SUPPLEMENTARY MATERIAL

Table S1. Sequences of the ZIP-code oligonucleotides used in the analyses described.

Table S2. ORF identifiers, trivial names and brief description of the 20 *Candida albicans* genes, whose variations in transcript levels between bastospore and hyphal growth are presented in Fig. 6.

Table S3. Sequences of primer pairs used for the amplification of the genomic regions of 21 SNPs from a case-control study on hay-fever. Also, the sequences of oligonucleotides are shown that were used as a control for the SNP-typing reaction, acting as a heterozygous template.

Figure S1. Quantification of the amount of oligonucleotide that was attached to an array surface. At each spot, a mixture of an excess of a D-formed oligonucleotide and a small quantity of the L-DNA ICP-sequence (ICP, 5`-TTCGGCTGTGAGAACGATCACGCA) was applied. Subsequently, the relative amount of oligonucleotide attached at each spot position was analysed by hybridisation of the fluorescence-labelled L-DNA complement of the ICP oligonucleotide. On the left half of the slide, the same pattern of D-formed ICP had been spotted. The hybridisation image shows that binding occurred only at positions of the L-DNA ICP. The relevant signal intensities were quantified and are shown in the panels on the right. At four spot positions, attachment had failed, so hybridisation produced only signals of or slightly above background, which is indicated by a horizontal line.

Table S1

ZIP-Code Sequence	Molecule Mass
AGCGAGCGGGAACAGGCCAA	7155.63
GGAACACCACGCAGCGCAGG	7092.32
GCAGTGCTCACCGTCCGCGA	7019.80
CGGAGTGGCACCAGCGGGAA	7159.22
GCAGCAGGCCAAAGCGAGCG	7128.12
GTCCGAGCCCTCACGCAGCG	7015.10
GCAGGACGACGCGGGTGGAA	7202.40
TGGCGGTCTGCTGAGCGGTC	7128.12
GTGGGTCCCGGAAGCGTGCT	7137.68
GCCTCGAGCCAACACCGCCT	6961.82
TGGCCGGACAGGAGACACGC	7124.53
GCCTGCCTTCACGAGCCCAA	6974.81
GTGGGCGAAGCGGGAACCTC	7141.50
CGGAGCGATCACGTGGCACC	7075.64
ACGCGACGCACCTGCTCCAA	6981.90
CCTCCCTCACGCGCCTGCAG	6925.26
GTGGACTGAGCGCGGATGGC	7197.60
CGAGGCAGACGCGTCCCACC	7023.36
TGGCCGAGACTGCAGGAGCG	7159.22
AGCGGACGACTGCGGACGAG	7167.60
GCCTGCGAAGACCCAAGCGA	7067.31
GAGCAGCGACGCCGAGGCAG	7147.25
GCGAGTCCCGAGGGTCCCAA	7075.64
GGAAAGCGAGCGGCAGCCAA	7167.60
TGGCGGAACAGGACTGCGGA	7173.60
TGGCGGGTTGCTCCTCGTGG	7111.40
GACGGCCTTGCTAGCGCGGA	7103.05
GCCTGCAGTGCTGGTCCGGA	7093.51
CCTCCGGAAGACCCTCGCGA	6993.74
GCGAGCAGCAGGGTGGACCA	7165.21
GCCTGAGCAGACGGTCGCGA	7117.37
GGGTGCCTAGCGGTCCAGCG	7122.14
CAGGACGCACCAACGCCCAA	6993.74
AGCGCACCCGGAACTGGAGC	7087.55
ACGCGTGGACTGCCTCGAGC	7068.50
ACGCCCTCCCAACCTCACGC	6879.40
CACCGCAGCCTCCCAACCAA	6908.78
GGGTTGGCGGAAGGTCGACG	7231.25
GCGAGCGAACCAGAGCGACG	7132.90
TGGCAGCGTCACGGGTCACC	7066.12
GGGTGACGAGCGCCAAGCCT	7114.98
GCGATGGCAGCGGTGGAGAC	7195.19
GCAGGCGATGGCTCACGACG	7120.95
GTCCTGCTGTGGGCGATGGC	7132.90
GGTCGTCCGGTCGCCTTGCT	7049.50
ACCAAGCGGCCTCCTCGTCC	6946.48
ACGCGGAAGGTCTGGCCAGG	7152.04
CCAACGGAGCGACGAGCAGG	7141.30
CGGACAGGGACGGCGATCAC	7118.56

GGTCGGGTCAGGCCTCGGAA	7147.25
CGGAAGCGCGAGACCACACC	7048.29
TCACCCTCTGGCGGAACGGA	7061.40
CCAAAGACAGCGGACGGCGA	7113.79
GGGTGGGTCGAGGCCTGGTC	7190.39
CGGAGTCCTGGCAGCGTGGC	7129.30
GCGAAGCGACCAAGACCGGA	7110.21
CAGGCACCCACCGCGAAGAC	7012.70
GTCCGCAGCCAACCAAACGC	6990.19
GCAGAGCGTGGCCGAGGTCC	7136.48
GTGGCGGACGGACGAGTGGC	7214.40
GCAGGTGGGACGGGTCGGGT	7238.60
AGACAGCGGCGAGAGCGGGT	7206.00
CGAGAGCGGTCCCGGAGGTC	7134.09
CCTCCGAGCACCGACGACGC	6981.91
ACGCCCAAACGCAGACCCAA	6983.09
GGTCCAGGTGGCGGTCGAGC	7165.21
AGCGTCACGAGCCAGGCGGA	7128.12
GAGCGTGGCGGAGGTCGGTC	7203.59
GACGGCGAGGGTGCAGGCAG	7227.60
CCTCGACGGTCCTGGCTGGC	7032.80
GAGCTGCTTGGCGCGACACC	7066.12
GCGACAGGCGGAGAGCGGAA	7216.80
GCAGTGGCGTCCGGGTGAGC	7159.20
CGAGGGAAGTGGGCAGCGGA	7242.20
TGGCGAGCGCAGTGGCAGAC	7150.80
CGAGGCCTGCAGGGAAAGCG	7162.81
CGAGGTCCGGGTGCGAGAGC	7167.60
GTGGGAGCGACGCAGGGCAG	7215.61
GGGTGCAGGCCTGTGGGTCC	7152.04
GCCTACGCGAGCGACGGAGC	7097.08
CACCGAGCTGCTGCCTTGGC	7016.24
GGGTGGAAAGCGGAGCGTGG	7275.85
CAGGCCAAGCAGACGCGACG	7089.9
GCGAGGGTGCGAGGGTTGCT	7218.00
AGCGGTCCGACGGCCTTCAC	7020.98
GTCCCGAGGCAGCGAGAGCG	7142.46
GCAGTCACGGTCAGCGGCCT	7067.31
GACGCCAACGGACGGAGGGT	7164.01
TCACGCGACACCCGGACACC	6963.00
CGAGCGGAGAGCGAGCCAGG	7192.79
AGCGTGCTGGTCGTGGGCCT	7128.12
AGCGCCAAGGGTCCTCGGGT	7111.40
CCAAAGCGAGACCGGAGCGA	7116.17
GACGCACCGAGCACGCACCA	7012.69
TCACCCAAGACGGCAGGCGA	7064.93
GGGTGGTCCGGAGCGAGCAG	7214.40
CCTCAGACGGGTAGCGGCGA	7128.10
GGAAGCAGCACCCGAGGCCT	7088.70
CCTCGTCCGTCCGGTCACCA	6931.70
GGGTGTGGACGCGGAAGCAG	7248.10
CGGAGAGCCCAAACGCGCAG	7089.40
ACGCGGTCGGAAGGGTGGTC	7183.80

Table S2

ORF Id.	Name	Description
orf19.4906		putative cell wall protein
orf19.5742	ALS9	agglutinin-like protein 9
orf19.1346	HYR6	hyphally regulated cell wall protein
orf19.1816	ALS3	agglutinin-like protein 3
orf19.715		hypothetical protein
orf19.3618	CWP1	putative cell wall protein
orf19.138	FIG1	integral membrane protein required for efficient mating
orf19.5188	CHS1	chitin synthase
orf19.4361	HYR2	hyphally regulated protein precursor
orf19.1690	TOS1	conserved hypothetical protein
orf19.1321	HWP1	hyphal wall protein
orf19.2767		hypothetical protein
orf19.6420		hypothetical membrane protein
orf19.7030	CCW14	cell wall mannoprotein | secretory stress response protein
orf19.5007	ACT1	actin
orf19.7218	PRY2	putative cell wall protein
orf19.930	PET9	ATP/ADP translocator
orf19.7114		putative cell wall protein
orf19.7362	SKN1	glucan synthase subunit involved in cell wall assembly
orf19.6771	UBI1	polyubiquitin involved in stress response system

Table S3

No.	Forward Primer	Reverse Primer	Lenght/nt
SNP 8, 9, 10	TGCCCCTCCCAGTCTAGTTCT	GCATCAAGGATACCCCTCACA	226
SNP 2	AACTCCTGTCTTGCATTGCA	TTCCATTCAAAATCATCTG	142
SNP 13	TGCTGATTGGCCCCAAGT	TTTGCAGTGACAATGTGAGGC	168
SNP 20	TTCCTTAGGTTGAGCTGGAGG	GTTCCATGCATTACGAGGAGC	164
SNP 24	TGCCTTGAGGAGAAAAGAGCT	TCGTTCAGCCTCTCACCTCT	151
SNP 26	GGAATGGGAAGCAGCTCAAG	AACAGGAATTTGGGGCTTTG	143
SNP 30	GGGTTGTGTGTTTATTTCACT	CCTGACACATTCAAGTTCTG	143
SNP 31	TTCAGACATTCACAATTGA	CCCAATGGTACAGGTTTT	163
SNP 38	AAAGCACACAACCTTGACCTG	GGGTGACACCTGGAAGTTGTA	144
SNP 41	TCGCCATCATGATAGCATCTG	TGGAGTATGACGAAATTTTCT	249
SNP 42	TTGCTTTGGTACAACATCC	TGGTAACCGTGGTCTCAATA	221
SNP 43	CTTCCGTGAGGACTGAATGA	TGCAAATAATGATGCTTTCGA	238
SNP 56	CCTTCGTTAGAACACCCATGA	AGACAGGGATTCTGGTTGTGA	123
SNP 61	CCTGGAGTGCACGAAGTTGT	ATAGATGGATGGGTGGGATG	150
SNP 66	CCCTCAACTCTTTCTCCCCTA	CAGGTGGATGTTTACCAATGA	142
SNP 72	TCCTTGTTTTCAGCTGCCCTA	GAGGGCTGATCCTACCACAAT	257
SNP 81	GAGCAGTTAACCAGCTTGTCT	TCACCTTGCTGCCTGCACATA	207
SNP 88	TAGAGAAAACCCGAGCATGA	TCCTAGGCCAATCTCACCTCA	150
SNP 90	TTCTTTTCCGTTTTGTGCAA	GTGCTGTCTTGAATCCTCTGC	150
Int-22-G	CGATCACACGTGTGGGCTCTGCA		
Int-22-A	CGATTACACGTGTGGGCTCTGCA		

Figure S1