG <u>GUCCACACAN</u> AUUGAGAGAA	120
[0891]	UCAUUACCAU UGGNUGUCUU UUUUAGAAAC AGAUUGNAGU AUGCUUUGUG CGGUAGAGAA	180
[0892]	GUCAAAGCCA UCAUGAUGCA ACAACACGUU CAAGUUGUCG GUAAAGUCAG AACUGAUACC	240
[0893]	ACCUACCC <u>AG CUGGUUUCAU GGAUGU</u> CAUC ACCUUGGAAG CUACCAACGA ACAUUUCA <u>GA</u>	300
[0894]	<u>UUAGCCUACG AUGUUA</u> AAGG UAAAUUCGCC GUUCACAGAA UUUCUGCUGA AGAAGCUGUC	360
[0895]	UACAAAUUGG GUAAAGUCA GAAAGUCCAA UUAGGUAAGA AAGGUGUUC AUACGUUGUU	420
[0896]	ACCCACGACG GU <u>AGAACUUA CAGAUACCCA GA</u> UCCAUUGA UCAGAGCUAA CGAUACCGUU	480
[0897]	AAAAUCGAUU UGGCUACCGG UAAGAUCGRU AGUUUCAUCA AAUUCGACAC UGGUAGAUUA	540
[0898]	GUUAUGGUUA CUGGUGGUAG AAAUUUGGGU AGAGUUGGUG UUAUUGUCCA CAGAGAAAAA	600
[0899]	CUCGAAGGAG GUUUCGAUUU GGUCCACAUC AAAGAUGCUU UGGAAAACAC UUUCGUUACC	660
[0900]	AGAUUGUCUA ACGUUUUUGU UAUUGGUACU GAAGCCGGUA AACCAUGGGU CUCAUUACCA	720
[0901]	AAGGGUAAAG GUAUCAAAU GUCUAUUUCU GAAGAAAGAG ACAGAAGAAN AGCUCAACAA	780
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[0911] ACCCACGACG GT **AGAACTAT CAGATACCCA GA** TCCATTGA TCAGAGCCAA CGATTCCGTT 480

[0912] AAGGTTGACT TAGCTACCGG TAAGATCACT GACTTTATCA GCTTTGACAC TGGTAGATTA 540

[0913] GTCATGGTTA CTGGTGGTCG TAACATGGGT AGAGTTGGTG TTATCACCCA CAGAGAAAAG 600

[0914] CACGAGGGTG GTTTCGATTT AGTCCACATC AAGGATTCTT TGGAAAACAC TTTCGTTACC 660

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[0916] AAGGGTAAGG GTATTAAGTT ATCCATCTCT GAAGAACGTG ACAGAAGAAG AAACCAACAA 780

[0917] CTTATCAACT AA 792

[0918] SEQ ID NO 201 ;RNA ;Debaryomyces hansenii

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[0924] **UUAUUCUAUG AUGUCA** AGGG UAGAUUCACU GUCCACAGAA UCACUGCUGA AGAAGCUUCU 360

[0925] UACAAGUUG CUAAGGUCAA GAAGGUCCAA UUAGGUAAGA GAGGUUUUCC AUACGUUGUC 420

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[0929] CACGAGGGUG GUUUCGAUUU AGUCCACAUC AAGGAUUCUU UGGAAAACAC UUUCGUUACC 660

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- [0944] AGATACCCAGATCCATTGATCAGAGCTAACGATACCGTTAAAATCGATTTGGCTACCGGTAAGATCGRTA
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[0950] TTGCTAACCTTCAATAAGTTGTT
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[0952] GAAUUCGUUGCUUGAGCAAGAGGAAAAGCUUACUAAAUUGAUAAAAGCAGGCAAAUAGAAAUAGUACUUGG
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[0969] SEQ ID NO 204 ;XM_446360.1 Candida glabrata CBS138, partial mRNA
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[0987] CUACCAACGAAAACUUCAGAUUGGUCUACGACGUCAGGGUAGAUUCGUGUCCACCGUAUCACUGACGA
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[0994] UCAACAAGGUUUUAAA
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[1028] SEQ ID NO 207 ;RNA *S. cerevisiae* ribosomal protein S7 gene ,exons 1 and 2
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- [1061] SEQ ID NO 208 ;M64294. A *S. cerevisiae* ribosomal protein S7 gene, exons 1 and 2
- [1062] GTAAGATTTAGAATAGTTTCTTTTCATATAACGTCGACTAAGTATAACAATAGATACACCACTATTGAGG
- [1063] AAAGATGGCTAGAGGACCGTATGTTGATTTCCACCTAAAAAATGAAGAGTTGGCAAAAACAAGATAATAG
- [1064] TTTTCTTTGAAGATGGGTACCCTCTCATGATTGGTACAAGTGATTTGCACCAAAGTGACGATGCGGACTA
- [1065] AAGAAAGAATATAAGAAGTTGTGTTTATCTATCGGAAGATAGAATTCTGATGAGAAAACTTTATCCTTGT
- [1066] TAAGAACAGATAAGCATTGCGGGATATTTTACTAACAAGAGTACGTTAATAATGTTAATACGATTTTT
- [1067] CATATAGAAAAGAAGCATCTAAAGAGATTAGCAGCTCCACACCATGGTTATTGGACAAGTTGTCCGGTTG
- [1068] TTACGCCCCAAGACCATCTGCTGGTCCACACAAAATTGCGTGAATCCTTGCCATTGATTGTCTTTCTAAGA
- [1069] AACAGATTAAGTATGCTTTGAACGGCCGTGAAGTCAAGGCTATCTTGATGCAACGTCACGTCAAAGTTG
- [1070] ACGGTAAGGTTAGAAGTACACCACCTACCCAGCTGGTTTCATGGACGTCATCACTCTAGATGCCACCAA
- [1071] TGAAAACCTTCAGATTGGTCTACGATGTCAAGGGTAGATTTCGCTGTCCACCGTATCACCGATGAAGAAGCC
- [1072] TCTTACAAATTGGGTAAGGTCAAGAAGGTTCAATTAGGTAAGAAGGGTGTTCATACGTTGTTACCCACG
- [1073] ATGGTAGAACTATCAGATACCCAGACCCAAACATCAAGGTCAATGACACTGTTAAGATTGATTTGGCCTC
- [1074] TGGTAAGATTACTGATTTTCATCAAGTTCGATGCCGGTAAGTTGGTTTACGTTACTGGTGGTCGTAACCTG
- [1075] GGTCGTATCGGTACTATCGTTCACAAGGAAAGACACGATGGTGGTTTCGATTTGGTTCACATCAAGGACT
- [1076] CCTTGGACAACACTTTCGTCACTAGATTGAACAATGTCTTCGTCATTGGTGAACAAGGTAAGCCTTACAT
- [1077] TTCTTTGCCAAAGGGTAAGGGTATCAAGTTGTCTATTGCTGAAGAACGTGACAGAAGAAGAGCTCAACAA
- [1078] GGTTTGTAAACATTTTAAATATTGTTATCTGCCCTCTCTTCGTCTTTTG
- [1079] SEQ ID NO 209 ;RNA A *S. cerevisiae* ribosomal protein S7 gene, exons 1 and 2
- [1080] GUAAGAUUUAGAAUAGUUUCUUUUCAUUAACGUCGACUAAGUAUAACAAUAGAUACACCACUAUUGAGG
- [1081] AAAGAUGGCUAGAGGACCGUAUGUUGAUUUCACCUCUAAAAAUGAAGAGUUGGCAAAAACAAGAUAAUAG
- [1082] UUUUCUUUGAAGAUGGGUACCCUCUCAUGAUUGGUACAAGUGAUUUGCACCAAAGUGACGAUGCGGACUA
- [1083] AAGAAAGAAUUAAGAAGUUGUUAUCUAUCGGAAGAUAGAAUUCUGAUGAGAAAAUUUUAUCCUUGU
- [1084] UAAGAACAGAUUAGCAUUGCGGGAUUUUUUACUAACAAGAGUACGUUUAAUAAUGUUAAUACGAUUUUU
- [1085] CAUAUAGAAAGAAGCAUCUAAAGAGAUUAGCAGCUCCACCAUUGGUUAUUGGACAAGUUGUCCGGUUG
- [1086] UUACGCCCCAAGACCAUCUGCUGGUCCACACAAAUUGCGUGAAUCCUUGCCAUUGAUUGUCUUUCUAAGA
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- [1088] ACGGUAAGGUUAGAACUGACACCACCUACCCAGCUGGUUUCUUGGACGUCACUCUAGAUGCCACCAA
- [1089] UGAAAACUUCAGAUUGGUCUACGAUGUCAAGGGUAGAUUCGUGUCCACCGUAUCACCGAUGAAGAAGCC
- [1090] UCUUACAAAUUGGGUAAGGUCAAGAAGGUUCAUUUAGGUUAGAAGGGUGUCCAUACGUUGUUACCCACG
- [1091] AUGGUAGAACUAUCAGAUACCCAGACCCAAACAUCAAGGUCAAUGACACUGUUAAGAUUGAUUUGGCCUC
- [1092] UGGUAAGAUUACUGAUUUCAUCAAGUUCGAUGCCGGUAAGUUGGUUUACGUUACUGGUGGUCGUAACUUG
- [1093] GGUCGUUACGGUACUAUCGUUCACAAGGAAAGACACGAUGGGUUGUUCGAUUUGGUUCACAUCAAGGACU
- [1094] CCUUGGACAACACUUUCGUCACUAGAUUGAACAAUGUCUUCGUCAUUGGUGAACAAAGGUAAGCCUUACAU
- [1095] UUCUUUGCCAAAGGGUAAGGGUACAAGUUGUCUUAUUGCUGAAGAACGUGACAGAAGAAGAGCUCACAAA
- [1096] GGUUUGUAAAACAUUUUAAAUAUUGUUAUCUGCCUCUCUUCGUCUUUUG
- [1097] SEQ ID NO 210
- [1098] XM_451697.1 *Kluyveromyces lactis* NRRL Y-1140, KLLA0B03652g predicted mRNA

- [1099] ATGGCTAGAGGACCAAAGAAGCATCTAAAGAGATTAGCAGCTCCACATCATTGGATGTTGGACAAGTTGT
[1100] CCGGTTGTTACGCACCAAGACCATCTGCTGGTCCACACAAGTTGCGTGAATCCTTGCCATTGATCGTTTT
[1101] CTTGAGAAACAGATTAAGTATGCTTTGAACGGTCGTGAAGTCAAGGCCATCTTGATGCAACGTCATGTC
[1102] AAGGTTGACGGTAAGGTCAGAACCGACACTACTTCCCAGCTGGTTTCATGGATGTTATCACCTTGAAG
[1103] CTACCAACGAAAACCTCAGATTGGTCTACGATGTTAAGGGTAGATTGCGTGTCCACCGTATCACTGATGA
[1104] AGAAGCTTCCTACAAGTTGGCTAAGGTCAAGAAGGTTCAACTAGGTAAGAAGGGTATTCCATACGTCGTT
[1105] ACCCACGACGGTAGAACCATCAGATACCCAGACCCAAACATCAAGGTTAACGACACCGTTAAGGTTGATT
[1106] TGGCTACTGGTACTATCACCGATTCATCAAATTCGACACTGGTAAGTTGGTTTTATGTTACCGGTGGTCG
[1107] TAACTTGGGTAGAGTTGGTACCATCGTCCACAGAGAAAGACACGAAGGTGGTTTTGATTTGGTTCACATC
[1108] AAGGATTCTTTGAAAACACTTTCGTCACCAGATTGAACAACGTTTTTCGTCATCGGTGAACCAGGTAGAC
[1109] CATGGATCTCCTTGCCAAAGGGTAAGGGTATCAAGTTGACCATCTCTGAAGAACGTGACCGTAGAAGAGC
[1110] TCAACATGGTTTGTA
[1111] SEQ ID NO 211
[1112] RNA *Kluyveromyces lactis* NRRL Y-1140, KLLA0B03652g predicted mRNA
[1113] AUGGCUAGAGGACCAAAGAAGCAUCUAAAGAGAUUAGCAGCUCCACAUCAUUGGAUGUUGGACAAGUUGU
[1114] CCGGUUGUUACGCACCAAGACCAUCUGCUGGUCCACACAAGUUGCGUGAAUCCUUGCCAUUGAUCGUUUU
[1115] CUUGAGAAACAGAUUAAAGUAUGCUUUGAACGGUCGUGAAGUCAAGGCCAUCUUGAUGCAACGUCAUGUC
[1116] AAGGUUGACGGUAAGGUCAGAACCGACACUACUUUCCCAGCUGGUUUCAUUGGAUGUUAUCACCUUGGAAG
[1117] CUACCAACGAAAACUUCAGAUUGGUCUACGAUGUUAAGGGUAGAUUCGUGUCCACCGUAUCACUGAUGA
[1118] AGAAGCUUCCUACAAGUUGGCUAAGGUCAAGAAGGUUCAACUAGGUAAGAAGGGUAUCCAUACGUCGUU
[1119] ACCCACGACGGUAGAACCAUCAGAUACCCAGACCCAAACAUCAAGGUUAAACGACACCGUUAAGGUUGAUU
[1120] UGGCUACUGGUACUUCACCGAUUUCAUCAAUUCGACACUGGUAAGUUGGUUUUUGUUUACCGGUGGUCG
[1121] UAACUUGGGUAGAGUUGGUACCAUCGUCCACAGAGAAAGACACGAAGGUGGUUUCGAUUUUGGUUCACAUC
[1122] AAGGAUUCUUUGGAAAACACUUUCGUCACCAGAUUGAACAAACGUUUUCGUCUACGGUGAACAGGUAGAC
[1123] CAUGGAUCUCCUUGCCAAAGGGUAAGGGUAUCAAGUUGACCAUCUCUGAAGAACGUGACCGUAGAAGAGC
[1124] UCAACAUGGUUUGUAA
[1125] SEQ ID NO 212 ;NM_209058.1|*Eremothecium gossypii* ADL391Cp (ADL391C), mRNA
[1126] ATGGCTAGAGGACCAAAGAAGCACCTGAAGAGATTGGCAGCTCCACACCACTGGTTGTTGGACAAGCTAT
[1127] CCGGCTGTTACGCTCCAAGACCATCCGCTGGTCCACACAAGTTGCGCGAGTCTTTGCCATTGATCGTCTT
[1128] CTTGAGAAACAGATTAAGTATGCTTTGAACGGTCGCGAGGTCAAGGCCATCCTAATGCAGCGTCATGTT
[1129] AAGGTTGACGGTAAGGTCAGAACTGACACTACCTACCCAGCTGGTTTCATGGATGTCATCACTCTAGAGG
[1130] CTACCAACGAGAACCTCAGATTGGTATACGATGTCAAGGGCAGATTTGCTGTCCACCGTATCACCGATGA
[1131] GGAGGCTACTTACAAGTTGGGTAAAGGTTAAGCGCGTTCAGCTAGGTAAGAAGGGTGTCCATACGTGGTC
[1132] ACTCACGACGGCAGAACCATCAGATACCCAGACCCAAACATCAAGGTTAACGACACCGTCAAGGTTGACC
[1133] TTGCTACTGGTAAGATTACCGACTTCATCAAGTTCGACACTGGTAAGTTGGTGTACGTCACCGGTGGCCG
[1134] TAACTTGGGCCGTATTGGTGTATCACCACAGAGAGAGACACGAGGGTGGCTTTGACTTGGTTCACATC
[1135] AAGGACTCCTTGAGAACAACCTTTCGTCACCAGATTGAACAACGTTTTTCGTCATCGGTGAGCAAGGTAGAC
[1136] CATGGATCTCCTTGCCAAGGGTAAGGGTATTAAGTTGTCCATTGCTGAGGAGCGTGACCGTAGAAGAGC
[1137] TCAACAAGGTTTGTA

- [1138] SEQ ID NO 213 ;RNA *Eremothecium gossypii* ADL391Cp (ADL391C), mRNA
- [1139] AUGGCUAGAGGACCAAAGAAGCACCUGAAGAGAUUGGCAGCUCCACACCACUGGUUGUUGGACAAGCUAU
- [1140] CCGGCUGUUACGCUCCAAGACCAUCCGCUGGUCCACACAAGUUGCGGAGUCUUUGCCAUUGAUCGUCUU
- [1141] CUUGAGAAACAGAUUAAAGUAUGCUUUGAACGGUCGCGAGGUCAAGGCCAUCCUAAUUGCAGCGUCAUGUU
- [1142] AAGGUUGACGGUAAGGUCAGAACUGACACUACCUACCCAGCUGGUUUCAUUGGAUGUCAUCACUCUAGAGG
- [1143] CUACCAACGAGAACUUCAGAUUGGUAUACGAUGUCAAGGGCAGAUUUGCUGUCCACCGUAUCACCGAUGA
- [1144] GGAGGCUACUUACAAGUUGGGUAAGGUUAAGCGCGUUCAGCUAGGUAGAAGGGUGUCCCAUACGUGGUC
- [1145] ACUCACGACGGCAGAACCAUCAGAUACCCAGACCCAAAACAUCAAGGUUAAACGACACCGUCAAGGUUGACC
- [1146] UUGCUACUGGUAAGAUUACCGACUUCAUCAAGUUCGACACUGGUAGUUGGUUACGUCACCGGUGGCCG
- [1147] UAACUUGGGCCGUUUGGUGUCAUACCCACAGAGAGACACGAGGGUGGCUUUGACUUGGUUCACAUC
- [1148] AAGGACUCCUUGGAGAACACUUUCGUCACCAGAUUGAACAACGUUUUCGUCAUCGGUGAGCAAGGUAGAC
- [1149] CAUGGAUCUCCUUGCCAAGGGGUAAGGGUAUUAAGUUGUCCAUUGCUGAGGAGCGUGACCGUAGAAGAGC
- [1150] UCAACAAGGUUUGUAA
- [1151] SEQ ID NO 214 ;XM_460509.1*Debaryomyces hansenii* CBS767 hypothetical
- [1152] protein(DEHA0F03674g)partial mRNA
- [1153] ATGGGTAGAGGTCAAAGAAGCACTTGAAGAGATTAGCAGCACCATCCCCTGGATGTTGGACAAAATTGT
- [1154] CCGGTACTTACGCACCAAGACCATCTGCTGGTCCCTACAAATTGAGAGAATCTTTACCATTGGTTATCTT
- [1155] CTTAAGAAACAGACTTAAGTATGCCTTAAACGGTAGAGAAGTCAAGGCCATCTTGATGCAAGAACACGTC
- [1156] AAGGTTGATGGTAAAGTTAGAACCGATGCTACTTCCCAGCTGGTTTCATGGATGTCATCACTTTAGAAG
- [1157] CTACCAACGAACACTTCAGATTAATCTATGATGTCAAGGGTAGATTCACTGTCCACAGAATCACTGCTGA
- [1158] AGAAGCTTCTTACAAGTTAGCTAAGGTCAAGAAGGTCCAATTAGGTAAGAGAGGTATTCCATACGTTGTC
- [1159] ACCCACGACGGTAGAACTATCAGATACCCAGATCCATTGATCAGAGCCAACGATTCCGTTAAGGTTGACT
- [1160] TAGCTACCGGTAAGATCACTGACTTTATCAGCTTTGACACTGGTAGATTAGTCATGGTTACTGGTGGTCG
- [1161] TAACATGGGTAGAGTTGGTGTATCACCACAGAGAAAAGCACGAGGGTGGTTTCGATTTAGTCCACATC
- [1162] AAGGATTCTTTGGAAAACACTTTCGTTACCAGATTAACCTAACGTCCTTCATCGTCGGTACTGAAGCTGGTA
- [1163] AGCCACACATTTCTTTACCAAAGGGTAAGGGTATTAAGTTATCCATCTCTGAAGAACGTGACAGAAGAAG
- [1164] AAACCAACAACCTTATCAACTAA
- [1165] SEQ ID NO 215 ;RNA *Debaryomyces hansenii* CBS767 hypothetical
- [1166] protein(DEHA0F03674g)partial mRNA
- [1167] AUGGGUAGAGGUCAAAGAAGCACUUGAAGAGAUUAGCAGCACCAUCCACUGGAUGUUGGACAAAUUGU
- [1168] CCGGUACUUACGCACCAAGACCAUCUGCUGGUCCUCACAAUUGAGAGAAUCUUUACCAUUGGUUAUCUU
- [1169] CUUAAGAAACAGACUUAAGUAUGCCUUAACGGUAGAGAAGUCAAGGCCAUUCUUGAUGCAAGAACACGUC
- [1170] AAGGUUGAUGGUAAAGUUAGAACCGAUGCUACUUUCCAGCUGGUUUCAUUGGAUGUCAUCUUUAGAAG
- [1171] CUACCAACGAACACUUCAGAUUAAUCUAUGAUGUCAAGGGUAGAUUCACUGUCCACAGAAUCACUGCUGA
- [1172] AGAAGCUUCUUACAAGUUAGCUAAGGUCAAGAAGGUCAAUUAGGUAAAGAGAGGUAAUCCAUCGUUGUC
- [1173] ACCCACGACGGUAGAACUUCAGAUACCCAGAUCCAUUGAUCAGAGCCAACGAUUCGUAAGGUUGACU
- [1174] UAGCUACCGGUAAGAUACUGACUUUUCAGCUUUGACACUGGUAGAUUAGUCAUGGUUACUGGUGGUCG
- [1175] UACAUGGGUAGAGUUGGUGUUUCACCCACAGAGAAAAGCACGAGGGUGGUUUCGAUUUAGUCCACAUC
- [1176] AAGGAUUCUUUGGAAAACACUUUCGUUACCAGAUUAAACUACGUCUUCUUCGUCGGUACUGAAGCUGGUA

[1177] AGCCACACAUUUUUUACCAAAGGGUAAGGGUAUUUAGUUUCCAUCUCUGAAGAACGUGACAGAAGAAG
[1178] AAACCAACAACUUAUCAACUAA
[1179] SEQ ID NO 216 ;XM_657428.1 *Aspergillus nidulans* FGSC A4 40S ribosomal
[1180] protein S7 (AN4916.2), mRNA
[1181] ATGGCTGCCATCAACAAGATCGCCCACAACCTCGCCGTCGAGGCAGAACCCTTCCGAGCTGGAGACCGCGA
[1182] TCGCGGGTGTCTCTCTCGACTTGGAGAGCAACACACAGGACCTGAAGGCTACTCTCCGGCCTCTGCAGTT
[1183] CGTGTCTGCTCGTGTGAGGTCGAGGTCGGCCACGGCAAGAAGGCTGTCATCATCTTCGTCCCCGTCCCTCTC
[1184] CTCCAGGCCTTCCACAAGATCCAGCAGCGCCTTACCCGTGAACTCGAGAAGAAGTTCTCGGACCGCCACG
[1185] TCCTCTTCGTGCTCAGCGCCGATCCTCCCCAAGCCCAAGCGTCCGTCAACTCCCGCACCAACCAGAA
[1186] GCAGAAGCGCCCCGTTCCTCGTACCCTTACTGCCGTTACGACGCCATCCTCGACGACCTCGTCTACCCC
[1187] GTTGAGATTGTTCGGCAAGCGCATCCGCACCAAGGAGGACGGCTCCAAGACCCCTCAAGGTCATCCTCGACG
[1188] AGAAGGAGCGTGGTGGTGTGACCACCGCCTCGACGCCCTACGGCGAGGTCTACCGTCTGACGGGTCG
[1189] TGCTGTGCTTTTTCGAGTTCCCCCAGGGTGGTGTCTGAGTTTTAA
[1190] SEQ ID NO 217 ;RNA *Aspergillus nidulans* FGSC A4 40S ribosomal
[1191] protein S7 (AN4916.2), mRNA
[1192] AUGGCUGCCAUCAACAAGAUUCGCCACAACUCGCCGUCGAGGCAGAACCCUUCGAGCUGGAGACCGCGA
[1193] UCGCGGGUGCUCUCUUCGACUUGGAGAGCAACACACAGGACCUGAAGGCUACUCUCCGGCCUCUGCAGUU
[1194] CGUGUCUGCUCGUGAGGUCGAGGUCGGCCACGGCAAGAAGGCUGUCAUCAUCUUCGUCCCCGUCCCUCUC
[1195] CUCCAGGCCUUCACAAGAUCCAGCAGCGCCUUACCCGUGAACUCGAGAAGAAGUUCUGGACCGCCACG
[1196] UCCUCUUCGUCGUCAGCGCCGCAUCCUCCCCAAGCCCAAGCGCUCCGUCAACUCCCGCACCAACCAGAA
[1197] GCAGAAGCGCCCCGUUCCCGUACCCUUCUGCCGUUCACGACGCCAUCCUCGACGACCUUGUCUACCCC
[1198] GUUGAGAUUGUCGGCAAGCGCAUCCGCACCAAGGAGGACGGCUCCAAGACCCUCAAGGUCUACCUUGACG
[1199] AGAAGGAGCGUGGUGGUUGUUGACCACCGCCUCGACGCCUACGGCGAGGUCUACCGUCGUCUGACGGGUCG
[1200] UGCUGUCGUUUUCGAGUUCCCCCAGGGUGGUCUUCUGAGUUUUAA
[1201] SEQ ID NO 218 ;> XM_749453.1 *Aspergillus fumigatus* Af293 ribosomal
[1202] protein S7e (Afu3g10730) partial mRNA
[1203] ATGGCTGCTATCAACAAGATCGCCCACAACCTCGCCATCGAGGCAGAACCCTTCCGAGCTGGAGACTGCGA
[1204] TCGCCGGCGCTCTCTACGACTTGGAGAGCAATACACAGGACCTGAAGGCCACCCTTCGGCCCCCTGCAGTT
[1205] TGTCTCTGCCCGTGAGGTTGAGGTCGGCCACGGCAAGAAGGCCGTTATCATCTTCGTCCCCGTCCCTCTC
[1206] CTCCAGGGCTTCCACAAGATCCAGCAGCGCCTGACCCGTGAGCTCGAGAAGAAGTTCTCCGACCGCCACG
[1207] TCCTCTTTGTTGCTCAGCGCCGATCCTGCCCGCCCTAAGCGCTCTGTCAACTCCCGCACCAACCAGAA
[1208] GCAGAAGCGTCCTCGCTCTCGCACCCCTGACCGCTGTCCACGACGCCATCCTCAACGACCTCGTTTACCCC
[1209] GTCGAGATCGTCGGCAAGCGTATCCGCACCAAGGAGGACGGCAGCAAGACTCTCAAGGTCATCCTGGACG
[1210] AGAAGGAGCGTGGTGGTGTGACCACAGACTCGATGCCTACGGCGAGGTTTACCGCCGACTAACCGGCCG
[1211] CTCTGTTGTCTTCGAGTTCCCCCAGAGCGGTGCCGCCGAGTACTAG
[1212] SEQ ID NO 219 ;RNA *Aspergillus fumigatus* Af293 ribosomal protein S7e
[1213] (Afu3g10730) partial mRNA
[1214] AUGGCUGCUAUCAACAAGAUUCGCCACAACUCGCCAUCGAGGCAGAACCCUUCGAGCUGGAGACUGCGA
[1215] UCGCGGGCGCUCUCUACGACUUGGAGAGCAAUACACAGGACCUGAAGGCCACCCUUCGGCCCCUGCAGUU

- [1216] UGUCUCUGCCCGUGAGGUUGAGGUCGGCCACGGCAAGAAGGCCGUUAUCAUCUUCGUCCCCGUCCCUCUC
[1217] CUCCAGGGCUUCCACAAGAUAUCCAGCAGCGCCUGACCCGUGAGCUCGAGAAGAAGUUCUCCGACCCGCCACG
[1218] UCCUCUUUGUUGCUCAGCGCCGCAUCCUGCCCCGCCUAAGCGCUCUGUCAACUCCCGCACCAACCAGAA
[1219] GCAGAAGCGUCCUCGCUCUCGCACCCUGACCCGUGUCCACGACGCCAUCCUCAACGACCCUCGUUUUACCCC
[1220] GUCGAGAUCGUCGGCAAGCGUAUCCGCACCAAGGAGGACGGCAGCAAGACUCUCAAGGUCAUCCUGGACG
[1221] AGAAGGAGCGUGGUGGUUUGACCACAGACUCGAUGCCUACGGCGAGGUUUUACCCGCCGACUAACCCGGCCG
[1222] CUCUGUUGUCUUCGAGUUCSCCCAGAGCGGUGCCGCCGAGUACUAG
[1223] SEQ ID NO 220 :> XM_001213780.1 *Aspergillus terreus* NIH2624 40S ribosomal
[1224] protein S7 (ATEG_04602)mRNA, complete cds
[1225] ATGGCTGCTATCAACAAGATCGCCACAACCTCGCCGTCTCGGCAGAACCCCTCCGAGCTGGAGACCCGCGA
[1226] TCGCCGGTGTCTGTTCGACCTCGAGAGCAACACCACCGACCTGAAGGCCACCCCTCCGCCCCCTTCAGTT
[1227] CGTGTCTGCTCGTGAGGTTGAGGTCGGCCACGGCAAGAAGGCCGTCATCATCTTCGTCCCTGTCCCTCTC
[1228] CTCCAGGGCTTCCACAAGATCCAGCAGCGTCTGACCCGTGAGCTCGAGAAGAAGTTCTCCGACCCGCCACG
[1229] TCCTCTTCGTTGCTCAGCGCCGATCCTGCCCGCCCCAAGCGCTCTGTCAACTCCCGCACCAACCAGAA
[1230] GCAGAAGCGTCCCCGTTCCCGCACTCTGACGGCCGTCCACGACGCCATCCTCACCGACCTCGTCTACCCC
[1231] GTCGAGATCGTCGGCAAGCGCATCCGCACCAAGGAGGACGGCTCCAAGACCCCTCAAGGTCATCCTCGACG
[1232] AGAAGGAGCGCGGCGGTGTCGACCACCGCCTCGATGCCTACGGCGAGGTCTACCGTCGTCTCACCGGCCG
[1233] TGCCGTCGTCTTCGAGTTCCCCCAGAGCGGTGCTGCTGACTACTAA
[1234] SEQ ID NO 221 ;RNA *Aspergillus terreus* NIH2624 40S ribosomal
[1235] protein S7 (AUEG_04602)mRNA, complete cds
[1236] AUGGCUGCUAUAACAAGAUCGCCACAACUCGCCGUCUCGGCAGAACCCCUCCGAGCUGGAGACCCGCGA
[1237] UCGCCGGUGCUCUGUUCGACCUUGAGAGCAACACCACCGACCCUGAAGGCCACCCUCCGCCCCUUCAGUU
[1238] CGUGUCUGCUCUGAGGUUGAGGUCGGCCACGGCAAGAAGGCCGUCAUCAUCUUCGUCCCCUGUCCCUCUC
[1239] CUCCAGGGCUUCCACAAGAUAUCCAGCAGCGUCUGACCCGUGAGCUCGAGAAGAAGUUCUCCGACCCGCCACG
[1240] UCCUCUUCGUUGCUCAGCGCCGCAUCCUGCCCCGCCCAAGCGCUCUGUCAACUCCCGCACCAACCAGAA
[1241] GCAGAAGCGUCCCCGUUCCCGCACUCUGACGGCCGUCCACGACGCCAUCCUCACCGACCCUCGUCUACCCC
[1242] GUCGAGAUCGUCGGCAAGCGCAUCCGCACCAAGGAGGACGGCUCCAAGACCCUCAAGGUCAUCCUCGACG
[1243] AGAAGGAGCGCGGCGGUGUCGACCACCGCCUCGAUGCCUACGGCGAGGUCUACCGUCGUCUACCCGGCCG
[1244] UGCCGUCGUCUUCGAGUUCSCCCAGAGCGGUGCUGCUGACUACUAA
[1245] SEQ NO 222 :*C. albicans* 1899
[1246] CATCACYTTGGAAGCTACCAACGAACATTTTCAGATTAGTCTACGATGTTAAAGGTAAATTYGCTGTTCA
CAGAATTTCTG
[1247] CTGAAGAAGCTGCCTACAAATTGGGTAAAGTCAAGAAAGTCCAATTAGGTAAGAAAGGTGTTCCATACG
TTGTTACCCAC
[1248] GACGGTAGAACYATCAGATACCCAGA
[1249] SEQ NO 223 :*C. albicans* 1899
[1250] CAUCACYUUGGAAGCUACCAACGAACAUUUCAGAUUAGUCUACGAUGUUAAAGGUAAAUYGCUGUUCA
CAGAAUUUCUG
[1251] CUGAAGAAGCUGCCUACAAAUUGGGUAAAAGUCAAGAAAGUCCAAUUAGGUAAGAAAGGUGUCCAUACG

UUGUUACCCAC

[1252] GACGGUAGAACYAUCAGAUACCCAGA

[1253] SEQ NO 224 *C. albicans* 2738

[1254] CATCACYTTGGAAGCTACCAACGAACATTTTCAGATTAGTCTACGATGTTAAAGGTAATTYGCTGTTCA
CAGAATYTCTG

[1255] STGAAGAAGCTGCCTAYAAAATTGGGTAAAGTCAAGAAAGTYCAATTAGGTAAGAAAGGTGTTCCATACG
TTGTTACCCAC

[1256] GACGGTAGAACYATCAGATACCCAGA

[1257] SEQ NO 225 *C. albicans* 2738

[1258] CAUCACYUUGGAAGCUACCAACGAACAUUUCAGAUUAGUCUACGAUGUUAAAGGUAAAUYGUGUUCA
CAGAAUYUCUG

[1259] SUGAAGAAGCUGCCUAYAAAUUGGGUAAAAGUCAAGAAAGUYCAAUUAGGUAAGAAAGGUGUCCAUACG
UUGUUACCCAC

[1260] GACGGUAGAACYAUCAGAUACCCAGA

[1261] SEQ NO 226 *C. albicans* 1912

[1262] CATCACYTTGGAAGCTACCAACGAACATTTTCAGATTAGTCTACGATGTTAAAGGTAATTCGCTGTTCA
CAGAATTTCTG

[1263] CTGAAGAAGCTGCCTACAAAATTGGGTAAAGTCAAGAAAGTCCAATTAGGTAAGAAAGGTGTTCCATACG
TTGTTACCCAC

[1264] GACGGTAGAACYATCAGATACCCAGA

[1265] SEQ NO 227 *C. albicans* 1912

[1266] CAUCACYUUGGAAGCUACCAACGAACAUUUCAGAUUAGUCUACGAUGUUAAAGGUAAAUCGUGUUCA
CAGAAUUUCUG

[1267] CUGAAGAAGCUGCCUACAAAUUGGGUAAAAGUCAAGAAAGUCCAAUUAGGUAAGAAAGGUGUCCAUACG
UUGUUACCCAC

[1268] GACGGUAGAACYAUCAGAUACCCAGA

[1269] SEQ NO 228 *C. parapsilosis* 6318

[1270] YATTACTTTGGAAGCCACYAATGAAAACTTTAGATTGATTTACGATGTCAAAGGTAGATTTGCTGTCCA
CAGAATCTCAG

[1271] CTGAAGAAGCCACTTACAAAATTGGGTAAAGTCAAGAGAGTCCAATTGGGTAAGAAGGGAATCCCATACG
TTGTCACCCAC

[1272] GATGGTAGAACYATCAGATACCCAGA

[1273] SEQ NO 229 *C. parapsilosis* 6318

[1274] YAUUACUUUGGAAGCCACYAAUGAAAACUUUAGAUUGAUUUACGAUGUCAAGGUAGAUUUGCUGUCCA
CAGAAUCUCAG

[1275] CUGAAGAAGCCACUUACAAAUUGGGUAAAAGUCAAGAGAGUCCAAUUGGGUAAGAAGGGAUCCCAUACG
UUGUCACCCAC

[1276] GAUGGUAGAACYAUCAGAUACCCAGA

[1277] SEQ NO 230 *C. parapsilosis* 6395

- [1278] CATCACTTTGGAAGCTACYAAAYGAACATTTTGMATTGATCTACGATGTYAAAGGTAGATTYGGCTGTYCA
YAGAATCTCTG
- [1279] CTGAAGAAGCCACYTACAAATTGGGTAAAGTTAAGAAAGTCCAATTAGGTAAAAAGGGAATYCCATACG
TTGTCACCCAC
- [1280] GATGGTAGAACYATCAGATACCCAG
- [1281] SEQ NO 231 :C. parapsilosis 6395
- [1282] CAUCACUUUGGAAGCUACYAAAYGAACAUUUUMGAUUGAUCUACGAUGUYAAAGGUAGAUUYGCUGUYCA
YAGAAUCUCUG
- [1283] CUGAAGAAGCCACYUACAAAUUGGGUAAAAGUUAAGAAAGUCCAUUAGGUAAAAAGGGAUYCCAUACG
UUGUCACCCAC
- [1284] GAUGGUAGAACYAUCAGAUACCCAG
- [1285] SEQ NO 232 :C. parapsilosis 96141
- [1286] CATTACTTTGGAAGCCACCAACGAACACTTTAGATTGATTTACGATGTTAARGGTAGATTYGGCTGTCCA
CAGAATYTCTG
- [1287] CTGARGAAGCCACCTACAAATTGGGTAAAGTTAAGAAAGTCCAATTAGGTAAAAAGGGAATCCCATACG
TTGTCACCCAC
- [1288] GATGGYAGAACYATCAGATACCCAG
- [1289] SEQ NO 233 :C. parapsilosis 96141
- [1290] CAUUACUUUGGAAGCCACCAACGAACACUUUAGAUUGAUUUACGAUGUUAARGGUAGAUUYGCUGUCCA
CAGAAUYUCUG
- [1291] CUGARGAAGCCACCUACAAAUUGGGUAAAAGUUAAGAAAGUCCAUUAGGUAAAAAGGGAUCCCAUACG
UUGUCACCCAC
- [1292] GAUGGYAGAACYAUCAGAUACCCAG
- [1293] SEQ 234 :C. parapsilosis 96137
- [1294] CATTACTTTGGAAGCCACCAATGAAAACCTTTAGATTGATTTACGATGTCAAAGGTAGATTTGCTGTCCA
CAGAATCTCAG
- [1295] CTGAAGAAGCCACTTACAAATTGGGTAAAGTCAAGAGAGTCCAATTGGGTAAGAAGGGAATCCCATACG
TTGTCACCCAC
- [1296] GATGGTAGAACCATCAGATACCCAG
- [1297] SEQ 235 :C. parapsilosis 96137
- [1298] CAUUACUUUGGAAGCCACCA AUGAAAACUUUAGAUUGAUUUACGAUGUCAAGGUAGAUUUGCUGUCCA
CAGAAUCUCAG
- [1299] CUGAAGAAGCCACUUACAAAUUGGGUAAAAGUCAAGAGAGUCCAUUUGGGUAAGAAGGGAUCCCAUACG
UUGUCACCCAC
- [1300] GAUGGUAGAACCAUCAGAUACCCAG
- [1301] SEQ 236 :C. parapsilosis 96143rep
- [1302] CATCACTTTGGAAGCTACYAAAYGAACATTTYAGATTGATCTACGATGTYAAAGGTAGATTYGGCTGTYCA
YAGAATCTCTG
- [1303] CTGAAGAAGCCACYTACAAATTGGGTAAAGTTAAGAAAGTCCAATTAGGTAAAAAGGGAATYCCATACG

TTGTCACCCAY

[1304] GATGGTAGAACYATCAGATACCCAG

[1305] SEQ 237 :C. parapsilosis 96143rep

[1306] CAUCACUUUGGAAGCUACYAAAYGAACAUUUYAGAUUGAUCUACGAUGUYAAAGGUAGAUUYGCUGUYCA
YAGAAUCUCUG

[1307] CUGAAGAAGCCACYUACAAAUUGGGUAAAAGUUAAGAAAGUCCAAUUAGGUAAAAAGGGAAUYCCAUACG
UUGUCACCCAY

[1308] GAUGGUAGAACYAUCAGAUACCCAG

[1309] SEQ 238 :C. parapsilosis 109

[1310] YAYTACTTTGGAAGCCACYAATGAAAACCTTTAGATTGATTTACGATGTCAAAGGTAGATTTGCTGTCCA
CAGAATCTCAG

[1311] CTGAAGAAGCCACTTACAAAATTGGGTAAAGTCAAGAGAGTCCAATTGGGTAAGAAGGGAATCCCATACG
TTGTCACCCAC

[1312] GATGGTAGAACTATCAGATACCCAGA

[1313] SEQ 239 :C. oarapsilosis 109

[1314] YAYUACUUUGGAAGCCACYAAUGAAAACUUUAGAUUGAUUUACGAUGUCAAGGUAGAUUUUGCUGUCCA
CAGAAUCUCAG

[1315] CUGAAGAAGCCACUUACAAAUUGGGUAAAAGUCAAGAGAGUCCAAUUGGGUAAGAAGGGAUCCCAUACG
UUGUCACCCAC

[1316] GAUGGUAGAACUAUCAGAUACCCAGA

[1317] SEQ 240 :C. parapsilosis2195

[1318] YATTACYTTGGAAGCYACYAAAYGAAAACCTTYAGATTGRITYACGAYGTCAARGGTAGATTYGCTGTCCA
CMGWATMTCWG

[1319] MYGAAGAAGCYWCYTACAARTTGGGTAARGTCAAGARRGTCCAATTGGGTAAGAAGGGWRITYCCATACG
TTGTCACYSAC

[1320] GATGGTAGAACYATCAGATACCCAGA

[1321] SEQ 241 :C. parapsilosis2195

[1322] YAUUACYUUGGAAGCYACYAAAYGAAAACUUUYAGAUUGRUUYACGAYGUCAARGGUAGAUUYGCUGUCCA
CMGWAUMUCWG

[1323] MYGAAGAAGCYWCYUACAARUUGGGUAARGUCAAGARRGUCCAAUUGGGUAAGAAGGGWRUYCCAUACG
UUGUCACYSAC

[1324] GAUGGUAGAACYAUCAGAUACCCAGA

[1325] SEQ 242 :C. parapsilosis 2315

[1326] CATCACTTTGGAAGCTACYAAAYGAACATTTYAGATTGATCTACGATGTYYAAAGGTAGATTYGCTGTCCA
CAGAATCTCTG

[1327] CTGAAGAAGCCACYTACAAAATTGGGTAAAGTTAAGAAAGTCCAATTAGGTAAAAAGGGAATYCCATACG
TTGTCACCCAY

[1328] GATGGTAGAACYATCAGATACCCAGA

[1329] SEQ 243 :C. parapsilosis 2315

- [1330] CAUCACUUUGGAAGCUACYAAAYGAACAUUUYAGAUUGAUCUACGAUGUYAAAGGUAGAUUYGCUGUCCA
CAGAAUCUCUG
- [1331] CUGAAGAAGCCACYUACAAAUUGGGUAAAAGUUAAGAAAGUCCAAUUAGGUAAAAAGGGAAUYCCAUACG
UUGUCACCCAY
- [1332] GAUGGUAGAACYAUCAGAUACCCAGA
- [1333] SEQ 244 :C. krusei 6199
- [1334] CATCACTTTAGAWGCAACCAACGAACACTTCAGATTAATCTATGACATCAAGGGTAGATTCGCAATCCA
CAGAATCACCC
- [1335] CAGAAGAAGCTGCATACAAGTTATGTAAGGTCAAGAAGGTCCAATTAGGTAAGAAGGGTATTCCTTATG
TTGTTACCCAC
- [1336] GATGGTAGAACYATCAGATACCCAG
- [1337] SEQ 245 :C. krusei 6199
- [1338] CAUCACUUUAGAWGCAACCAACGAACACUUCAGAUUAAUCUAUGACAUCAAGGGUAGAUUCGCAAUCCA
CAGAAUCACCC
- [1339] CAGAAGAAGCUGCAUACAAGUUAUGUAAGGUCAAGAAGGUCCAAUUAGGUAGAAGGGUAAUCCUUAUG
UUGUUACCCAC
- [1340] GAUGGUAGAACYAUCAGAUACCCAG
- [1341] SEQ 246 :C. tropicalis 8072
- [1342] CATTACCTTGGAAGCTACCAACGAACACTTCAGATTGATTTACGATGTTAAAGGTAAATTCGCTGTTCA
CAGAATTTCTG
- [1343] CTGAAGAAGCTTCTTACAAATTAGGTAAAGTCAAGAAGGTTCAATTAGGTAAAAAGGTGTTCCATACG
TTGTCACCCAC
- [1344] GATGGTAGAACYATCAGATACCCAGA
- [1345] SEQ 247 :C. tropicalis 8072
- [1346] CAUUACCUUGGAAGCUACCAACGAACACUUCAGAUUGAUUUACGAUGUUAAAGGUAAAAUUCGUGUUCA
CAGAAUUUCUG
- [1347] CUGAAGAAGCUUCUUACAAAUUAGGUAAAAGUCAAGAAGGUCAAUUAGGUAAAAAGGUGUCCAUCG
UUGUCACCCAC
- [1348] GAUGGUAGAACYAUCAGAUACCCAGA
- [1349] SEQ 248 :C. tropicalis 2316
- [1350] CATCACTTTTRGAWGCWACCAACGAACAYTTCAGATTAATCTACGAYGTCAAGGGTAAATTCGCTGTCCA
CAGAATCACYG
- [1351] CTGAAGAAGCTGCCTMCAAATTGGTTAARGTMAAGAAAGTCCAATTAGGTAAGARAGGTGTTCCWTACG
TTGTTACCCAC
- [1352] GAYGGTAGAACYATCAGATACCCAGA
- [1353] SEQ 249 :C. tropicalis 2316
- [1354] CAUCACUUURGAWGCWACCAACGAACAYUUCAGAUUAAUCUACGAYGUCAAGGGUAAAAUUCGUGUCCA
CAGAAUCACYG
- [1355] CUGAAGAAGCUGCCUMCAAAAUUGGUUAARGUMAAGAAAGUCCAAUUAGGUAGAARAGGUGUCCWUACG

UUGUUACCCAC

[1356] GAYGGUAGAACYAUCAGAUACCCAGA

[1357] SEQ 250 :C. dubliniensis 16971

[1358] CATYACYTTRGAAGCTACYAAAYGAACATTTTCAGATTAGTWTACGATGTTAAAGGTAAATTYGCGYTTCA
YAGAATCTCTG

[1359] CTGAAGAAGCTKCCTACAAATTGGGTAAAGTYAARAAAGTCCAATTRGGTAARAAAGGTGTTCCATAYG
TTGTTACCCAC

[1360] GACGGTAGAACYATCAGATACCCAG

[1361] SEQ 251 :C. dubliniensis 16971

[1362] CAUYACYUURGAAGCUACYAAAYGAACAUUUCAGAUUAGUWUACGAUGUUAAAGGUAAAUYGCGYUUCA
YAGAAUCUCUG

[1363] CUGAAGAAGCUKCCUACAAAUUGGGUAAAAGUYAARAAAGUCCA AUURGGUAARAAAGGUGUUCCAUAYG
UUGUUACCCAC

[1364] GACGGUAGAACYAUCAGAUACCCAG

[1365] SEQ 252 :C. dubliniensis 16721

[1366] CATYACYTTRGAAGCTACYAAAYGAACATTTTCAGATTAGTWTACGATGTTAAAGGTAAATTYGCGYTTCA
YAGAATCTCTG

[1367] CTGAAGAAGCTKCCTACAAATTGGGTAAAGTYAAGAAAGTCCAATTRGGTAARAAAGGTGTTCCATACG
TTGTTACCCAC

[1368] GACGGTAGAACYATCAGATACCCAG

[1369] SEQ 253 :C. dubliniensis 16721

[1370] CAUYACYUURGAAGCUACYAAAYGAACAUUUCAGAUUAGUWUACGAUGUUAAAGGUAAAUYGCGYUUCA
YAGAAUCUCUG

[1371] CUGAAGAAGCUKCCUACAAAUUGGGUAAAAGUYAAGAAAGUCCA AUURGGUAARAAAGGUGUUCCAUACG
UUGUUACCCAC

[1372] GACGGUAGAACYAUCAGAUACCCAG

[1373] SEQ 254 :C. dubliniensis 16197

[1374] CATYACYTTRGAAGCTACYAAAYGAACATTTTCAGATTAGTWTACGATGTTAAAGGTAAATTYRCYGTTC
YAGAATCTCTG

[1375] CTGAAGAAGCTKCCTACAAATTGGGTAAAGTYAARAAAGTCCAATTRGGTAARAAAGGTGTTCCATACG
TTGTTACCCAC

[1376] GACGGTAGAACYATCAGATACCCAGA

[1377] SEQ 255 :C. dubliniensis 16197

[1378] CAUYACYUURGAAGCUACYAAAYGAACAUUUCAGAUUAGUWUACGAUGUUAAAGGUAAAUYRCYUUCA
YAGAAUCUCUG

[1379] CUGAAGAAGCUKCCUACAAAUUGGGUAAAAGUYAARAAAGUCCA AUURGGUAARAAAGGUGUUCCAUACG
UUGUUACCCAC

[1380] GACGGUAGAACYAUCAGAUACCCAGA

[1381] SEQ 256 :C. norvegenesis 2145

- [1382] TATCACTTTAGAAGCAACCAACGAAAACCTCAGATTAATCTACGACATCAAGGGTAGATTCGCAATTCA
CAGAATCACTC
- [1383] CTGAAGAAGCAGCATAACAAGTTATGTAAGATCAAGAAGGTCCAATTAGGTAAGAAGGGTATTCCATAYG
TTGTTACACAC
- [1384] GACGGTAGAACYATCAGATACCCAGA
- [1385] SEQ 257 :C. norvegenesis 2145
- [1386] UAUCACUUUAGAAGCAACCAACGAAAACUUCAGAUUAAUCUACGACAUCAAGGGUAGAUUCGCAAUUC
CAGAAUCACUC
- [1387] CUGAAGAAGCAGCAUACAAGUUUGUAAGAUCAAGAAGGUCCAUUAGGUAAGAAGGGUAAUCCAUYG
UUGUUACACAC
- [1388] GACGGUAGAACYAUCAGAUACCCAGA
- [1389] SEQ 258 :C. guilliermondii 23
- [1390] CATCACCTTGGAGGCCACCAACGAGCACTTYAGATTGGTGTACGACGTCAAGGGTAGATTTGCTGTCCA
CAGAATCACCG
- [1391] CTGAGGAGGCTTCTACAAGTTGGGTAAGGTCAAGAAGGTTCAATTGGGYAAGAGAGGTATTCCATACG
TTGTGACCCAC
- [1392] GACGGTAGAACTATCAGATACCCAGA
- [1393] SEQ 259 :C. guilliermondii 23
- [1394] CAUCACCUUGGAGGCCACCAACGAGCACUUYAGAUUGGUGUACGACGUCAAGGGUAGAUUUGCUGUCCA
CAGAAUCACCG
- [1395] CUGAGGAGGCUUCCUACAAGUUGGGUAAGGUCAAGAAGGUCAAUUGGGYAAGAGAGGUAAUCCAUACG
UUGUGACCCAC
- [1396] GACGGUAGAACUAUCAGAUACCCAGA
- [1397] SEQ 260 :C. guilliermondii 8167
- [1398] ATCACCTTGGAGGCTACCAACGAGCACTTCAGATTGGTGTACGATGTCAAGGGTAGATTTGCTGTCCAC
AGAATCACCGC
- [1399] TGAAGAGGCTTCTACAAGTTGGGTAAGGTCAAGAAGGTTCAATTGGGTAAGAGAGGTATTCCATACGT
TGTTACCCACG
- [1400] ACGGTAGAACCATCAGATACCCAG
- [1401] SEQ 261 :C. guilliermondii 8167
- [1402] AUCACCUUGGAGGCUACCAACGAGCACUUCAGAUUGGUGUACGAUGUCAAGGGUAGAUUUGCUGUCCAC
AGAAUCACCGC
- [1403] UGAAGAGGCUUCCUACAAGUUGGGUAAGGUCAAGAAGGUCAAUUGGGUAAGAGAGGUAAUCCAUACGU
UGUUACCCACG
- [1404] ACGGUAGAACCAUCAGAUACCCAG
- [1405] SEQ 262 :C. lusitaniae 64
- [1406] CACCTTGGARGCCACCAACGAAAACCTCAGATTGGTGTACGACATCAAGGGTAGATTTACTGTCCACAG
AATCACCGCTG
- [1407] ARGAAGGTTCTACAAGTTGGGTAAGGTCAAGAAGATYGCTTTGGGCAAGAAGGCTATCCCATACGTGG

TTACCCACGAY

[1408] GGTAGAACTATCAGATACCCAG

[1409] SEQ 263 :C. lusitaniae 64

[1410] CACCUUGGARGCCACCAACGAAAACUUCAGAUUGGUGUACGACAUCAAGGGUAGAUUCACUGUCCACAG
AAUCACCGCUG

[1411] ARGAAGGUUCCUACAAGUUGGGUAAGGUCAAGAAGAUYGCUUUGGGCAAGAAGGCUAUCCCAUACGUGG
UUACCCACGAY

[1412] GGUAGAACUAUCAGAUACCCAG

[1413] SEQ 264 :C. lipolytica 112

[1414] CAGATTGGTGTACGACGTCAAGGGTAGATTCGCCGTGCACAGAATCACCGCCGAGGAGTCCACCTACAA
GTTGGCCAAGA

[1415] TCAAGAAGGTCCAGTTGGGCAAGAAGAGTATCCCCTACGCCGTCACCCACGACGGTAGAACTATCAGAT
ACCCAGA

[1416] SEQ 265 :C. lipolytica 112

[1417] CAGAUUGGUGUACGACGUCAAGGGUAGAUUCGCCGUGCACAGAAUCACCGCCGAGGAGUCCACCUACAA
GUUGGCCAAGA

[1418] UCAAGAAGGUCCAGUUGGGCAAGAAGAGUAUCCCCUACGCCGUCACCCACGACGGUAGAACUAUCAGAU
ACCCAGA

[1419] SEQ 266 :C. lipolytica 31

[1420] CATCACCTTGRRGCCACCAACGAAAACCTCAGATTGGTGTACGACATCAAGGGTAGATTCAGTGTCCA
CAGAATCACCG

[1421] CTGAGGAAGGTTCTTACAAGTTGGGTAAGGTCAAGAAGATYGCTTTGGGCAAGAAGGCTATCCCATACG
TGGTTACCCAC

[1422] GAYGGTAGAACTATCAGATACCCAGA

[1423] SEQ 267 :C. lipolytica 31

[1424] CAUCACCUUGRRGCCACCAACGAAAACUUCAGAUUGGUGUACGACAUCAAGGGUAGAUUCACUGUCCA
CAGAAUCACCG

[1425] CUGAGGAAGGUUCCUACAAGUUGGGUAAGGUCAAGAAGAUYGCUUUGGGCAAGAAGGCUAUCCCAUACG
UGGUUACCCAC

[1426] GAYGGUAGAACUAUCAGAUACCCAGA

[1427] SEQ 268 :C. lipolytica 113

[1428] TTCAGATTGGTGTACGACGTCAAGGGTAGATTCGCCGTGCACAGAATCACCGCCGAGGAGTCCACCTAC
AAGTTGGCCAA

[1429] GATCAAGAAGGTCCAGTTGGGCAAGAAGAGTATCCCCTACGCCGTCACCCACGACGGTAGAACTATCAG
ATACCCAGA

[1430] SEQ 269 :C. lipolytica 113

[1431] UUCAGAUUGGUGUACGACGUCAAGGGUAGAUUCGCCGUGCACAGAAUCACCGCCGAGGAGUCCACCUAC
AAGUUGGCCAA

[1432] GAUCAAGAAGGUCCAGUUGGGCAAGAAGAGUAUCCCCUACGCCGUCACCCACGACGGUAGAACUAUCAG

AUACCCAGA

[1433] SEQ 270 :C. rugosa 85

[1434] CTTGAGCTACCAACGAAAACCTTCASMTTGATCTACGACGTCAAGGGTAGATTTGCCGTCCACAGAATCA
CCGCTGAAGAA

[1435] GCTTCGTACAAGTTGGSYAAGGTYAAGTCCGTCCAATTGGGYAAGMGMSKKATYCCTTACGCYGT TACY
CACGAYGGTAG

[1436] AACTATCAGATACCCAGA

[1437] SEQ 271 :C. rugosa 85

[1438] CUUGAGCUACCAACGAAAACUUCASMUUGAUCUACGACGUCAAGGGUAGAUUUGCCGUCCACAGAAUCA
CCGCUGAAGAA

[1439] GCUUCGUACAAGUUGGSYAAGGUYAAGUCCGUCCA AUUGGGYAAGMGMSKKAUYCCUUACGCYUUACY
CACGAYGGUAG

[1440] AACUAUCAGAUACCCAGA

[1441] SEQ 272 :C. rugosa 613

[1442] CCTTGGAAGCTACCAACGAAAACCTTCAGATTGATCTACGACGTCAAGGGTAGATTTGCCGTCCACAGAA
TCACCGCTGAA

[1443] GAAGCTTCGTACAAGTTGGSYAAGGTYAAGTCCGTCCAATTGGGYAAGMGMSKKATTCCCTTACGCYGT T
ACYCACGAYGG

[1444] TAGAACYATCAGATACCCAGA

[1445] SEQ 273 :C. rugosa 613

[1446] CCUUGGAAGCUACCAACGAAAACUUCAGAUUGAUCUACGACGUCAAGGGUAGAUUUGCCGUCCACAGAA
UCACCGCUGAA

[1447] GAAGCUUCGUACAAGUUGGSYAAGGUYAAGUCCGUCCA AUUGGGYAAGMGMSKKAUUCUUACGCYUU
ACYCACGAYGG

[1448] UAGAACYAUCAGAUACCCAGA

[1449] SEQ 274 :C. rugosa 41

[1450] CATCTCGCTTGAAGCCACCAACGAAAACCTTCAGATTGATCTACGACGTCAAGGGTAGATTTGCCGTCCA
CAGAATCACCG

[1451] CYGAAGWGGCYTCGTACAAGTTGGSYAAGGTYAAGTCCGTCCAATTGGGYAAGMGMSKKATYCCTTACG
CYGTYACYCAC

[1452] GACGGTAGAACTAYCAGATACCCAG

[1453] SEQ 275 :C. rugosa 41

[1454] CAUCUCGCUUGAAGCCACCAACGAAAACUUCAGAUUGAUCUACGACGUCAAGGGUAGAUUUGCCGUCCA
CAGAAUCACCG

[1455] CYGAAGWGGCYUCGUACAAGUUGGSYAAGGUYAAGUCCGUCCA AUUGGGYAAGMGMSKKAUYCCUUACG
CYGUYACYCAC

[1456] GACGGUAGAACUAYCAGAUACCCAG

[1457] SEQ 276 :C. rugosa 44

[1458] TCGCTTGAGCCACCAACGAAAACCTTCAGATTGATCTACGACGTCAAGGGTAGATTTGCCGTCCACAGAA

TCACCGCTGAA

[1459] GAGGCYTCGTACAAGTTGGSYAAGGTYAAGTCCGTCCAATTGGGYAAGMGMSKKATYCCTTACGCGYTY
ACYCACGACGG

[1460] TAGAACTATCAGATACCCAG

[1461] SEQ 277 :C. rugosa 44

[1462] UCGCUUGAGCCACCAACGAAAAACUUCAGAUUGAUCUACGACGUCAAGGGUAGAUUUGCCGUCCACAGAA
UCACCGCUGAA

[1463] GAGGCYUCGUACAAGUUGGSYAAGGUYAAGUCCGUCCA AUUGGGYAAGMGMSKKAUYCCUUACGCGYGY
ACYCACGACGG

[1464] UAGAACUAUCAGAUACCCAG

[1465] SEQ 278 :C. rugosa 46

[1466] TCGCTTGAGCCACCAACGAAAACTTCAGATTGATCTACGACGTCAAGGGTAGATTTGCCGTCCACAGAA
TCACCGCTGAA

[1467] GAGGCYTCGTACAAGTTGGSYAAGGTYAAGTCCGTCCAATTGGGYAAGMGMSKKATYCCTTACGCGYTY
ACYCACGACGG

[1468] TAGAACTATCAGATACCCAG

[1469] SEQ 279 :C. rugosa 46

[1470] UCGCUUGAGCCACCAACGAAAAACUUCAGAUUGAUCUACGACGUCAAGGGUAGAUUUGCCGUCCACAGAA
UCACCGCUGAA

[1471] GAGGCYUCGUACAAGUUGGSYAAGGUYAAGUCCGUCCA AUUGGGYAAGMGMSKKAUYCCUUACGCGYGY
ACYCACGACGG

[1472] UAGAACUAUCAGAUACCCAG

[1473] SEQ 280 :C. famata 1

[1474] CATCACTTTAGAAGCYACCAACGAACACTTCAGATTAATCTAYGAYGTCAAGGGTAGATTCACTGTYCA
CAGAATCACCG

[1475] CYGAAGAAGCTTCTTACAAGTTAGCTAAGGTYAAGAAGGTYCAATTAGGTAAGAGWGGTATTCCATACG
TTGTYACCCAC

[1476] GATGGTAGAACTATCAGATACCCAG

[1477] SEQ 281 :C. famata 1

[1478] CAUCACUUUAGAAGCYACCAACGAACACUUCAGAUUAAUCUAYGAYGUCAAGGGUAGAUUCACUGUYCA
CAGAAUCACCG

[1479] CYGAAGAAGCUUCUUACAAGUUAGCUAAGGUYAAGAAGGUYCAAUUAGGUAAGAGWGGUAAUCCAUACG
UUGUYACCCAC

[1480] GAUGGUAGAACUAUCAGAUACCCAG

[1481] SEQ 282 :C. famata 2

[1482] CATCACYTTAGAAGCYACCAACGAACACTTCAGATTRATCTATGAYGTCAAGGGTAGATTCACTGTCCA
CAGAATCACYG

[1483] CTGAAGAAGCTTCTTACAAGTTAGCYAAGGTCAAGAAGGTCCAATTAGGTAAGAGAGGTATTCCATACG
YTGTYACWCAC

- [1484] GAYGGTAGAACTATCAGATACCCAG
[1485] SEQ 283 :C. famata 2
[1486] CAUCACYUUAGAAGCYACCAACGAACACUUCAGAUURAUCUAUGAYGUCAAGGGUAGAUUCACUGUCCA
CAGAAUCACYG
[1487] CUGAAGAAGCUUCUUACAAGUUAGCYAAGGUCAAGAAGGUCCAUUAGGUAAGAGAGGUUUCCAUACG
YUGUYACWCAC
[1488] GAYGGUAGAACUAUCAGAUACCCAG
[1489] SEQ 284 :C. famata 3
[1490] CATCACTTTAGAAGCYACCAACGAACACTTCAGATTAATCTAYGAYGTCAAGGGTAGATTCACTGTYCA
CAGAATCACCG
[1491] CYGAAGAAGCTTCTTACAAGTTAGCTAAGGTYAAGAAGGTYCAATTAGGTAAGAGRGGTATTCCATACG
TTGTYACCCAC
[1492] GATGGTAGAACTATCAGATACCCAG
[1493] SEQ 285 :C. famata 3
[1494] CAUCACUUUAGAAGCYACCAACGAACACUUCAGAUUUAUCUAYGAYGUCAAGGGUAGAUUCACUGUYCA
CAGAAUCACCG
[1495] CYGAAGAAGCUUCUUACAAGUUAGCUAAGGUYAAGAAGGUYCAUUAGGUAAGAGRGGUAAUCCAUACG
UUGUYACCCAC
[1496] GAUGGUAGAACUAUCAGAUACCCAG
[1497] SEQ 286 :C. famata 4
[1498] CATCACYTTAGAAGCYACCAACGAACACTTCAGATTRATCTATGAYGTCAAGGGTAGATTCACTGTCCA
CAGAATCACYG
[1499] CTGAAGAAGCTTCTTACAAGTTAGCYAAGGTCAAGAAGGTCCAATTAGGTAAGAGAGGTATTCCATAYG
YTGTYACWCAC
[1500] GAYGGTAGAACTATCAGATACCCAG
[1501] SEQ 287 :C. famata 4
[1502] CAUCACYUUAGAAGCYACCAACGAACACUUCAGAUURAUCUAUGAYGUCAAGGGUAGAUUCACUGUCCA
CAGAAUCACYG
[1503] CUGAAGAAGCUUCUUACAAGUUAGCYAAGGUCAAGAAGGUCCAUUAGGUAAGAGAGGUUUCCAUAYG
YUGUYACWCAC
[1504] GAYGGUAGAACUAUCAGAUACCCAG
[1505] SEQ 288 :C. famata 5
[1506] CATCACTTTAGAAGCYACCAACGAACACTTCAGATTRATCTATGAYGTCAAGGGTAGATTCACTGTCCA
CAGAATCACYG
[1507] CTGAAGAAGCTTCTTACAAGTTAGCYAAGGTCAAGAAGGTCCAATTAGGTAAGAGAGGTATTCCATACG
TTGTYACMCAC
[1508] GAYGGTAGAACTATCAG
[1509] SEQ 289 :C. famata 5
[1510] CAUCACUUUAGAAGCYACCAACGAACACUUCAGAUURAUCUAUGAYGUCAAGGGUAGAUUCACUGUCCA

CAGAAUCACYG

[1511] CUGAAGAAGCUUCUUACAAGUUAGCYAAGGUCAAGAAGGUCCAUUAGGUAAGAGAGGUUUCCAUACG
UUGUYACMCAC

[1512] GAYGGUAGAACUAUCAG

[1513] SEQ 290 :C. haemuloni 52

[1514] CACCTTGGAGGCCACCAACGAGAACTTCAGATTGGTGTACGATGTCAAGGGTAGATTCACTGTCCACAG
AATCACCGCTG

[1515] AGGAGGCTTCTTACAAGCTCGGTAAGGTCARGAAGATCGCTTTGGGTAAGAGAGGTGTTCCATACGTTG
TCACCCACGAC

[1516] GGTAGAACTATCAGATACCCAG

[1517] SEQ 291 :C. haemuloni 52

[1518] CACCUUGGAGGCCACCAACGAGAAUUCAGAUUGGUGUACGAUGUCAAGGGUAGAUUCACUGUCCACAG
AAUCACCGCUG

[1519] AGGAGGCUUCCUACAAGCUCGGUAAGGUCARGAAGAUCGCUUUGGGUAAGAGAGGUGUCCAUACGUUG
UCACCCACGAC

[1520] GGUAGAACUAUCAGAUACCCAG

[1521] SEQ 292 :C. haemulonii 53

[1522] CACCTTGGAGGCCACCAACGAGAACTTCAGATTGGTGTACGAYGTCAAGGGTAGATTCACTGTCCACAG
AATCACCGCTG

[1523] AGGAGGCTTCTTACAAGCTCGGTAAGGTCAGAAAGATCGCYTTGGGTAAGAGAGGTATYCCATACGTTG
TCACCCACGAC

[1524] GGTAGAACTATCAGATACCCAG

[1525] SEQ 293 :C. haemulonii 53

[1526] CACCUUGGAGGCCACCAACGAGAAUUCAGAUUGGUGUACGAYGUCAAGGGUAGAUUCACUGUCCACAG
AAUCACCGCUG

[1527] AGGAGGCUUCUUACAAGCUCGGUAAGGUCAGAAAGAUCGCUUUGGGUAAGAGAGGUUUYCCAUACGUUG
UCACCCACGAC

[1528] GGUAGAACUAUCAGAUACCCAG

[1529] SEQ 294 :C. pulcherrima 36

[1530] GATCACTTTGGAGGCYACCAACGAGAACTTYAGATTGATCTAYGACGTVAAGGGTAGATTYACTGTGCA
CAGAATCACSR

[1531] CCGAGGAGGSCTCKTACAAGTTGGGYAAGGTCAGAAAGATCGCCTTGGGYAAGAGAGGYGTCCTTACG
CYGTSACCCAC

[1532] GACGGTAGAACTATCAGATACCCAG

[1533] SEQ 295 :C. pulcherrima 36

[1534] GAUCACUUUGGAGGCYACCAACGAGAAUUYAGAUUGAUCUAYGACGUVAAGGGUAGAUUYACUGUGCA
CAGAAUCACSR

[1535] CCGAGGAGGSCUCKUACAAGUUGGGYAAGGUCAGAAAGAUCGCCUUGGGYAAGAGAGGYGUKCCUUACG
CYGUSACCCAC

- [1536] GACGGUAGAACUAUCAGAUACCCAG
[1537] SEQ 296 :C.pulcherrima 37
[1538] GATCACTTTGGAGGCYACCAACGAGAACTTCAGATTGATCTAYGACGTMAAGGGTAGATTYACTGTGCA
CAGAATCACCG
[1539] CCGAGGAGGSCTCKTACAAGTTGGGYAAGGTCAGAAAGATYGCCTTGGGYAAGAGAGGYGTCCTTACG
CYGTVACYCAC
[1540] GACGGTAGAACTATCAGATACCCAG
[1541] SEQ 297 :C.pulcherrima 37
[1542] GAUCACUUUGGAGGCYACCAACGAGAACUUCAGAUUGAUCUAYGACGUMAAGGGUAGAUUYACUGUGCA
CAGAAUCACCG
[1543] CCGAGGAGGSCUCKUACAAGUUGGGYAAGGUCAGAAAGAUYGCCUUGGGYAAGAGAGGYGUKCCUUACG
CYGUVACYCAC
[1544] GACGGUAGAACUAUCAGAUACCCAG
[1545] SEQ 298 :C.pulcherrima 38
[1546] GATCACTTTGGAGGCYACCAACGAGAACTTYAGATTGATCTAYGACGTVAAGGGTAGATTYACTGTGCA
CAGAATCACCG
[1547] CCGAGGAGGSCTCKTACAAGTTGGGYAAGGTCAGAAAGATCGCCTTGGGYAAGAGAGGYGTCCTTACG
CYGTSACYCAC
[1548] GACGGTAGAACTATCAGATACCCAG
[1549] SEQ 299 :C.pulcherrima 38
[1550] GAUCACUUUGGAGGCYACCAACGAGAACUUYAGAUUGAUCUAYGACGUVAAGGGUAGAUUYACUGUGCA
CAGAAUCACCG
[1551] CCGAGGAGGSCUCKUACAAGUUGGGYAAGGUCAGAAAGAUCGCCUUGGGYAAGAGAGGYGUKCCUUACG
CYGUSACYCAC
[1552] GACGGUAGAACUAUCAGAUACCCAG
[1553] SEQ 300 :C.pulcherrima 39
[1554] GATCACTTTGGAGGCCACCAACRAGAACTTCAGATTGATCTAYGACGTMAAGGGTAGATTACYGTGCA
CAGAATCACCG
[1555] CCGAGGAGGCCTCKTACAAGTTGGGYAAGGTCAGAAAGATCGCCTTGGGYAAGAGAGGYGTCCTTACG
CYGTMACYCAC
[1556] GACGGTAGAACTATCAGATACCCAG
[1557] SEQ 301 :C.pulcherrima 39
[1558] GAUCACUUUGGAGGCCACCAACRAGAACUUCAGAUUGAUCUAYGACGUMAAGGGUAGAUUCACYGUGCA
CAGAAUCACCG
[1559] CCGAGGAGGCCUCKUACAAGUUGGGYAAGGUCAGAAAGAUCGCCUUGGGYAAGAGAGGYGUKCCUUACG
CYGUMACYCAC
[1560] GACGGUAGAACUAUCAGAUACCCAG
[1561] SEQ 302 :C.pulcherrima 40
[1562] GATCACTTTGGAGGCCACCAACGAGAACTTYAGATTGATCTAYGACG TSAAGGGTAGATTYACTGTGCA

CAGAATCACCG

[1563] CCGAGGAGGSCTCKTACAAGTTGGGYAAGGTCAGAAAGATYGCCTTGGGYAAGAGWGGYGTKCCTTACG
CYGTSACYCAC

[1564] GACGGTAGAACTATCAGATACCCAG

[1565] SEQ 303 :C. pulcherrima 40

[1566] GAUCACUUUGGAGGCCACCAACGAGAACUUYAGAUUGAUCUAYGACGUSAAGGGUAGAUUYACUGUGCA
CAGAAUCACCG

[1567] CCGAGGAGGSCUCKUACAAGUUGGGYAAGGUCAGAAAGAUYGCCUUGGGYAAGAGWGGYGUKCCUUACG
CYGUSACYCAC

[1568] GACGGUAGAACUAUCAGAUACCCAG

[1569] SEQ 304 :C. utilis 50

[1570] CTTGGAGGCCACCAACGAGAACTTCAGATTGGTCTACGATGTCAAGGGTAGATTTGCTGTCCACAGAAT
CACCGATGATG

[1571] AAGCTTCTTACAAGCTTGCTAAGGTCAAGAAGGTTCAATTGGGTAAGAGAGGTATCCCATACGTTGTTA
CCCACGACGGT

[1572] AGAACTATCAGATACCCAG

[1573] SEQ 305 :C. utilis 50

[1574] CUUGGAGGCCACCAACGAGAACUUCAGAUUGGUCUACGAUGUCAAGGGUAGAUUUGCUGUCCACAGAAU
CACCGAUGAUG

[1575] AAGCUUCUUACAAGCUUGCUAAGGUCAAGAAGGUUCAUUGGGUAAGAGAGGUAUCCCAUACGUUGUUA
CCCACGACGGU

[1576] AGAACUAUCAGAUACCCAG

[1577] SEQ 306 :C. utilis 51

[1578] CTTGGAGGCCACCAACGAGAACTTCAGATTGGTCTACGATGTCAAGGGTAGATTTGCTGTCCACAGAAT
CACCGATGATG

[1579] AAGCTTCTTACAAGCTTGCTAAGGTCAAGAAGGTTCAATTGGGTAAGAGAGGTATCCCATACGTTGTTA
CCCACGACGGT

[1580] AGAACTATCAGATACCCAG

[1581] SEQ 307 :C. utilis 51

[1582] CUUGGAGGCCACCAACGAGAACUUCAGAUUGGUCUACGAUGUCAAGGGUAGAUUUGCUGUCCACAGAAU
CACCGAUGAUG

[1583] AAGCUUCUUACAAGCUUGCUAAGGUCAAGAAGGUUCARUUGGGUAAGAGAGGUAUCCCAUACGUUGUUA
CCCACGACGGU

[1584] AGAACUAUCAGAUACCCAG

[1585] SEQ 308 :C. kefyr 59

[1586] CACCTTGGACRCTACCAAMGAAACTTCAGATTGGTCTACGACGTTAAGGGTAGATTCGCTGTCCACCG
TATCACCGACG

[1587] AAGAAGCTTCTTACAAATTGGGTAAGGTCAGAAAGGTCCAAGGTAAGAAGGGTATTCCATACGTTG
TTACCCACGAC

- [1588] GGTAGAACTATCAGATACCCAG
[1589] SEQ 309 :C. kefyr 59
[1590] CACCUUGGACRCUACCAAMGAAAACUUCAGAUUGGUCUACGACGUUAAGGGUAGAUUCGCUGUCCACCG
UAUCACCGACG
[1591] AAGAAGCUUCUUACAAAUUGGGUAAGGUCAGAAAGGUCCAACUAGGUAAGAAGGGUAUCCAUACGUUG
UUACCCACGAC
[1592] GGUAGAACUAUCAGAUACCCAG
[1593] SEQ 310 :C. kefyr 3898
[1594] TGTCACCTTGGACGCTACCAACGAAAACCTTCAGATTGGTCTACGACGTTAAGGGTAGATTCGCTGTCCA
CCGTATCACCG
[1595] ACGAAGAAGCTTCTTACAAATTGGGTAAGGTCAGAAAGGTCCAACCTAGGTAAGAAGGGTATTCCATACG
TTGTTACCCAC
[1596] GACGGTAGAACYATCAGATACCCAG
[1597] SEQ 311 :C. kefyr 3898
[1598] UGUCACCUUGGACGCUACCAACGAAAACUUCAGAUUGGUCUACGACGUUAAGGGUAGAUUCGCUGUCCA
CCGUUACCCG
[1599] ACGAAGAAGCUUCUUACAAAUUGGGUAAGGUCAGAAAGGUCCAACUAGGUAAGAAGGGUAUCCAUACG
UUGUUACCCAC
[1600] GACGGUAGAACYAUCAGAUACCCAG
[1601] SEQ 312 :C. viswanathii 92
[1602] CATCACCTTGAAGCCACCAACGAACACTTCAGATTGGTCTACGACGTCAAGGGTAGATTTGCTGTCCA
CAGAATCTCCG
[1603] CTGAAGAAGCYTCTTACAAGTTGGGCAAGGTCAAGAAGGTTGCYTTGGGTAAGAAGGGTGTTCCTTACG
TTGTCACCCAC
[1604] GACGGTAGAACTATCAGATACCCAGA
[1605] SEQ 313 :C. viswanathii 92
[1606] CAUCACCUUGGAAGCCACCAACGAACACUUCAGAUUGGUCUACGACGUCAAGGGUAGAUUUGCUGUCCA
CAGAAUCUCCG
[1607] CUGAAGAAGCYUCCUACAAGUUGGGCAAGGUCAAGAAGGUUGCYUUGGGUAAGAAGGGUGUCCUUACG
UUGUCACCCAC
[1608] GACGGUAGAACUAUCAGAUACCCAGA
[1609] SEQ 314 :C. viswanathii 93
[1610] YAYTACTTTGAAGCCACYAATGAAAACCTTAGATTGATTTACGATGTCAAAGGTAGATTTGCTGTCCA
CAGAATCTCAG
[1611] CTGAAGAAGCCACTTACAAATTGGGTAAGTCAAGAGAGTCCAATTGGGTAAGAAGGGAATCCCATACG
TTGTCACCCAC
[1612] GATGGTAGAACTATCAGATACCCAGA
[1613] SEQ 315 :C. viswanathii 93
[1614] YAYUACUUUGGAAGCCACYAAUGAAAACUUUAGAUUGAUUUACGAUGUCAAGGUAGAUUUGCUGUCCA

CAGAAUCUCAG

[1615] CUGAAGAAGCCACUUACAAAUUGGGUAAAAGUCAAGAGAGUCCAAUUGGGUAAGAAGGGAAUCCCAUACG
UUGUCACCCAC

[1616] GAUGGUAGAACUAUCAGAUACCCAGA

[1617] SEQ 316 :C. zeylanoides 74

[1618] TCTTGAGGCTACCAACGAGCACTTCAGATTGGTGTACGACGTCAAGGGTAGATTCGCCGTGCACAGAAT
CACCGCCGAGG

[1619] AGTCCACCTACAAGTTGGCCAAGATCAAGAAGGTCCAGTTGGGCAAGAAGAGTATCCCCTACGCCGTCA
CCCACGACGGT

[1620] AGAACTATCAGATACCCAGA

[1621] SEQ 317 :C. zeylanoides 74

[1622] UCUUGAGGCUACCAACGAGCACUUCAGAUUGGUGUACGACGUCAAGGGUAGAUUCGCCGUGCACAGAAU
CACCGCCGAGG

[1623] AGUCCACCUACAAGUUGGCAAGAUCAAGAAGGUCCAGUUGGGCAAGAAGAGUAUCCCCUACGCCGUCA
CCCACGACGGU

[1624] AGAACUAUCAGAUACCCAGA

[1625] SEQ 318 :C. zeylanoides 67

[1626] TCTCTCTTGAGCCACCAAYGAGCACTTCAGATTGGTGTAYGACGTMAAGGGTAGATTYGCYGTGCACAG
AATCACCGCKG

[1627] AGGAGTCSAMYTACAAGTTGGCCAARATCAAGAAGGTKCASTTRGGCAAGAARAGCATCCCYTACGCY
TCACCCAYGAY

[1628] GGYAGAACTATCAGATACCCAG

[1629] SEQ 319 :C. zeylanoides 67

[1630] UCUCUCUUGAGCCACCAAYGAGCACUUCAGAUUGGUGUAYGACGUMAAGGGUAGAUUYGCYUGGCACAG
AAUCACCGCKG

[1631] AGGAGUCSAMYUACAAGUUGGCAARAUCAAGAAGGUKCASUURGGCAAGAARAGCAUCCCYUACGCY
UCACCCAYGAY

[1632] GGYAGAACUAUCAGAUACCCAG

[1633] SEQ 320 :C. zeylanoides 69

[1634] TCTCTCTTGAGCCACCAAYGAGCACTTCAGATTGGTGTAYGACGTMAAGGGTAGATTYGCYGTGCACAG
AATCACCGCSG

[1635] AGGAGTCSAMYTACAAGTTGGCCAARATCAAGAAGGTKCASTTRGGCAAGAARAGCATCCCYTACGCY
TCACCCAYGAY

[1636] GGYAGAACTATCAGATACCCAG

[1637] SEQ 321 :C. zeylanoides 69

[1638] UCUCUCUUGAGCCACCAAYGAGCACUUCAGAUUGGUGUAYGACGUMAAGGGUAGAUUYGCYUGGCACAG
AAUCACCGCSG

[1639] AGGAGUCSAMYUACAAGUUGGCAARAUCAAGAAGGUKCASUURGGCAAGAARAGCAUCCCYUACGCY
UCACCCAYGAY

- [1640] GGYAGAACUAUCAGAUACCCAG
[1641] SEQ 322 :C. zeylanoides 68
[1642] TCTCTCTTGAGCCWCCAACGAGCACTTCAGATTGGTGTACGACGTCAAGGGTAGATTCCGCCGTGCACAG
AATCACCCGCCG
[1643] AGGAGTCCACCTACAAGTTGGCCAAGATCAAGAAGGTCCAGTTGGGCAAGAAGAGTATCCCCTACGCCG
TCACCCACGAC
[1644] GGTAGAACTATCAGATAACCCAG
[1645] SEQ 323 :C. zeylanoides 68
[1646] UCUCUCUUGAGCCWCCAACGAGCACUUCAGAUUGGUGUACGACGUCAAGGGUAGAUUCGCCGUGCACAG
AAUCACCCGCCG
[1647] AGGAGUCCACCUACAAGUUGGCCAAGAUAAGAAGGUCCAGUUGGGCAAGAAGAGUAUCCCCUACGCCG
UCACCCACGAC
[1648] GGUAGAACUAUCAGAUACCCAG
[1649] SEQ 324 :C. zeylanoides 70
[1650] CTACCAACRAACACTTCAGATTGATTTACGATGTTAAAGGTAAATTCGCTGTTACAGAAATTTCTGCTG
AAGAAGCTTCT
[1651] TACAAATTAGGTAAAGTCAAGAAGGTTCAATTAGGTAAAAAAGGTGTTCCATACGTTGTCACCCACGAT
GGTAGAACTAT
[1652] CAGATAACCCAG
[1653] SEQ 325 :C. zeylanoides 70
[1654] CUACCAACRAACACUUCAGAUUGAUUUACGAUGUUAAAGGUAAAUUCGUGUUCACAGAAUUUCUGCUG
AAGAAGCUUCU
[1655] UACAAAUUAGGUAAAAGUCAAGAAGGUUCAAUUAGGUAAAAAAGGUGUUCCAUACGUUGUCACCCACGAU
GGUAGAACUAU
[1656] CAGAUACCCAG
[1657] SEQ 326 :A. fumigatus2204
[1658] GTCGCTCAGCGCCGCATCCTGCCCGCCCCAAGCGCTCTGTCAACTCCCGCACCAACCAGAAGCAGAAG
CGTCCTCGCTC
[1659] TCGCACCTGACCGCTGTCCACGACGCCATCCTCAACGACCTCGTTTACCCCGTCGAGATCGTCGGCAA
GCGTATCCGCA
[1660] CCAAGGAGGACGGCAGCAAGACTCTCAAGGTCGTTCTGGACGAGAAGGAGCGTGGTGGTGTGACCACA
GACTCGATGCC
[1661] TACGGCGAGGTTTACCGCCGACTAACCGGCCGCTCTGTTGTTTTCGAGTTCCCCCAGAG
[1662] SEQ 327 :A. fumigatus2204
[1663] GUCGCUCAGCGCCGAUCCUGCCCCGCCCAAGCGCUCUGUCAACUCCCGCACCAACCAGAAGCAGAAG
CGUCCUCGCUC
[1664] UCGCACCCUGACCGCUGUCCACGACGCCAUCCUCAACGACCUCGUUUACCCCGUCGAGAUUCGUCGGCAA
GCGUAUCCGCA
[1665] CCAAGGAGGACGGCAGCAAGACUCUCAAGGUCGUUCUGGACGAGAAGGAGCGUGGUGGUGUUGACCACA

GACUCGAUGCC

[1666] UACGGCGAGGUUUACCGCCGACUAACCGGCCGCUCUGUUGUUUCGAGUUCSCCAGAG

[1667] SEQ 328 :A. fumigatus5062

[1668] CGTCGCTCAGCGCCGCATCCTGCCCGCCCCAAGCGCTCTGTCAACTCCCGCACCAACCAGAAGCAGAA
GCGTCCTCGCT

[1669] CTCGCACCCTGACCGCTGTCCACGACGCCATCCTCACCGACCTCGTTTACCCCGTCGAGATCGTCGGCA
AGCGTATCCGC

[1670] ACCAAGGAGGACGGCAGCAAGACTCTCAAGGTCATCCTGGACGAGAAGGAGCGTGGTGGTGTGACCAC
AGACTCGATGC

[1671] CTACGGCGAGGTTTACCGCCGACTAACCGGCCGCTCTGTTGTCTTCGAGTTCCSCCAGAG

[1672] SEQ 329 :A. fumigatus5062

[1673] CGUCGCUCAGCGCCGCAUCCUGCCCCGCCCAAGCGCUCUGUCAACUCCCGCACCAACCAGAAGCAGAA
GCGUCCUCGCU

[1674] CUCGCACCCUGACCGCUGUCCACGACGCCAUCCUCACCGACCUCGUUUACCCCGUCGAGAUCGUCGGCA
AGCGUAUCCGC

[1675] ACCAAGGAGGACGGCAGCAAGACUCUCAAGGUCAUCCUGGACGAGAAGGAGCGUGGUGUGUUGACCAC
AGACUCGAUGC

[1676] CUACGGCGAGGUUUACCGCCGACUAACCGGCCGCUCUGUUGUCUUCGAGUUCSCCAGAG

[1677] SEQ 330 :A. fumigatus133. 61

[1678] TGTTGCTCAGCGCCGCATCCTGCCCGCCCTAAGCGCTCTGTCAACTCCCGCACCAACCAGAAGCAGAA
GCGTCCTCGCT

[1679] CTCGCACCCTGACCGCTGTCCACGACGCCATCCTCAACGACCTCGTTTACCCCGTCGAGATCGTCGGCA
AGCGTATCCGC

[1680] ACCAAGGAGGACGGCAGCAAGACTCTCAAGGTCATCCTGGACGAGAAGGAGCGTGGTGGTGTGACCAC
AGACTCGATGC

[1681] CTACGGCGAGGTTTACCGCCGACTAACCGGCCGCTCTGTTGTCTTCGAGTTCCSCCAGAG

[1682] SEQ 331 :A. fumigatus133. 61

[1683] UGUUGCUCAGCGCCGCAUCCUGCCCCGCCUAAGCGCUCUGUCAACUCCCGCACCAACCAGAAGCAGAA
GCGUCCUCGCU

[1684] CUCGCACCCUGACCGCUGUCCACGACGCCAUCCUCAACGACCUCGUUUACCCCGUCGAGAUCGUCGGCA
AGCGUAUCCGC

[1685] ACCAAGGAGGACGGCAGCAAGACUCUCAAGGUCAUCCUGGACGAGAAGGAGCGUGGUGUGUUGACCAC
AGACUCGAUGC

[1686] CUACGGCGAGGUUUACCGCCGACUAACCGGCCGCUCUGUUGUCUUCGAGUUCSCCAGAG

[1687] SEQ 332 :A. fumigatus419. 64

[1688] TGTTGCTCAGCGCCGCATCCTGCCCGCCCTAAGCGCTCTGTCAACTCCCGCACCAACCAGAAGCAGAA
GCGTCCTCGCT

[1689] CTCGCACCCTGACCGCTGTCCACGACGCCATCCTCAACGACCTCGTTTACCCCGTCGAGATCGTCGGCA
AGCGTATCCGC

- [1690] ACCAAGGAGGACGGCAGCAAGACTCTCAAGGTCATCCTGGACGAGAAGGAGCGTGGTGGTGTGACCAC
AGACTCGATGC
- [1691] CTACGGCGAGGTTTACCGCCGACTAACCGGCCGCTCTGTTATCTTCGAGTTCCCCCAGAG
- [1692] SEQ 333 :A. fumigatus419. 64
- [1693] UGUUGCUCAGCGCCGCAUCCUGCCCCGCCCUAAGCGCUCUGUCAACUCCCGCACCAACCAGAAGCAGAA
GCGUCCUCGCU
- [1694] CUCGCACCCUGACCGCUGUCCACGACGCCAUCCUCAACGACCUCGUUUACCCCGUCGAGAUCGUCGGCA
AGCGUAUCCGC
- [1695] ACCAAGGAGGACGGCAGCAAGACUCUCAAGGUCAUCCUGGACGAGAAGGAGCGUGGUGUGUUGACCAC
AGACUCGAUGC
- [1696] CUACGGCGAGGUUUACCGCCGACUAACCGGCCGUCUGUUAUCUUCGAGUUCSCCAGAG
- [1697] SEQ 334 :A. terreus2729
- [1698] CGTTGCTCAGCGCCGATCCTGCCCGCCCCAAGCGCTCTGTCAACTCCCGCACCAACCAGAAGCAGAA
GCGTCCCCGTT
- [1699] CCCGACTCTGACGGCCGTCCACGACGCCATCCTCACCGACCTCGTCTACCCCGTCGAGATCGTCGGCA
AGCGCATCCGC
- [1700] ACCAAGGAGGACGGTCCAAGACCTCAAGGTCATCCTCGACGAGAAGGAGCGCGGGCGGTGTCGACCAC
CGCCTCGATGC
- [1701] CTACGGCGAGGTCTACCGTCTCACC GGCCGTGCCGTCGTCTTCGAGTTCCCCCAGAG
- [1702] SEQ 335 :A. terreus2729
- [1703] CGUUGCUCAGCGCCGCAUCCUGCCCCGCCCUAAGCGCUCUGUCAACUCCCGCACCAACCAGAAGCAGAA
GCGUCCCCGUU
- [1704] CCCGCACUCUGACGGCCGUCCACGACGCCAUCCUCACCGACCUCGUCUACCCCGUCGAGAUCGUCGGCA
AGCGCAUCCGC
- [1705] ACCAAGGAGGACGGCUCCAAGACCCUCAAGGUCAUCCUCGACGAGAAGGAGCGCGGGUGUCGACCAC
CGCCUCGAUGC
- [1706] CUACGGCGAGGUCUACCGUCGUCUACCGGCCGUGCCGUCGUCUUCGAGUUCSCCAGAG
- [1707] SEQ 336 :A. flavus108. 30
- [1708] CGTCGCTCAGCGCCGATCCTGCCCAAGCCCAAGCGCTCTGTCAACTCCCGCACCAACCAGAAGCAGAA
GCGTCCCCGTT
- [1709] CCCGACTCTGACTGCTGTCCACGACGCCATCCTCGGCGACCTGGTCTACCCCGTTGAGATCGTCGGCA
AGCGCATCCGC
- [1710] ACCAAGGAGGATGGCAGCAAGACCTCAAGGTCATCCTGGATGAGAAGGAGCGTGGTGGTGTGACCAC
CGTCTCGATGC
- [1711] CTACGGCGAGGTCTACCGCGTTTGACCGGCCGCAACGTCGTCTTCGAGTTCCCCCAGAG
- [1712] SEQ 337 :A. flavus108. 30
- [1713] CGUCGUCAGCGCCGCAUCCUGCCCCAAGCCCAAGCGCUCUGUCAACUCCCGCACCAACCAGAAGCAGAA
GCGUCCCCGUU
- [1714] CCCGCACUCUGACUGCUGUCCACGACGCCAUCCUCGGCGACCUGGUCUACCCCGUUGAGAUCGUCGGCA

AGCGCAUCCGC

[1715] ACCAAGGAGGAUGGCAGCAAGACCCUCAAGGUCAUCCUGGAUGAGAAGGAGCGUGGUGUGUUGACCAC
CGUCUCGAUGC

[1716] CUACGGCGAGGUCUACCGCCGUUUGACCGGCCGCAACGUCGUCUUCGAGUUCSCCAGAG

[1717] SEQ 338 :A. flavus117.62

[1718] CGTCGCTCAGCGCCGCATCCTGCCCAAGCCCAAGCGCTCTGTCAACTCCCGCACCAACCAGAAGCAGAA
GCGTCCCGTT

[1719] CCCGCACTCTGACTGCTGTCCACGACGCCATCCTCGGGACCTGGTCTACCCCGTTGAGATCGTCGGCA
AGCGCATCCGC

[1720] ACCAAGGAGGACGGCAGCAAGACCCCTCAAGGTCATCCTGGATGAGAAGGAGCGTGGTGGTGTGACCAC
CGTCTCGATGC

[1721] CTACGGCGAGGTCTACCGCCGTTTGACCGGCCGCAACGTCGTCTTCGAGTTCCSCCAGAG

[1722] SEQ 339 :A. flavus117.62

[1723] CGUCGCUCAGCGCCGCAUCCUGCCCAAGCCCAAGCGCUCUGUCAACUCCCGCACCAACCAGAAGCAGAA
GCGUCCCGUU

[1724] CCCGCACUCUGACUGCUGUCCACGACGCCAUCCUCGGCGACCUGGUCUACCCCGUUGAGAUCGUCGGCA
AGCGCAUCCGC

[1725] ACCAAGGAGGACGGCAGCAAGACCCUCAAGGUCAUCCUGGAUGAGAAGGAGCGUGGUGUGUUGACCAC
CGUCUCGAUGC

[1726] CUACGGCGAGGUCUACCGCCGUUUGACCGGCCGCAACGUCGUCUUCGAGUUCSCCAGAG

[1727] SEQ 340 :A. nidulans5231

[1728] CGTCGCTCAGCGCCGCATCCTTCCCAAGCCCAAGCGTCCGTCAACTCCCGCACCAACCAGAAGCAGAA
GCGCCCCGTT

[1729] CCCGTACCCTCACTGCTGTTACGATGCCATCCTTGACGACCTCGTCTACCCCGTTGAGATTGTGCGCA
AGCGCATCCGC

[1730] ACCAAGGAGGACGGCTCCAAGACTCTCAAGGTTATCCTCGACGAGAAGGAGCGTGGTGGTGTGACCAC
CGCCTCGACGC

[1731] CTACGGCGAGGTCTACCGTCGTCTGACGGGTCGTGCTGTCGTTTTCGAGTTCCSCCAGAG

[1732] SEQ 341 :A. nidulans5231

[1733] CGUCGCUCAGCGCCGCAUCCUCCCAAGCCCAAGCGCUCGGUCAACUCCCGCACCAACCAGAAGCAGAA
GCGCCCCGUU

[1734] CCCGUACCCUCACUGCUGUUCACGAUGCCAUCCUUGACGACCUCGUCUACCCCGUUGAGAUUGUCGGCA
AGCGCAUCCGC

[1735] ACCAAGGAGGACGGCUCCAAGACUCUCAAGGUUAUCCUCGACGAGAAGGAGCGUGGUGUGUUGACCAC
CGCCUCGACGC

[1736] CUACGGCGAGGUCUACCGUCGUCUGACGGGUCGUGCUGUCGUUUUCGAGUUCSCCAGAG

[1737] SEQ 342 :A. nidulans4190

[1738] CGTCGCTCAGCGCCGCATCCTCCCAAGCCCAAGCGTCCGTCAACTCCCGCACCAACCAGAAGCAGAA
GCGCCCCGTT

- [1739] CCCGTACCCTTACTGCCGTTACGACGCCATCCTCGACGACCTCGTCTACCCCGTTGAGATTGTCGGCA
AGCGCATCCGC
- [1740] ACCAAGGAGGACGGCTCCAAGACCTCAAGGTCATCCTCGACGAGAAGGAGCGTGGTGGTGTGACCAC
CGCCTCGACGC
- [1741] CTACGGCGAGGTCTACCGTCGTCTGACGGGTCGTGCTGTCGTTTTTCGAGTTCCCCCAGAG
- [1742] SEQ 343 :A. nidulans4190
- [1743] CGUCGCUCAGCGCCGCAUCCUCCCCAAGCCCAAGCGUCUCCGUCAACUCCCGCACCAACCAGAAGCAGAA
GCGCCCCCGUU
- [1744] CCCGUACCCUUACUGCCGUUCACGACGCCAUCCUCGACGACCUCGUCUACCCCGUUGAGAUUGUCGGCA
AGCGCAUCCGC
- [1745] ACCAAGGAGGACGGCUCCAAGACCCUCAAGGUCAUCCUCGACGAGAAGGAGCGUGGUGUGUUGACCAC
CGCCUCGACGC
- [1746] CUACGGCGAGGUCUACCGUCGUCUGACGGGUCGUGCUGUCGUUUUCGAGUUCSCCAGAG
- [1747] SEQ 344 :A. nidulans100.2
- [1748] CGTCGCTCAGCGCCGCATCCTCCCCAAGCCCAAGCGTCCGTCAACTCCCGCACCAACCAGAAGCAGAA
GCGCCCCCGTT
- [1749] CCCGTACCCTTACTGCCGTTACGACGCCATCCTCGACGACCTCGTCTACCCCGTTGAGATTGTCGGCA
AGCGCATCCGC
- [1750] ACCAAGGAGGACGGCTCCAAGACCTCAAGGTCATCCTCGACGAGAAGGAGCGTGGTGGTGTGACCAC
CGCCTCGACGC
- [1751] CTACGGCGAGGTCTACCGTCGTCTGACGGGTCGTGCTGTCGTTTTTCGAGTTCCCCCAGAG
- [1752] SEQ 345 :A. nidulans100.2
- [1753] CGUCGCUCAGCGCCGCAUCCUCCCCAAGCCCAAGCGUCUCCGUCAACUCCCGCACCAACCAGAAGCAGAA
GCGCCCCCGUU
- [1754] CCCGUACCCUUACUGCCGUUCACGACGCCAUCCUCGACGACCUCGUCUACCCCGUUGAGAUUGUCGGCA
AGCGCAUCCGC
- [1755] ACCAAGGAGGACGGCUCCAAGACCCUCAAGGUCAUCCUCGACGAGAAGGAGCGUGGUGUGUUGACCAC
CGCCUCGACGC
- [1756] CUACGGCGAGGUCUACCGUCGUCUGACGGGUCGUGCUGUCGUUUUCGAGUUCSCCAGAG
- [1757] SEQ 346 :A. versicolor1323
- [1758] CGTCGCTCAGCGCCGCATCCTTCCCCAAGCCCAAGCGTCCGTCAACTCTCGCACCAACCAGAAGCAGAA
GCGCCCTCGTT
- [1759] CTCGCACCCTGACGGCTGTCCACGACTCCATCCTTGACGACCTCGTCTACCCCGTTGAGATCGTCGGCA
AGCGTACCCGC
- [1760] ACCAAGGAGGACGGCAGCAAGACGCTCAAGGTCATCCTCGACGAGAAGGAGCGCGGCGGCGTTGACCAC
CGCCTCGACGC
- [1761] CTACGGCGAGGTCTACCGTCGTTTTGACGGGTCGTGCTGTTGTTTTTCGAGTTCCCCCAGAG
- [1762] SEQ 347 :A. versicolor1323
- [1763] CGUCGCUCAGCGCCGCAUCCUCCCCAAGCCCAAGCGUCUCCGUCAACUCUCGCACCAACCAGAAGCAGAA

GCGCCCUCGUU

[1764] CUCGCACCCUGACGGCUGUCCACGACUCCAUCCUUGACGACCUCGUCUACCCCGUUGAGAUCGUCGGCA
AGCGUACCCGC

[1765] ACCAAGGAGGACGGCAGCAAGACGCUCAAGGUCAUCCUCGACGAGAAGGAGCGCGGGCGGCGUUGACCAC
CGCCUCGACGC

[1766] CUACGGCGAGGUCUACCGUCGUUUGACCGGUCGUGCUGUUGUUUCGAGUUCSCCAGAG

[1767] SEQ 348 :A. versicolor2196

[1768] CGTCGCTCAGCGCCGCATCCTTCCTAAGCCCAAGCGCTCCGTCAACTCCCGCACCAACCAGAAGCAGAA
GCGCCCTCGTT

[1769] CTCGCACTCTGACGGCTGTCCACGACTCCATCCTTGACGACCTCGTCTACCCCGTTGAGATCGTCGGCA
AGCGTACCCGC

[1770] ACCAAGGAGGACGGCAGCAAGACGCTCAAGGTCATCCTCGACGAGAAGGAGCGCGGGCGGCTTGACCAC
CGCCTCGACGC

[1771] CTACGGCGAGGTCTACCGTCGTTTGACCGGTCGTGCTGTTGTTTTCGAGTTCCSCCAGAG

[1772] SEQ 349 :A. versicolor2196

[1773] CGUCGCUCAGCGCCGCAUCCUCCUAAGCCCAAGCGUCUCCGUCAACUCCCGCACCAACCAGAAGCAGAA
GCGCCCUCGUU

[1774] CUCGCACUCUGACGGCUGUCCACGACUCCAUCCUUGACGACCUCGUCUACCCCGUUGAGAUCGUCGGCA
AGCGUACCCGC

[1775] ACCAAGGAGGACGGCAGCAAGACGCUCAAGGUCAUCCUCGACGAGAAGGAGCGCGGGCGGCGUUGACCAC
CGCCUCGACGC

[1776] CUACGGCGAGGUCUACCGUCGUUUGACCGGUCGUGCUGUUGUUUCGAGUUCSCCAGAG

[1777] SEQ 350 :A. versicolor5058

[1778] CGTCGCTCAGCGCCGCATCCTTCCTAAGCCTAAGCGCTCCGTCAACTCCCGCACCAACCAGAAGCAGAA
GCGCCCCCGTT

[1779] CCCGCACCCTGACGGCCGTCCACGATGCTATCCTTGACGACCTCGTCTACCCCGTTGAGATCGTCGGCA
AGCGTACCCGC

[1780] ACCAAGGAGGACGGCAGCAAGACGCTCAAGATCATCCTCGACGAGAAGGAGCGCGGGCGGCTTGACCAC
CGCCTTGACGC

[1781] CTACGGCGAGGTCTACCGTCGTTTGACTGGTCGTGCTGTTGTTTTCGAGTTCCSCCAGAG

[1782] SEQ 351 :A. versicolor5058

[1783] CGUCGCUCAGCGCCGCAUCCUCCUAAGCCUAAGCGUCUCCGUCAACUCCCGCACCAACCAGAAGCAGAA
GCGCCCCCGUU

[1784] CCCGCACCCUGACGGCCGUCCACGAUGCUAUCUUGACGACCUCGUCUACCCCGUUGAGAUCGUCGGCA
AGCGUACCCGC

[1785] ACCAAGGAGGACGGCAGCAAGACGCUCAAGAUAUCCUCGACGAGAAGGAGCGCGGGCGGCGUUGACCAC
CGCCUUGACGC

[1786] CUACGGCGAGGUCUACCGUCGUUUGACUGGUCGUGCUGUUGUUUCGAGUUCSCCAGAG

[1787] SEQ 352 :A. versicolor6898

- [1788] CGTCGCTCAGCGCCGCATCCTTCCTAAGCCCAAGCGCTCCGTCAACTCCCGCACCAACCAGAAGCAGAA
GCGCCCCCGTT
- [1789] CCCGCACCCTGACGGCCGTCCACGATGCCATCCTTGACGACCTCGTCTACCCCGTTGAGATCGTCGGCA
AGCGTACCCGC
- [1790] ACCAAGGAGGACGGCAGCAAGACGCTCAAGATCATCCTCGACGAGAAGGAGCGCGGGCGGCGTTGACCAC
CGCCTTGACGC
- [1791] CTACGGCGAGGTCTACCGTCGTTTGACTGGTCGTGCTGTTGTTTTCGAGTTCCCCCAGAG
- [1792] SEQ 353 :A. versicolor6898
- [1793] CGUCGCUCAGCGCCGCAUCCUCCUAAGCCCAAGCGUCUCCGUCAACUCCCGCACCAACCAGAAGCAGAA
GCGCCCCCGUU
- [1794] CCCGCACCCUGACGGCCGUCCACGAUGCCAUCCUUGACGACCUCGUCUACCCCGUUGAGAUCGUCGGCA
AGCGUACCCGC
- [1795] ACCAAGGAGGACGGCAGCAAGACGCUCAAGAUCAUCCUCGACGAGAAGGAGCGCGGGCGGUUGACCAC
CGCCUUGACGC
- [1796] CUACGGCGAGGUCUACCGUCGUUUGACUGGUCGUGCUGUUGUUUCGAGUUCSCCAGAG
- [1797] SEQ 354 :A. versicolor111.32
- [1798] CGTTGCTCAGCGCCGCATCCTTCCTAAGCCTAAGCGCTCCGTCAACTCCCGCACCAACCAGAAGCAGAA
GCGCCCCCGTT
- [1799] CCCGCACCCTGACGGCCGTCCACGATGCTATCCTTGACGACCTCGTCTACCCCGTTGAGATCGTCGGCA
AGCGTACCCGC
- [1800] ACCAAGGAGGACGGCAGCAAGACGCTCAAGATCATCCTCGACGAGAAGGAGCGCGGGCGGCGTTGACCAC
CGCCTTGACGC
- [1801] CTACGGCGAGGTCTACCGTCGTTTGACTGGTCGTGCTGTTGTTTTCGAGTTCCCCCAGAG
- [1802] SEQ 355 :A. versicolor111.32
- [1803] CGUUGCUCAGCGCCGCAUCCUCCUAAGCCUAAGCGUCUCCGUCAACUCCCGCACCAACCAGAAGCAGAA
GCGCCCCCGUU
- [1804] CCCGCACCCUGACGGCCGUCCACGAUGCUAUCUUGACGACCUCGUCUACCCCGUUGAGAUCGUCGGCA
AGCGUACCCGC
- [1805] ACCAAGGAGGACGGCAGCAAGACGCUCAAGAUCAUCCUCGACGAGAAGGAGCGCGGGCGGUUGACCAC
CGCCUUGACGC
- [1806] CUACGGCGAGGUCUACCGUCGUUUGACUGGUCGUGCUGUUGUUUCGAGUUCSCCAGAG
- [1807] SEQ 356 :A. clavatus7944
- [1808] CGTCGCTCAGCGCCGCATCCTGCCCGCCCCAAGCGCTCTGTCAACTCCCGCACCAACCAGAAGCAGAA
GCGTCCTCGCT
- [1809] CCCGCACCCTGACTGCCGTTACGACGCCATCCTCACCGACCTCGTCTACCCCGTCGAGATCGTCGGCA
AGCGCACCCGC
- [1810] ACCAAGGAGGACGGCTCCAAGACCTCAAGGTCGTCCTTGACGAGAAGGAGCGTGGCGGTGTTGACCAC
AGACTCGATGC
- [1811] CTACGGCGAGGTCTACCGCCGTTTAAACCGCCGCTCCGTTGTCTTCGAGTTCCCCCAGAG

- [1812] SEQ 357 :A. clavatus7944
[1813] CGUCGCUCAGCGCCGCAUCCUGCCCCGCCCCAAGCGCUCUGUCAACUCCCGCACCAACCAGAAGCAGAA
GCGUCCUCGCU
[1814] CCCGCACCCUGACUGCCGUUCACGACGCCAUCCUCACCGACCUCGUCUACCCCGUCGAGAUCGUCGGCA
AGCGCACCCGC
[1815] ACCAAGGAGGACGGCUCCAAGACCCUCAAGGUCGUCCUUGACGAGAAGGAGCGUGGCGGUGUUGACCAC
AGACUCGAUGC
[1816] CUACGGCGAGGUCUACCGCCGUUUAACCGGCCGUCUCCGUUGUCUUCGAGUUCSCCAGAG
[1817] SEQ 358 :A. clavatus2391
[1818] CGTCGCTCAGCGCCGCATCCTGCCCCGCCCCAAGCGCTCCGTCAACTCCCCTCCAACCAGAAGCAGAA
GCGCCCTCGCT
[1819] CCCGCACTCTGACCGCTGTTACGACGCCATCCTCACTGATCTCGTCTTCCCCGTCGAGATCGTCGGCA
AGCGCACCCGC
[1820] ACCAAGGAGGACGGCTCCAAGACCCCTCAAGGTCATCCTTGACGAGAAGGAGCGTGGTGGTGTGACCAC
AGACTCGATGC
[1821] CTACGGCGAGGTCTACCGCCGTTAACCGGCCGCTCCGTTGTCTTCGAGTTCCCCCAGAG
[1822] SEQ 359 :A. clavatus2391
[1823] CGUCGCUCAGCGCCGCAUCCUGCCCCGCCCCAAGCGCUCUGUCAACUCCCGCUCCAACCAGAAGCAGAA
GCGCCUCGCU
[1824] CCCGCACUCUGACCGCUGUUCACGACGCCAUCCUCACUGAUCUCGUCUUCSCCGUCGAGAUCGUCGGCA
AGCGCACCCGC
[1825] ACCAAGGAGGACGGCUCCAAGACCCUCAAGGUCAUCCUUGACGAGAAGGAGCGUGGUGGUGUUGACCAC
AGACUCGAUGC
[1826] CUACGGCGAGGUCUACCGCCGUUUAACCGGCCGUCUCCGUUGUCUUCGAGUUCSCCAGAG
[1827] SEQ 360 :A. candidus9695
[1828] CGTCGCTCAGCGCCGCATCCTGTGCGCCCCAAGCGCTCCGTCAACTCGCGCACCAACCAGAAGCAGAA
GCGCCCCGCT
[1829] CGCGCACTCTGACCGCGTGCACGACAACATCCTGACCGACCTGGTCTACCCCGTCGAGATCGTCGGCA
AGCGCATCCGC
[1830] ACCAAGGAGGACGGCAGCAAGACCCCTCAAGGTTATCCTGGACGAGAAGGAGCGCGGCGGCGTTGACCAC
CGCCTGGACGC
[1831] CTACGGCGAGGTCTACCGCCGACTGACGGGCCGCAACGTTGTCTTCGAGTTCCCCCAGAG
[1832] SEQ 361 :A. candidus9695
[1833] CGUCGCUCAGCGCCGCAUCCUGUCGCGCCCCAAGCGCUCUGUCAACUCGCGCACCAACCAGAAGCAGAA
GCGCCCCGCU
[1834] CGCGCACUCUGACCGCCGUGCACGACAACAUCUGACCGACCUGGUCUACSCCGUCGAGAUCGUCGGCA
AGCGCAUCCGC
[1835] ACCAAGGAGGACGGCAGCAAGACCCUCAAGGUUAUCCUGGACGAGAAGGAGCGCGGCGGCGUUGACCAC
CGCCUGGACGC

- [1836] CUACGGCGAGGUCUACCGCCGACUGACGGGCCGCAACGUUGUCUUCGAGUUCSCCCAGAG
- [1837] SEQ 362 :A. candidus567.65
- [1838] CGTCGCTCAGCGCCGCATCCTGTCGCGCCCCAAGCGCTCCGTCAACTCGCGACCAACCAGAAGCAGAA
GCGCCCCGCT
- [1839] CGCGCACTCTGACCGCCGTGCACGACAACATCCTGACCGACCTTGTCTACCCCGTCGAGATCGTCGGCA
AGCGCGTCCGC
- [1840] ACCAAGGAGGACGGCAGCAAGACCCCTCAAGGTTATCCTGGACGAGAAGGAGCGTGGCGGCGTTGACCAC
CGTCTGGACGC
- [1841] CTACGGCGAGGTCTACCGCCGACTGACGGGCCGCAACGTTGTCTTCGAGTTSCCCAGAG
- [1842] SEQ 363 :A. candidus567.65
- [1843] CGUCGCUCAGCGCCGCAUCCUGUCGCGCCCCAAGCGUCUCCGUCAACUCGCGACCAACCAGAAGCAGAA
GCGCCCCGCU
- [1844] CGCGCACUCUGACCGCCGUGCACGACAACAUCCUGACCGACCUUGUCUACCCCGUCGAGAUCGUCGGCA
AGCGCGUCCGC
- [1845] ACCAAGGAGGACGGCAGCAAGACCCUCAAGGUUAUCCUGGACGAGAAGGAGCGUGGCGGCGUUGACCAC
CGUCUGGACGC
- [1846] CUACGGCGAGGUCUACCGCCGACUGACGGGCCGCAACGUUGUCUUCGAGUUCSCCCAGAG
- [1847] SEQ 364 :A. candidus225.80
- [1848] CGTCGCTCAGCGCCGCATCCTGTCGCGCCCCAAGCGCTCCGTCAACTCGCGACCAACCAGAAGCAGAA
GCGCCCCGCT
- [1849] CGCGCACTCTGACCGCCGTGCACGACAACATCCTGACCGACCTCGTCTACCCCGTCGAGATCGTCGGCA
AGCGCGTCCGC
- [1850] ACCAAGGAGGACGGCAGCAAGACCCCTCAAGGTTATCCTGGACGAGAAGGAGCGCGGCGGCGTTGACCAC
CGCCTGGACGC
- [1851] CTACGGCGAGGTCTACCGCCGACTACCGGCCGCAACGTTGTCTTCGAGTTSCCCAGAG
- [1852] SEQ 365 :A. Candidus225.80
- [1853] CGUCGCUCAGCGCCGCAUCCUGUCGCGCCCCAAGCGUCUCCGUCAACUCGCGACCAACCAGAAGCAGAA
GCGCCCCGCU
- [1854] CGCGCACUCUGACCGCCGUGCACGACAACAUCCUGACCGACCUUGUCUACCCCGUCGAGAUCGUCGGCA
AGCGCGUCCGC
- [1855] ACCAAGGAGGACGGCAGCAAGACCCUCAAGGUUAUCCUGGACGAGAAGGAGCGCGGCGGCGUUGACCAC
CGCCUGGACGC
- [1856] CUACGGCGAGGUCUACCGCCGACUCACCGGCCGCAACGUUGUCUUCGAGUUCSCCCAGAG
- [1857] SEQ 366 :A. glaucus2425
- [1858] CGTCGCTCAGCGCCGCATCCTCTCCCGCCCCAAGCGCTCCGTCAACTCGCGACCAACCAGACCCAGAA
GCGTCCCCGTT
- [1859] CGCGTACTCTGACCGCTGTCCACGACTCCATCCTCACCGACCTCGTCTACCCCGTCGAGATCGTTGGCA
AGCGCATCCGC
- [1860] ACCAAGGAGGACGGCAGCAAGACCATCAAGGTTGTTCTCGACGAGAAGGAGCGCGGTGGTGTGACCAC

AGACTTGATGC

[1861] CTACGGCGAGGTCTACCGCAGACTGACCGGCCGTGCCGTTGTCTTCGAGTTCCCCCAGAG

[1862] SEQ 367 :A. glaucus2425

[1863] CGUCGCUCAGCGCCGCAUCCUCUCCCGCCCCAAGCGCUCGGUCAACUCGCGCACCAACCAGACCCAGAA
GCGUCCCCGUU

[1864] CGCGUACUCUGACCGCUGUCCACGACUCCAUCCUCACCGACCUCGUCUACCCCGUCGAGAUCGUUGGCA
AGCGCAUCCGC

[1865] ACCAAGGAGGACGGCAGCAAGACCAUCAAGGUUGUUCUCGACGAGAAGGAGCGCGGUGUGUUGACCAC
AGACUUGAUGC

[1866] CUACGGCGAGGUCUACCGCAGACUGACCGGCCGUGCCGUUGUCUUCGAGUUCCCCCAGAG

[1867] SEQ 368 :A. glaucusMA542

[1868] CATCGCTCAGCGCCGCATCCTCTCCCGCCCCAAGCGCTCCGTCAACTCGCGCACCAACCAGACCCAGAA
GCGTCCCCGTT

[1869] CCCGACTCTGACCGCTGTCCACGACTCCATCCTCACTGACCTCGTCTACCCCGTCGAGATCGTTGGCA
AGCGCATCCGC

[1870] ACCAAGGAGGACGGCAGCAAGACCATCAAGTTGTTCTCGACGAGAAGGAGCGCGGTGGTGTGACCAC
AGACTCGATGC

[1871] CTACGGCGAGGTCTACCGCAGACTGACCGGCCGTGCCGTTGTCTTCGAGTTCCCCCAGAG

[1872] SEQ 369 :A. glaucusMA542

[1873] CAUCGCUCAGCGCCGCAUCCUCUCCCGCCCCAAGCGCUCGGUCAACUCGCGCACCAACCAGACCCAGAA
GCGUCCCCGUU

[1874] CCCGCACUCUGACCGCUGUCCACGACUCCAUCCUCACUGACCUCGUCUACCCCGUCGAGAUCGUUGGCA
AGCGCAUCCGC

[1875] ACCAAGGAGGACGGCAGCAAGACCAUCAAGGUUGUUCUCGACGAGAAGGAGCGCGGUGUGUUGACCAC
AGACUCGAUGC

[1876] CUACGGCGAGGUCUACCGCAGACUGACCGGCCGUGCCGUUGUCUUCGAGUUCCCCCAGAG

[1877] SEQ 370 :A. glaucusMA5279

[1878] CATCGCTCAGCGCCGCATCCTCTCCCGCCCCAAGCGCTCCGTCAACTCGCGCACCAACCAGACCCAGAA
GCGTCCCCGTT

[1879] CCCGACTCTGACTGCTGTCCACGACTCCATCCTCACCGACCTCGTCTACCCCGTCGAGATCGTTGGCA
AGCGTATCCGC

[1880] ACCAAGGAGGACGGCAGCAAGACCATCAAGTTGTTCTCGACGAGAAGGAGCGCGGTGGTGTGACCAC
AGACTCGATGC

[1881] CTACGGCGAGGTCTACCGCAGACTGACCGGCCGTGCCGTTGTCTTCGAGTTCCCCCAGAG

[1882] SEQ 371 :A. glaucusMA5279

[1883] CAUCGCUCAGCGCCGCAUCCUCUCCCGCCCCAAGCGCUCGGUCAACUCGCGCACCAACCAGACCCAGAA
GCGUCCCCGUU

[1884] CCCGCACUCUGACUGCUGUCCACGACUCCAUCCUCACCGACCUCGUCUACCCCGUCGAGAUCGUUGGCA
AGCGUAUCCGC

- [1885] ACCAAGGAGGACGGCAGCAAGACCAUCAAGGUUGUUCUCGACGAGAAGGAGCGCGGUGGUGUUGACCAC
AGACUCGAUGC
- [1886] CUACGGCGAGGUCUACCGCAGACUGACCGGCCGUGCCGUUGUCUUCGAGUUCSCCAGAG
- [1887] SEQ 372 :A. glaucus117314
- [1888] CGCTCAGCGCCGCATCCTCTCCCGCCCAAGCGCTCCGTCAACTCGCGACCAACCAGACCCAGAAGCG
TCCCCGTTCCC
- [1889] GCACTCTGACCGCTGTCCACGACTCCATCCTCACCGACCTCGTCTACCCCGTCGAGATCGTTGGCAAGC
GCATCCGCACC
- [1890] AAGGAGGACGGCAGCAAGACCATCAAGGTTGTTCTTGACGAGAAGGAGCGCGGTGGTGTGACCACAGA
CTCGATGCCTA
- [1891] CGGCGAGGTCTACCGCAGACTGACCGGCCGTGCCGTTGTCTTCGAGTTCCCCCAGAG
- [1892] SEQ 373 :A. glaucus117314
- [1893] CGCUCAGCGCCGAUCCUCUCCCGCCCCAAGCGCUCCGUCAACUCGCGCACCAACCAGACCCAGAAGCG
UCCCCGUUCCC
- [1894] GCACUCUGACCGCUGUCCACGACUCCAUCCUCACCGACCUCGUCUACCCCGUCGAGAUCGUUGGCAAGC
GCAUCCGCACC
- [1895] AAGGAGGACGGCAGCAAGACCAUCAAGGUUGUUCUUGACGAGAAGGAGCGCGGUGGUGUUGACCACAGA
CUCGAUGCCUA
- [1896] CGGCGAGGUCUACCGCAGACUGACCGGCCGUGCCGUUGUCUUCGAGUUCSCCAGAG
- [1897] SEQ 374 :A. glaucus297. 71
- [1898] CGCTCAGCGCCGCATCCTCTCCCGCCCAAGCGCTCCGTCAACTCGCGACCAACCAGACCCAGAAGCG
TCCCCGTTCCC
- [1899] GCACTCTGACTGCTGTCCACGASTCCATCCTCACCGACCTCGTCTACCCCGTCGACATCGTTGGCAAGC
GTATCCGCACC
- [1900] AAGGAGGACGGCAGCAAGACCATCAAGGTTGTTCTCGACGAGAAGGAGCGCGGTGGTGTGACCACAGA
CTCGATGCCTA
- [1901] CGGCGAGGTCTACCGCAGACTGACCGGCCGTGCCGTTGTCTTCGAGTTCCCCCAGAG
- [1902] SEQ 375 :A. glaucus297. 71
- [1903] CGCUCAGCGCCGAUCCUCUCCCGCCCCAAGCGCUCCGUCAACUCGCGCACCAACCAGACCCAGAAGCG
UCCCCGUUCCC
- [1904] GCACUCUGACUGCUGUCCACGASUCCAUCCUCACCGACCUCGUCUACCCCGUCGAGAUCGUUGGCAAGC
GUAUCCGCACC
- [1905] AAGGAGGACGGCAGCAAGACCAUCAAGGUUGUUCUCGACGAGAAGGAGCGCGGUGGUGUUGACCACAGA
CUCGAUGCCUA
- [1906] CGGCGAGGUCUACCGCAGACUGACCGGCCGUGCCGUUGUCUUCGAGUUCSCCAGAG
- [1907] SEQ 376 :A. niger124. 49
- [1908] CGTTGCTCAGCGCCGCATCCTGCCCGCCCCAAGCGCTCCGCCAGCTCTCGTTCCAACCAGAAGCAGAA
GCGTCCCCGTT
- [1909] CCCGCACTCTGACTGCTGTCCACGACGCCATCCTCACCGACCTCGTCTACCCCGTCGAGATCGTCGGCA

AGCGTACCCGC

[1910] ACCAAGGAGGACGGCTCCAAGACCCCTCAAGGTCATCCTGGACGAGAAGGAGCGTGGTGGTGTGACCAC
CGCCTTGATGC

[1911] CTACGGCGAGGTCTACCGTCGGTTGACTGGCCGTGCTGTTGTCTTTGAATTCCCCCAGGG

[1912] SEQ 377 :A.niger124.49

[1913] CGUUGCUCAGCGCCGCAUCCUGCCCCGCCCAAGCGCUCGCCAGCUCUCGUUCCAACCAGAAGCAGAA
GCGUCCCCGUU

[1914] CCCGCACUCUGACUGCUGUCCACGACGCCAUCCUCACCGACCUCGUCUACCCCGUCGAGAUCGUCGGCA
AGCGUACCCGC

[1915] ACCAAGGAGGACGGCUCCAAGACCCUCAAGGUCAUCCUGGACGAGAAGGAGCGUGGUGUGUUGACCAC
CGCCUUGAUGC

[1916] CUACGGCGAGGUCUACCGUCGGUUGACUGGCCGUGCUGUUGUCUUUGAAUCCCCCAGGG

[1917] SEQ 378 :Alb1

[1918] 5' attgtctacgatgttaaaggtaaattc 3'

[1919] SEQ 379 :Alb1

[1920] 5' gaatttacctttaacatcgtagacaat 3'

[1921] SEQ 380 :Alb2

[1922] 5' agaatt tctgctgaagaagctgcct 3'

[1923] SEQ 381 :Alb2

[1924] 5' aggcagettcttcagcagaaattct 3'

[1925] SEQ 382 :Alb3a

[1926] 5' tcagattagtctacgatgttaaaggtaaa3'

[1927] SEQ 383 :Alb3a

[1928] 5' ttacctttaacatcgtagactaatctga 3'

[1929] SEQ 384 :Alb3

[1930] 5' tcagattagtctacgatgttaaaggtaaattc 3'

[1931] SEQ 385 :Alb3

[1932] 5' gaatttacctttaacatcgtagactaatctga 3'

[1933] SEQ 386 :kru2

[1934] 5' agctgcatacaagttatgtaaggtc 3'

[1935] SEQ 387 :kru2

[1936] 5' gaccttacataacttgatgcagct 3'

[1937] SEQ 388 :Kru1

[1938] 5' tcaccccagaagaagctgeat 3'

[1939] SEQ 389 :Kru1

[1940] 5' atgcagettcttctgggggtga 3'

[1941] SEQ 390 :Parap1

[1942] 5' aaagtagatttgcttgcac 3'

[1943] SEQ 391 :Parap1

- [1944] 5' gtggcaagcaaactactttt 3'
[1945] SEQ 392 :Parap2
[1946] 5' aagggaatcccatacgttgta 3'
[1947] SEQ 393 :Parap2
[1948] 5' tgacaacgtatgggattccctt 3'
[1949] SEQ 394 :Trop1
[1950] 5' taccaacgaacacttcagattgattta 3'
[1951] SEQ 395 :Trop1
[1952] 5' taaatcaatctgaagtgttcggttgta 3'
[1953] SEQ 396 :Trop2
[1954] 5' ttctgctgaagaagcttcttataca 3'
[1955] SEQ 397 :Trop2
[1956] 5' ttgtaagaagcttcttcagcagaa 3'
[1957] SEQ 398 :Trop3
[1958] 5' acagaatttctgctgaagaagcttcttataca 3'
[1959] SEQ 399 :Trop3
[1960] 5' ttgtaagaagcttcttcagcagaaattctgt 3'
[1961] SEQ 400 :Trop4
[1962] 5' cgaacacttcagattgatttacgatgttaaa 3'
[1963] SEQ 401 :Trop4
[1964] 5' tttaacatcgtaaataatctgaagtgttcg 3'
[1965] SEQ 402 :Trop6
[1966] 5' tttaacatcgtaaataatctgaagtgttcg3'
[1967] SEQ 403 :Trop6
[1968] 5' cgaacacttcagattgatttacgatgttaaa 3'
[1969] SEQ 404 :Trop9
[1970] 5' ttaccttaacatcgtaaataatctgaagtgttcggttggt 3'
[1971] SEQ 405 :Trop9
[1972] 5' accaacgaacacttcagattgatttacgatgttaaaggtaa 3'
[1973] SEQ 406 :Glab1
[1974] 5' tatcactgacgaagaagcttc 3'
[1975] SEQ 407 :Glab1
[1976] 5' gaagcttcttcgtagtgata 3'
[1977] SEQ 408 :Glab2
[1978] 5' ttgggtaaggtaagaaggccaatt 3'
[1979] SEQ 409 :Glab2
[1980] 5' aattggaccttcttgaccttaccata 3'
[1981] SEQ 410 :Glab3
[1982] 5' tatcactgacgaagaagcttcttataca 3'

- [1983] SEQ 411 :Glab3
[1984] 5' ttgtaggaagcttcttcgtcagtgata 3'
[1985] SEQ 412 :Glab 5
[1986] 5' atacgttgactgacgatggt 3'
[1987] SEQ 413 :Glab 5
[1988] 5' accatcgtcagtgacaacgtat 3'
[1989] SEQ 414 :MycoSEQ AF1F
[1990] 5' GACCGCCACGTCCTCTT 3'
[1991] SEQ 415 :MycoSEQ AF1R
[1992] 5' CTCTGGGGGAACTCGAA 3'
[1993] SEQ 416 :MycoSEQ NIG1R
[1994] 5' CCCTGGGGGAATTCAAA 3'
[1995] SEQ 417 :MycoSEQ NIG1F
[1996] 5' GACCGCCACGTTCTCTT 3'
[1997] SEQ 418 :AF6 FOW
[1998] 5' AGCAAGACTCTCAAGGTC 3'
[1999] SEQ 419 :ASP2
[2000] 5' AGGTTTACCGCCGACTAACC 3'
[2001] SEQ 420 :ASP2
[2002] 5' GGTTAGTCGGCGGTAAACCT 3'
[2003] SEQ 421 :AFUM1
[2004] 5' CGCTGTCCACGACGCCATCCTCA 3'
[2005] SEQ 422 :AFUM1
[2006] 5' TGAGGATGGCGTCGTGGACAGCG 3'
[2007] SEQ 423 :AFUM2
[2008] 5' CCGACTAACCGCCGCTCTG 3'
[2009] SEQ 424 :AFUM2
[2010] 5' CAGAGCGGCCGGTTAGTCGG 3'
[2011] SEQ 425 :ACAN1
[2012] 5' CGTGACGACAACATCCTGACCGA 3'
[2013] SEQ 426 :ACAN1
[2014] 5' TCGGTCAGGATGTTGTCGTGCACG 3'
[2015] SEQ 427 :ACAN2
[2016] 5' CGGCGGCGTTGACCACCGCCTGGAC 3'
[2017] SEQ 428 :ACAN2
[2018] 5' GTCCAGGCGGTGGTCAACGCCGCCG 3'
[2019] SEQ 429 :ATERR1
[2020] 5' CGGCGGTGTCGACCACCGCCTC 3'
[2021] SEQ 430 :ATERR1

- [2022] 5' GAGGCGGTGGTCGACACCGCCG 3'
[2023] SEQ 431 :ATERR2
[2024] 5' CGTCTACCGGCCGTGCCGTCGTC 3'
[2025] SEQ 432 :ATERR2
[2026] 5' GACGACGGCACGGCCGGTGAGACG 3'
[2027] SEQ 433 :AVER1
[2028] 5' CTTGACGACCTCGTCTACCCCGTTG 3'
[2029] SEQ 434 :AVER1
[2030] 5' CAACGGGGTAGACGAGGTCGTCAAG 3'
[2031] SEQ 435 :AVER2
[2032] 5' CTACCGTCGTTTGACCGGTCGTGCTGTTG 3'
[2033] SEQ 436 :AVER2
[2034] 5' CAACAGCACGACCGGTCAAACGACGGTAG 3'
[2035] SEQ 437 :ANID1
[2036] 5' GTACCCTCACTGCTGTTCACGATGC 3'
[2037] SEQ 438 :ANID1
[2038] 5' GCATCGTGAACAGCAGTGAGGGTAC 3'
[2039] SEQ 439 :ANID2
[2040] 5' GTCGTCTGACGGGTCGTGCTGTC 3'
[2041] SEQ 440 :ANID2
[2042] 5' GACAGCACGACCCGTCAGACGAC 3'
[2043] SEQ 441 :AFLAV1
[2044] 5' GCCGTTTGACCGGCCGCAACGTCGTC 3'
[2045] SEQ 442 :AFLAV1
[2046] 5' GACGACGTTGCGGCCGGTCAAACGGC 3'
[2047] SEQ 443 :ACLAV1
[2048] 5' CGAGATCGTCGGCAAGCGCAC 3'
[2049] SEQ 444 :ACLAV1
[2050] 5' GTGCGCTTGCCGACGATCTCG 3'
[2051] SEQ 445 :ACLAV2
[2052] CGGCCGCTCCGTTGTCTTCGAG 3'
[2053] SEQ 446 :ACLAV2
[2054] 5' CTCGAAGACAACGGAGCGGCCG 3'
[2055] SEQ 447 :ACLAV3
[2056] 5' CGCCGTTTAACCGGCCGCTCCGTTGTC 3'
[2057] SEQ 448 :ACLAV3
[2058] 5' GACAACGGAGCGGCCGGTTAAACGGCG 3'
[2059] SEQ 449 :S.cerevisiae 33
[2060] CATCACTCTAGATGCCACCAATGAAAACTTCAGATTGGTCTACGATGTCAAGGGTAGATTCGCTGTCCA

CCGTATCACCG

[2061] ATGAAGAAGCYTCTTACAARTTGGGTAAGGTCAAGAAGGTYCAATTAGGTAAGAAGGGTGTTCATACG
TTGTTACCCAC

[2062] GATGGTAGAACTATCAGATACCCAG

[2063] SEQ 450 :*S. cerevisiae* 33

[2064] CAUCACUCUAGAUGCCACCAAUGAAAACUUCAGAUUGGUCUACGAUGUCAAGGGUAGAUUCGCUGUCCA
CCGUAUCACCG

[2065] AUGAAGAAGCYUCUUACAARUUGGGUAAGGUCAAGAAGGUYCAAUUAGGUAAGAAGGGUGUCCAUACG
UUGUUACCCAC

[2066] GAUGGUAGAACUAUCAGAUACCCAG

[2067] SEQ 451 :*C. neoformans*114

[2068] GGTGTACGATGTCAAGGGTAGATTACACYSTSCACAGAATCACCGCYGAGGAGKCTWCCTACAAGYTSGS
YAAGRTCARGA

[2069] AGRTCMTTGGGYAAGAGRRGTRTYCCMTACGYYGTCASCCACGACGGTAGAACTATCAGATACCCA
GA

[2070] SEQ 452 :*C. neoformans*114

[2071] GGUGUACGAUGUCAAGGGUAGAUUCACYSUSCACAGAAUCACCGCYGAGGAGKCUWCCUACAAGYUSGS
YAAGRUCARGA

[2072] AGRUCSMKUUGGGYAAGAGRRGURUYCCMUACGYYGUCASCCACGACGGUAGAACUAUCAGAUACCCA
GA

[2073] SEQ 453 :*A. fischeri*_131700

[2074] CGTCGCTCAGCGCCGCATCCTGCCCCGCCCAAGCGCTCCGTCAACTCCCGCACCAACCAGAAGCAGAA
GCGTCCTCGCT

[2075] CTCGCACCCTGACCGCCGTCCACGACGCCATCCTCAACGACCTCGTTTACCCCGTCGAGATCGTCGGCA
AGCGTACCCGC

[2076] ACCAAGGAAGACGGCAGCAAGACTCTCAAGGTCATCCTCGACGAGAAGGAGCGTGGCGGTGTTGACCAC
AGACTCGATGC

[2077] CTACGGCGAGGTCTACCGCCGACTGACCGGCCGCTCTGTTGTCTTCGAGTTCCCCCAGAG

[2078] SEQ 454 :*A. fischeri*_131700

[2079] CGUCGCUCAGCGCCGCAUCCUGCCCCGCCCAAGCGUCUCCGUCAACUCCCGCACCAACCAGAAGCAGAA
GCGUCCUCGCU

[2080] CUCGCACCCUGACCGCCGUCCACGACGCCAUCCUCAACGACCUCGUUUACCCCGUCGAGAUCGUCGGCA
AGCGUACCCGC

[2081] ACCAAGGAAGACGGCAGCAAGACUCUCAAGGUCAUCCUCGACGAGAAGGAGCGUGGCGGUGUUGACCAC
AGACUCGAUGC

[2082] CUACGGCGAGGUCUACCGCCGACUGACCGGCCGUCUGUUGUCUUCGAGUUCSSCCAGAG

[2083] SEQ 455 :*A. fischeri*_211390

[2084] CGTCGCTCAGCGCCGCATCCTGCCCCGCCCAAGCGCTCTGTCAACTCCCGCACCAACCAGAAGCAGAA
GCGTCCTCGCT

- [2085] CTCGCACCCTGACCGCTGTCCACGATGCCATCCTCAACGACCTCGTTTACCCCGTCGAGATCGTCGGCA
AGCGTATCCGC
- [2086] ACCAAGGAGGACGGCAGCAAGACTCTCAAGGTCATCCTGGACGAGAAGGAGCGTGGTGGTGTGACCAC
AGACTCGATGC
- [2087] CTACGGCGAGGTTTACCGCCGACTAACTGGCCGCTCTGTTGTCTTCGAGTTCCCCCAGAG
- [2088] SEQ 456 :A. fischeri_211390
- [2089] CGUCGCUCAGCGCCGCAUCCUGCCCCGCCCAAGCGCUCUGUCAACUCCCGCACCAACCAGAAGCAGAA
GCGUCCUCGCU
- [2090] CUCGCACCCUGACCGCUGUCCACGAUGCCAUCCUCAACGACCUCGUUUACCCCGUCGAGAUCGUCGGCA
AGCGUAUCCGC
- [2091] ACCAAGGAGGACGGCAGCAAGACUCUCAAGGUCAUCCUGGACGAGAAGGAGCGUGGUGUGUUGACCAC
AGACUCGAUGC
- [2092] CUACGGCGAGGUUUACCGCCGACUAAUCUGGCCGCUUGUUGUCUUCGAGUUCSCCAGAG
- [2093] SEQ 457 :A. fischeri_214525
- [2094] CGTCGCTCAGCGCCGATCCTGCCCGCCCCAAGCGCTCTGTCAACTCCCGCACCAACCAGAAGCAGAA
GCGTCCTCGCT
- [2095] CTCGCACCCTGACCGCTGTCCACGATGCCATCCTCAACGACCTCGTTTACCCCGTCGAGATCGTCGGCA
AGCGTATCCGC
- [2096] ACCAAGGAGGACGGCAGCAAGACTCTCAAGGTCATCCTGGACGAGAAGGAGCGTGGTGGTGTGACCAC
AGACTCGATGC
- [2097] CTACGGCGAGGTTTACCGCCGACTAACTGGCCGCTCTGTTGTCTTCGAGTTCCCCCAGAG
- [2098] SEQ 458 :A. fischeri_214525
- [2099] CGUCGCUCAGCGCCGCAUCCUGCCCCGCCCAAGCGCUCUGUCAACUCCCGCACCAACCAGAAGCAGAA
GCGUCCUCGCU
- [2100] CUCGCACCCUGACCGCUGUCCACGAUGCCAUCCUCAACGACCUCGUUUACCCCGUCGAGAUCGUCGGCA
AGCGUAUCCGC
- [2101] ACCAAGGAGGACGGCAGCAAGACUCUCAAGGUCAUCCUGGACGAGAAGGAGCGUGGUGUGUUGACCAC
AGACUCGAUGC
- [2102] CUACGGCGAGGUUUACCGCCGACUAAUCUGGCCGCUUGUUGUCUUCGAGUUCSCCAGAG
- [2103] SEQ 459 :N. fischeri_1085
- [2104] CGCTCAGCGCCGATCCTGCCCGCCCCAAGCGTCCGTCAACTCCCGCACCAACCAGAAGCAGAAGCG
CCCTCGCTCCC
- [2105] GCACCCTGACCGCTGTCCACGACGCCATCCTCAACGACCTCGTTTACCCCGTCGAGATCGTCGGCAAGC
GTATCCGCACC
- [2106] AAGGAGGACGGCAGCAAGACTCTCAAGGTCATCCTGGACGAGAAGGAGCGTGGCGGTGTTGACCACAGA
CTCGATGCCTA
- [2107] CGGCGAGGTTTACCGCCGACTAACCGGCCGCTCTGTTGTCTTCGAGTTCCCCCAGAG
- [2108] SEQ 460 :N. fischeri_1085
- [2109] CGCUCAGCGCCGCAUCCUGCCCCGCCCAAGCGCUCUGUCAACUCCCGCACCAACCAGAAGCAGAAGCG

CCCUCGCUCCC

[2110] GCACCCUGACCGCUGUCCACGACGCCAUCCUCAACGACCUCGUUUACCCCGUCGAGAUCGUCGGCAAGC
GUAUCCGCACC

[2111] AAGGAGGACGGCAGCAAGACUCUCAAGGUCAUCCUGGACGAGAAGGAGCGUGGCGGUGUUGACCACAGA
CUCGAUGCCUA

[2112] CGGCGAGGUUUACCGCCGACUAACCGGCCGCUCUGUUGUCUUCGAGUUCSCCAGAG

[2113] SEQ 461 :N. fischeri_14726

[2114] TGCTCAGCGCCGCATCCTGCCCGCCCAAGCGCTCTGTCAACTCCCGCACCAACCAGAAGCAGAAGCG
CCCTCGCTCTC

[2115] GCACCCTGACCGCTGTCCACGACGCCATCCTCACCACCTCGTTTACCCCGTCGAGATCGTCGGCAAGC
GTATCCGCACC

[2116] AAGGAGGACGGCAGCAAGACTCTCAAGGTCATCCTGGACGAGAAGGAGCGTGGCGGTGTTGACCACAGA
CTCGATGCCTA

[2117] CGGCGAGGTCTACCGCCGACTAACCGGCCGCCTGTGTTGTCTTCGAGTTCCSCCAGAG

[2118] SEQ 462 :N. fischeri_14726

[2119] UGCUCAGCGCCGCAUCCUGCCCGCCCAAGCGCUCUGUCAACUCCCGCACCAACCAGAAGCAGAAGCG
CCCUCGCUCUC

[2120] GCACCCUGACCGCUGUCCACGACGCCAUCCUCACCGACCUCGUUUACCCCGUCGAGAUCGUCGGCAAGC
GUAUCCGCACC

[2121] AAGGAGGACGGCAGCAAGACUCUCAAGGUCAUCCUGGACGAGAAGGAGCGUGGCGGUGUUGACCACAGACUCGAUGCCUA

[2122] CGGCGAGGUUUACCGCCGACUAACCGGCCGCUCUGUUGUCUUCGAGUUCSCCAGAG

[2123] SEQ 463 :N. fischeri_19426

[2124] TGCTCAGCGCCGCATCCTGCCACGCCCAAGCGCTCTGTCAACTCCCGCACCAACCAGAAGCAGAAGCG
CCCTCGCTCTC

[2125] GCACCCTGACCGCCGTCCACGACGCCATCCTCGACGACCTCGTTTACCCCGTCGAGATCGTCGGCAAGC
GTATCCGCACC

[2126] AAGGAGGACGGCAGCAAGACTCTCAAGGTCATCCTGGACGAGAAGGAGCGTGGCGGTGTTGACCACAGA
CTCGATGCCTA

[2127] CGGCGAGGTCTACCGCCGACTAACCGGCCGCCTGTGTTGTCTTCGAGTTCCSCCAGAG

[2128] SEQ 464 :N. fischeri_19426

[2129] UGCUCAGCGCCGCAUCCUGCCACGCCCAAGCGCUCUGUCAACUCCCGCACCAACCAGAAGCAGAAGCG
CCCUCGCUCUC

[2130] GCACCCUGACCGCCGUCCACGACGCCAUCCUCGACGACCUCGUUUACCCCGUCGAGAUCGUCGGCAAGC
GUAUCCGCACC

[2131] AAGGAGGACGGCAGCAAGACUCUCAAGGUCAUCCUGGACGAGAAGGAGCGUGGCGGUGUUGACCACAGA
CUCGAUGCCUA

[2132] CGGCGAGGUUUACCGCCGACUAACCGGCCGUGCUGUUGUCUUCGAGUUCSCCAGAG

[2133] SEQ 465 :N. fischeri_20179

[2134] TGCTCAGCGCCGCATCCTGCCACGCCCAAGCGCTCTGTCAACTCCCGCACCAACCAGAAGCAGAAGCG

CCCTCGCTCTC

[2135] GCACCCTGACCGCCGTCCACGACGCCATCCTCGACGACCTCGTTTACCCCGTCGAGATCGTCGGCAAGC
GTATCCGCACC

[2136] AAGGAGGACGGCAGCAAGACTCTCAAGGTCATCCTGGACGAGAAGGAGCGTGGCGGTGTTGACCACAGA
CTCGATGCCTA

[2137] CGGCGAGGTCTACCGCCGACTAACCGGCCGTGCTGTTGTCTTCGAGTTCCCCCAGAG

[2138] SEQ 466 :N. fischeri_20179

[2139] UGCUCAGCGCCGAUCCUGCCACGCCCAAGCGCUCUGUCAACUCCCGCACCAACCAGAAGCAGAAGCG
CCCUCGCUCUC

[2140] GCACCCUGACCGCCGUCCACGACGCCAUCCUCGACGACCUCGUUUACCCCGUCGAGAUCGUCGGCAAGC
GUAUCCGCACC

[2141] AAGGAGGACGGCAGCAAGACUCUCAAGGUCAUCCUGGACGAGAAGGAGCGUGGCGGUGUUGACCACAGA
CUCGAUGCCUA

[2142] CGGCGAGGUCUACCGCCGACUAAACCGGCCGUGCUGUUGUCUUCGAGUCCCCCAGAG

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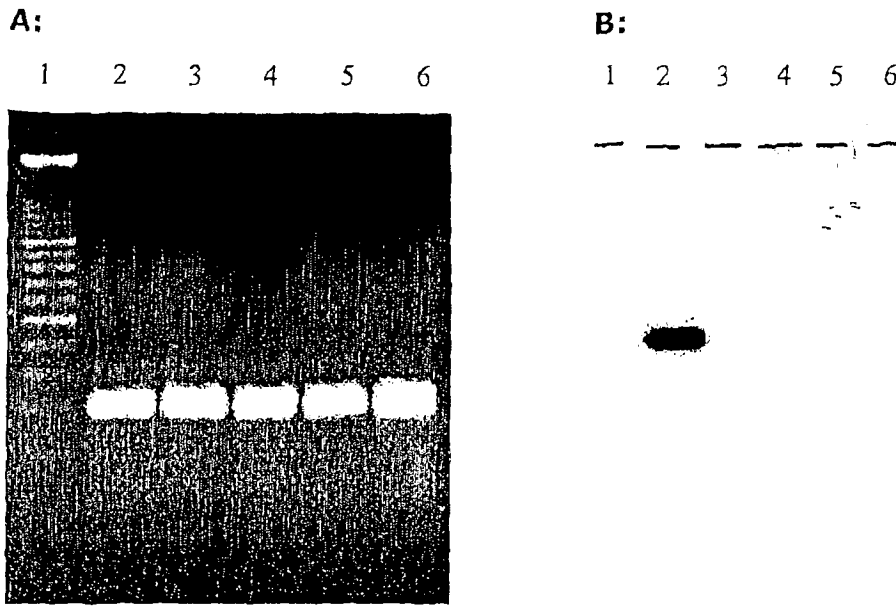
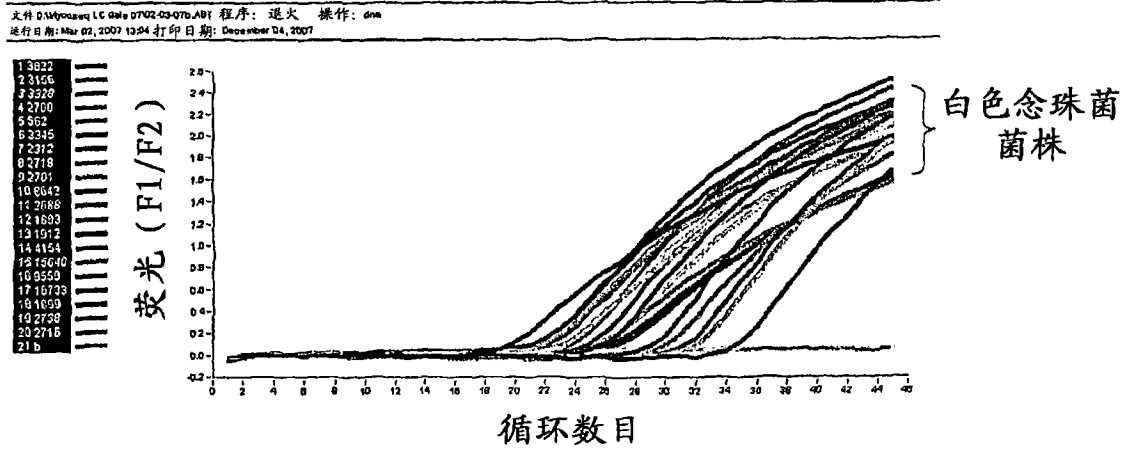


图 1A 和 B



基线调整: 算法 嘈杂带指针: N/A 分析方法: 二阶导数量大值
颜色补偿: 关

图 2

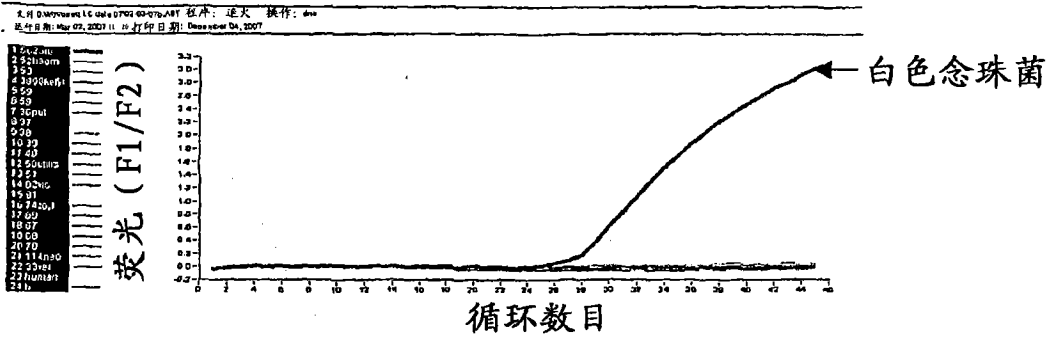


图 3

基线调整:算法 嘈声带指针:N/A 分析方法:二阶导数量大值颜色补偿:关

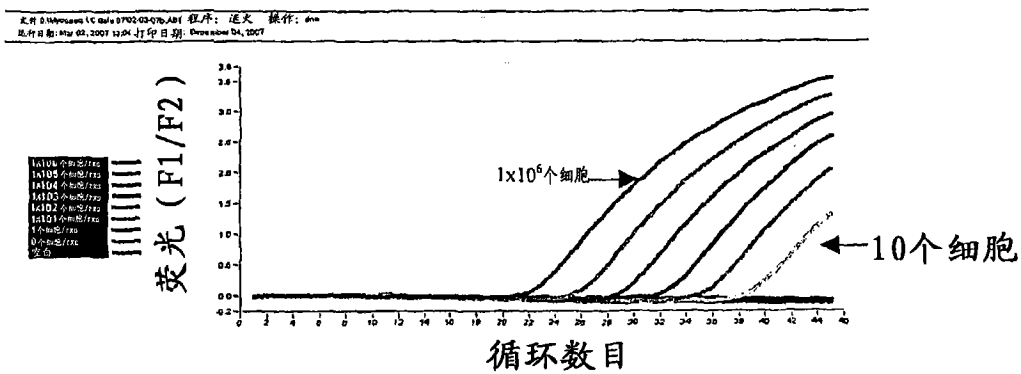


图 4

基线调整:算法 嘈声带指针:N/A 分析方法:二阶导数量大值颜色补偿:关

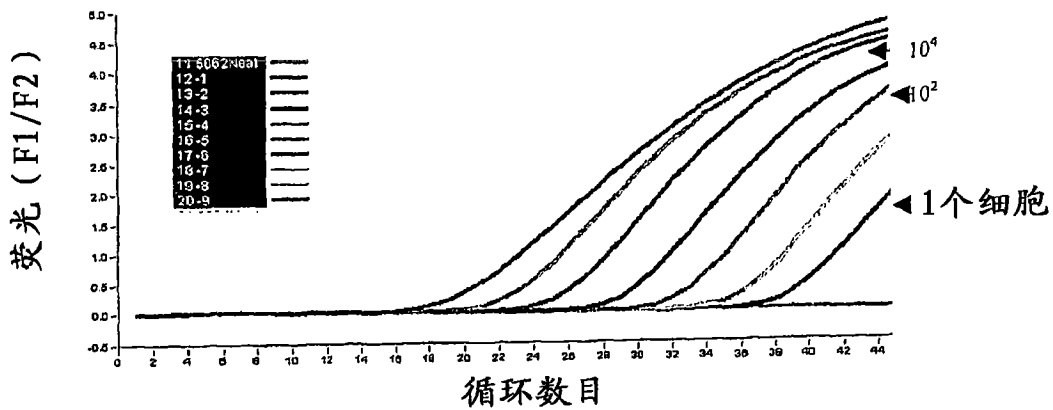


图 5

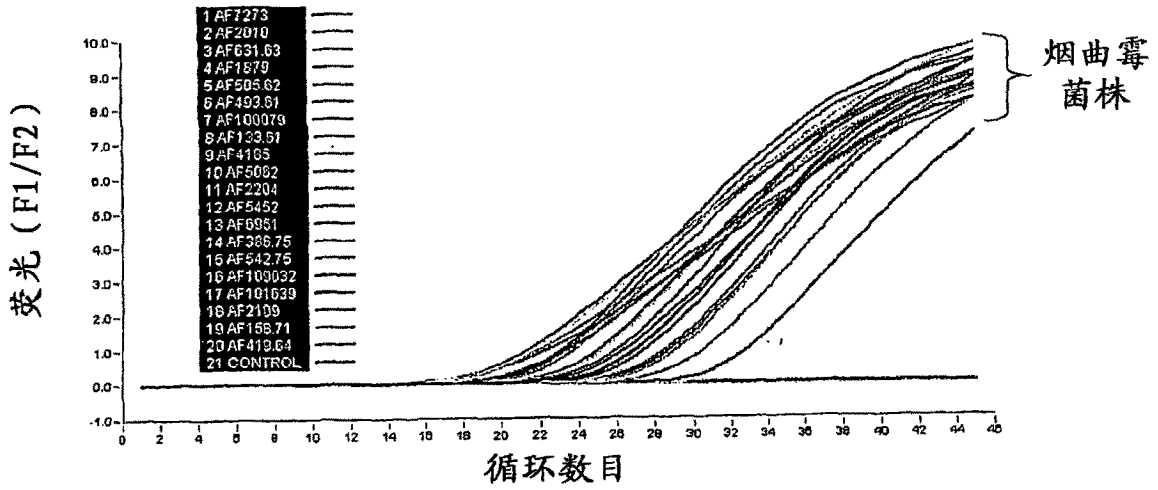


图 6

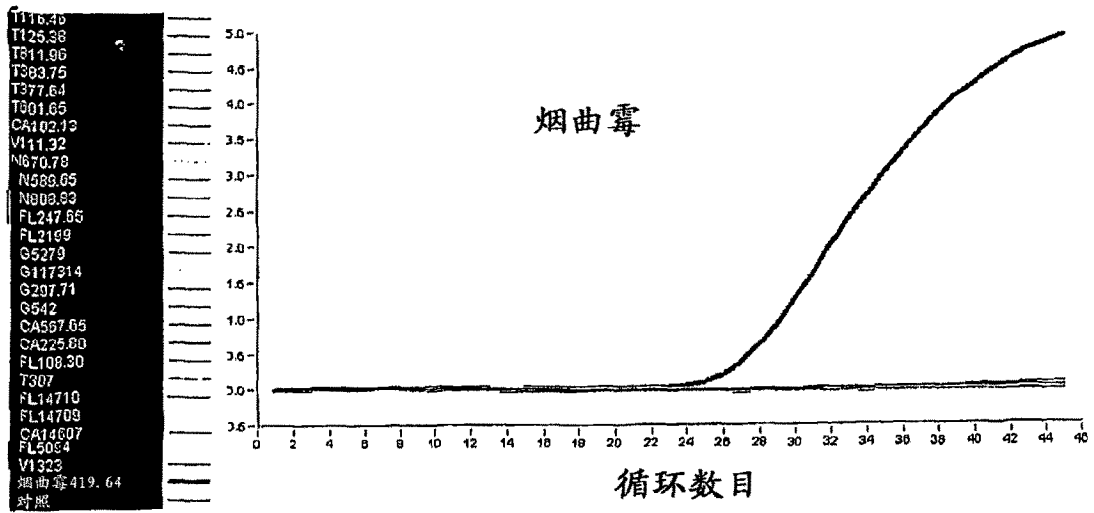


图 7