|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Contig 19#** | **Location** | **Log2 pseudo-median signal intensity** | **Target** | **CGD Gene name** | **Description** |
| Contig19-10194 | 4621..5701 | 1.438 | orf19.3895 | *CHT2* | Chitinase, required for normal filamentous growth; mRNA binds to She3p and is localized to buds of yeast-form cells and hyphal tips; downregulated in core caspofungin response; induced in yeast-form cells; Cyr1p-, Efg1p-, pH-regulated |
| Contig19-10194 | 5821..6181 | 1.281 | orf19.3897 |  | Predicted ORF in Assemblies 19, 20 and 21; decreased transcription is observed upon fluphenazine treatment or in an azole-resistant strain that overexpresses CDR1 and CDR2; transcription is repressed in response to alpha pheromone in SpiderM medium |
| Contig19-10194 | 57181..57421 | 1.263 | orf19.3928 and orf19.3929 |  | Putative transcription factor with zinc finger DNA-binding motif |
| Contig19-10198 | 17881..18361 | 1.184 |  |  |  |
| Contig19-2513 | 118741..119221 | 1.182 | orf19.7391 | *OCH1* | alpha-1,6-mannosyltransferase; initiates N-glycan outer chain branch addition; similar to S. cerevisiae Och1p; required for wild-type virulence in mouse intravenous infection; fungal-specific (no human or murine homolog) |
| Contig19-10186 | 57721..58021 | 1.128 |  |  |  |
| Contig19-10202 | 208561..209221 | 1.119 | orf19.4336 | *RPS5* | Predicted ribosomal protein; macrophage/pseudohyphal-induced after 16 h; genes encoding cytoplasmic ribosomal subunits, translation factors, and tRNA synthetases are downregulated upon phagocytosis by murine macrophage |
| Contig19-2500 | 98521..99061 | 1.021 |  |  |  |
| Contig19-10198 | 1..841 | 1.013 |  |  |  |
| Contig19-10105 | 16441..16801 | 1.005 |  |  |  |
| Contig19-10170 | 40021..40261 | 1.004 | orf19.3178 |  |  |
| Contig19-10170 | 46321..46561 | 1.002 |  |  |  |
| Contig19-10202 | 61741..62161 | 0.997 | orf19.4250 and orf19.4251 | 2) *ZCF22* | 2) Predicted zinc-finger protein of unknown function |
| Contig19-10198 | 2821..3001 | 0.961 | orf19.4132 |  |  |
| Contig19-10093 | 22381..22561 | 0.958 | orf19.1117 |  | Predicted ORF in Assemblies 19, 20 and 21; similar to Candida boidinii formate dehydrogenase; virulence-group-correlated expression |
| Contig19-10202 | 60421..61021 | 0.951 |  |  |  |
| Contig19-10170 | 66061..66661 | 0.943 | orf19.3195 | *HIP1* | Alkaline upregulated; flucytosine induced; regulated by Plc1p, Gcn2p and Gcn4p; fungal-specific (no human or murine homolog) |
| Contig19-10170 | 44101..44281 | 0.937 | orf19.3183 and orf19.3184 |  |  |
| Contig19-10198 | 1561..1981 | 0.935 |  |  |  |
| Contig19-10202 | 221941..222301 | 0.924 |  |  |  |
| Contig19-10234 | 54241..56161 | 0.922 | orf19.5808 |  |  |
| Contig19-10212 | 274741..275041 | 0.915 |  |  |  |
| Contig19-10137 | 52801..53221 | 0.906 | orf19.1957 | *CYC3* | Cytochrome c heme lyase, mitochondrial; gene also encodes antigenic cell-wall protein; mRNA more abundant in filaments than yeast-form; induced on polystyrene adherence, interaction with macrophage; N-glycosylation, 2 heme-binding motifs |
| Contig19-2449 | 26041..26641 | 0.900 |  |  |  |
| Contig19-2456 | 721..1921 | 0.899 | orf19.6614 |  | Deleted in assembly 21 |
| Contig19-10202 | 56281..56641 | 0.878 | orf19.4246 |  | Protein with similarity to S. cerevisiae Ykr070wp; transposon mutation affects filamentous growth; Hog1p-downregulated; shows colony morphology-related gene regulation by Ssn6p; induced during cell wall regeneration; possibly essential gene |
| Contig19-2511 | 38221..38941 | 0.872 | orf19.7302 |  |  |
| Contig19-10247 | 80821..82441 | 0.869 |  |  |  |
| Contig19-10192 | 117961..119701 | 0.866 |  |  |  |
| Contig19-10119 | 95281..95701 | 0.865 |  |  |  |
| Contig19-10137 | 11281..11521 | 0.862 | orf19.1932 | *CFL4* | Similar to ferric reductase, C-terminal region; expression greater in low iron; transcription is negatively regulated by Sfu1p; ciclopirox olamine induced; shows colony morphology-related gene regulation by Ssn6p |
| Contig19-2511 | 128581..128761 | 0.857 |  |  |  |
| Contig19-10202 | 109261..109561 | 0.840 |  |  |  |
| Contig19-10212 | 68941..70621 | 0.838 | orf19.4597 |  | Predicted ORF in Assemblies 19, 20 and 21; possibly an essential gene, disruptants not obtained by UAU1 method |
| Contig19-1876 | 5341..5941 | 0.835 |  |  |  |
| Contig19-10202 | 14941..15241 | 0.834 | orf19.4227 |  |  |
| Contig19-10176 | 74401..74821 | 0.828 |  |  |  |
| Contig19-10238 | 37501..39901 | 0.827 |  |  |  |
| Contig19-10216 | 175801..176161 | 0.820 |  |  |  |
| Contig19-10104 | 4861..5341 | 0.817 |  |  |  |
| Contig19-10104 | 99241..101341 | 0.812 |  |  |  |
| Contig19-10203 | 80041..81901 | 0.812 | orf19.4388 |  | Predicted ORF in Assemblies 19, 20 and 21; has histone fold domain; similar to TAFII47 proteins from S. cerevisiae, Danio rerio, Drosophila melanogaster, human, and mouse |
| Contig19-10137 | 59641..59941 | 0.811 | orf19.1958 |  |  |
| Contig19-10080 | 21421..21601 | 0.803 |  |  |  |
| Contig19-10184 | 47881..48181 | 0.803 |  |  |  |
| Contig19-10202 | 152281..152581 | 0.802 |  |  |  |
| Contig19-10080 | 20761..21121 | 0.795 |  |  |  |
| Contig19-10132 | 10441..10861 | 0.793 |  |  |  |
| Contig19-10203 | 109081..109450 | 0.791 | orf19.4401 | *YVH1* | Putative dual specificity phosphatase (phosphoserine/threonine and phosphotyrosine phosphatase); similar to S. cerevisiae Yvh1p; required for wild-type growth rate and for wild-type virulence in mouse model of systemic infection |
| Contig19-10227 | 152881..153531 | 0.783 | orf19.5475 |  |  |
| Contig19-10206 | 39181..40261 | 0.778 |  |  |  |
| Contig19-1859 | 8101..8530 | 0.776 |  |  |  |
| Contig19-10065 | 18721..19321 | 0.771 |  |  |  |
| Contig19-10104 | 361..901 | 0.770 | orf19.1227 | *ZCF4* | Putative transcription factor with zinc cluster DNA-binding motif; possibly spurious ORF (Annotation Working Group prediction) |
| Contig19-10198 | 16981..17341 | 0.766 | orf19.4144 |  | Predicted ORF in Assemblies 19, 20 and 21; clade-associated gene expression |
| Contig19-10194 | 24001..24241 | 0.765 |  |  |  |
| Contig19-10216 | 110341..110761 | 0.765 | orf19.4956 | *RPN1* | Predicted ORF in Assemblies 19, 20 and 21; regulated by Gcn2p and Gcn4p |
| Contig19-1086 | 421..961 | 0.762 |  |  |  |
| Contig19-10123 | 1..481 | 0.760 |  |  |  |
| Contig19-10119 | 192541..192721 | 0.751 |  |  |  |
| Contig19-10090 | 27961..28441 | 0.750 |  |  |  |
| Contig19-10123 | 56221..56401 | 0.737 | orf19.1630 |  |  |
| Contig19-10237 | 76081..76321 | 0.736 |  |  |  |
| Contig19-2456 | 12061..13021 | 0.733 |  |  |  |
| Contig19-10202 | 102241..102541 | 0.732 | orf19.4271 |  |  |
| Contig19-10212 | 123061..123361 | 0.729 |  |  |  |
| Contig19-10233 | 481..961 | 0.725 |  |  |  |
| Contig19-10198 | 40081..40441 | 0.721 |  |  |  |
| Contig19-10194 | 215221..215521 | 0.720 | orf19.4007 |  |  |
| Contig19-1914 | 661..1501 | 0.720 |  |  |  |
| Contig19-10202 | 218761..219061 | 0.710 |  |  |  |
| Contig19-10126 | 12601..13081 | 0.709 |  |  |  |
| Contig19-10202 | 223381..223681 | 0.708 | orf19.4342 |  |  |
| Contig19-2500 | 2401..2641 | 0.707 |  |  |  |
| Contig19-10123 | 238201..238681 | 0.706 |  |  |  |
| Contig19-10202 | 39901..40441 | 0.704 |  |  |  |
| Contig19-10202 | 220981..221401 | 0.704 |  |  |  |
| Contig19-10158 | 210901..211081 | 0.701 |  |  |  |
| Contig19-10170 | 85201..85681 | 0.701 |  |  |  |
| Contig19-10227 | 150121..152281 | 0.700 | orf19.5474 and orf19.5475 |  | 1) Predicted ORF in Assemblies 19, 20 and 21; possibly spurious ORF (Annotation Working Group prediction); transcriptionally activated by Mnl1p under weak acid stress |
| Contig19-10202 | 165841..166741 | 0.695 |  |  |  |
| Contig19-2456 | 9061..11221 | 0.695 |  |  |  |
| Contig19-10065 | 19621..20101 | 0.692 |  |  |  |
| Contig19-10087 | 43441..44161 | 0.692 |  |  |  |
| Contig19-10176 | 95881..96241 | 0.692 | orf19.3435 |  |  |
| Contig19-10202 | 244441..244621 | 0.692 |  |  |  |
| Contig19-10123 | 217201..217921 | 0.688 | orf19.1707 |  |  |
| Contig19-10123 | 8341..8641 | 0.687 | orf19.1608 |  |  |
| Contig19-10220 | 10261..10441 | 0.678 |  |  |  |
| Contig19-10198 | 7261..7501 | 0.677 |  |  |  |
| Contig19-10198 | 23521..23941 | 0.677 |  |  |  |
| Contig19-10070 | 10081..10681 | 0.673 |  |  |  |
| Contig19-10202 | 192181..192601 | 0.668 |  |  |  |
| Contig19-10202 | 219661..220081 | 0.668 |  |  |  |
| Contig19-10233 | 98341..99541 | 0.667 | orf19.5752 |  |  |
| Contig19-10155 | 28561..28801 | 0.663 | orf19.2649 | *PCL1* | Cyclin homolog; expression induced upon filamentous growth; transcription is induced in response to alpha pheromone in SpiderM medium |
| Contig19-10202 | 39061..39241 | 0.660 |  |  |  |
| Contig19-10137 | 44941..45241 | 0.657 | orf19.1950 |  |  |
| Contig19-10225 | 30421..30841 | 0.655 |  |  |  |
| Contig19-10063 | 12841..13741 | 0.653 | orf19.639 |  | Predicted ORF in Assemblies 19, 20 and 21; decreased transcription is observed upon fluphenazine treatment or in an azole-resistant strain that overexpresses CDR1 and CDR2 |
| Contig19-10070 | 32341..32581 | 0.648 |  |  |  |
| Contig19-10236 | 309181..309541 | 0.648 |  |  |  |
| Contig19-2134 | 5401..7321 | 0.647 |  |  |  |
| Contig19-10162 | 68161..68761 | 0.646 |  |  |  |
| Contig19-10227 | 141901..142981 | 0.644 |  |  |  |
| Contig19-10237 | 194161..194941 | 0.641 | orf19.6114 |  |  |
| Contig19-10057 | 1201..1441 | 0.638 | orf19.567 | *TFB3* | Putative transcription factor with C3HC4 zinc finger DNA-binding motif; transcription is positively regulated by Tbf1p |
| Contig19-10186 | 34801..36241 | 0.638 | orf19.3673 |  | In S.c. TRS23 One of 10 subunits of the transport protein particle (TRAPP) complex of the cis-Golgi which mediates vesicle docking and fusion; involved in endoplasmic reticulum (ER) to Golgi membrane traffic; human homolog is TRAPPC4 |
| Contig19-2500 | 80041..81121 | 0.638 |  |  |  |
| Contig19-10150 | 45361..45661 | 0.637 |  |  |  |
| Contig19-10127 | 9241..9481 | 0.634 |  |  |  |
| Contig19-10202 | 54781..55081 | 0.633 | orf19.4245 |  |  |
| Contig19-10035 | 61141..61441 | 0.631 |  |  |  |
| Contig19-10123 | 248941..249121 | 0.629 | orf19.1721 and orf19.1720 | 1) *NCE103* | 1) Carbonic anhydrase involved in the conversion of carbon dioxide to bicarbonate; essential for pathogenesis in host niches with limited CO2, wild-type white-opaque switching; biofilm induced; activated by Mnl1p under weak acid stress |
| Contig19-10225 | 142741..143701 | 0.628 |  |  |  |
| Contig19-10137 | 108001..108241 | 0.626 |  |  |  |
| Contig19-1859 | 6901..7501 | 0.625 |  |  |  |
| Contig19-10230 | 162601..163741 | 0.623 |  |  |  |
| Contig19-10212 | 147661..147961 | 0.622 | orf19.4641 | *NMT1* | Myristoyl-CoA:protein N-myristoyltransferase; attaches the fatty acid myristate to a small number of proteins at an N-terminal Gly; essential; antifungal drug target; functional homolog of S. cerevisiae Nmt1p |
| Contig19-10170 | 26521..26821 | 0.621 | orf19.3172 and orf19.3173 |  |  |
| Contig19-10202 | 108481..108781 | 0.621 |  |  |  |
| Contig19-10185 | 20881..21361 | 0.614 |  |  |  |
| Contig19-10201 | 30421..32221 | 0.607 |  |  |  |
| Contig19-10198 | 4981..5221 | 0.605 |  |  |  |
| Contig19-1127 | 1861..2050 | 0.604 |  |  |  |
| Contig19-10194 | 266941..268021 | 0.602 | orf19.4054 | *CTA24* | Putative transcriptional activator, downregulated by Efg1p; member of a family of telomere-proximal genes; transcription is upregulated in an RHE model of oral candidiasis |
| Contig19-10215 | 113161..113641 | 0.601 |  |  |  |
| Contig19-10171 | 7321..7681 | 0.600 |  |  |  |
| Contig19-10140 | 56461..57061 | 0.599 |  |  |  |
| Contig19-2405 | 28861..29041 | 0.598 | orf19.6192 |  | Predicted ORF in Assemblies 19, 20 and 21; Plc1p-regulated; possibly spurious ORF |
| Contig19-2413 | 17761..18661 | 0.598 |  |  |  |
| Contig19-1876 | 1081..1381 | 0.597 |  |  |  |
| Contig19-10090 | 30181..30601 | 0.594 |  |  |  |
| Contig19-10171 | 28021..28261 | 0.587 | orf19.3219 |  |  |
| Contig19-10212 | 50581..51121 | 0.587 |  |  |  |
| Contig19-10225 | 32461..33241 | 0.584 | orf19.5306 |  |  |
| Contig19-1859 | 5521..6781 | 0.583 |  |  |  |
| Contig19-10241 | 65281..66481 | 0.580 | orf19.6227 |  |  |
| Contig19-10237 | 191581..192541 | 0.579 |  |  |  |
| Contig19-10237 | 196201..196621 | 0.579 | orf19.6115 |  |  |
| Contig19-2506 | 1141..2101 | 0.578 |  |  |  |
| Contig19-2506 | 4501..5281 | 0.578 |  |  |  |
| Contig19-2506 | 2761..3001 | 0.577 |  |  |  |
| Contig19-10166 | 2761..4081 | 0.573 |  |  |  |
| Contig19-1472 | 1741..2101 | 0.571 |  |  |  |
| Contig19-10136 | 16081..17161 | 0.570 | orf19.1825 |  | Protein not essential for viability; filament induced; regulated by Nrg1p, Rfg1p, Tup1p |
| Contig19-10139 | 124921..125281 | 0.570 | orf19.2061 |  |  |
| Contig19-2516 | 164701..165841 | 0.570 |  |  |  |
| Contig19-1888 | 3541..4441 | 0.568 |  |  |  |
| Contig19-2518 | 136501..137101 | 0.568 |  |  |  |
| Contig19-10014 | 33421..33661 | 0.567 |  |  |  |
| Contig19-10202 | 13261..13561 | 0.567 |  |  |  |
| Contig19-10237 | 198781..199081 | 0.566 |  |  |  |
| Contig19-10170 | 17881..18061 | 0.559 | orf19.3170 |  |  |
| Contig19-10170 | 99961..100400 | 0.558 |  |  |  |
| Contig19-10186 | 59461..59881 | 0.558 | orf19.3683 | *AGE3* | Putative ADP-ribosylation factor GTPase activating protein, functional ortholog of S. cerevisiae GCS1; mutation affects endocytosis, hyphal growth, chemical and drug resistance, and sensitivity to cell wall inhibitors |
| Contig19-10194 | 269461..269701 | 0.558 |  |  |  |
| Contig19-2500 | 30601..31081 | 0.556 |  |  |  |
| Contig19-10209 | 58321..58681 | 0.555 |  |  |  |
| Contig19-2134 | 4681..5221 | 0.555 |  |  |  |
| Contig19-10131 | 6061..6361 | 0.554 |  |  |  |
| Contig19-10131 | 8461..8641 | 0.554 |  |  |  |
| Contig19-1996 | 2221..2881 | 0.554 |  |  |  |
| Contig19-10237 | 197521..198121 | 0.552 |  |  |  |
| Contig19-10194 | 270121..270541 | 0.551 |  |  |  |
| Contig19-2456 | 13201..13450 | 0.549 |  |  |  |
| Contig19-1472 | 2641..2890 | 0.548 |  |  |  |
| Contig19-10057 | 7021..7621 | 0.547 |  |  |  |
| Contig19-2516 | 167101..167410 | 0.545 |  |  |  |
| Contig19-10202 | 224641..224941 | 0.543 |  |  |  |
| Contig19-10215 | 80341..80581 | 0.543 |  |  |  |
| Contig19-10057 | 34861..35341 | 0.542 |  |  |  |
| Contig19-2507 | 51961..53041 | 0.537 |  |  |  |
| Contig19-10228 | 38221..38401 | 0.534 |  |  |  |
| Contig19-10254 | 98581..98761 | 0.532 | orf19.9773 |  |  |
| Contig19-10202 | 31741..31921 | 0.523 |  |  |  |
| Contig19-2134 | 2821..3001 | 0.521 |  |  |  |
| Contig19-2201 | 16981..17161 | 0.517 |  |  |  |
| Contig19-10202 | 60061..60301 | 0.509 |  |  |  |
| Contig19-10072 | 15061..15301 | 0.508 | orf19.741 |  |  |
| Contig19-10194 | 258061..258361 | 0.502 | orf19.4043 |  |  |
| Contig19-10194 | 95641..95821 | 0.460 | orf19.3952 |  |  |