**Supplementary Table S2. Genes containing KojR1-70 binding region in 1000 b upstream of the initiation codon.**

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| Peak Region | Gene ID | Original description |
| Chr5\_A\_oryzae\_RIB40:4372485-4372683 | AO090113000138 | Putative transporter; present in the kojic acid biosynthetic gene cluster |
| Chr5\_A\_oryzae\_RIB40:1165268-1165466 | AO090701000448 | Has domain(s) with predicted heme binding activity |
| Chr3\_A\_oryzae\_RIB40:2038063-2038261 | AO090023000783 | Has domain(s) with predicted catalytic activity, nitronate monooxygenase activity and role in oxidation-reduction process |
| Chr3\_A\_oryzae\_RIB40:3419755-3419953 | AO090026000613 | Ortholog(s) have ATP binding, ATPase activity, metallopeptidase activity, role in protein complex assembly, proteolysis, signal peptide processing and m-AAA complex, mitochondrial inner boundary membrane localization |
| Chr2\_A\_oryzae\_RIB40:2312210-2312408 | AO090003000082 | Ortholog of Aspergillus flavus NRRL 3357 : AFL2T\_02865 |
| Chr5\_A\_oryzae\_RIB40:3813614-3813812 | AO090120000422 | Ortholog(s) have DNA-directed DNA polymerase activity, role in DNA replication initiation, telomere capping and alpha DNA polymerase:primase complex, cytosol, nuclear envelope localization |
| Chr5\_A\_oryzae\_RIB40:3813614-3813812 | AO090120000421 | Ortholog(s) have phosphatidylinositol transporter activity, role in cellular response to drug, phospholipid biosynthetic process, phospholipid transport, sterol biosynthetic process and lipid particle, plasma membrane localization |
| Chr6\_A\_oryzae\_RIB40:953-1151 | AO090020000719 | Ortholog of *A. nidulans* FGSC A4 : AN2370, AN10160, AN0323, *A. fumigatus* Af293 : Afu1g02440, Afu4g02760, *A. niger* CBS 513.88 : An01g05750, An12g09350, An13g03290 and *A. oryzae* RIB40 : AO090005000852 |
| Chr8\_A\_oryzae\_RIB40:266490-266688 | AO090103000394 | Has domain(s) with predicted transmembrane transporter activity, role in transmembrane transport and integral component of membrane localization |
| Chr6\_A\_oryzae\_RIB40:3584722-3584920 | AO090038000029 | Has domain(s) with predicted peroxiredoxin activity and role in oxidation-reduction process |
| Chr1\_A\_oryzae\_RIB40:485924-486122 | AO090009000181 | Protein of unknown function |
| Chr3\_A\_oryzae\_RIB40:4007711-4007909 | AO090026000392 | Ortholog(s) have mitochondrion localization |
| Chr4\_A\_oryzae\_RIB40:4473364-4473562 | AO090102000028 | Has domain(s) with predicted ATP binding, ATPase activity, ATPase activity, coupled to transmembrane movement of substances, nucleoside-triphosphatase activity, nucleotide binding activity and role in transport |
| Chr3\_A\_oryzae\_RIB40:1724542-1724740 | AO090023000653 | Ortholog(s) have ferrous iron binding activity, role in peptidyl-diphthamide biosynthetic process from peptidyl-histidine and cytosol, nucleus localization |
| Chr2\_A\_oryzae\_RIB40:624894-625092 | AO090001000256 | Has domain(s) with predicted DNA binding, zinc ion binding activity, role in transcription, DNA-templated and nucleus localization |
| Chr3\_A\_oryzae\_RIB40:1546518-1546716 | AO090023000583 | Ortholog of *A. nidulans* FGSC A4 : AN7052, *A. fumigatus* Af293 : Afu4g09510, Afu4g03945, *A. niger* CBS 513.88 : An14g00940, An07g04990, An04g08460 and *A. oryzae* RIB40 : AO090011000324, AO090005000036 |

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