**Supplementary Table S3. DEGs detected by RNA-Seq using *A. oryzae*** *Δ****kojR* and RIB40.**

|  |  |  |  |
| --- | --- | --- | --- |
| Gene ID | Up or Down\* | FDR | Original description |
| AO090113000136 | + | 9.06E-33 | FAD-dependent oxidoreductase; present in the kojic acid biosynthetic gene cluster |
| AO090005000583 | - | 1.84E-31 | Ortholog of *A. nidulans* FGSC A4 : AN1549, *A. fumigatus* Af293 : Afu8g05600, *A. niger* CBS 513.88 : An16g07080, *Aspergillus wentii* : Aspwe1\_0187131 and *Aspergillus sydowii* : Aspsy1\_0086712 |
| AO090023000589 | - | 3.79E-23 | Ortholog of *A. niger* CBS 513.88 : An11g03810, *Neosartorya fischeri* NRRL 181 : NFIA\_063740, NFIA\_095150 and *Aspergillus wentii* : Aspwe1\_0038630, Aspwe1\_0045728 |
| AO090026000254 | - | 3.79E-23 | Ortholog(s) have pyruvate dehydrogenase (acetyl-transferring) kinase activity, role in carbon utilization, peptidyl-serine phosphorylation and mitochondrion localization |
| AO090009000166 | - | 9.46E-22 | Ortholog of *A. nidulans* FGSC A4 : AN3724, *A. fumigatus* Af293 : Afu6g12460, *A. niger* CBS 513.88 : An06g01620, *Aspergillus wentii* : Aspwe1\_0033694 and *Aspergillus sydowii* : Aspsy1\_0044118 |
| AO090012000670 | - | 3.21E-16 | Ortholog of *A. fumigatus* Af293 : Afu3g14260, *A. niger* CBS 513.88 : An09g04240, *Neosartorya fischeri* NRRL 181 : NFIA\_063040 and *Aspergillus wentii* : Aspwe1\_0038047 |
| AO090010000443 | - | 4.75E-16 | Ortholog of *Aspergillus flavus* NRRL 3357 : AFL2T\_11611 |
| AO090010000444 | - | 2.64E-15 | Predicted phosphofructokinase subunit with role in glycolysis; transcription is repressed by glucose; upregulated under hypoxic growth conditions |
| AO090102000620 | + | 7.95E-15 | Ortholog(s) have ATPase activity, coupled, chaperone binding, unfolded protein binding activity |
| AO090003000546 | + | 7.95E-15 | Ortholog(s) have DNA binding, bending, RNA polymerase I transcription factor binding and RNA polymerase I transcription factor recruiting transcription factor activity, more |
| AO090023000918 | + | 9.34E-13 | Ortholog of *A. nidulans* FGSC A4 : AN4379, *A. fumigatus* Af293 : Afu4g06670/aspf7, *Neosartorya fischeri* NRRL 181 : NFIA\_109540 and *Aspergillus wentii* : Aspwe1\_0023301 |
| AO090120000112 | + | 1.92E-12 | Ortholog(s) have IgE binding, thioredoxin peroxidase activity and extracellular region, peroxisome localization |
| AO090701000343 | - | 2.40E-11 | Ortholog of *A. nidulans* FGSC A4 : AN10977, A. fumigatus Af293 : Afu2g00790, *Aspergillus wentii* : Aspwe1\_0052113 and *Aspergillus sydowii* : Aspsy1\_0048752 |
| AO090003001182 | + | 2.89E-11 | Ortholog of *A. nidulans* FGSC A4 : AN2000/ubi4, A. fumigatus Af293 : Afu4g10350/ubiD, A. niger CBS 513.88 : An04g06510, *Aspergillus wentii* : Aspwe1\_0047475 and *Aspergillus sydowii* : Aspsy1\_0053937 |
| AO090103000022 | + | 3.62E-11 | Ortholog(s) have choline:oxygen 1-oxidoreductase activity, role in choline catabolic process and intracellular localization |
| AO090701000742 | + | 4.94E-11 | Ortholog(s) have role in cellular response to biotic stimulus, cellular response to farnesol, cellular response to heat, cellular response to hydrogen peroxide and cellular response to starvation, more |
| AO090038000465 | - | 1.67E-09 | Has domain(s) with predicted protein disulfide oxidoreductase activity |
| AO090012000495 | + | 3.53E-08 | Ortholog(s) have role in DNA methylation, global genome nucleotide-excision repair, mitotic spindle assembly checkpoint, rRNA transcription, regulation of DNA methylation, sexual sporulation resulting in formation of a cellular spore |
| AO090020000540 | + | 1.36E-07 | Ortholog(s) have cytoplasm localization |
| AO090003000458 | - | 1.71E-07 | Ortholog(s) have uracil DNA N-glycosylase activity and nucleus localization |
| AO090011000201 | - | 2.17E-07 | Ortholog of *A. nidulans* FGSC A4 : AN3215, AN7166, AN8609, *A. fumigatus* Af293 : Afu3g14210, Afu4g03360, Afu4g12510 and *A. niger* CBS 513.88 : An09g04200, An14g01840 |
| AO090113000138 | + | 4.99E-07 | Putative transporter; present in the kojic acid biosynthetic gene cluster |
| AO090003000457 | - | 1.59E-06 | Ortholog(s) have role in RNA metabolic process and cytosol, nucleus localization |
| AO090026000547 | - | 2.31E-06 | Ortholog(s) have 3'-tyrosyl-DNA phosphodiesterase activity, role in single strand break repair and nucleus localization |
| AO090120000183 | - | 3.56E-06 | Protein of unknown function |
| AO090009000715 | + | 3.56E-06 | Ortholog(s) have role in maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) and 90S preribosome, cytosol, extracellular region localization |
| AO090003000018 | + | 4.12E-06 | Hsp30-like protein; positively regulated by XlnR |
| AO090003000919 | - | 1.22E-05 | Ortholog of *A. fumigatus* Af293 : Afu1g04300, *A. niger* CBS 513.88 : An01g03130, *A. oryzae* RIB40 : AO090701000446, *Aspergillus wentii* : Aspwe1\_0025379 and *Aspergillus terreus* NIH2624 : ATET\_06531 |
| AO090038000286 | - | 1.33E-05 | Ortholog of *A. nidulans* FGSC A4 : AN9073, AN1160, A. fumigatus Af293 : Afu1g11220, Afu7g02460, *A. niger* CBS 513.88 : An12g00140 and *Aspergillus wentii* : Aspwe1\_0173751 |
| AO090102000506 | - | 1.63E-05 | Protein of unknown function |
| AO090012000521 | - | 1.69E-05 | Ortholog(s) have intracellular localization |
| AO090038000287 | + | 1.86E-05 | Ortholog(s) have guanyl-nucleotide exchange factor activity, translation elongation factor activity, role in translational elongation and cell surface, cytosol, eukaryotic translation elongation factor 1 complex, ribosome localization |
| AO090038000395 | - | 1.86E-05 | Predicted 3-phosphoglycerate kinase with role in glycolysis |
| AO090003000947 | + | 4.76E-05 | Ortholog(s) have role in protein ubiquitination, ribosome biogenesis and cytosol, extracellular region, membrane, mitochondrion, nucleolus localization |
| AO090005001291 | + | 5.59E-05 | Ortholog(s) have role in rRNA processing and 90S preribosome, box C/D snoRNP complex, small-subunit processome localization |
| AO090012000821 | - | 6.34E-05 | Ortholog of *A. nidulans* FGSC A4 : AN10356, AN0435, *A. fumigatus* Af293 : Afu1g04510, Afu3g13080, *A. niger* CBS 513.88 : An01g03600 and *A. oryzae* RIB40 : AO090003000870 |
| AO090102000351 | - | 7.92E-05 | Putative membrane protein |
| AO090102000336 | - | 0.000123 | Has domain(s) with predicted catalytic activity |
| AO090012000496 | + | 0.000151 | Histone |
| AO090009000288 | + | 0.000288 | Ortholog(s) have histone demethylase activity (H3-K9 specific), nucleosome binding activity and role in antisense RNA transcription, histone H3-K9 demethylation, positive regulation of transcription, DNA-templated, regulation of meiosis |
| AO090009000557 | + | 0.000288 | Malate synthase; upregulated under hypoxic growth conditions |
| AO090120000322 | - | 0.0003 | DNA ligase IV homolog involved in the final step of nonhomologous end joining |
| AO090003000984 | - | 0.000305 | Has domain(s) with predicted heme binding, iron ion binding, oxygen binding activity and role in oxygen transport |
| AO090011000518 | + | 0.000384 | Ortholog of *A. nidulans* FGSC A4 : AN4622, *A. fumigatus* Af293 : Afu2g02380, *A. niger* CBS 513.88 : An07g06420, *Aspergillus wentii* : Aspwe1\_0168908 and *Aspergillus sydowii* : Aspsy1\_0155773 |
| AO090010000221 | - | 0.000384 | Bacterial rhodopsin family G-protein coupled receptor-like protein |
| AO090003000150 | + | 0.000558 | Ortholog of *A. nidulans* FGSC A4 : AN3310, AN1449, AN7654, *A. fumigatus* Af293 : Afu2g01140, Afu3g00880, Afu8g04370 and *A. niger* CBS 513.88 : An15g07790, An10g00430 |
| AO090701000554 | - | 0.000558 | Heat shock protein |
| AO090005001207 | + | 0.000708 | Ortholog of *A. nidulans* FGSC A4 : AN0860, *A. fumigatus* Af293 : Afu1g15260, *A. niger* CBS 513.88 : An01g13370, *A. oryzae* RIB40 : AO090103000449 and *Aspergillus wentii* : Aspwe1\_0111296 |
| AO090026000179 | - | 0.000963 | Ortholog of *A. nidulans* FGSC A4 : AN6380, *A. fumigatus* Af293 : Afu2g13930, *A. niger* CBS 513.88 : An02g05120, *Neosartorya fischeri* NRRL 181 : NFIA\_089090 and *Aspergillus versicolor* : Aspve1\_0052622 |
| AO090009000459 | + | 0.00108 | Ortholog(s) have RNA polymerase II transcription factor binding transcription factor activity involved in negative regulation of transcription, more |
| AO090020000043 | + | 0.00112 | Has domain(s) with predicted sequence-specific DNA binding RNA polymerase II transcription factor activity, zinc ion binding activity, role in regulation of transcription, DNA-templated and nucleus localization |
| AO090020000512 | - | 0.00246 | Protein of unknown function |
| AO090003001244 | - | 0.0026 | Has domain(s) with predicted phosphoric diester hydrolase activity and role in lipid metabolic process |
| AO090023000141 | + | 0.00276 | Has domain(s) with predicted hydrolase activity |
| AO090011000309 | - | 0.00313 | Ortholog of *A. nidulans* FGSC A4 : AN7139, *A. fumigatus* Af293 : Afu4g03730, *A. niger* CBS 513.88 : An14g01430, *Aspergillus wentii* : Aspwe1\_0030342 and *Aspergillus sydowii* : Aspsy1\_0034590 |
| AO090005000428 | + | 0.0033 | Ortholog(s) have ATPase activity, translation elongation factor activity, role in translational elongation and cell surface, cytosolic ribosome, plasma membrane, yeast-form cell wall localization |
| AO090701000206 | + | 0.00353 | 4-aminobutyrate transaminase, GABA transaminase; predominantly expressed in the basal region of hyphae |
| AO090012000768 | + | 0.00353 | GATA-type transcription factor |
| AO090009000117 | - | 0.00353 | Ortholog(s) have hydrolase activity, acting on glycosyl bonds, transferase activity, transferring glycosyl groups activity and role in carbohydrate metabolic process |
| AO090009000405 | + | 0.00353 | Ortholog(s) have ATP:ADP antiporter activity |
| AO090002000060 | - | 0.00396 | Ortholog(s) have cytochrome-c oxidase activity, role in aerobic respiration, mitochondrial electron transport, cytochrome c to oxygen and mitochondrial respiratory chain complex IV localization |
| AO090026000812 | + | 0.00439 | Ortholog of *A. fumigatus* Af293 : Afu7g04020, *A. niger* CBS 513.88 : An13g00480, *Aspergillus wentii* : Aspwe1\_0429172, *Aspergillus sydowii* : Aspsy1\_0154048 and *Aspergillus terreus* NIH2624 : ATET\_04283 |
| AO090103000456 | - | 0.00527 | Has domain(s) with predicted N,N-dimethylaniline monooxygenase activity, NADP binding, flavin adenine dinucleotide binding activity and role in oxidation-reduction process |
| AO090023000570 | + | 0.00527 | Glutathione S-transferase; upregulated in *A. oryzae* and *A. nidulans* under hypoxic growth conditions |
| AO090003000805 | + | 0.00557 | Ortholog(s) have large ribosomal subunit rRNA binding activity, role in ribosomal large subunit assembly and 90S preribosome, cytosol, preribosome, large subunit precursor localization |
| AO090011000266 | - | 0.00572 | Protein of unknown function |
| AO090038000281 | - | 0.00642 | Ortholog of *A. nidulans* FGSC A4 : AN8776, *A. niger* CBS 513.88 : An08g03560, *Aspergillus wentii* : Aspwe1\_0508022, *Aspergillus sydowii* : Aspsy1\_0035009 and *Aspergillus terreus* NIH2624 : ATET\_00334 |
| AO090003000922 | + | 0.00865 | Ca2+/H+ antiporter family protein |
| AO090005000278 | - | 0.00905 | Protein of unknown function |
| AO090005001030 | - | 0.00955 | Ortholog of *Aspergillus flavus* NRRL 3357 : AFL2T\_00992 |
| AO090023000571 | + | 0.00967 | Has domain(s) with predicted flavin adenine dinucleotide binding, oxidoreductase activity, acting on CH-OH group of donors activity and role in oxidation-reduction process |
| AO090003000043 | + | 0.00969 | Ortholog of *A. nidulans* FGSC A4 : AN5764, *A. fumigatus* Af293 : Afu6g06670, *A. niger* CBS 513.88 : An18g06390, *Aspergillus wentii* : Aspwe1\_0170253 and *Aspergillus sydowii* : Aspsy1\_0030199 |
| AO090003000631 | + | 0.0109 | Ortholog(s) have glutathione peroxidase activity, glutathione transferase activity and role in cellular response to metal ion, cellular response to xenobiotic stimulus |
| AO090001000237 | + | 0.0113 | Ortholog of *A. nidulans* VeA, a global gene regulator involved in light-sensitive control of differentiation and secondary metabolism; positively regulates penicillin production of *A. oryzae* |
| AO090005001622 | - | 0.0152 | Ortholog of *A. nidulans* FGSC A4 : AN1378, *A. fumigatus* Af293 : Afu1g09030, *A. niger* CBS 513.88 : An08g00540, *Aspergillus wentii* : Aspwe1\_0024518 and *Aspergillus sydowii* : Aspsy1\_0138364 |
| AO090023000516 | + | 0.0163 | Ortholog(s) have cytosol, nucleus localization |
| AO090005001117 | - | 0.0177 | Ortholog(s) have fatty acid alpha-hydroxylase activity, role in cellular response to cadmium ion, detoxification of cadmium ion, mannosyl-inositol phosphorylceramide metabolic process and endoplasmic reticulum, membrane localization |
| AO090026000184 | - | 0.0177 | Has domain(s) with predicted calcium ion binding, calcium-dependent phospholipid binding activity |
| AO090020000513 | - | 0.0181 | Has domain(s) with predicted N-acetyltransferase activity |
| AO090011000215 | - | 0.0181 | bHLH transcription factor with a role in hyphal morphology, asexual conidiospore formation, and the promotion of sclerotial production |
| AO090102000352 | - | 0.0181 | Ortholog(s) have cytosol, mitotic spindle pole body, nucleus localization |
| AO090011000414 | - | 0.0186 | Ortholog(s) have glyceraldehyde-3-phosphate dehydrogenase (NAD+) (phosphorylating) activity and extracellular region, intracellular, membrane localization |
| AO090002000050 | + | 0.0202 | Ortholog of *A. nidulans* FGSC A4 : AN20013 and *A. fumigatus* Af293 : AfuMt00070 |
| AO090003001054 | - | 0.0204 | Ortholog(s) have Rpd3L complex, Rpd3L-Expanded complex, Rpd3S complex, cytosol localization |
| AO090011000118 | + | 0.0228 | Ribonuclease T1; secreted protein |
| AO090003000575 | - | 0.026 | Ortholog(s) have role in cellular response to drug, secondary metabolite biosynthetic process |
| AO090701000169 | - | 0.0261 | Ortholog of *A. nidulans* FGSC A4 : AN2183, *A. fumigatus* Af293 : Afu6g03800, *A. niger* CBS 513.88 : An15g01720, *Aspergillus wentii* : Aspwe1\_0035996 and *Aspergillus sydowii* : Aspsy1\_0084971 |
| AO090020000517 | + | 0.0297 | Ortholog(s) have serine-type endopeptidase activity |
| AO090005000736 | - | 0.0297 | Ortholog(s) have mitochondrion, nucleus localization |
| AO090011000634 | - | 0.0297 | Protein of unknown function |
| AO090120000432 | - | 0.0305 | Ortholog of *A. nidulans* FGSC A4 : AN6859, *A. fumigatus* Af293 : Afu5g13070, *A. niger* CBS 513.88 : An14g06090, *Aspergillus wentii* : Aspwe1\_0107789 and *Aspergillus sydowii* : Aspsy1\_0085559 |
| AO090038000466 | + | 0.0367 | Ortholog(s) have cytosol, nuclear envelope, nuclear membrane, nucleolus localization |
| AO090005000833 | + | 0.0367 | Ortholog(s) have cytosol, nucleolus localization |
| AO090120000145 | - | 0.0392 | Phosphoglycerate mutase; upregulated in *A. oryzae* and *A. nidulans* under hypoxic growth conditions |
| AO090011000656 | - | 0.0392 | Ortholog(s) have cytoplasm localization |
| AO090012000887 | + | 0.0424 | Has domain(s) with predicted FMN binding, oxidoreductase activity and role in oxidation-reduction process |
| AO090012000247 | + | 0.0451 | Protein of unknown function |
| AO090003000415 | + | 0.0451 | Aconitate hydratase |
| AO090003000750 | + | 0.0464 | Ortholog of *A. nidulans* FGSC A4 : AN2861, *A. fumigatus* Af293 : Afu3g11870, *A. niger* CBS 513.88 : An02g07700, *Aspergillus wentii* : Aspwe1\_0105255 and *Aspergillus sydowii* : Aspsy1\_0042742 |
| AO090011000308 | - | 0.0496 | Has domain(s) with predicted catalytic activity, glutamate-ammonia ligase activity and role in nitrogen compound metabolic process |

\*+, Significant increase in expression in the RIB40 compared to the *ΔkojR* strain; -, Significant decrease in expression in the RIB40 compared to the *ΔkojR* strain.

\*\* Original description is based on information provided by the Comprehensive *Aspergillus oryzae* Genome Database (CAoGD) (<<https://nribf21.nrib.go.jp/CAoGD/>>.