# Genome Sequencing and Metabolic Potential Analysis of *Irpex lacteus*

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**Table S1.** The analyzed PKSs in phylogenetic tree.

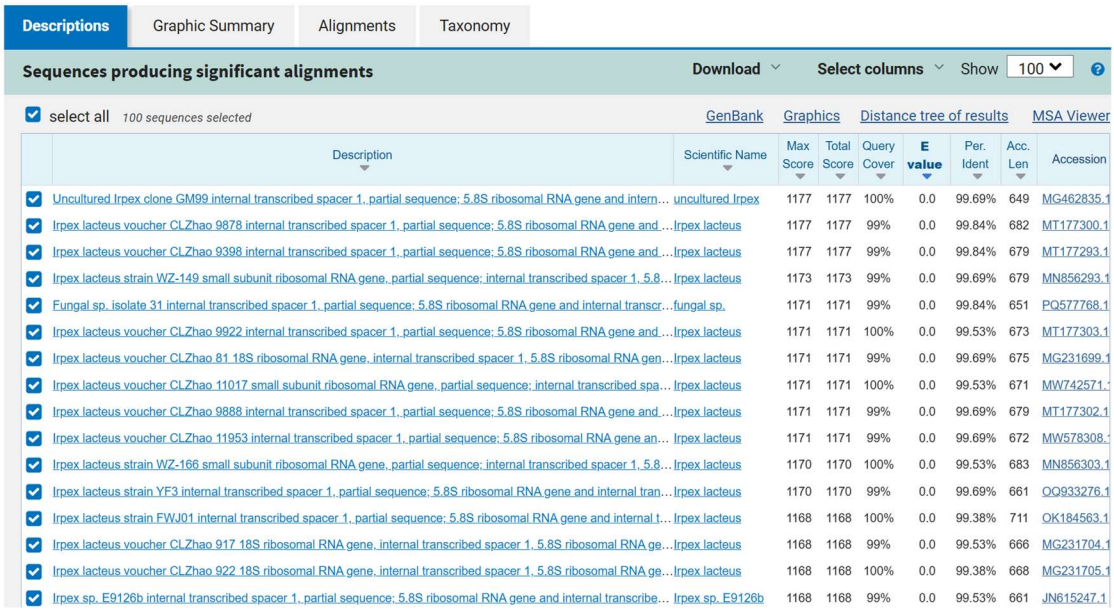
| Organism | Enzyme | Accession number | Proposed domain structure |
|---|---|---|---|
| *Antrodia cinnamomea* | PKS63787 | AST08390.1 | SAT KS AT PT ACP ACP TE |
| *Armillaria mellea* | ArmB | I3ZNU9.1 | SAT KS AT PT ACP ACP TE |
| *Aspergillus fumigatus* | Alb1 | AAC39471.1 | SAT KS AT PT ACP ACP TE |
| *Aspergillus fumigatus* | FccA | Q4WA61.1 | SAT KS AT DH ACP |
| *Aspergillus nidulans* | WA | CAA46695.2 | SAT KS AT PT ACP ACP TE |
| *Aspergillus nidulans* | MdpG | Q5BH30.1 | SAT KS AT DH ACP |
| *Aspergillus nidulans* | AptA | XP_663604.1 | SAT KS AT PT ACP |
| *Aspergillus niger* | AdaA | G3KLH6.1 | SAT KS AT DH ACP |
| *Aspergillus nidulans* | PkfA | Q5B8A0.1 | SAT KS AT DH ACP |
| *Aspergillus niger* | AlbA | A2QUI2.1 | SAT KS AT DH ACP ACP TE |
| *Aspergillus parasiticus* | AflC | Q12053.1 | SAT KS AT PT ACP TE |
| *Aspergillus terreus* | ACAS | XP_001217072.1 | SAT KS AT PT ACP |
| *Coprinopsis cinerea* | CC1G | XP_001835415.2 | KS AT PT ACP TE |
| *Cortinarius odorifer* | CoPKS1 | P9WES1 | KS AT DH ACP AB |
| *Cortinarius odorifer* | CoPKS4 | P9WES2 | KS AT DH ACP AB |
| *Penicillium aethiopicum* | GsfA | D7PI15.1 | SAT KS AT DH ACP |
| *Penicillium brevicompactum* | MpaC | F1DBA9.1 | ACP KS AT DH ACP AB |
| *BY1* | PKS1 | APH07629.1 | SAT KS AT DH ACP TE |
| *BY1* | PKS2 | APH07628.1 | SAT KS AT DH ACP ACPACP TE |
| *Aspergillus oryzae* | PKSA | BAE71314.1 | SAT KS AT PT ACP TE |
| *Agaricus bisporus var. bisporus H97 v2.0* | PKS1 | 202648 | SAT KS AT PT ACP ACP ACP |
| *Auricularia delicata SS-5* | PKS1 | 167360 | KS AT DH KR ACP RED |
| *Fomitiporia mediterranea* | PKS1 | 144436 | X KS AT PT ACP TE |
| *Ganoderma sp.10597* | PKS1 | 86609 | KS AT PT ACP TE |
| *Fomitopsis pinicola SS1* | PKS1 | 83434 | SAT KS AT PT ACP TE |
| *Laccaria bicolor* | PKS1 | XP_001876029.1 | SAT KS AT PT ACP TE |
| *Schizophyllum commune* | PKS1 | XP_003038401.1 | SAT KS AT PT ACP TE |
| *Ustilago maydis* | PKS3 | XP_011390610.1 | KS X PT ACP ACP TE |
| *Laetiporus sulphureus* | LpaA | QNJ99675.1 | KS AT DH MT ER KR ACP TE |
| *Trametes versicolor* | PKS1 | XP_008041566.1 | KS AT DH ACP ACP TE |
| *Trametes chinabarina* | PKS1 | CDO73915.1 | KS AT PT ACP ACP TE |
| *Stereum hirsutum* | PKS1 | XP_007307184.1 | SAT KS AT DH ACP ACP ACP TE |
| *Fibroporia radiculosa* | PKS1 | XP_012179384.1 | SAT KS AT PT ACP ACP TE |
| *Amanita muscaria* | PKS1 | KIL57002.1 | SAT KS AT PT ACP ACP |
| *Grifola frondosa* | PKS1 | BAO20284.1 | SAT KS AT DH ACP ACP TE |

**Table S2.** Identification of cytochrome P450 genes in *I. lacteus* genome.

| Query | Hit type | PSSM-ID | From | To | E-Value | Bitscore | Accession | Short name |
|---|---|---|---|---|---|---|---|---|
| 79_t | specific | 410688 | 64 | 490 | 0 | 543.324 | cd11065 | CYP64-like |
| 83_t | specific | 410688 | 80 | 489 | 3.17E-176 | 502.108 | cd11065 | CYP64-like |
| 854_t | specific | 410693 | 148 | 551 | 9.52E-106 | 325.053 | cd11070 | CYP56-like |
| 1016_t | specific | 410688 | 81 | 496 | 1.30E-170 | 488.241 | cd11065 | CYP64-like |
| 1017_t | specific | 410688 | 79 | 491 | 2.47E-155 | 449.335 | cd11065 | CYP64-like |
| 1126_t | specific | 410688 | 65 | 512 | 4.08E-176 | 502.878 | cd11065 | CYP64-like |
| 1144_t | specific | 410688 | 1 | 391 | 1.73E-146 | 422.757 | cd11065 | CYP64-like |
| 1145_t | specific | 410688 | 85 | 515 | 5.73E-156 | 451.647 | cd11065 | CYP64-like |
| 1146_t | specific | 410688 | 80 | 508 | 6.15E-168 | 481.692 | cd11065 | CYP64-like |
| 1609_t | specific | 410667 | 64 | 501 | 4.02E-175 | 499.897 | cd11041 | CYP503A1-like |
| 1612_t | specific | 410667 | 64 | 503 | 5.15E-162 | 466.385 | cd11041 | CYP503A1-like |
| 1613_t | specific | 410667 | 64 | 501 | 2.35E-164 | 472.548 | cd11041 | CYP503A1-like |
| 1657_t | specific | 410685 | 486 | 862 | 3.39E-128 | 392.002 | cd11062 | CYP58-like |
| 1658_t | specific | 410685 | 7 | 376 | 3.64E-133 | 387.765 | cd11062 | CYP58-like |
| 1684_t | specific | 410685 | 77 | 489 | 2.60E-151 | 438.611 | cd11062 | CYP58-like |
| 1852_t | superfamily | 372343 | 206 | 370 | 1.89E-16 | 76.2663 | cl24253 | CYP67-like |
| 1934_t | specific | 410688 | 79 | 503 | 4.58E-167 | 479.381 | cd11065 | CYP64-like |
| 1958_t | specific | 410688 | 66 | 478 | 5.64E-165 | 473.218 | cd11065 | CYP64-like |
| 1961_t | specific | 410688 | 74 | 501 | 3.70E-168 | 482.463 | cd11065 | CYP64-like |
| 1962_t | specific | 410692 | 66 | 530 | 5.72E-143 | 419.367 | cd11069 | CYP_FUM15-like |
| 2517_t | specific | 410692 | 84 | 536 | 2.03E-168 | 484.851 | cd11069 | CYP_FUM15-like |
| 2524_t | specific | 410692 | 83 | 535 | 1.08E-166 | 480.229 | cd11069 | CYP_FUM15-like |
| 2525_t | specific | 410692 | 71 | 522 | 1.24E-169 | 487.162 | cd11069 | CYP_FUM15-like |
| 2554_t | specific | 410688 | 76 | 504 | 2.11E-141 | 414.282 | cd11065 | CYP64-like |
| 2739_t | specific | 410688 | 65 | 482 | 2.52E-154 | 445.483 | cd11065 | CYP64-like |
| 2839_t | specific | 410692 | 65 | 527 | 3.28E-143 | 420.138 | cd11069 | CYP_FUM15-like |
| 2846_t | specific | 410688 | 1229 | 1657 | 2.82E-173 | 528.301 | cd11065 | CYP64-like |
| 2966_t | specific | 410692 | 71 | 531 | 5.95E-140 | 411.663 | cd11069 | CYP_FUM15-like |
| 3822_t | specific | 410688 | 62 | 485 | 1.02E-170 | 487.855 | cd11065 | CYP64-like |
| 3896_t | specific | 410688 | 65 | 481 | 3.42E-164 | 473.603 | cd11065 | CYP64-like |
| 4217_t | specific | 410692 | 65 | 525 | 2.33E-150 | 438.242 | cd11069 | CYP_FUM15-like |
| 4226_t | specific | 410688 | 68 | 488 | 6.27E-161 | 481.307 | cd11065 | CYP64-like |
| 4227_t | specific | 410688 | 79 | 506 | 1.66E-155 | 450.106 | cd11065 | CYP64-like |
| 4236_t | specific | 410688 | 1 | 420 | 1.48E-165 | 472.447 | cd11065 | CYP64-like |
| 4237_t | specific | 410688 | 69 | 498 | 0 | 522.908 | cd11065 | CYP64-like |
| 4238_t | specific | 410688 | 70 | 497 | 9.13E-155 | 447.795 | cd11065 | CYP64-like |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| 4240_t | specific | 410688 | 64 | 491 | 2.79E-162 | 467.055 | cd11065 | CYP64-like |
| 4371_t | specific | 410688 | 64 | 482 | 8.51E-150 | 435.083 | cd11065 | CYP64-like |
| 4372_t | specific | 410688 | 62 | 486 | 9.80E-159 | 457.425 | cd11065 | CYP64-like |
| 4497_t | specific | 410688 | 69 | 498 | 1.43E-173 | 495.945 | cd11065 | CYP64-like |
| 4523_t | specific | 410688 | 68 | 523 | 2.60E-176 | 503.648 | cd11065 | CYP64-like |
| 4524_t | specific | 410688 | 69 | 493 | 1.13E-167 | 480.537 | cd11065 | CYP64-like |
| 4708_t | specific | 410688 | 84 | 569 | 4.57E-147 | 430.075 | cd11065 | CYP64-like |
| 5308_t | specific | 410686 | 130 | 601 | 1.76E-166 | 480.902 | cd11063 | CYP52 |
| 5541_t | specific | 410688 | 79 | 498 | 1.28E-162 | 468.21 | cd11065 | CYP64-like |
| 6102_t | specific | 410684 | 85 | 546 | 2.64E-141 | 415.083 | cd11061 | CYP67-like |
| 6139_t | specific | 410684 | 85 | 545 | 6.81E-133 | 393.897 | cd11061 | CYP67-like |
| 6224_t | specific | 410691 | 25 | 451 | 0 | 570.666 | cd11068 | CYP120A1 |
| 6561_t | specific | 410686 | 126 | 592 | 3.10E-175 | 507.866 | cd11063 | CYP52 |
| 6562_t | specific | 410686 | 129 | 595 | 4.91E-173 | 497.465 | cd11063 | CYP52 |
| 6566_t | specific | 410686 | 129 | 595 | 1.52E-176 | 506.325 | cd11063 | CYP52 |
| 6629_t | specific | 410693 | 82 | 497 | 3.24E-107 | 326.979 | cd11070 | CYP56-like |
| 6840_t | specific | 410688 | 1 | 389 | 2.39E-150 | 432.387 | cd11065 | CYP64-like |
| 7003_t | specific | 410691 | 25 | 459 | 0 | 561.806 | cd11068 | CYP120A1 |
| 7013_t | specific | 410691 | 25 | 452 | 0 | 663.499 | cd11068 | CYP120A1 |
| 7021_t | specific | 410668 | 83 | 539 | 0 | 545.659 | cd11042 | CYP51-like |
| 7177_t | specific | 410692 | 73 | 547 | 1.51E-149 | 437.086 | cd11069 | CYP_FUM15-like |
| 7955_t | specific | 410688 | 99 | 530 | 3.35E-162 | 468.21 | cd11065 | CYP64-like |
| 7972_t | specific | 410688 | 80 | 507 | 3.47E-166 | 477.455 | cd11065 | CYP64-like |
| 7974_t | specific | 410688 | 29 | 376 | 3.50E-136 | 395.407 | cd11065 | CYP64-like |
| 7988_t | specific | 410688 | 76 | 490 | 1.58E-157 | 454.343 | cd11065 | CYP64-like |
| 7993_t | specific | 410688 | 86 | 533 | 9.55E-173 | 495.174 | cd11065 | CYP64-like |
| 7994_t | specific | 410688 | 98 | 525 | 7.63E-156 | 451.647 | cd11065 | CYP64-like |
| 7995_t | specific | 410688 | 101 | 529 | 0 | 544.094 | cd11065 | CYP64-like |
| 8000_t | specific | 410688 | 1 | 388 | 5.44E-151 | 434.313 | cd11065 | CYP64-like |
| 8001_t | specific | 410688 | 98 | 525 | 5.53E-180 | 513.278 | cd11065 | CYP64-like |
| 8036_t | specific | 410688 | 62 | 487 | 2.34E-166 | 478.225 | cd11065 | CYP64-like |
| 8037_t | specific | 410688 | 115 | 540 | 2.79E-165 | 477.84 | cd11065 | CYP64-like |
| 8039_t | specific | 410688 | 62 | 487 | 1.09E-171 | 492.093 | cd11065 | CYP64-like |
| 8394_t | specific | 410688 | 62 | 504 | 6.96E-173 | 494.404 | cd11065 | CYP64-like |
| 8486_t | specific | 410688 | 1 | 416 | 2.18E-149 | 431.231 | cd11065 | CYP64-like |
| 8741_t | specific | 410684 | 133 | 569 | 1.03E-128 | 383.497 | cd11061 | CYP67-like |
| 8742_t | specific | 410684 | 131 | 546 | 2.35E-126 | 376.563 | cd11061 | CYP67-like |
| 8746_t | specific | 410667 | 57 | 513 | 2.03E-163 | 470.622 | cd11041 | CYP503A1-like |
| 8832_t | specific | 410684 | 129 | 550 | 5.82E-131 | 388.119 | cd11061 | CYP67-like |
| 8843_t | specific | 410684 | 130 | 570 | 3.11E-127 | 379.645 | cd11061 | CYP67-like |
| 8844_t | specific | 410684 | 130 | 549 | 2.10E-133 | 394.668 | cd11061 | CYP67-like |
| 8846_t | specific | 410684 | 80 | 565 | 5.93E-134 | 396.979 | cd11061 | CYP67-like |
| 8847_t | specific | 410684 | 80 | 549 | 1.63E-139 | 410.461 | cd11061 | CYP67-like |
| 9122_t | specific | 410686 | 116 | 580 | 1.46E-169 | 488.22 | cd11063 | CYP52 |
| 9268_t | specific | 410688 | 59 | 480 | 6.95E-142 | 414.282 | cd11065 | CYP64-like |
| 9362_t | specific | 410703 | 92 | 501 | 0 | 591.143 | cd11082 | CYP61_CYP710 |
| 9807_t | specific | 410667 | 60 | 482 | 3.34E-154 | 445.969 | cd11041 | CYP503A1-like |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| 9858_t | superfamily | 475119 | 674 | 768 | 0.000236734 | 43.7159 | cd11065 | CYP64-like |
| 10076_t | specific | 410688 | 73 | 500 | 0 | 563.354 | cd11065 | CYP64-like |
| 10895_t | specific | 410688 | 81 | 504 | 1.29E-176 | 503.648 | cd11065 | CYP64-like |
| 10931_t | specific | 410691 | 36 | 455 | 0 | 618.815 | cd11068 | CYP120A1 |
| 10956_t | specific | 410688 | 62 | 483 | 0 | 535.235 | cd11065 | CYP64-like |
| 10958_t | specific | 410688 | 63 | 487 | 4.87E-167 | 480.151 | cd11065 | CYP64-like |
| 11332_t | specific | 410688 | 70 | 495 | 2.25E-178 | 507.886 | cd11065 | CYP64-like |
| 11450_t | specific | 410688 | 60 | 503 | 1.69E-172 | 493.248 | cd11065 | CYP64-like |
| 11811_t | specific | 410684 | 133 | 553 | 8.60E-130 | 385.808 | cd11061 | CYP67-like |
| 11892_t | specific | 410684 | 126 | 556 | 2.41E-127 | 379.26 | cd11061 | CYP67-like |
| 12184_t | specific | 410684 | 124 | 518 | 2.67E-115 | 365.778 | cd11061 | CYP67-like |
| 12258_t | specific | 410688 | 69 | 508 | 1.62E-161 | 464.743 | cd11065 | CYP64-like |
| 12443_t | specific | 410688 | 62 | 485 | 9.75E-165 | 472.833 | cd11065 | CYP64-like |
| 12448_t | specific | 410688 | 63 | 475 | 1.17E-157 | 454.343 | cd11065 | CYP64-like |
| 12478_t | specific | 410688 | 62 | 486 | 1.17E-164 | 472.447 | cd11065 | CYP64-like |
| 12480_t | specific | 410688 | 140 | 565 | 1.58E-162 | 470.136 | cd11065 | CYP64-like |
| 12481_t | specific | 410688 | 73 | 496 | 4.17E-162 | 466.669 | cd11065 | CYP64-like |
| 12482_t | specific | 410688 | 62 | 466 | 1.25E-154 | 446.254 | cd11065 | CYP64-like |
| 12487_t | specific | 410688 | 63 | 487 | 6.55E-154 | 445.483 | cd11065 | CYP64-like |
| 12501_t | specific | 410691 | 35 | 430 | 0 | 548.709 | cd11068 | CYP120A1 |
| 12502_t | specific | 410691 | 26 | 459 | 0 | 598.4 | cd11068 | CYP120A1 |
| 12503_t | specific | 410691 | 25 | 455 | 0 | 621.127 | cd11068 | CYP120A1 |
| 12589_t | specific | 410688 | 68 | 497 | 4.59E-177 | 504.804 | cd11065 | CYP64-like |



Descriptions | Graphic Summary | Alignments | Taxonomy

**Sequences producing significant alignments** — Download — Select columns — Show 100

select all *100 sequences selected* — GenBank — Graphics — Distance tree of results — MSA Viewer

| Description | Scientific Name | Max Score | Total Score | Query Cover | E value | Per. Ident | Acc. Len | Accession |
|---|---|---|---|---|---|---|---|---|
| Uncultured Irpex clone GM99 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and intern… | uncultured Irpex | 1177 | 1177 | 100% | 0.0 | 99.69% | 649 | MG462835.1 |
| Irpex lacteus voucher CLZhao 9878 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and … | Irpex lacteus | 1177 | 1177 | 99% | 0.0 | 99.84% | 682 | MT177300.1 |
| Irpex lacteus voucher CLZhao 9398 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and … | Irpex lacteus | 1177 | 1177 | 99% | 0.0 | 99.84% | 679 | MT177293.1 |
| Irpex lacteus strain WZ-149 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8… | Irpex lacteus | 1173 | 1173 | 99% | 0.0 | 99.69% | 679 | MN856293.1 |
| Fungal sp. isolate 31 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcr… | fungal sp. | 1171 | 1171 | 99% | 0.0 | 99.84% | 651 | PQ577768.1 |
| Irpex lacteus voucher CLZhao 9922 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and … | Irpex lacteus | 1171 | 1171 | 100% | 0.0 | 99.53% | 673 | MT177303.1 |
| Irpex lacteus voucher CLZhao 81 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gen… | Irpex lacteus | 1171 | 1171 | 99% | 0.0 | 99.69% | 675 | MG231699.1 |
| Irpex lacteus voucher CLZhao 11017 small subunit ribosomal RNA gene, partial sequence; internal transcribed spa… | Irpex lacteus | 1171 | 1171 | 100% | 0.0 | 99.53% | 671 | MW742571.1 |
| Irpex lacteus voucher CLZhao 9888 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and … | Irpex lacteus | 1171 | 1171 | 99% | 0.0 | 99.69% | 679 | MT177302.1 |
| Irpex lacteus voucher CLZhao 11953 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene an… | Irpex lacteus | 1171 | 1171 | 99% | 0.0 | 99.69% | 672 | MW578308.1 |
| Irpex lacteus strain WZ-166 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8… | Irpex lacteus | 1170 | 1170 | 100% | 0.0 | 99.53% | 683 | MN856303.1 |
| Irpex lacteus strain YF3 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal tran… | Irpex lacteus | 1170 | 1170 | 99% | 0.0 | 99.69% | 661 | OQ933276.1 |
| Irpex lacteus strain FWJ01 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal t… | Irpex lacteus | 1168 | 1168 | 100% | 0.0 | 99.38% | 711 | OK184563.1 |
| Irpex lacteus voucher CLZhao 917 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA ge… | Irpex lacteus | 1168 | 1168 | 99% | 0.0 | 99.53% | 666 | MG231704.1 |
| Irpex lacteus voucher CLZhao 922 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA ge… | Irpex lacteus | 1168 | 1168 | 100% | 0.0 | 99.38% | 668 | MG231705.1 |
| Irpex sp. E9126b internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribe… | Irpex sp. E9126b | 1168 | 1168 | 99% | 0.0 | 99.53% | 661 | JN615247.1 |

**Figure S1.** ITS alignment of the strain Y1.The ITS of strain Y1 was aligned to the nr database of NCBI.

The ITS of strain Y1

CGAGTTTTGACGGGTTGTAGCTGGCCTCTCACGAGGCATGTGCACGCCTGGCTCA
TCCACTCTTAACCTCTGTGCACTTTATGTAAGAGAAAAAAATGGTGGAAGCTTCC
AGGATCTCGCGAGAGGTCTTCGGTTGAACAAGCCGTTTTTCTTTCTTATGTTTTACT
ACAAACGCTTCAGTTATAGAATGTCAACTGTGTATAACACATTTATATACAACTTT
CAGCAACGGATCTCTTGGCTCTCGCATCGATGAAGAACGCAGCGAAATGCGATA
AGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCA
CTCCTTGGTATTCCGAGGAGTATGCCTGTTTGAGTCTCATGGTATTCTCAACCCCT
AAATTTTTGTAATGAAGGTTTAGCGGGCTTGGACTTGGAGGTTGTGTCGGCCCTTG
TCGGTCGACTCCTCTGAAATGCATTAGCGTGAATCTTACGGATCGCCTTCAGTGTG
ATAATTATCTGCGCTGTGGTGTTGAAGTATTTATGGTGTTCATGCTTCGAACCGTC
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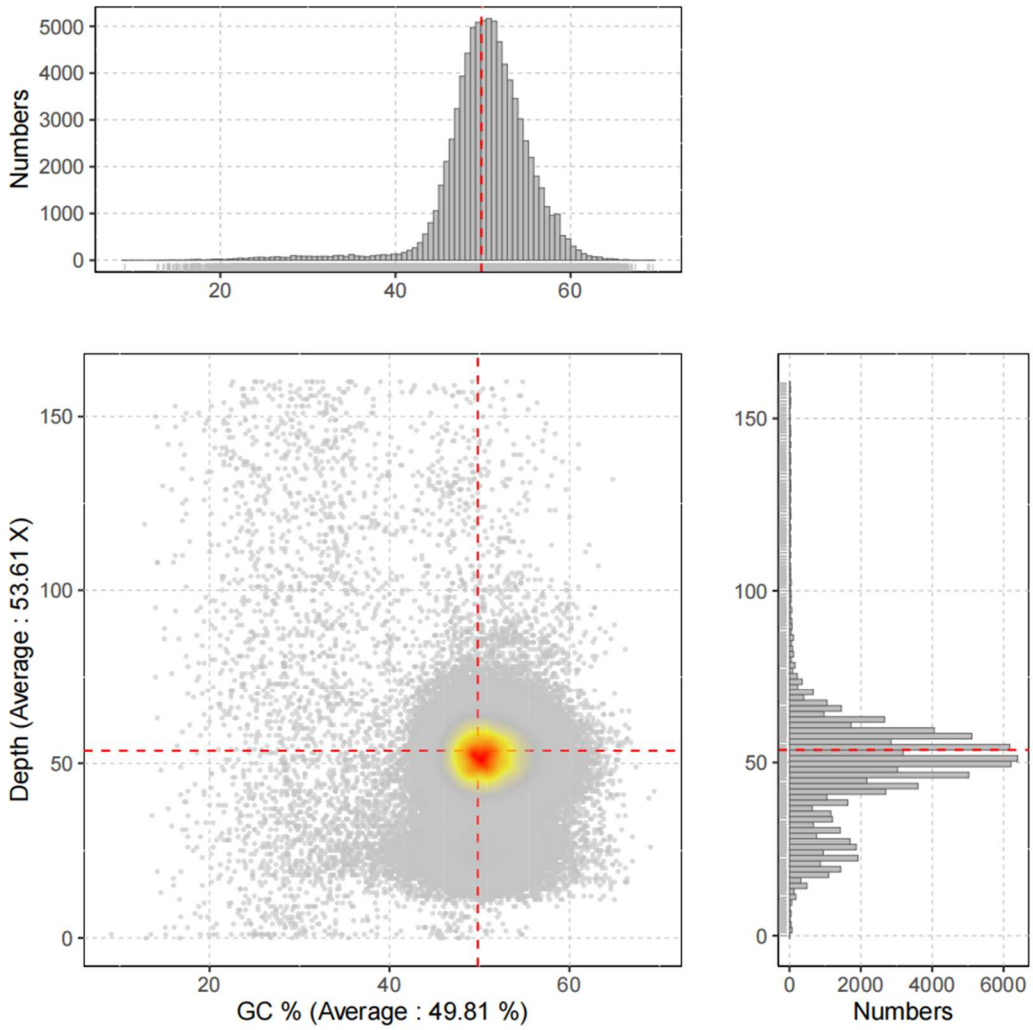



**Figure S2.** GC content and coverage correlation analysis.

The horizontal coordinate is the GC content and the vertical coordinate is the mean depth. The scatterplot exhibits a shape approximating a Poisson distribution, indicating that the GC bias during sequencing was not severe.

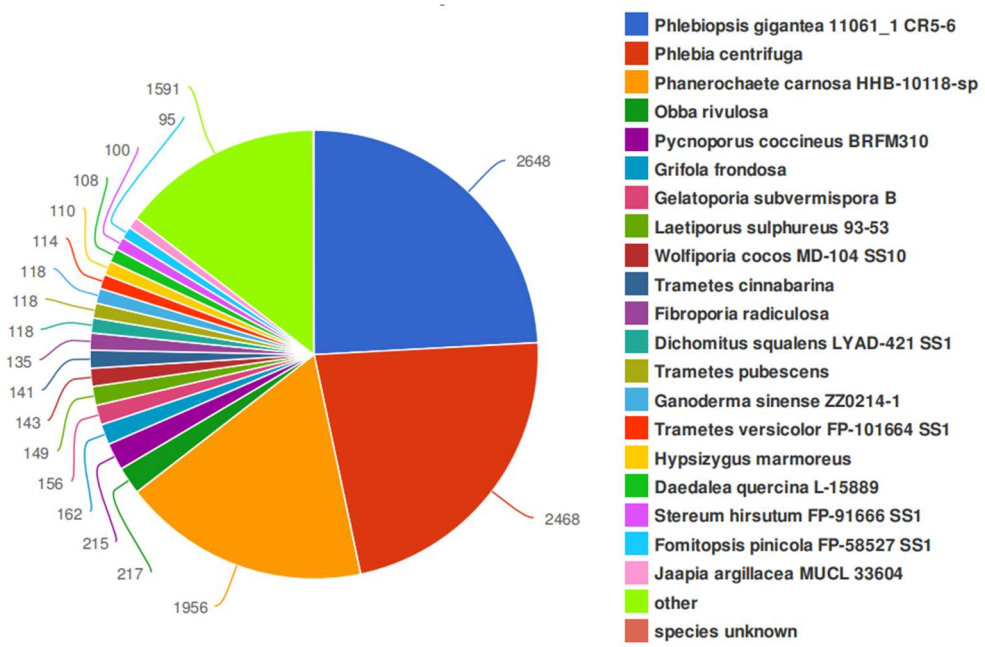



**Figure S3.** Species distribution map of Nr database alignment to sequences.

According to the results of the Nr library match, the top 10 species were counted and the rest were classified as other species, and the distribution of these species was mapped according to their proportion.

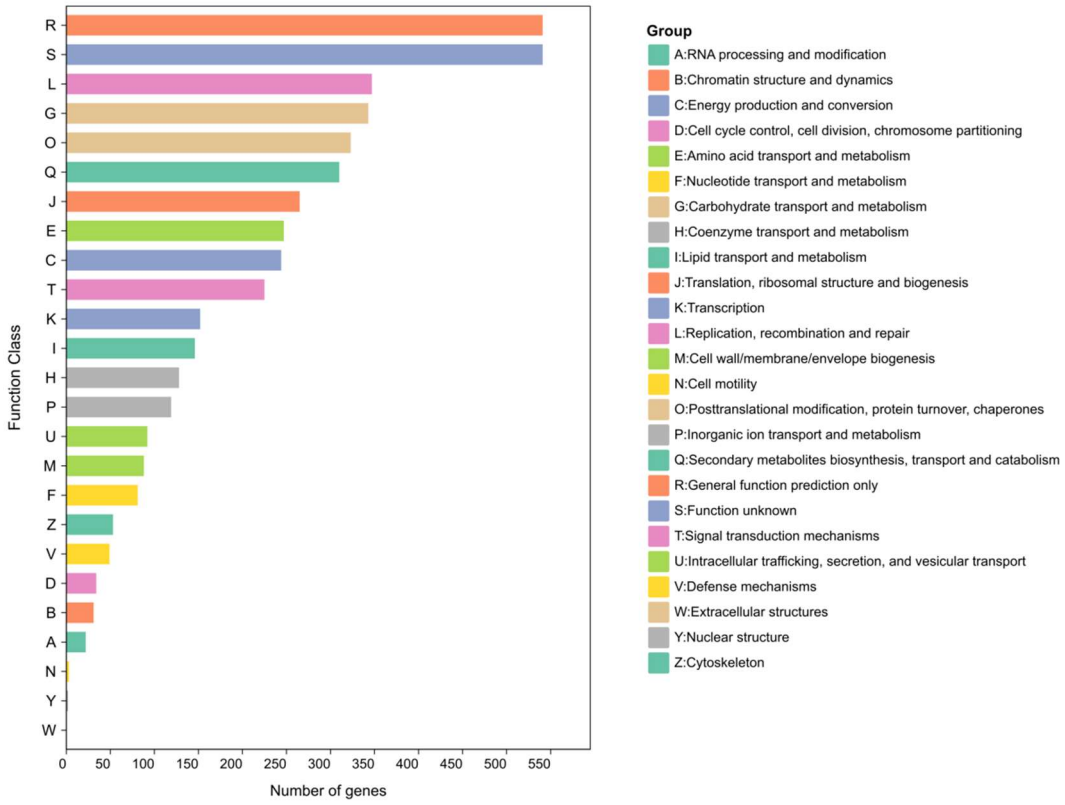



**Figure S4.** Cluster of Orthologous Groups of proteins (COG).

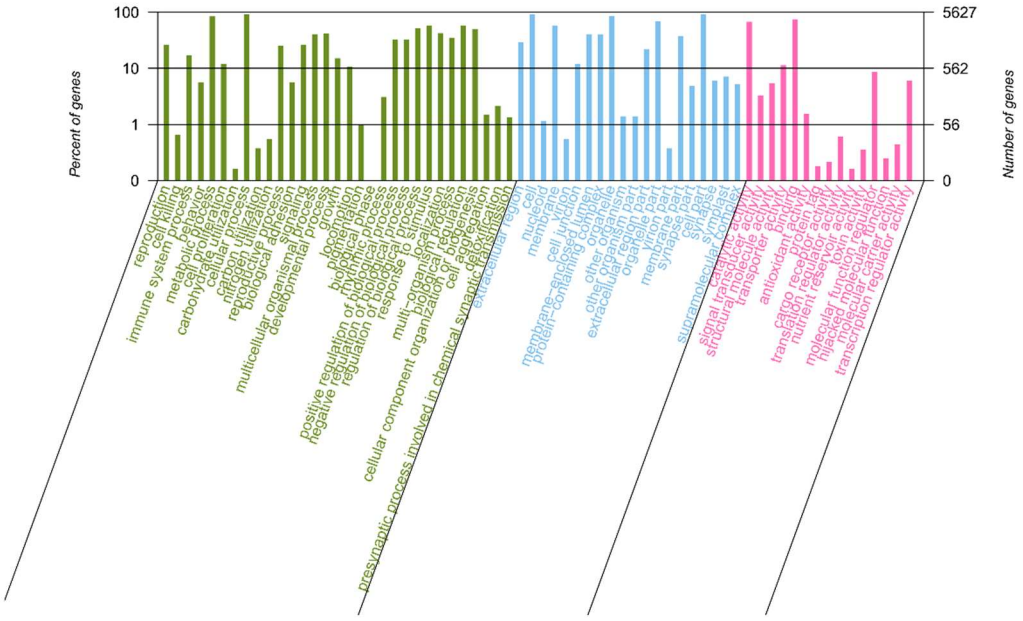



**Figure S5.** Statistical map of functional annotation classification based on GO database.

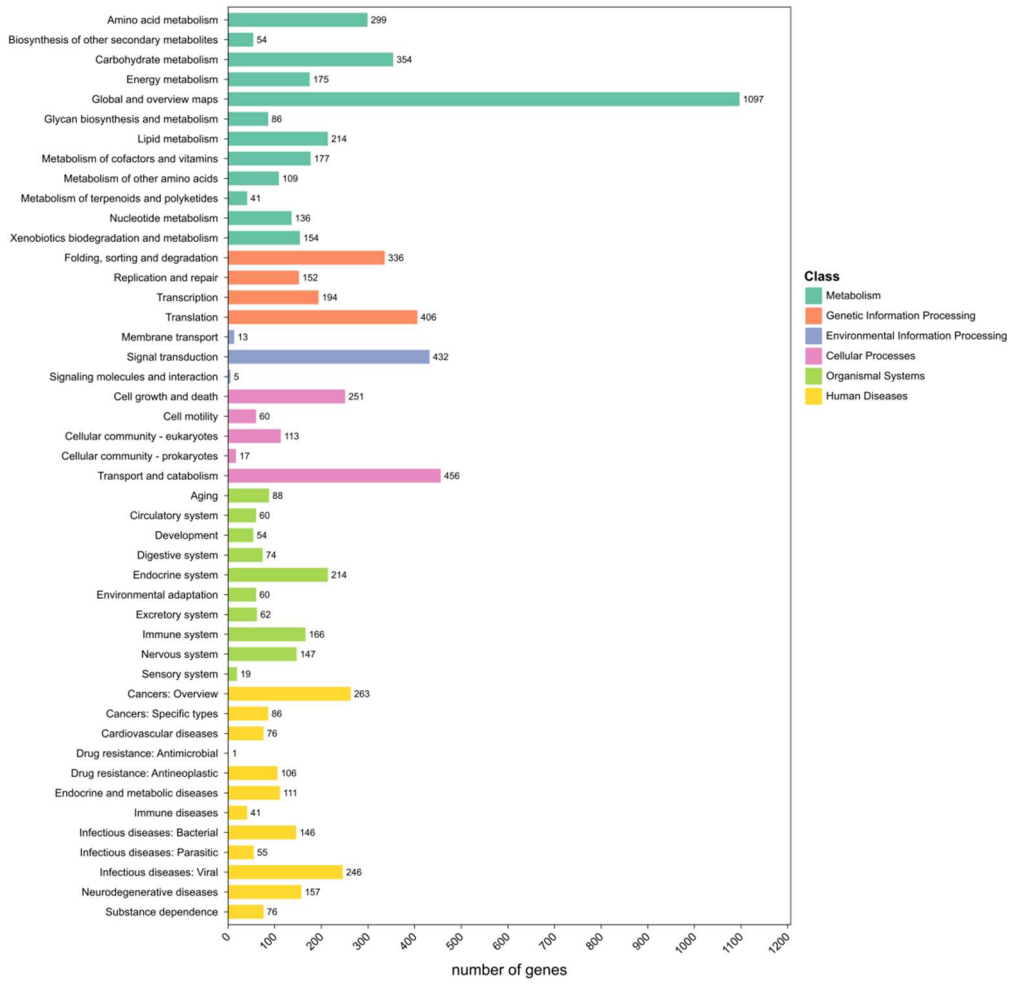



**Figure S6.** Kyoto Encyclopedia of Genes and Genomes (KEGG).

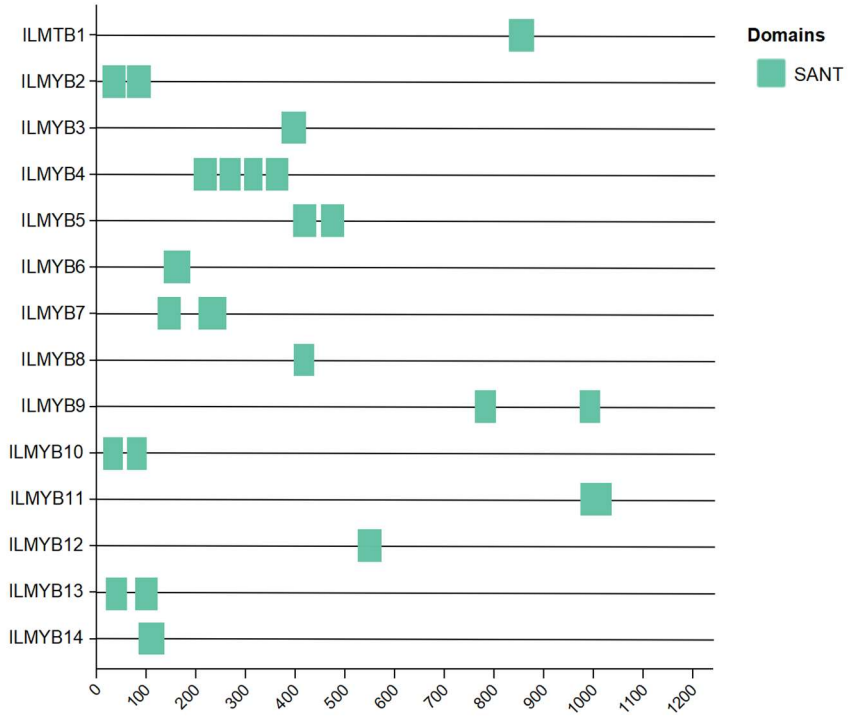



**Figure S7.** Schematic diagram of the predicted structural domains of the MYB transcription factor SANT in *I. lacteus*. The number of squares represents the number of structural domains possessed.

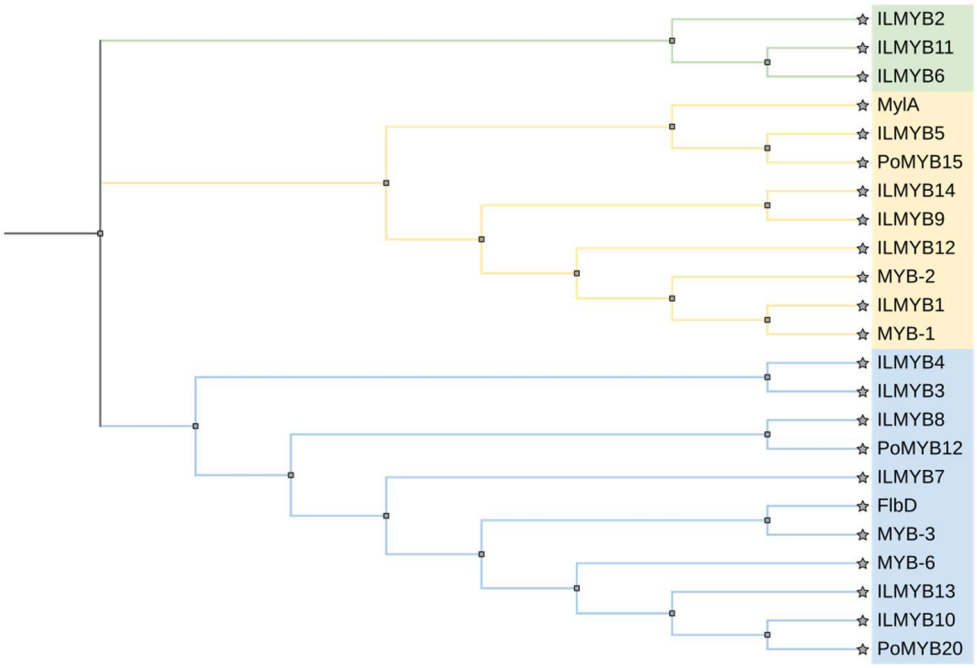



**Figure S8.** Phylogenetic tree of MYB proteins with known functions in *I. lacteus* and some fungi.