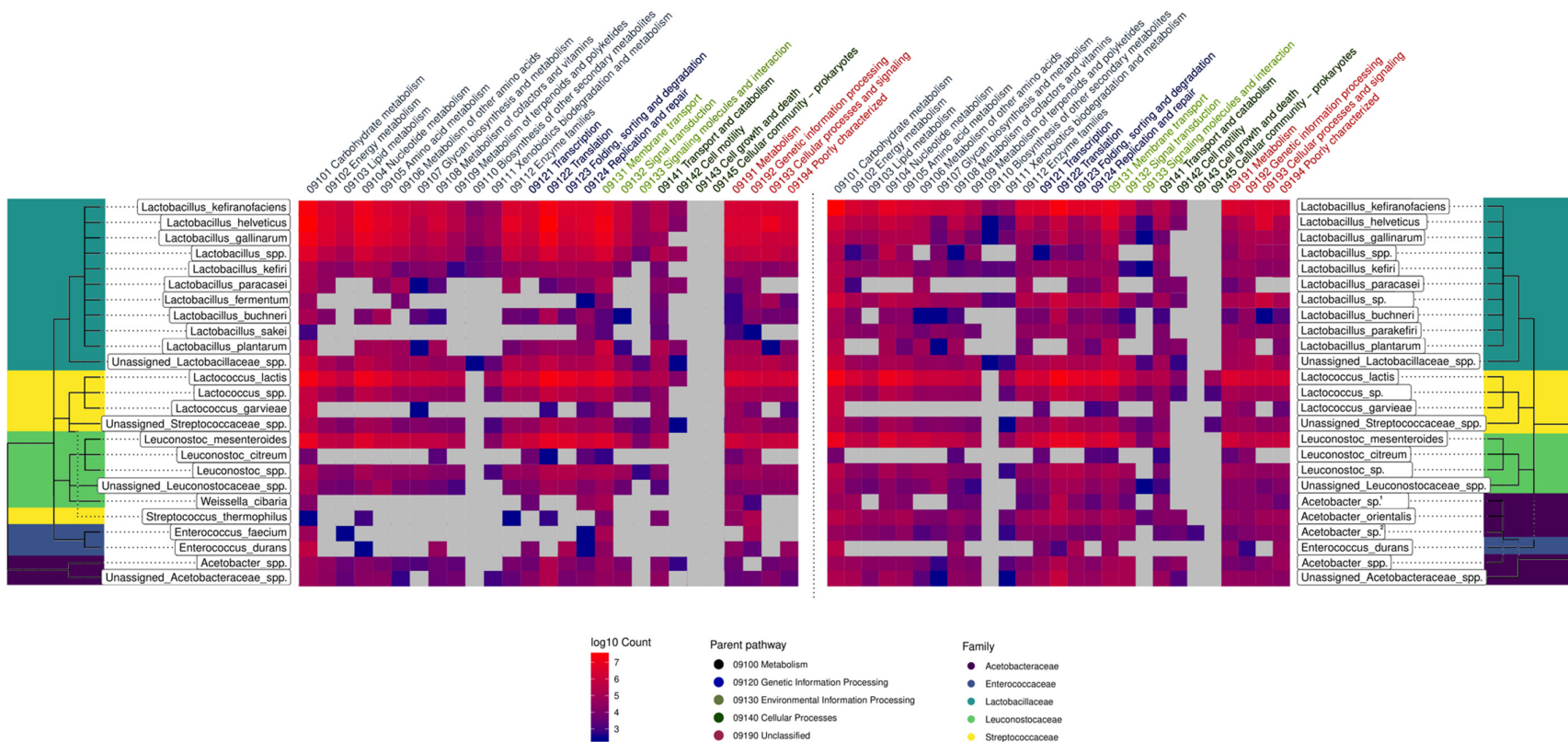


1 **Supplementary:**
2 **Metatranscriptomic Analysis of Argentinian Kefirs**
3 **Varying in Apparent Viscosity**

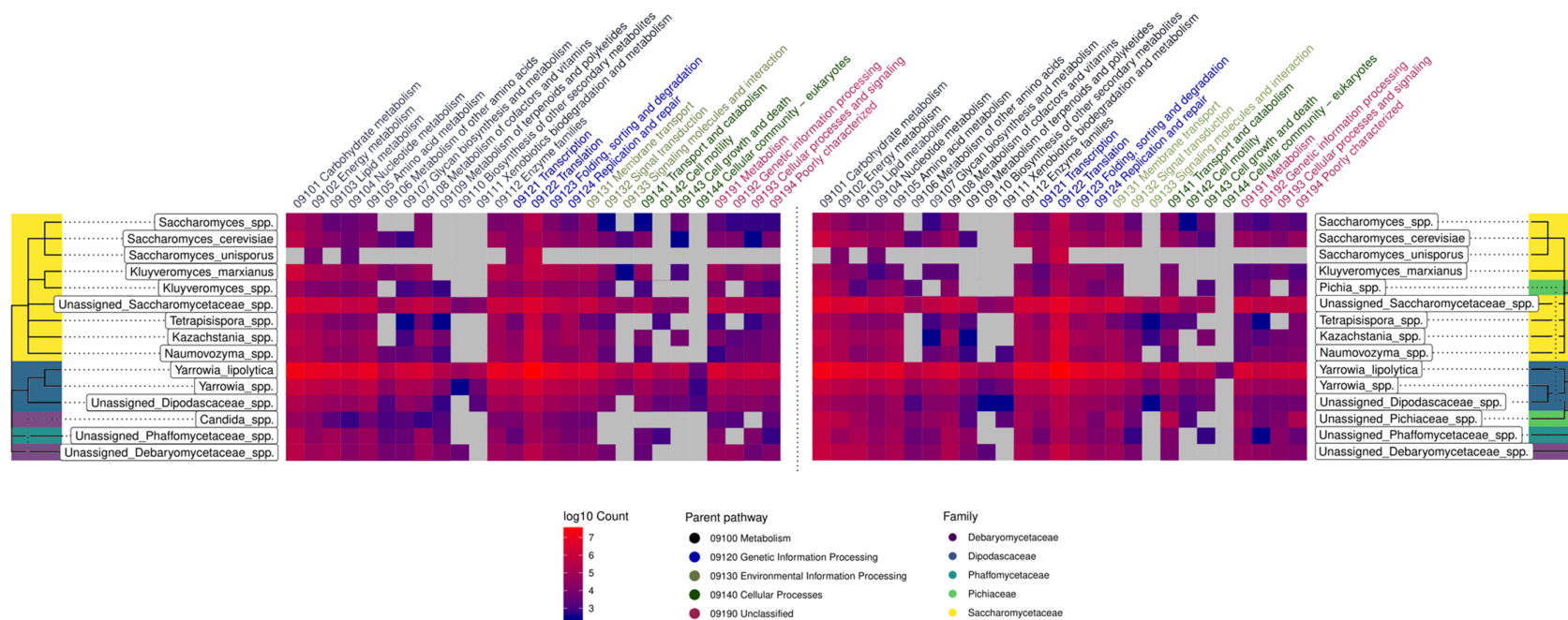
4 Diego Lisboa Rios ^{1,2}, Ana Agustina Bengoa ³, Patrícia Costa Lima da Silva ¹, César Silva Santana Moura
5 ¹, Graciela Liliana Garrote ³, Analía Graciela Abraham ^{3,4,*}, Gabriel da Rocha Fernandes ⁵, Jacques Robert
6 Nicoli ⁶, Elisabeth Neumann ⁶ and Álvaro Cantini Nunes ^{1,*}

7

8 .

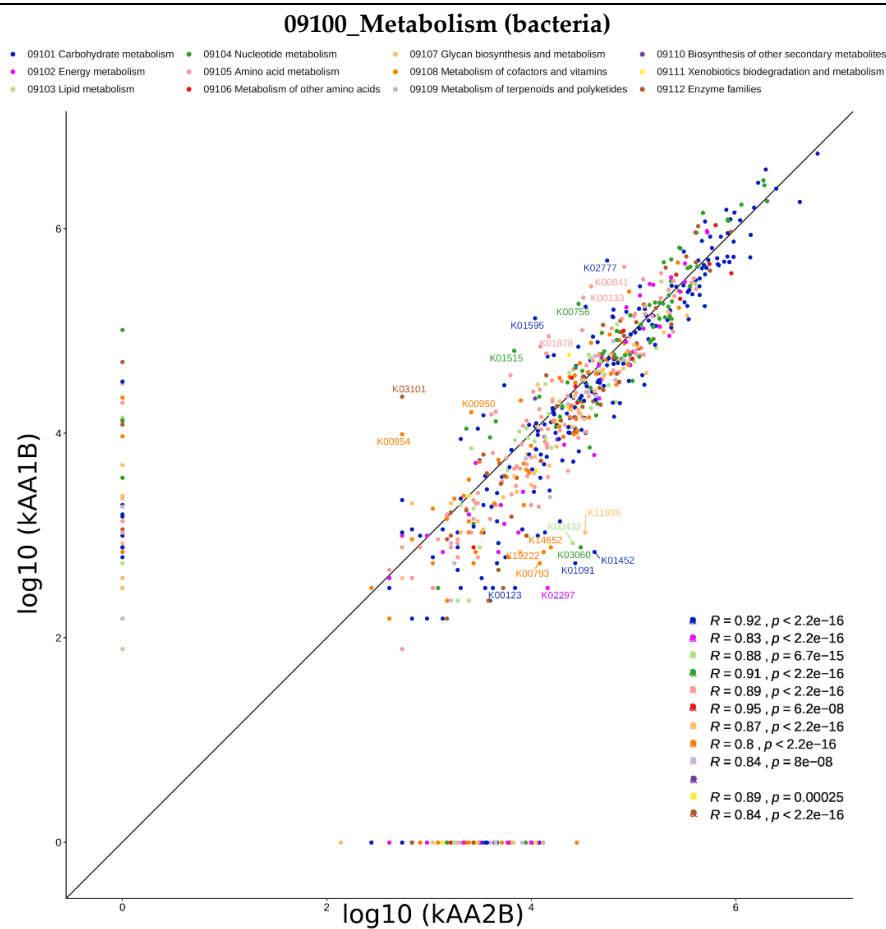


(A)

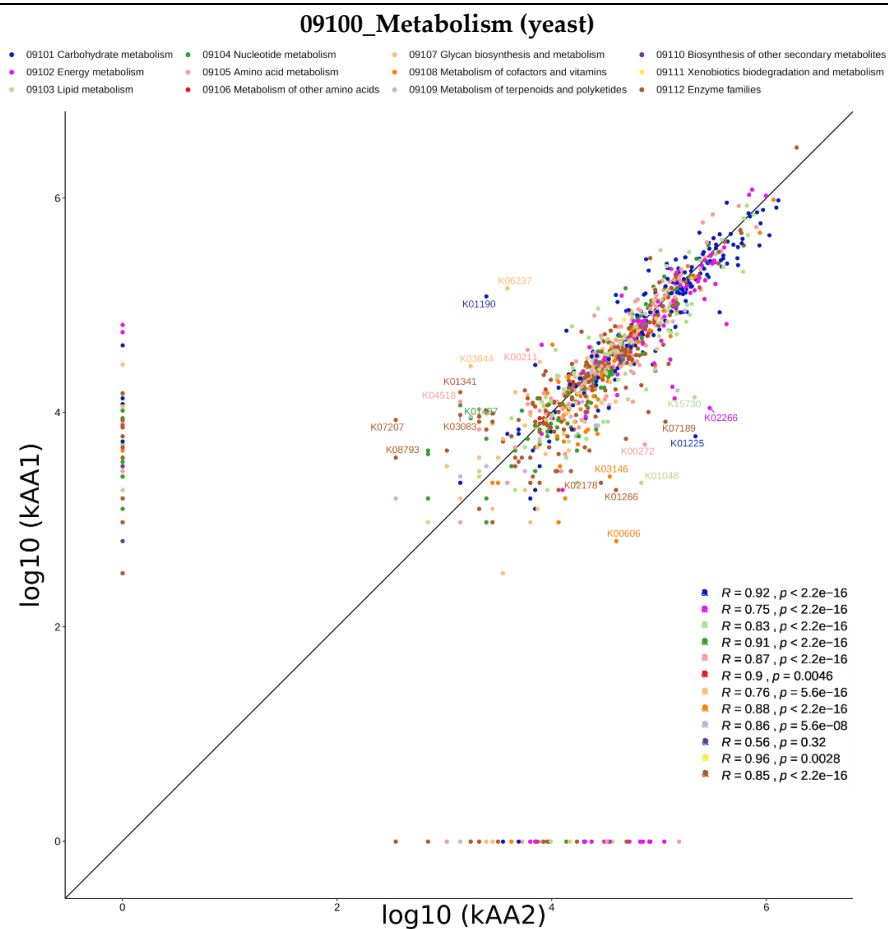


(B)

Figure S1. Relative expression levels of functional orthologs genes mapped by the KEGG database (KO) for bacteria (A) and yeasts (B) communities of milk kefir MKAA1 and MKAA2. The chart is a side-by-side comparison of the libraries, showing the path_a and path_b of the KO, a coloured cladogram for the family, and the heatmap of normalised expression in the log10 of absolute normalised reads. The bacterial and yeast heatmaps had the limit of 25 and 15 most expressed species, respectively.

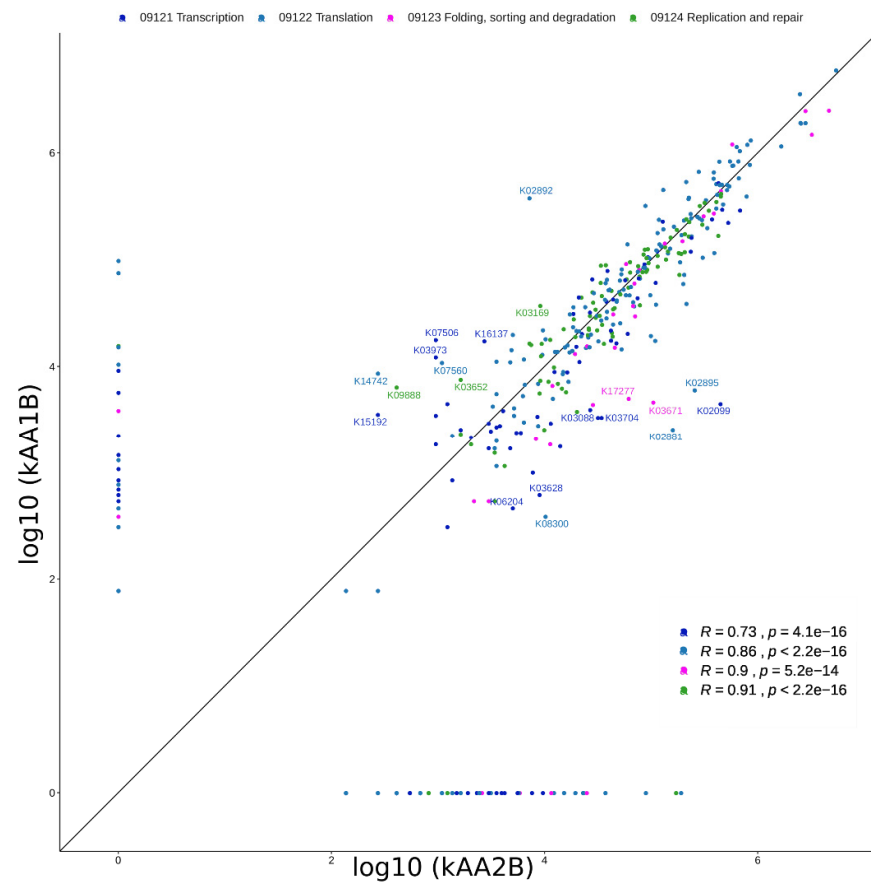


09120_Genetic Information Processing (bacteria)



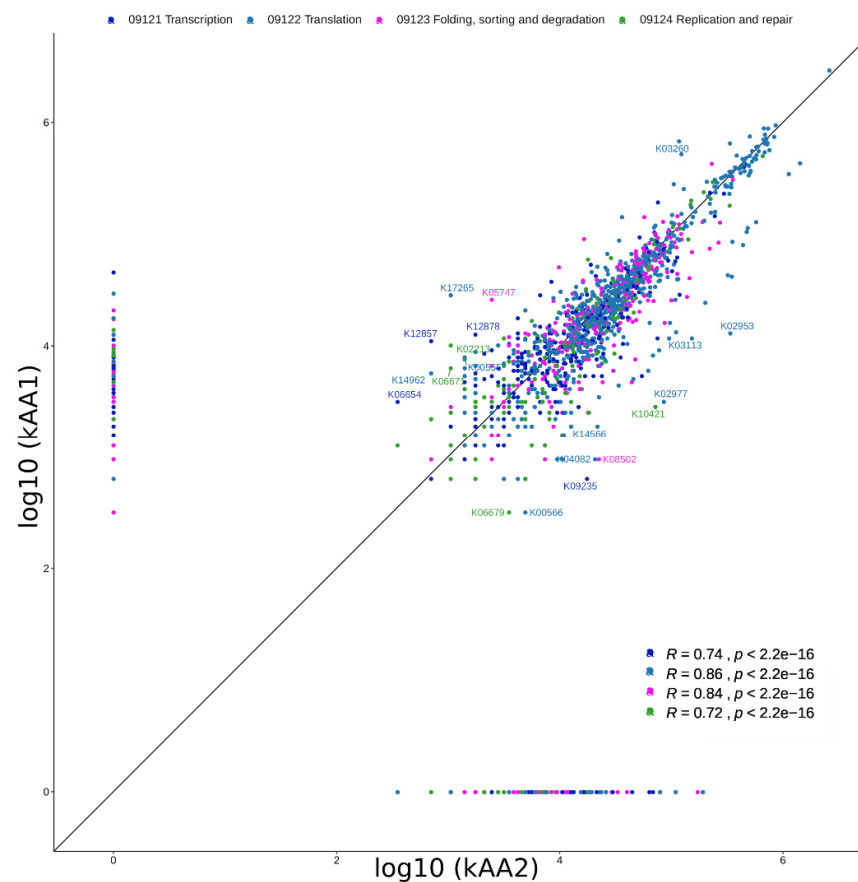
09120_Genetic Information Processing (yeast)

(A)



09130_Environmental Information Processing (bacteria)

(B)



09130_Environmental Information Processing (yeast)

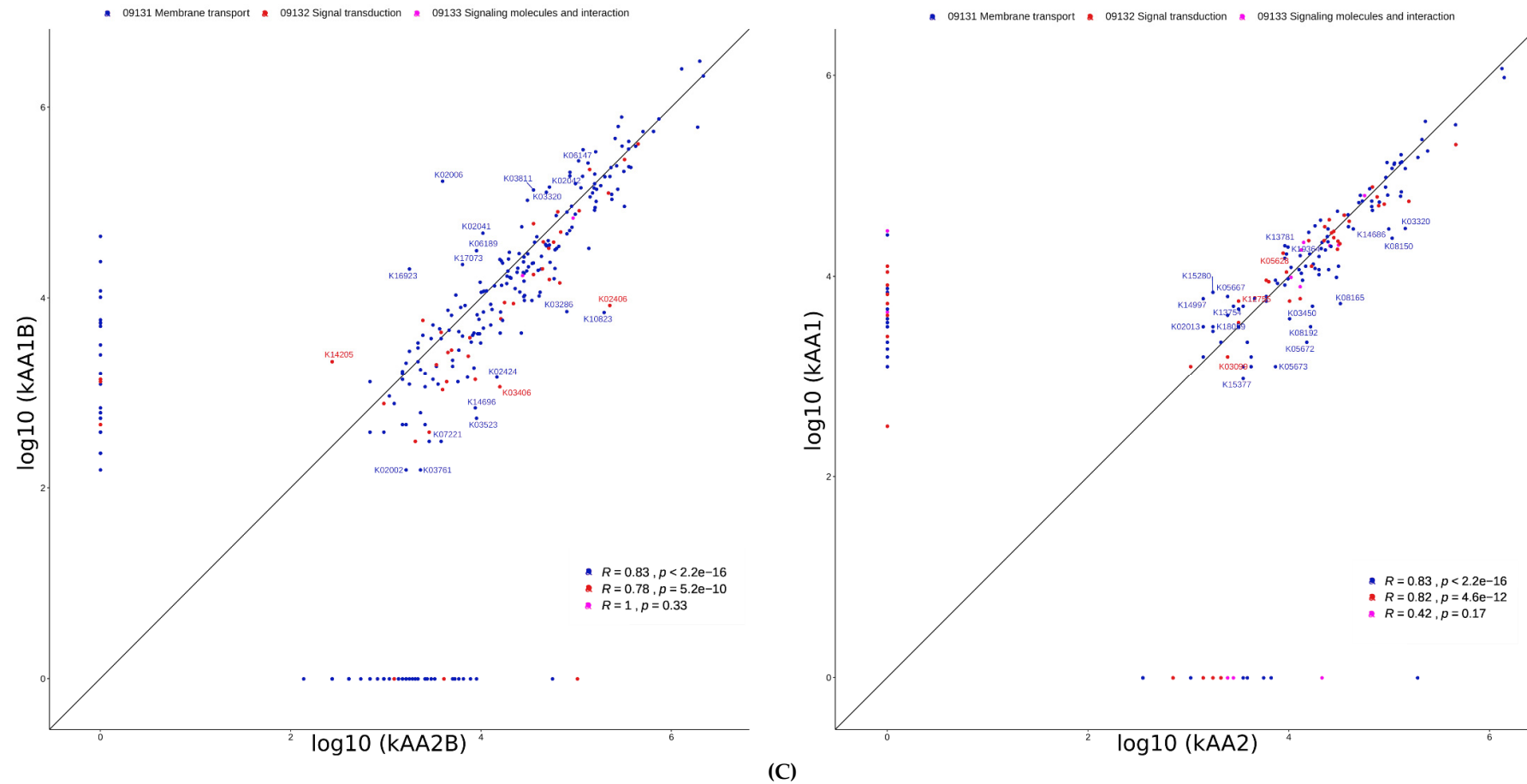
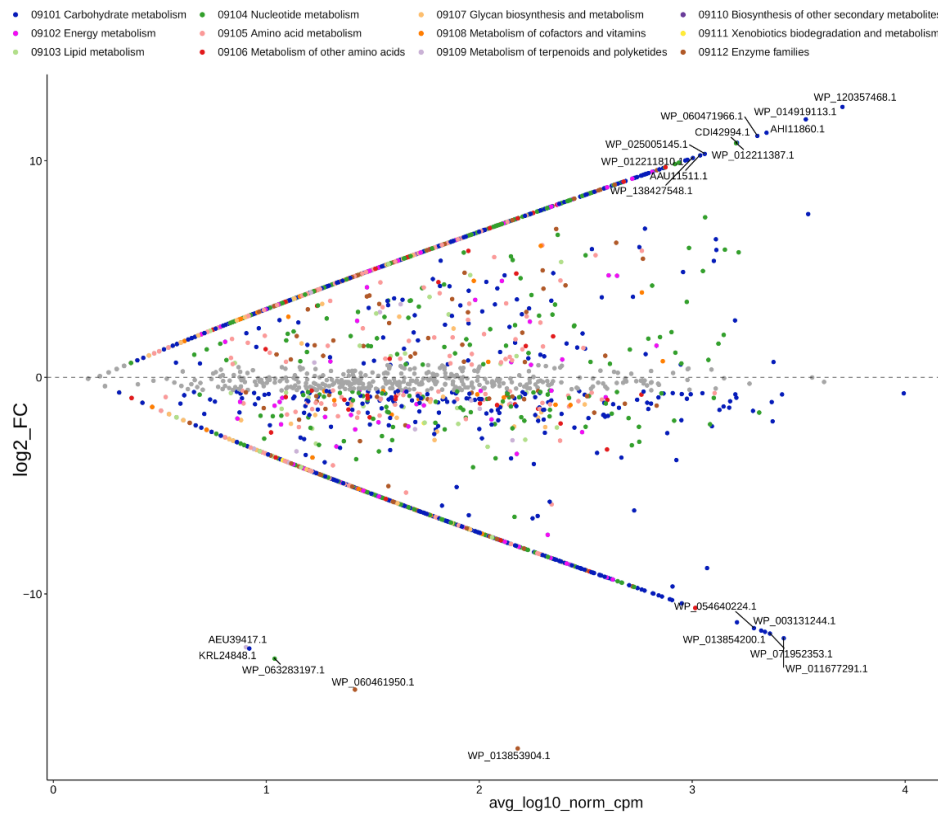


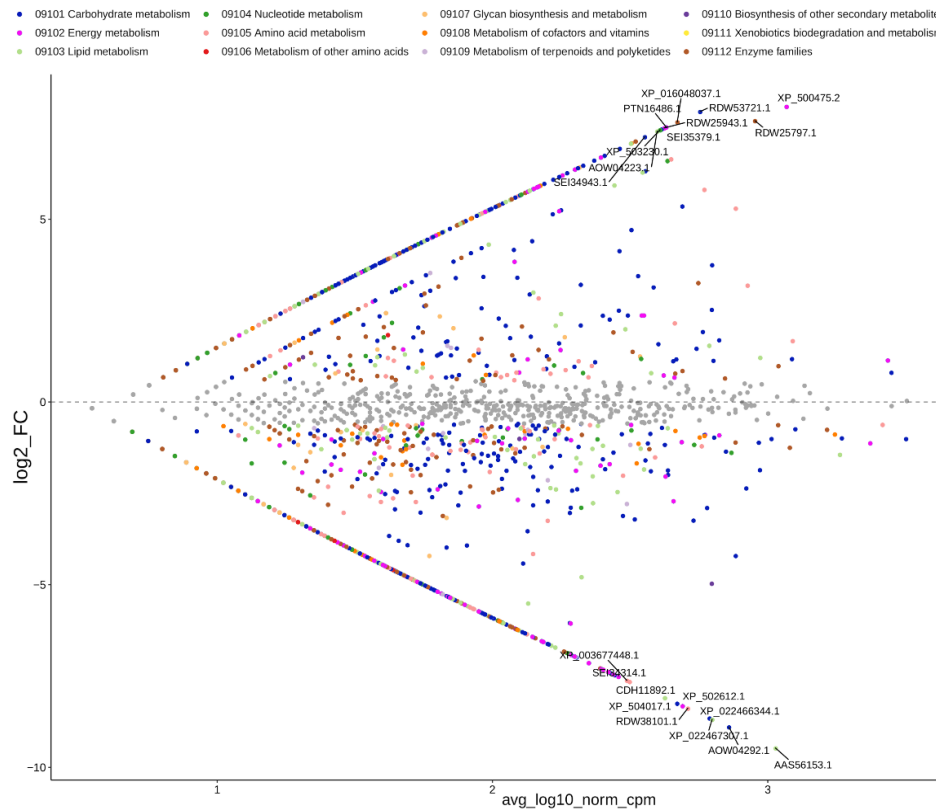
Figure S2. Pearson's correlation coefficient (R) between the relative abundance of annotated reads by the KEGG database of MKAA1 vs MKAA2 bacteria and yeasts concerning **A.** Metabolism processing, **B.** Genetic Information Processing, **C.** Environmental Information Processing.

09100_Metabolism (bacteria)



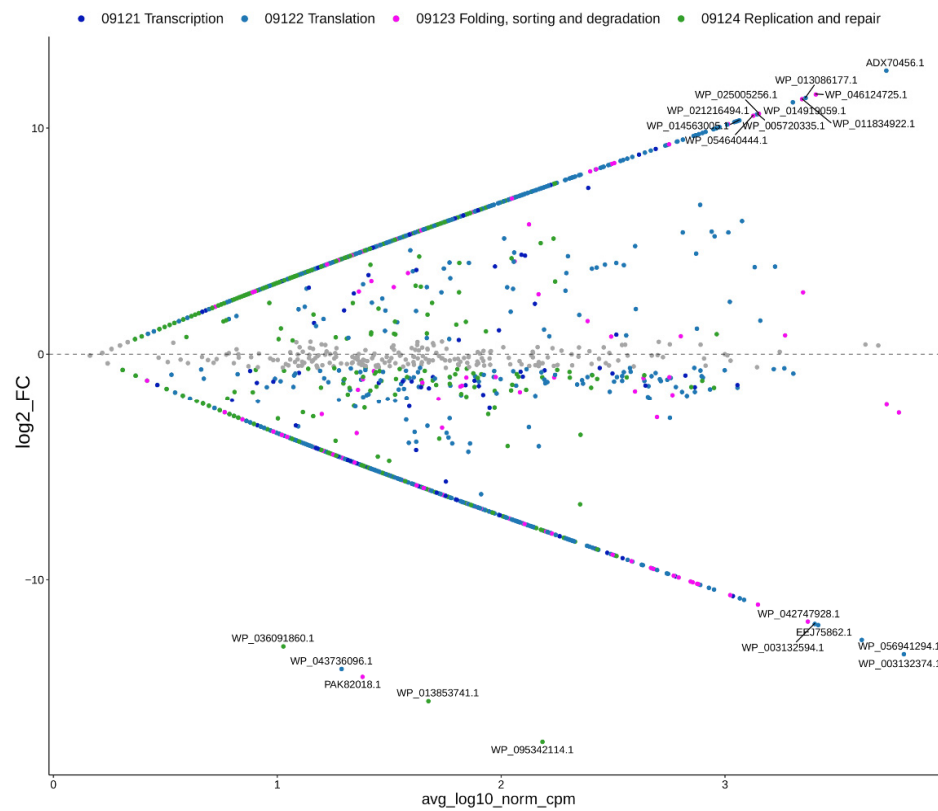
09120_Genetic Information Processing (bacteria)

09100_Metabolism (yeast)



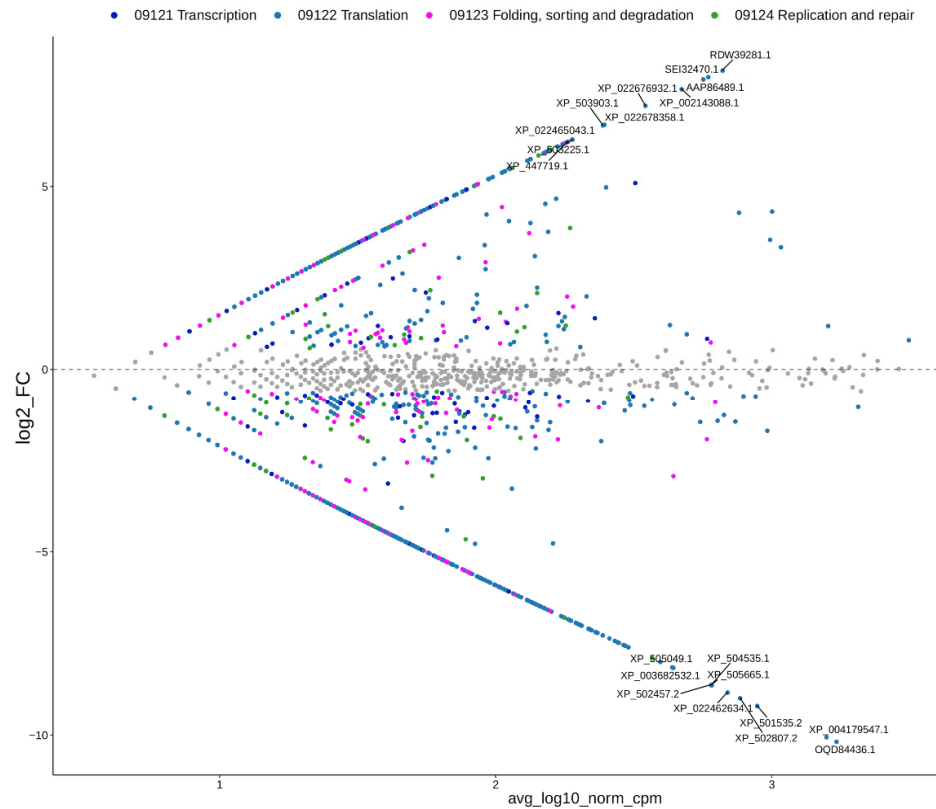
09120_Genetic Information Processing (yeast)

(A)



09130_Environmental Information Processing (bacteria)

(B)



09130_Environmental Information Processing (yeast)

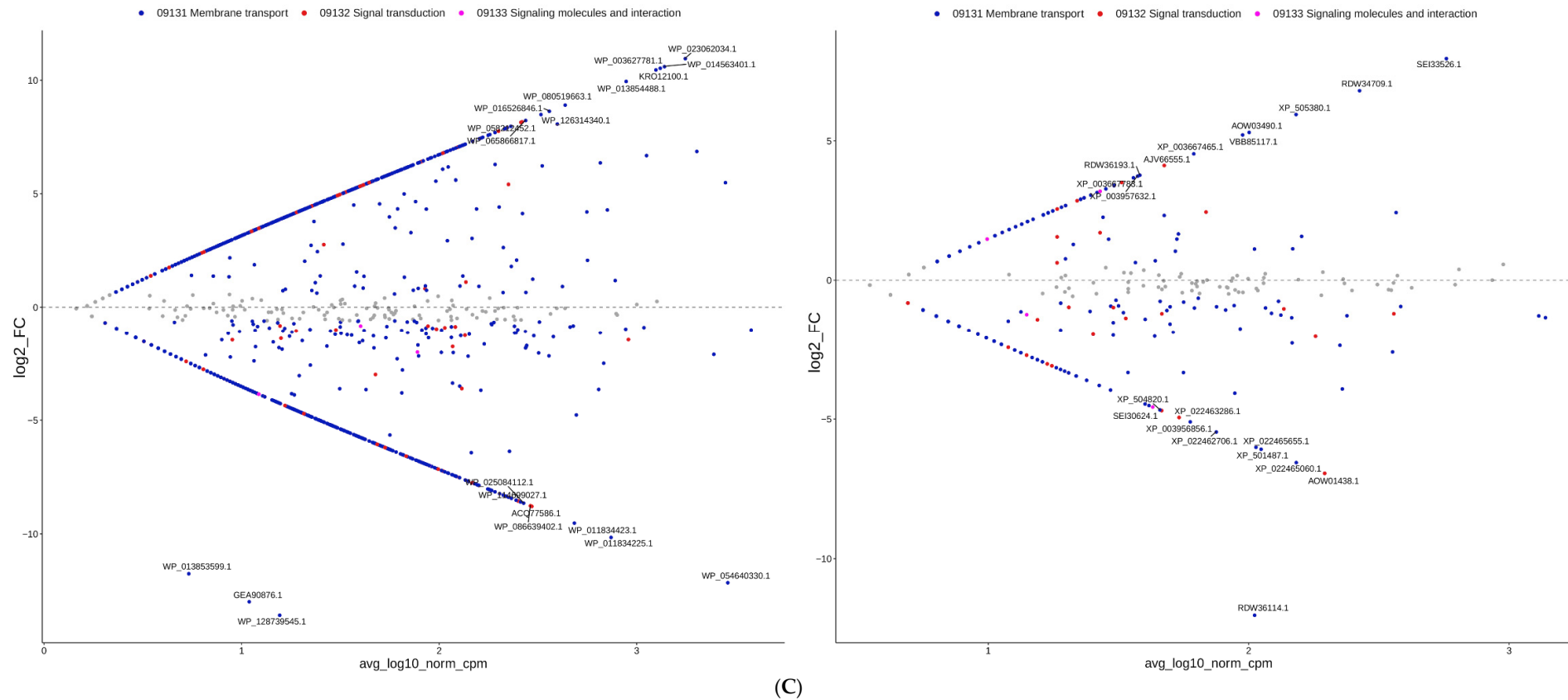


Figure S3. MA plot between the relative abundance of **MKAA1** vs **MKAA2** bacteria and yeasts annotated reads by the KEGG database concerning **A.** Metabolism Processing, **B.** Genetic Information Processing, **C.** Environmental Information Processing.

Table S1. List of KEGG ortholog entries in MKAA1 vs MKAA2 bacterial libraries.

Names	total	KO
MKAA1_Bacteria	1390	K01154 K14061 K11616 K02279 K02026 K09861 K03695 K00689 K03495
		K03737 K09952 K01989 K00997 K16925 K08724 K02048 K00924 K17073
MKAA2_Bacteria		K01736 K19222 K07040 K01372 K03686 K02028 K04567 K00931 K00297
		K11244 K01613 K09987 K02057 K00656 K01439 K00031 K08234 K07461
		K07010 K03439 K10040 K03502 K01744 K03705 K00588 K05916 K02041
		K00869 K03584 K17472 K01803 K11717 K04066 K03231 K16923 K05946
		K00823 K01657 K01662 K07171 K00549 K04771 K01783 K00114 K19268
		K01256 K18692 K01286 K05794 K15531 K09692 K01207 K03702 K03484
		K06200 K02052 K00765 K00763 K03210 K03711 K00954 K03699 K01304
		K10254 K02000 K10439 K03811 K08311 K01607 K00872 K18891 K02483
		K03572 K03216 K02598 K00788 K01092 K05847 K10120 K02808 K00849
		K01775 K15580 K00058 K09790 K01925 K01687 K02111 K06286 K01838
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		K18104 K13695 K01963 K02809 K00812 K01738 K09888 K01101 K02768
		K00298 K06966 K03722 K11085 K03703 K07738 K03830 K07720 K02434
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Table S2. List of KEGG ortholog entries KEGG orthologs in MKAA1 vs MKAA2 yeast libraries.

Names	total	KO
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MKAA2_Yeast (unique)	291	K15690 K00689 K17916 K17338 K12187 K04771 K12593 K12183 K17275 K10524 K12833 K11484 K11767 K17430 K11881 K09456 K14013 K12160 K03858 K11084 K15119 K08501 K02908 K02982 K08073 K15590 K07893 K10694 K09562 K09537 K02529 K15154 K01674 K15033 K19027 K15145 K17774 K16197 K07824 K07197 K12592 K18155 K03939 K07976 K02903 K15724 K13122 K17842 K08252 K17634 K11403 K03661 K03407 K10840 K15902 K03349 K03946 K12574 K17292 K02649 K18463 K15220 K00804 K09780 K06024 K07001 K05669 K11092 K09521 K14814 K08855 K07898 K11213 K11553 K10570 K06656 K18736 K08188 K18615 K15008 K12260 K11377 K14321 K11126 K16368 K12627 K12741 K15042 K01424 K09229 K01826 K18753 K00420 K08726 K15223 K07756 K11346 K09705 K10246 K08770 K11170 K02740 K18369 K05962 K00517 K18441 K03941 K18084 K09238 K09249 K04349 K11151 K03446 K06999 K04393 K11482 K12871 K15108 K12189 K11135 K18638 K11378 K11774 K02365 K03112 K15901 K01379 K03859 K01534 K00123 K10144 K17661 K15385 K10526 K07198 K03959 K14635 K06998 K15453 K03824 K19307 K14263 K14317 K13856 K03872 K07248 K12161 K03539 K00456 K07114 K02152 K17667 K03868 K03937 K12846 K13239 K11647 K01175 K12578 K18647 K04755 K17570 K10587 K07890 K01185 K06568 K10392 K10080 K09105 K06687 K15543 K17868 K11798 K08805 K18081 K00062 K11887 K07443 K18720 K12877 K17780 K03016 K13102 K13867 K18170 K01894 K09506 K13954 K11678 K06658 K06683 K10393 K10868 K07902 K17914 K12847 K04392 K00274 K17336 K00331 K18667 K14526 K01127 K12035 K10802 K00338 K14652 K10971 K09550 K13119 K04882 K11366 K13870 K15614 K07055 K18658 K06644 K06640 K15188 K05528 K15977 K15153 K07182 K00038 K05019 K11497 K09648 K08235 K03284 K15278 K15130 K06546 K13924 K12824 K15181 K10751 K00661 K01673 K12594 K18626 K19294 K12549 K01315 K08762 K12575 K14381 K06836 K15593 K02621 K11399

		K08509 K02971 K01263 K08966 K13171 K10669 K14543 K04422 K01273 K02678 K16570 K11651 K06130 K12478 K15219 K03498 K12754 K12345 K10740 K10297 K10276 K07541 K11247 K15451 K03012 K00537 K10739 K01250 K11276 K02143 K14853 K05545 K00412 K12399 K11558 K18177 K18188 K19202 K12626 K19371 K16946
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Table S3. KEGG orthologs exclusive in MKAA1 or MKAA2 bacteria library.

Kefir sample	Exclusive KOs
MKAA1	<p>ko00001 KEGG Orthology (KO) (137)</p> <p>K00844 HK; hexokinase [EC:2.7.1.1]</p> <p>K01812 uxaC; glucuronate isomerase [EC:5.3.1.12]</p> <p>K03079 ulaE; L-ribulose-5-phosphate 3-epimerase [EC:5.1.3.22]</p> <p>K19355 MAN; mannan endo-1,4-beta-mannosidase [EC:3.2.1.78]</p> <p>K02770 PTS-Fru-EIIC; PTS system, fructose-specific IIC component</p> <p>K05350 bglB; beta-glucosidase [EC:3.2.1.21]</p> <p>K05342 E2.4.1.64; alpha,alpha-trehalose phosphorylase [EC:2.4.1.64]</p> <p>K01209 abfA; alpha-L-arabinofuranosidase [EC:3.2.1.55]</p> <p>K07248 aldA; lactaldehyde dehydrogenase/glycolaldehyde dehydrogenase [EC:1.2.1.22 1.2.1.21]</p> <p>K01577 oxc; oxalyl-CoA decarboxylase [EC:4.1.1.8]</p> <p>K14729 FOX2; multifunctional beta-oxidation protein [EC:4.2.1.- 1.1.1.-]</p> <p>K00368 nirK; nitrite reductase (NO-forming) [EC:1.7.2.1]</p> <p>K15397 KCS; 3-ketoacyl-CoA synthase [EC:2.3.1.199]</p> <p>K11175 purN; phosphoribosylglycinamide formyltransferase 1 [EC:2.1.2.2]</p> <p>K11541 URA2; carbamoyl-phosphate synthase/aspartate carbamoyltransferase [EC:6.3.5.5 2.1.3.2]</p> <p>K02823 pyrDII; dihydroorotate dehydrogenase electron transfer subunit</p> <p>K01494 dcd; dCTP deaminase [EC:3.5.4.13]</p> <p>K09020 rutB; ureidoacrylate peracid hydrolase [EC:3.5.1.110]</p> <p>K00558 DNMT1; DNA (cytosine-5)-methyltransferase 1 [EC:2.1.1.37]</p> <p>K01523 hisE; phosphoribosyl-ATP pyrophosphohydrolase [EC:3.6.1.31]</p> <p>K11755 hisIE; phosphoribosyl-ATP pyrophosphohydrolase / phosphoribosyl-AMP cyclohydrolase [EC:3.6.1.31 3.5.4.19]</p> <p>K00743 GGTA1; N-acetyllactosaminide 3-alpha-galactosyltransferase [EC:2.4.1.87]</p> <p>K00796 folP; dihydropteroate synthase [EC:2.5.1.15]</p> <p>K03182 ubiD; 4-hydroxy-3-polyprenylbenzoate decarboxylase [EC:4.1.1.98]</p> <p>K03186 ubiX; flavin prenyltransferase [EC:2.5.1.129]</p> <p>K15889 PCME; prenylcysteine alpha-carboxyl methylesterase [EC:3.1.1.-]</p> <p>K16124 tycC; tyrocidine synthetase III</p> <p>K02947 RP-S10e; small subunit ribosomal protein S10e</p> <p>K02975 RP-S25e; small subunit ribosomal protein S25e</p> <p>K02925 RP-L3e; large subunit ribosomal protein L3e</p> <p>K03257 EIF4A; translation initiation factor 4A</p> <p>K17244 chiE; putative chitobiose transport system substrate-binding protein</p> <p>K05815 ugpE; sn-glycerol 3-phosphate transport system permease protein</p> <p>K16963 yxeO; putative S-methylcysteine transport system ATP-binding protein</p> <p>K01997 livH; branched-chain amino acid transport system permease protein</p> <p>K01995 livG; branched-chain amino acid transport system ATP-binding protein</p> <p>K11706 mtsB; iron/zinc/manganese/copper transport system ATP-binding protein</p> <p>K11051 ABC-2.CYL.P; multidrug/hemolysin transport system permease protein</p> <p>K18231 msrA; macrolide transport system ATP-binding/permease protein</p> <p>K11016 shlA; hemolysin</p> <p>K07696 nreC; two-component system, NarL family, response regulator NreC</p>

[K11624](#) ydfI; two-component system, NarL family, response regulator YdfI
[K16692](#) etk-wzc; tyrosine-protein kinase Etk/Wzc [EC:2.7.10.-]
[K07207](#) TSC2; tuberous sclerosis 2
[K10917](#) aphA; PadR family transcriptional regulator, regulatory protein AphA
[K11041](#) eta; exfoliative toxin A/B
[K05520](#) pfpl; protease I [EC:3.5.1.124]
[K03152](#) thiJ; protein deglycase [EC:3.5.1.124]
[K12941](#) abgB; aminobenzoyl-glutamate utilization protein B
[K17734](#) aprX; serine protease AprX [EC:3.4.21.-]
[K04088](#) hflK; modulator of FtsH protease HflK
[K19354](#) waaH; heptose III glucuronosyltransferase [EC:2.4.1.-]
[K12994](#) wbdB; mannosyl-N-acetyl-alpha-D-glucosaminyl-diphospho-
ditrans,octakis-undecaprenol 3-alpha-mannosyltransferase / alpha-1,3-
rhamnosyltransferase [EC:2.4.1.349 2.4.1.-]
[K17248](#) pglJ; N-acetylgalactosamine-N,N'-diacetylbaicillosaminyl-
diphospho-undecaprenol 4-alpha-N-acetylgalactosaminyltransferase
[EC:2.4.1.291]
[K16698](#) tuaG; teichuronic acid biosynthesis glycosyltransferase TuaG
[EC:2.4.-.-]
[K16702](#) amsE; amylovoran biosynthesis glycosyltransferase AmsE [EC:2.4.-.-]
]

[K13012](#) wbqP; O-antigen biosynthesis protein WbqP
[K13635](#) cbl; LysR family transcriptional regulator, cys regulon transcriptional
activator
[K02436](#) gatR; DeoR family transcriptional regulator, galactitol utilization
operon repressor
[K02081](#) agaR; DeoR family transcriptional regulator, aga operon
transcriptional repressor
[K07726](#) putative transcriptional regulator
[K11365](#) SGF73; SAGA-associated factor 73
[K14763](#) NAF1; H/ACA ribonucleoprotein complex non-core subunit NAF1
[K14835](#) NOP2; 25S rRNA (cytosine2870-C5)-methyltransferase [EC:2.1.1.310]
[K03773](#) fklB; FKBP-type peptidyl-prolyl cis-trans isomerase FklB [EC:5.2.1.8]
[K07390](#) grxD; monothiol glutaredoxin
[K11369](#) RTG2; retrograde regulation protein 2
[K02100](#) araE; MFS transporter, SP family, arabinose:H⁺ symporter
[K02429](#) fucP; MFS transporter, FHS family, L-fucose permease
[K03449](#) MFS.CP; MFS transporter, CP family, cyanate transporter
[K06199](#) crcB; fluoride exporter
[K07279](#) yfaL; autotransporter family porin
[K12684](#) esp; serine protease autotransporter [EC:3.4.21.-]
[K12685](#) ssp; subtilase-type serine protease [EC:3.4.21.-]
[K16210](#) togT; oligogalacturonide transporter
[K11735](#) gabP; GABA permease
[K16235](#) mmuP; S-methylmethionine transporter
[K03756](#) potE; putrescine:ornithine antiporter
[K03832](#) tonB; periplasmic protein TonB
[K02221](#) yggT; YggT family protein
[K02243](#) comGA; competence protein ComGA
[K02248](#) comGF; competence protein ComGF
[K17286](#) STOM; erythrocyte band 7 integral membrane protein
[K09951](#) cas2; CRISPR-associated protein Cas2
[K07452](#) mcrB; 5-methylcytosine-specific restriction enzyme B [EC:3.1.21.-]

[K06218](#) relE; mRNA interferase RelE/StbE
[K18843](#) hicB; antitoxin HicB
[K09162](#) cld; chlorite dismutase [EC:1.13.11.49]
[K00573](#) E2.1.1.77; protein-L-isoaspartate(D-aspartate) O-methyltransferase [EC:2.1.1.77]
[K03827](#) yjaB; putative acetyltransferase [EC:2.3.1.-]
[K06898](#) larB; pyridinium-3,5-biscarboxylic acid mononucleotide synthase [EC:2.5.1.143]
[K18673](#) bglK; beta-glucoside kinase [EC:2.7.1.85]
[K13932](#) mdcD; malonate decarboxylase beta subunit [EC:4.1.1.87]
[K13727](#) pdc; phenolic acid decarboxylase [EC:4.1.1.-]
[K07459](#) ybjD; putative ATP-dependent endonuclease of the OLD family
[K03458](#) TC.NCS2; nucleobase:cation symporter-2, NCS2 family
[K07214](#) fes; enterochelin esterase and related enzymes
[K07001](#) NTE family protein
[K08981](#) putative membrane protein
[K09775](#) uncharacterized protein
[K09927](#) uncharacterized protein
[K09976](#)
[K00242](#) sdhD; succinate dehydrogenase/fumarate reductase, membrane anchor subunit
[K01625](#) eda; 2-dehydro-3-deoxyphosphogluconate aldolase / (4S)-4-hydroxy-2-oxoglutarate aldolase [EC:4.1.2.14 4.1.3.42]
[K00078](#) DHDH; dihydrodiol dehydrogenase / D-xylose 1-dehydrogenase (NADP) [EC:1.3.1.20 1.1.1.179]
[K03475](#) PTS-Ula-EIIC; PTS system, ascorbate-specific IIC component
[K03881](#) ND4; NADH-ubiquinone oxidoreductase chain 4 [EC:7.1.1.2]
[K01046](#) lip; triacylglycerol lipase [EC:3.1.1.3]
[K10804](#) tesA; acyl-CoA thioesterase I [EC:3.1.2.- 3.1.2.2 3.1.1.2 3.1.1.5]
[K01753](#) dsdA; D-serine dehydratase [EC:4.3.1.18]
[K00486](#) KMO; kynurenine 3-monooxygenase [EC:1.14.13.9]
[K01935](#) bioD; dethiobiotin synthetase [EC:6.3.3.3]
[K02960](#) RP-S16e; small subunit ribosomal protein S16e
[K14327](#) UPF2; regulator of nonsense transcripts 2
[K16961](#) yxeM; putative S-methylcysteine transport system substrate-binding protein
[K17076](#) lysY; putative lysine transport system ATP-binding protein [EC:3.6.3.-]
[K01998](#) livM; branched-chain amino acid transport system permease protein
[K11332](#) nblR; two-component system, OmpR family, response regulator NblR
[K11531](#) lsrR; lsr operon transcriptional repressor
[K02054](#) ABC.SP.P1; putative spermidine/putrescine transport system permease protein
[K02393](#) flgH; flagellar L-ring protein precursor FlgH
[K09017](#) rutR; TetR/AcrR family transcriptional regulator
[K11923](#) cueR; MerR family transcriptional regulator, copper efflux regulator
[K03483](#) mtlR; mannitol operon transcriptional antiterminator
[K03493](#) bglG1; transcriptional antiterminator
[K03684](#) rnd; ribonuclease D [EC:3.1.13.5]
[K15460](#) yfiC; tRNA¹Val (adenine37-N6)-methyltransferase [EC:2.1.1.223]
[K10696](#) BRE1; E3 ubiquitin-protein ligase BRE1 [EC:2.3.2.27]
[K06212](#) focA; formate transporter

	<p>K02236 comC; leader peptidase (prepilin peptidase) / N-methyltransferase [EC:3.4.23.43 2.1.1.-]</p> <p>K07451 mcrA; 5-methylcytosine-specific restriction enzyme A [EC:3.1.21.-]</p> <p>K00984 aadA; streptomycin 3"-adenylyltransferase [EC:2.7.7.47]</p> <p>K13714 atl; bifunctional autolysin [EC:3.5.1.28 3.2.1.96]</p> <p>K07047 nfdA; N-substituted formamide deformylase [EC:3.5.1.91]</p> <p>K07038 inner membrane protein</p> <p>K06929 uncharacterized protein</p> <p>K07149 uncharacterized protein</p>
MKAA2	<p>ko00001 KEGG Orthology (KO) (351)</p> <p>K02446 glpX; fructose-1,6-bisphosphatase II [EC:3.1.3.11]</p> <p>K00128 ALDH; aldehyde dehydrogenase (NAD+) [EC:1.2.1.3]</p> <p>K00116 mqo; malate dehydrogenase (quinone) [EC:1.1.5.4]</p> <p>K01959 pycA; pyruvate carboxylase subunit A [EC:6.4.1.1]</p> <p>K17744 GalDH; L-galactose dehydrogenase [EC:1.1.1.316]</p> <p>K12373 HEXA_B; hexosaminidase [EC:3.2.1.52]</p> <p>K00102 LDHD; D-lactate dehydrogenase (cytochrome) [EC:1.1.2.4]</p> <p>K00029 E1.1.1.40; malate dehydrogenase (oxaloacetate-decarboxylating)(NADP+) [EC:1.1.1.40]</p> <p>K00050 ttuD; hydroxypyruvate reductase [EC:1.1.1.81]</p> <p>K00127 fdoI; formate dehydrogenase subunit gamma</p> <p>K01720 prpD; 2-methylcitrate dehydratase [EC:4.2.1.79]</p> <p>K01704 leuD; 3-isopropylmalate/(R)-2-methylmalate dehydratase small subunit [EC:4.2.1.33 4.2.1.35]</p> <p>K01114 plc; phospholipase C [EC:3.1.4.3]</p> <p>K02300 cyoD; cytochrome o ubiquinol oxidase subunit IV</p> <p>K02275 coxB; cytochrome c oxidase subunit II [EC:1.9.3.1]</p> <p>K15229 mauB; methylamine dehydrogenase heavy chain [EC:1.4.9.1]</p> <p>K02575 NRT; MFS transporter, NNP family, nitrate/nitrite transporter</p> <p>K04091 ssuD; alkanesulfonate monooxygenase [EC:1.14.14.5]</p> <p>K00957 cysD; sulfate adenylyltransferase subunit 2 [EC:2.7.7.4]</p> <p>K01082 cysQ; 3'(2'), 5'-bisphosphate nucleotidase [EC:3.1.3.7]</p> <p>K00641 metX; homoserine O-acetyltransferase/O-succinyltransferase [EC:2.3.1.31 2.3.1.46]</p> <p>K00769 gpt; xanthine phosphoribosyltransferase [EC:2.4.2.22]</p> <p>K00643 E2.3.1.37; 5-aminolevulinate synthase [EC:2.3.1.37]</p> <p>K01457 atzF; allophanate hydrolase [EC:3.5.1.54]</p> <p>K00145 argC; N-acetyl-gamma-glutamyl-phosphate reductase [EC:1.2.1.38]</p> <p>K00681 ggt; gamma-glutamyltranspeptidase / glutathione hydrolase [EC:2.3.2.2 3.4.19.13]</p> <p>K02535 lpxC; UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase [EC:3.5.1.108]</p> <p>K03147 thiC; phosphomethylpyrimidine synthase [EC:4.1.99.17]</p> <p>K03517 nadA; quinolinate synthase [EC:2.5.1.72]</p> <p>K00606 panB; 3-methyl-2-oxobutanoate hydroxymethyltransferase [EC:2.1.2.11]</p> <p>K03638 moaB; molybdopterin adenylyltransferase [EC:2.7.7.75]</p> <p>K01698 hemB; porphobilinogen synthase [EC:4.2.1.24]</p> <p>K01749 hemC; hydroxymethylbilane synthase [EC:2.5.1.61]</p> <p>K09882 cobS; cobaltochelatase CobS [EC:6.6.1.2]</p> <p>K02234 cobW; cobalamin biosynthesis protein CobW</p> <p>K00355 NQO1; NAD(P)H dehydrogenase (quinone) [EC:1.6.5.2]</p>

[K00919](#) ispE; 4-diphosphocytidyl-2-C-methyl-D-erythritol kinase [EC:2.7.1.148]
[K01252](#) entB; bifunctional isochorismate lyase/aryl carrier protein [EC:3.3.2.1 6.3.2.14]
[K10680](#) nemA; N-ethylmaleimide reductase [EC:1.-.-.]
[K00528](#) fpr; ferredoxin/ferredoxin---NADP+ reductase [EC:1.18.1.2 1.19.1.1]
[K03138](#) TFIIF1; transcription initiation factor TFIIF subunit alpha
[K02930](#) RP-L4e; large subunit ribosomal protein L4e
[K02866](#) RP-L10e; large subunit ribosomal protein L10e
[K03117](#) tatB; sec-independent protein translocase protein TatB
[K00970](#) pcnB; poly(A) polymerase [EC:2.7.7.19]
[K01159](#) ruvC; crossover junction endodeoxyribonuclease RuvC [EC:3.1.22.4]
[K02067](#) mlaD; phospholipid/cholesterol/gamma-HCH transport system substrate-binding protein
[K10009](#) tcyB; L-cystine transport system permease protein
[K09693](#) tagH; teichoic acid transport system ATP-binding protein [EC:7.5.2.4]
[K09810](#) lolD; lipoprotein-releasing system ATP-binding protein [EC:3.6.3.-]
[K07091](#) lptF; lipopolysaccharide export system permease protein
[K05338](#) lrgA; holin-like protein
[K07708](#) glnL; two-component system, NtrC family, nitrogen regulation sensor histidine kinase GlnL [EC:2.7.13.3]
[K11103](#) dctA; aerobic C4-dicarboxylate transport protein
[K13587](#) cckA; two-component system, cell cycle sensor histidine kinase and response regulator CckA [EC:2.7.13.3]
[K01991](#) wza; polysaccharide biosynthesis/export protein
[K01381](#) PEP4; saccharopepsin [EC:3.4.23.25]
[K01173](#) ENDOG; endonuclease G, mitochondrial
[K11931](#) pgaB; poly-beta-1,6-N-acetyl-D-glucosamine N-deacetylase [EC:3.5.1.-]
[K02408](#) fliE; flagellar hook-basal body complex protein FliE
[K11498](#) CENPE; centromeric protein E
[K13013](#) wbqV; O-antigen biosynthesis protein WbqV
[K02116](#) atpI; ATP synthase protein I
[K17737](#) dhcR; LysR family transcriptional regulator, carnitine catabolism transcriptional activator
[K06075](#) slyA; MarR family transcriptional regulator, transcriptional regulator for hemolysin
[K13643](#) iscR; Rrf2 family transcriptional regulator, iron-sulfur cluster assembly transcription factor
[K14761](#) ybcJ; ribosome-associated protein
[K15333](#) TRM3; tRNA guanosine-2'-O-methyltransferase [EC:2.1.1.34]
[K13628](#) iscA; iron-sulfur cluster assembly protein
[K04080](#) ibpA; molecular chaperone IbpA
[K10402](#) KIF20; kinesin family member 20
[K01669](#) phrB; deoxyribodipyrimidine photo-lyase [EC:4.1.99.3]
[K08994](#) yneE; ion channel-forming bestrophin family protein
[K16088](#) TC.FEV.OM1; outer-membrane receptor for ferric coprogen and ferric-rhodotorulic acid
[K07267](#) oprB; porin
[K07278](#) tamA; translocation and assembly module TamA
[K05595](#) marC; multiple antibiotic resistance protein
[K02246](#) comGD; competence protein ComGD
[K19167](#) abiQ; protein AbiQ

[K00897](#) aphA; kanamycin kinase [EC:2.7.1.95]
[K05882](#) E1.1.1.91; aryl-alcohol dehydrogenase (NADP+) [EC:1.1.1.91]
[K00327](#) POR; NADPH-ferrihemoprotein reductase [EC:1.6.2.4]
[K08255](#) cdr; CoA-disulfide reductase [EC:1.8.1.14]
[K00633](#) lacA; galactoside O-acetyltransferase [EC:2.3.1.18]
[K03828](#) yjgM; putative acetyltransferase [EC:2.3.1.-]
[K00982](#) glnE; [glutamine synthetase] adenylyltransferase / [glutamine synthetase]-adenylyl-L-tyrosine phosphorylase [EC:2.7.7.42 2.7.7.89]
[K03928](#) yvaK; carboxylesterase [EC:3.1.1.1]
[K01073](#) E3.1.2.20; acyl-CoA hydrolase [EC:3.1.2.20]
[K01144](#) E3.1.11.5; exodeoxyribonuclease V [EC:3.1.11.5]
[K03924](#) moxR; MoxR-like ATPase [EC:3.6.3.-]
[K04755](#) fdx; ferredoxin, 2Fe-2S
[K06191](#) nrdH; glutaredoxin-like protein NrdH
[K07290](#) yhjG; AsmA family protein
[K09153](#) small membrane protein
[K03670](#) mdoG; periplasmic glucans biosynthesis protein
[K06192](#) pqiB; paraquat-inducible protein B
[K06136](#) pqqB; pyrroloquinoline quinone biosynthesis protein B
[K03748](#) sanA; SanA protein
[K06923](#) uncharacterized protein
[K06940](#) uncharacterized protein
[K09806](#) uncharacterized protein
[K15633](#) gpml; 2,3-bisphosphoglycerate-independent phosphoglycerate mutase [EC:5.4.2.12]
[K00235](#) SDHB; succinate dehydrogenase (ubiquinone) iron-sulfur subunit [EC:1.3.5.1]
[K00040](#) uxuB; fructuronate reductase [EC:1.1.1.57]
[K00971](#) manC; mannose-1-phosphate guanylyltransferase [EC:2.7.7.13]
[K16148](#) glgM; alpha-maltose-1-phosphate synthase [EC:2.4.1.342]
[K01198](#) xynB; xylan 1,4-beta-xylosidase [EC:3.2.1.37]
[K01003](#) bcpA; oxaloacetate decarboxylase [EC:4.1.1.112]
[K00822](#) E2.6.1.18; beta-alanine--pyruvate transaminase [EC:2.6.1.18]
[K01659](#) prpC; 2-methylcitrate synthase [EC:2.3.3.5]
[K00336](#) nuoG; NADH-quinone oxidoreductase subunit G [EC:7.1.1.2]
[K00343](#) nuoN; NADH-quinone oxidoreductase subunit N [EC:7.1.1.2]
[K00411](#) UQCRFS1; ubiquinol-cytochrome c reductase iron-sulfur subunit [EC:7.1.1.8]
[K00405](#) ccoO; cytochrome c oxidase cbb3-type subunit II
[K15576](#) nrtA; nitrate/nitrite transport system substrate-binding protein
[K01897](#) ACSL; long-chain acyl-CoA synthetase [EC:6.2.1.3]
[K00222](#) TM7SF2; Delta14-sterol reductase [EC:1.3.1.70]
[K04097](#) HPGDS; prostaglandin-H2 D-isomerase / glutathione transferase [EC:5.3.99.2 2.5.1.18]
[K01768](#) E4.6.1.1; adenylyl cyclase [EC:4.6.1.1]
[K01428](#) ureC; urease subunit alpha [EC:3.5.1.5]
[K17723](#) preA; dihydropyrimidine dehydrogenase (NAD+) subunit PreA [EC:1.3.1.1]
[K00639](#) kbl; glycine C-acetyltransferase [EC:2.3.1.29]
[K00274](#) MAO; monoamine oxidase [EC:1.4.3.4]
[K00548](#) metH; 5-methyltetrahydrofolate--homocysteine methyltransferase [EC:2.1.1.13]
[K08963](#) mtnA; methylthioribose-1-phosphate isomerase [EC:5.3.1.23]

[K02501](#) hisH; imidazole glycerol-phosphate synthase subunit HisH [EC:4.3.2.10]
[K00285](#) dadA; D-amino-acid dehydrogenase [EC:1.4.5.1]
[K05358](#) quiA; quinate dehydrogenase (quinone) [EC:1.1.5.8]
[K03823](#) pat; phosphinothricin acetyltransferase [EC:2.3.1.183]
[K06048](#) gshA; glutamate---cysteine ligase / carboxylate-amine ligase [EC:6.3.2.2 6.3.-.-]
[K00799](#) GST; glutathione S-transferase [EC:2.5.1.18]
[K00748](#) lpxB; lipid-A-disaccharide synthase [EC:2.4.1.182]
[K03273](#) gmhB; D-glycero-D-manno-heptose 1,7-bisphosphate phosphatase [EC:3.1.3.82 3.1.3.83]
[K03276](#) waaR; UDP-glucose/galactose:(glucosyl)LPS alpha-1,2-glucosyl/galactosyltransferase [EC:2.4.1.-]
[K00946](#) thiL; thiamine-monophosphate kinase [EC:2.7.4.16]
[K00228](#) CPOX; coproporphyrinogen III oxidase [EC:1.3.3.3]
[K02188](#) cbiD; cobalt-precorrin-5B (C1)-methyltransferase [EC:2.1.1.195]
[K02226](#) cobC; alpha-ribazole phosphatase [EC:3.1.3.73]
[K12506](#) ispDF; 2-C-methyl-D-erythritol 4-phosphate cytidyltransferase / 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase [EC:2.7.7.60 4.6.1.12]
[K02523](#) ispB; octaprenyl-diphosphate synthase [EC:2.5.1.90]
[K02291](#) crtB; 15-cis-phytoene synthase [EC:2.5.1.32]
[K01061](#) E3.1.1.45; carboxymethylenebutenolidase [EC:3.1.1.45]
[K14564](#) NOP56; nucleolar protein 56
[K03075](#) secG; preprotein translocase subunit SecG
[K02726](#) PSMA2; 20S proteasome subunit alpha 2 [EC:3.4.25.1]
[K06861](#) lptB; lipopolysaccharide export system ATP-binding protein [EC:3.6.3.-]
[K12340](#) tolC; outer membrane protein
[K07799](#) mdtA; membrane fusion protein, multidrug efflux system
[K18326](#) mdtD; MFS transporter, DHA2 family, multidrug resistance protein
[K07667](#) kdpE; two-component system, OmpR family, KDP operon response regulator KdpE
[K00990](#) glnD; [protein-PII] uridylyltransferase [EC:2.7.7.59]
[K03407](#) cheA; two-component system, chemotaxis family, sensor kinase CheA [EC:2.7.13.3]
[K13590](#) dgcB; diguanylate cyclase [EC:2.7.7.65]
[K18139](#) oprM; outer membrane protein, multidrug efflux system
[K03411](#) cheD; chemotaxis protein CheD [EC:3.5.1.44]
[K02391](#) flgF; flagellar basal-body rod protein FlgF
[K02386](#) flgA; flagella basal body P-ring formation protein FlgA
[K10357](#) MYO5; myosin V
[K16308](#) CIT; citron Rho-interacting kinase [EC:2.7.11.1]
[K02482](#) two-component system
[K01284](#) dcp; peptidyl-dipeptidase Dcp [EC:3.4.15.5]
[K16135](#) dmlR; LysR family transcriptional regulator, transcriptional activator for dmlA
[K18900](#) bpeT; LysR family transcriptional regulator, regulator for bpeEF and oprC
[K08365](#) merR; MerR family transcriptional regulator, mercuric resistance operon regulatory protein
[K06168](#) miaB; tRNA-2-methylthio-N6-dimethylallyl-adenosine synthase [EC:2.8.4.3]
[K03770](#) ppiD; peptidyl-prolyl cis-trans isomerase D [EC:5.2.1.8]
[K11323](#) JMJD6; histone arginine demethylase JMJD6 [EC:1.14.11.-]

[K14160](#) imuA; protein ImuA
[K02532](#) lacY; MFS transporter, OHS family, lactose permease
[K08156](#) araJ; MFS transporter, DHA1 family, arabinose polymer utilization protein
[K08167](#) smvA; MFS transporter, DHA2 family, multidrug resistance protein
[K08217](#)
[K05802](#) mscK; potassium-dependent mechanosensitive channel
[K03559](#) exbD; biopolymer transport protein ExbD
[K16263](#) yjeH; amino acid efflux transporter
[K15726](#) czcA; cobalt-zinc-cadmium resistance protein CzcA
[K15270](#) sam; S-adenosylmethionine uptake transporter
[K02168](#) betT; choline/glycine/proline betaine transport protein
[K11747](#) kefB; glutathione-regulated potassium-efflux system protein KefB
[K03321](#) TC.SULP; sulfate permease, SulP family
[K07230](#) p19; periplasmic iron binding protein
[K03641](#) tolB; TolB protein
[K12206](#) icmB; intracellular multiplication protein IcmB [EC:7.2.4.8]
[K02479](#) two-component system
[K07062](#) fitB; toxin FitB [EC:3.1.-.-]
[K03564](#) BCP; peroxiredoxin Q/BCP [EC:1.11.1.15]
[K00664](#) ATF; alcohol O-acetyltransferase [EC:2.3.1.84]
[K16869](#) lipL; octanoyl-[GcvH]:protein N-octanoyltransferase [EC:2.3.1.204]
[K01567](#) pdaA; peptidoglycan-N-acetylmuramic acid deacetylase [EC:3.5.1.-]
[K09022](#) ridA; 2-iminobutanoate/2-iminopropanoate deaminase [EC:3.5.99.10]
[K01802](#) E5.2.1.8; peptidylprolyl isomerase [EC:5.2.1.8]
[K07443](#) ybaZ; methylated-DNA-protein-cysteine methyltransferase related protein
[K07445](#) putative DNA methylase
[K03453](#) TC.BASS; bile acid:Na⁺ symporter, BASS family
[K03457](#) TC.NCS1; nucleobase:cation symporter-1, NCS1 family
[K06287](#) maf; septum formation protein
[K07289](#) asmA; AsmA protein
[K07146](#) UPF0176 protein
[K08972](#) putative membrane protein
[K07003](#) uncharacterized protein
[K09799](#) uncharacterized protein
[K09857](#) uncharacterized protein
[K09985](#) uncharacterized protein
[K01568](#) PDC; pyruvate decarboxylase [EC:4.1.1.1]
[K00121](#) frmA; S-(hydroxymethyl)glutathione dehydrogenase / alcohol dehydrogenase [EC:1.1.1.284 1.1.1.1]
[K00241](#) sdhC; succinate dehydrogenase/fumarate reductase, cytochrome b subunit
[K00034](#) gdh; glucose 1-dehydrogenase [EC:1.1.1.47]
[K01087](#) otsB; trehalose 6-phosphate phosphatase [EC:3.1.3.12]
[K01703](#) leuC; 3-isopropylmalate/(R)-2-methylmalate dehydratase large subunit [EC:4.2.1.33 4.2.1.35]
[K00329](#) E7.1.1.2; NADH dehydrogenase [EC:7.1.1.2]
[K00342](#) nuoM; NADH-quinone oxidoreductase subunit M [EC:7.1.1.2]
[K00356](#) E1.6.99.3; NADH dehydrogenase [EC:1.6.99.3]
[K02133](#) ATPeF1B; F-type H⁺-transporting ATPase subunit beta [EC:7.1.2.2]
[K15228](#) mauA; methylamine dehydrogenase light chain [EC:1.4.9.1]

[K00370](#) narG; nitrate reductase/nitrite oxidoreductase, alpha subunit [EC:1.7.5.1 1.7.99.-]
[K00459](#) ncd2; nitronate monooxygenase [EC:1.13.12.16]
[K01725](#) cynS; cyanate lyase [EC:4.2.1.104]
[K01673](#) cynT; carbonic anhydrase [EC:4.2.1.1]
[K15555](#) ssuB; sulfonate transport system ATP-binding protein [EC:3.6.3.-]
[K10764](#) metZ; O-succinyl homoserine sulfhydrylase [EC:2.5.1.-]
[K05881](#) dhaM; phosphoenolpyruvate---glycerone phosphotransferase subunit DhaM [EC:2.7.1.121]
[K00980](#) tagD; glycerol-3-phosphate cytidyltransferase [EC:2.7.7.39]
[K13481](#) xdhA; xanthine dehydrogenase small subunit [EC:1.17.1.4]
[K01485](#) codA; cytosine/creatinine deaminase [EC:3.5.4.1 3.5.4.21]
[K03465](#) thyX; thymidylate synthase (FAD) [EC:2.1.1.148]
[K00758](#) deoA; thymidine phosphorylase [EC:2.4.2.4]
[K01920](#) gshB; glutathione synthase [EC:6.3.2.3]
[K01593](#) DDC; aromatic-L-amino-acid/L-tryptophan decarboxylase [EC:4.1.1.28 4.1.1.105]
[K13829](#) aroKB; shikimate kinase / 3-dehydroquinate synthase [EC:2.7.1.71 4.2.3.4]
[K03786](#) aroQ; 3-dehydroquinate dehydratase II [EC:4.2.1.10]
[K05364](#) pbpA; penicillin-binding protein A
[K12553](#) pbp3; penicillin-binding protein 3 [EC:3.4.-.-]
[K00953](#) FLAD1; FAD synthetase [EC:2.7.7.2]
[K03637](#) moaC; cyclic pyranopterin monophosphate synthase [EC:4.6.1.17]
[K03185](#) ubiH; 2-octaprenyl-6-methoxyphenol hydroxylase [EC:1.14.13.-]
[K00099](#) dxr; 1-deoxy-D-xylulose-5-phosphate reductoisomerase [EC:1.1.1.267]
[K06045](#) shc; squalene-hopene/tetraprenyl-beta-curcumen cyclase [EC:5.4.99.17 4.2.1.129]
[K01821](#) praC; 4-oxalocrotonate tautomerase [EC:5.3.2.6]
[K04114](#) bcrA; benzoyl-CoA reductase subunit A [EC:1.3.7.8]
[K02894](#) RP-L23e; large subunit ribosomal protein L23e
[K02942](#) RP-LP1; large subunit ribosomal protein LP1
[K04566](#) lysK; lysyl-tRNA synthetase, class I [EC:6.1.1.6]
[K03072](#) secD; preprotein translocase subunit SecD
[K11996](#) MOCS3; adenylyltransferase and sulfurtransferase [EC:2.7.7.80 2.8.1.11]
[K12605](#) CNOT2; CCR4-NOT transcription complex subunit 2
[K11960](#) urtB; urea transport system permease protein
[K07788](#) mdtB; multidrug efflux pump
[K07670](#) mtrA; two-component system, OmpR family, response regulator MtrA
[K03412](#) cheB; two-component system, chemotaxis family, protein-glutamate methyltransferase/glutaminase [EC:3.1.1.61 3.5.1.44]
[K03234](#) EEF2; elongation factor 2
[K09823](#) zur; Fur family transcriptional regulator, zinc uptake regulator
[K10918](#) aphB; LysR family transcriptional regulator, transcriptional activator AphB
[K02416](#) fliM; flagellar motor switch protein FliM
[K02557](#) motB; chemotaxis protein MotB
[K02396](#) flgK; flagellar hook-associated protein 1 FlgK
[K02390](#) flgE; flagellar hook protein FlgE
[K02394](#) flgI; flagellar P-ring protein precursor FlgI
[K02387](#) flgB; flagellar basal-body rod protein FlgB

[K18164](#) NDUFAF7; NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 7
[K13771](#) nsrR; Rrf2 family transcriptional regulator, nitric oxide-sensitive transcriptional repressor
[K15125](#) fhaB; filamentous hemagglutinin
[K01273](#) DPEP; membrane dipeptidase [EC:3.4.13.19]
[K03568](#) tldD; TldD protein
[K12995](#) wbdC; N-acetyl-alpha-D-glucosaminyl-diphospho-ditrans,octakisundecaprenol 3-alpha-mannosyltransferase / rhamnosyltransferase [EC:2.4.1.348 2.4.1.-]
[K19338](#) nac; LysR family transcriptional regulator, nitrogen assimilation regulatory protein
[K07979](#) ytrA; GntR family transcriptional regulator
[K03719](#) lrp; Lrp/AsnC family transcriptional regulator, leucine-responsive regulatory protein
[K00989](#) rph; ribonuclease PH [EC:2.7.7.56]
[K05516](#) cbpA; curved DNA-binding protein
[K03771](#) surA; peptidyl-prolyl cis-trans isomerase SurA [EC:5.2.1.8]
[K03163](#) TOP1; DNA topoisomerase I [EC:5.6.2.1]
[K17675](#) SUPV3L1; ATP-dependent RNA helicase SUPV3L1/SUV3 [EC:3.6.4.13]
[K07277](#) SAM50; outer membrane protein insertion porin family
[K17792](#) TIM54; mitochondrial import inner membrane translocase subunit TIM54
[K07152](#) SCO1_2; protein SCO1/2
[K02049](#) ABC.SN.A; NitT/TauT family transport system ATP-binding protein
[K13864](#) SLC7A2; solute carrier family 7 (cationic amino acid transporter), member 2
[K08137](#) galP; MFS transporter, SP family, galactose:H⁺ symporter
[K03288](#) citA; MFS transporter, MHS family, citrate/tricarballoylate:H⁺ symporter
[K08178](#) JEN; MFS transporter, SHS family, lactate transporter
[K08196](#) muck; MFS transporter, AAHS family, cis,cis-muconate transporter
[K03562](#) tolQ; biopolymer transport protein TolQ
[K16090](#) fiu; catecholate siderophore receptor
[K18903](#)
[K09800](#) tamB; translocation and assembly module TamB
[K15549](#) mdtN; membrane fusion protein, multidrug efflux system
[K15727](#) czcB; membrane fusion protein, cobalt-zinc-cadmium efflux system
[K02283](#) cpaF; pilus assembly protein CpaF [EC:7.4.2.8]
[K02415](#) fliL; flagellar FliL protein
[K01155](#) E3.1.21.4; type II restriction enzyme [EC:3.1.21.4]
[K19159](#) yefM; antitoxin YefM
[K19163](#) ccdB; toxin CcdB
[K07302](#) iorA; isoquinoline 1-oxidoreductase subunit alpha [EC:1.3.99.16]
[K07303](#) iorB; isoquinoline 1-oxidoreductase subunit beta [EC:1.3.99.16]
[K01536](#) ENA; P-type Na⁺/K⁺ transporter [EC:7.2.2.3 7.2.2.-]
[K06891](#) clpS; ATP-dependent Clp protease adaptor protein ClpS
[K03187](#) ureE; urease accessory protein
[K07460](#) yraN; putative endonuclease
[K07481](#) transposase
[K04754](#) mlaA; phospholipid-binding lipoprotein MlaA
[K02200](#) ccmH; cytochrome c-type biogenesis protein CcmH
[K07002](#) uncharacterized protein

[K07018](#) uncharacterized protein
[K07157](#) uncharacterized protein
[K09005](#) uncharacterized protein
[K01057](#) PGLS; 6-phosphogluconolactonase [EC:3.1.1.31]
[K01686](#) uxuA; mannonate dehydratase [EC:4.2.1.8]
[K01195](#) uidA; beta-glucuronidase [EC:3.2.1.31]
[K12972](#) ghrA; glyoxylate/hydroxypyruvate reductase [EC:1.1.1.79 1.1.1.81]
[K01433](#) purU; formyltetrahydrofolate deformylase [EC:3.5.1.10]
[K00330](#) nuoA; NADH-quinone oxidoreductase subunit A [EC:7.1.1.2]
[K00412](#) CYTB; ubiquinol-cytochrome c reductase cytochrome b subunit
[K02299](#) cyoC; cytochrome o ubiquinol oxidase subunit III
[K00390](#) cysH; phosphoadenosine phosphosulfate reductase [EC:1.8.4.8 1.8.4.10]
[K01620](#) ltaE; threonine aldolase [EC:4.1.2.48]
[K00772](#) mtaP; 5'-methylthioadenosine phosphorylase [EC:2.4.2.28]
[K00821](#) argD; acetylmethionine/N-succinyl diaminopimelate aminotransferase [EC:2.6.1.11 2.6.1.17]
[K01814](#) hisA; phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase [EC:5.3.1.16]
[K00979](#) kdsB; 3-deoxy-manno-octulosonate cytidylyltransferase (CMP-KDO synthetase) [EC:2.7.7.38]
[K00275](#) pdxH; pyridoxamine 5'-phosphate oxidase [EC:1.4.3.5]
[K01950](#) E6.3.5.1; NAD⁺ synthase (glutamine-hydrolysing) [EC:6.3.5.1]
[K01012](#) bioB; biotin synthase [EC:2.8.1.6]
[K03801](#) lipB; lipoyl(octanoyl) transferase [EC:2.3.1.181]
[K09457](#) queF; 7-cyano-7-deazaguanine reductase [EC:1.7.1.13]
[K06042](#) cobH-cbiC; precorrin-8X/cobalt-precorrin-8 methylmutase [EC:5.4.99.61 5.4.99.60]
[K00768](#) E2.4.2.21; nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase [EC:2.4.2.21]
[K18199](#) inhA; cyclohexyl-isocyanide hydratase [EC:4.2.1.103]
[K02984](#) RP-S3Ae; small subunit ribosomal protein S3Ae
[K07323](#) mlaC; phospholipid transport system substrate-binding protein
[K02471](#) bacA; vitamin B12/bleomycin/antimicrobial peptide transport system ATP-binding/permease protein
[K14981](#) chvI; two-component system, OmpR family, response regulator ChvI
[K11621](#) liaG; lia operon protein LiaG
[K02389](#) flgD; flagellar basal-body rod modification protein FlgD
[K02392](#) flgG; flagellar basal-body rod protein FlgG
[K03585](#)
[K08309](#) slt; soluble lytic murein transglycosylase [EC:4.2.2.-]
[K14261](#) alaC; alanine-synthesizing transaminase [EC:2.6.1.-]
[K02444](#) glpR; DeoR family transcriptional regulator, glycerol-3-phosphate regulon repressor
[K11475](#) vanR; GntR family transcriptional regulator, vanillate catabolism transcriptional regulator
[K02427](#) rlmE; 23S rRNA (uridine2552-2'-O)-methyltransferase [EC:2.1.1.166]
[K03536](#) rnpA; ribonuclease P protein component [EC:3.1.26.5]
[K15255](#) PIF1; ATP-dependent DNA helicase PIF1 [EC:3.6.4.12]
[K03560](#) tolR; biopolymer transport protein TolR
[K17713](#) bamB; outer membrane protein assembly factor BamB
[K04744](#) lptD; LPS-assembly protein
[K02244](#) comGB; competence protein ComGB
[K18829](#) mvpT; antitoxin VapB

K17870	nox1; NADH oxidase (H ₂ O ₂ -forming) [EC:1.6.3.3]
K05524	fdxA; ferredoxin
K03642	rlpA; rare lipoprotein A
K07217	Mn-containing catalase

Table S4. KEGG orthologs exclusive in AA1 or AA2 Yeast libraries.

Kefir sample	Exclusive KOs
MKAA1	<p>ko00001 KEGG Orthology (KO) (242)</p> <p>K17738 ARD; D-arabinitol 2-dehydrogenase [EC:1.1.1.250]</p> <p>K01218 gmuG; mannan endo-1,4-beta-mannosidase [EC:3.2.1.78]</p> <p>K10218 ligK; 4-hydroxy-4-methyl-2-oxoglutarate aldolase [EC:4.1.3.17]</p> <p>K18082 MTMR3_4; myotubularin-related protein 3/4 [EC:3.1.3.48 3.1.3.64 3.1.3.95]</p> <p>K00994 CHPT1; diacylglycerol cholinephosphotransferase [EC:2.7.8.2]</p> <p>K00720 UGCG; ceramide glucosyltransferase [EC:2.4.1.80]</p> <p>K01817 trpF; phosphoribosylanthranilate isomerase [EC:5.3.1.24]</p> <p>K05530 VAN1; mannan polymerase I complex VAN1 subunit [EC:2.4.1.-]</p> <p>K12555 pbp2A; penicillin-binding protein 2A [EC:2.4.1.129 3.4.16.4]</p> <p>K18278 THI5; pyrimidine precursor biosynthesis enzyme</p> <p>K00604 MTFMT; methionyl-tRNA formyltransferase [EC:2.1.2.9]</p> <p>K15777 DOPA; 4,5-DOPA dioxygenase extradiol [EC:1.13.11.-]</p> <p>K04127 cefD; isopenicillin-N epimerase [EC:5.1.1.17]</p> <p>K11091 SNRPA; U1 small nuclear ribonucleoprotein A</p> <p>K12822 RBM25; RNA-binding protein 25</p> <p>K12832 SF3B5; splicing factor 3B subunit 5</p> <p>K12624 LSM5; U6 snRNA-associated Sm-like protein LSM5</p> <p>K12848 SNU23; U4/U6.U5 tri-snRNP component SNU23</p> <p>K03537 POP5; ribonuclease P/MRP protein subunit POP5 [EC:3.1.26.5]</p> <p>K09517 DNAJB11; DnaJ homolog subfamily B member 11</p> <p>K10598 PPIL2; peptidyl-prolyl cis-trans isomerase-like 2 [EC:5.2.1.8]</p> <p>K14443 TOB; protein Tob/BTG</p> <p>K02327 POLD1; DNA polymerase delta subunit 1 [EC:2.7.7.7]</p> <p>K03504 POLD3; DNA polymerase delta subunit 3</p> <p>K10743 RNASEH2A; ribonuclease H2 subunit A [EC:3.1.26.4]</p> <p>K03657 uvrD; DNA helicase II / ATP-dependent DNA helicase PcrA [EC:3.6.4.12]</p> <p>K10958 RAD57; DNA repair protein RAD57</p> <p>K03165 TOP3; DNA topoisomerase III [EC:5.6.2.1]</p> <p>K10885 XRCC5; ATP-dependent DNA helicase 2 subunit 2</p> <p>K03508 POLZ2; DNA polymerase zeta [EC:2.7.7.7]</p> <p>K05668 ABCC5; ATP-binding cassette, subfamily C (CFTR/MRP), member 5</p> <p>K07678 barA; two-component system, NarL family, sensor histidine kinase BarA [EC:2.7.13.3]</p> <p>K06277 RAPGEF1; Rap guanine nucleotide exchange factor 1</p> <p>K02555 MIH1; M-phase inducer tyrosine phosphatase [EC:3.1.3.48]</p> <p>K03085 SIC1; substrate and inhibitor of the cyclin-dependent protein kinase CDC28</p> <p>K02515 HSL1; serine/threonine-protein kinase HSL1, negative regulator of Swe1 kinase [EC:2.7.11.-]</p> <p>K03114 SWE1; mitosis inhibitor protein kinase SWE1 [EC:2.7.11.1]</p> <p>K08731 BIRC5; baculoviral IAP repeat-containing protein 5</p> <p>K07191 SLC2A4; MFS transporter, SP family, solute carrier family 2 (facilitated glucose transporter), member 4</p> <p>K07207 TSC2; tuberous sclerosis 2</p> <p>K04952 CNGB1; cyclic nucleotide gated channel beta 1</p> <p>K09183 GATA4; GATA-binding protein 4</p> <p>K11825 AP2B1; AP-2 complex subunit beta-1</p> <p>K12190 VPS36; ESCRT-II complex subunit VPS36</p> <p>K10396 KIF5; kinesin family member 5</p>

[K18191](#) FMC1; ATP synthase assembly factor FMC1, mitochondrial
[K02332](#) POLG; DNA polymerase gamma 1 [EC:2.7.7.7]
[K02214](#) CDC7; cell division control protein 7 [EC:2.7.11.1]
[K02307](#) DAM1; DASH complex subunit DAM1
[K02179](#) BUB2; cell cycle arrest protein BUB2
[K06667](#) CAK1; serine/threonine-protein kinase CAK1 [EC:2.7.11.22]
[K18669](#) DYRK2_3_4; dual specificity tyrosine-phosphorylation-regulated kinase 2/3/4 [EC:2.7.12.1]
[K06678](#) YCG1; condensin complex subunit 3
[K01358](#) clpP; ATP-dependent Clp protease, protease subunit [EC:3.4.21.92]
[K12765](#) IME2; meiosis induction protein kinase IME2/SME1 [EC:2.7.11.1]
[K13709](#) ARHGAP5; Rho GTPase-activating protein 5
[K05748](#) WASF2; WAS protein family, member 2
[K02032](#) ABC.PE.A1; peptide/nickel transport system ATP-binding protein
[K10380](#) ANK; ankyrin
[K06002](#) PGA; pepsin A [EC:3.4.23.1]
[K10426](#) DCTN4; dynactin 4
[K04574](#) NEFH; neurofilament heavy polypeptide
[K17576](#) PPP1R37; protein phosphatase 1 regulatory subunit 37
[K09191](#) GTF3A; general transcription factor IIIA
[K10494](#) ZBTB7; zinc finger and BTB domain-containing protein 7
[K09407](#) FOXN; forkhead box protein N
[K15564](#) CTK2; CTD kinase subunit beta
[K16466](#) CETN3; centrin-3
[K09710](#) ybeB; ribosome-associated protein
[K15323](#) TSEN34; tRNA-splicing endonuclease subunit Sen34 [EC:4.6.1.16]
[K00685](#) ATE1; arginyl-tRNA---protein transferase [EC:2.3.2.8]
[K09568](#) FKBP1; FK506-binding protein 1 [EC:5.2.1.8]
[K11982](#) RNF115_126; E3 ubiquitin-protein ligase RNF115/126 [EC:2.3.2.27]
[K07880](#) RAB4B; Ras-related protein Rab-4B
[K16276](#) BTS; zinc finger protein-like protein
[K10301](#) FBXO21; F-box protein 21
[K11134](#) ELG1; telomere length regulation protein
[K11268](#) ESCO; N-acetyltransferase [EC:2.3.1.-]
[K11274](#) WDHD1; chromosome transmission fidelity protein 4
[K10753](#) ASF1; histone chaperone ASF1
[K11401](#) SAS2; histone acetyltransferase SAS2 [EC:2.3.1.48]
[K11402](#) SAS4; something about silencing protein 4
[K11547](#) NDC80; kinetochore protein NDC80
[K16488](#) SDCCAG8; serologically defined colon cancer antigen 8
[K16803](#) CKAP5; cytoskeleton-associated protein 5
[K17660](#) CBP1; cytochrome b pre-mRNA-processing protein 1
[K17784](#) MINOS1; mitochondrial inner membrane organizing system protein 1
[K18914](#) FDXR; adrenodoxin-NADP+ reductase [EC:1.18.1.6]
[K15283](#) SLC35E1; solute carrier family 35, member E1
[K14715](#) SLC39A9; solute carrier family 39 (zinc transporter), member 9
[K08137](#) galP; MFS transporter, SP family, galactose:H+ symporter
[K13021](#) ttuB; MFS transporter, ACS family, tartrate transporter
[K08167](#) smvA; MFS transporter, DHA2 family, multidrug resistance protein
[K10400](#) KIF15; kinesin family member 15
[K18599](#) JNM1; nuclear migration protein JNM1
[K06792](#) AGC1; aggrecan 1
[K01066](#) aes; acetyl esterase [EC:3.1.1.-]
[K13357](#) SPO1; putative meiotic phospholipase SPO1 [EC:3.1.1.-]

[K01533](#) copB; P-type Cu²⁺ transporter [EC:7.2.2.9]
[K03187](#) ureE; urease accessory protein
[K06377](#) spo0M; sporulation-control protein
[K06907](#)
[K05351](#) E1.1.1.9; D-xylulose reductase [EC:1.1.1.9]
[K00045](#) E1.1.1.67; mannitol 2-dehydrogenase [EC:1.1.1.67]
[K18982](#) gli; D-galactarolactone isomerase [EC:5.4.1.4]
[K01236](#) treZ; maltotrioglycyltrehalose trehalohydrolase [EC:3.2.1.141]
[K02267](#) COX6B; cytochrome c oxidase subunit 6b
[K02272](#) COX7C; cytochrome c oxidase subunit 7c
[K15397](#) KCS; 3-ketoacyl-CoA synthase [EC:2.3.1.199]
[K01081](#) E3.1.3.5; 5'-nucleotidase [EC:3.1.3.5]
[K01239](#) iunH; purine nucleosidase [EC:3.2.2.1]
[K01514](#) PRUNE; exopolyphosphatase [EC:3.6.1.11]
[K13761](#) PDE9; high affinity cGMP-specific 3',5'-cyclic phosphodiesterase 9 [EC:3.1.4.35]
[K16856](#) ugl; ureidoglycolate lyase [EC:4.3.2.3]
[K01493](#) comEB; dCMP deaminase [EC:3.5.4.12]
[K16330](#) pseudouridylate synthase/pseudouridine kinase [EC:4.2.1.70 2.7.1.83]
[K00547](#) mmuM; homocysteine S-methyltransferase [EC:2.1.1.10]
[K00868](#) pdxK; pyridoxine kinase [EC:2.7.1.35]
[K11414](#) SIRT4; NAD⁺-dependent protein deacetylase sirtuin 4 [EC:2.3.1.286]
[K03342](#) pabBC; para-aminobenzoate synthetase / 4-amino-4-deoxychorismate lyase [EC:2.6.1.85 4.1.3.38]
[K01934](#) MTHFS; 5-formyltetrahydrofolate cyclo-ligase [EC:6.3.3.2]
[K00355](#) NQO1; NAD(P)H dehydrogenase (quinone) [EC:1.6.5.2]
[K00485](#) FMO; dimethylaniline monooxygenase (N-oxide forming) [EC:1.14.13.8]
[K03025](#) RPC6; DNA-directed RNA polymerase III subunit RPC6
[K12839](#) SMNDC1; survival of motor neuron-related-splicing factor 30
[K12867](#) SYF1; pre-mRNA-splicing factor SYF1
[K14530](#) RPP40; ribonucleases P/MRP protein subunit RPP40 [EC:3.1.26.5]
[K14292](#) TGS1; trimethylguanosine synthase [EC:2.1.1.-]
[K13130](#) GEMIN2; gem associated protein 2
[K13137](#) STRAP; serine-threonine kinase receptor-associated protein
[K13917](#) RNGTT; mRNA-capping enzyme [EC:2.7.7.50 3.6.1.-]
[K14397](#) NUDT21; cleavage and polyadenylation specificity factor subunit 5
[K14022](#) CUE1; coupling of ubiquitin conjugation to ER degradation protein 1
[K10583](#) UBE2S; ubiquitin-conjugating enzyme E2 S [EC:2.3.2.23]
[K10609](#) CUL4; cullin 4
[K03352](#) APC5; anaphase-promoting complex subunit 5
[K03357](#) APC10; anaphase-promoting complex subunit 10
[K02335](#) polA; DNA polymerase I [EC:2.7.7.7]
[K02684](#) PRI1; DNA primase small subunit [EC:2.7.7.102]
[K03506](#) POLE4; DNA polymerase epsilon subunit 4 [EC:2.7.7.7]
[K02540](#) MCM2; DNA replication licensing factor MCM2 [EC:3.6.4.12]
[K08737](#) MSH6; DNA mismatch repair protein MSH6
[K04482](#) RAD51; DNA repair protein RAD51
[K10875](#) RAD54L; DNA repair and recombination protein RAD54 and RAD54-like protein [EC:3.6.4.-]
[K03406](#) mcp; methyl-accepting chemotaxis protein
[K17633](#) RASAL2; RAS protein activator-like 2
[K09237](#) TTK; tramtrack
[K06649](#) SWI4; regulatory protein SWI4
[K05760](#) PXN; paxillin

[K18953](#) NSMAF; factor associated with neutral sphingomyelinase activation
[K06236](#) COL1A; collagen, type I, alpha
[K12489](#) ACAP; Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein
[K12494](#) PSD; PH and SEC7 domain-containing protein
[K10089](#) M6PR; cation-dependent mannose-6-phosphate receptor
[K13349](#) MPV17L; Mpv17-like protein
[K02174](#) BR-C; broad-complex core protein
[K02557](#) motB; chemotaxis protein MotB
[K13908](#) MUC5B; mucin-5B
[K08187](#) SLC16A10; MFS transporter, MCT family, solute carrier family 16 (monocarboxylic acid transporters), member 10
[K02156](#) AUB; aubergine
[K11643](#) CHD4; chromodomain-helicase-DNA-binding protein 4 [EC:3.6.4.12]
[K08825](#) DYRK1; dual specificity tyrosine-phosphorylation-regulated kinase 1 [EC:2.7.12.1]
[K11853](#) USP34; ubiquitin carboxyl-terminal hydrolase 34 [EC:3.4.19.12]
[K06833](#) ADAM2; disintegrin and metalloproteinase domain-containing protein 2 [EC:3.4.24.-]
[K08609](#) ADAM20; disintegrin and metalloproteinase domain-containing protein 20 [EC:3.4.24.-]
[K14960](#) CXXC1; COMPASS component SPP1
[K09200](#) SP-N; transcription factor Sp, invertebrate
[K09245](#) UGA3; transcriptional activator protein UGA3
[K09366](#) POU4F; POU domain transcription factor, class 4
[K09401](#) FOXI; forkhead box protein I
[K09404](#) FOXK; forkhead box protein K
[K10778](#) ada; AraC family transcriptional regulator, regulatory protein of adaptative response / methylated-DNA-[protein]-cysteine methyltransferase [EC:2.1.1.63]
[K11758](#) RSC3_30; chromatin structure-remodeling complex subunit RSC3/30
[K03086](#) rpoD; RNA polymerase primary sigma factor
[K13210](#) FUBP; far upstream element-binding protein
[K18759](#) EDC1_2; enhancer of mRNA-decapping protein 1/2
[K18849](#) BMT2; 25S rRNA (adenine2142-N1)-methyltransferase [EC:2.1.1.286]
[K19308](#) BMT6; 25S rRNA (uracil2843-N3)-methyltransferase [EC:2.1.1.312]
[K06970](#) rlmF; 23S rRNA (adenine1618-N6)-methyltransferase [EC:2.1.1.181]
[K06927](#) DPH6; diphthine-ammonia ligase [EC:6.3.1.14]
[K18469](#) TBC1D5; TBC1 domain family member 5
[K11971](#) RNF14; E3 ubiquitin-protein ligase RNF14 [EC:2.3.2.31]
[K19041](#) RNF38_44; E3 ubiquitin-protein ligase RNF38/44 [EC:2.3.2.27]
[K16275](#) BAH; E3 ubiquitin-protein ligase BAH [EC:2.3.2.27]
[K15068](#) DIA2; protein DIA2
[K11801](#) DCAF11; DDB1- and CUL4-associated factor 11
[K10736](#) MCM10; minichromosome maintenance protein 10
[K11269](#) CTF18; chromosome transmission fidelity protein 18
[K11271](#) DSCC1; sister chromatid cohesion protein DCC1
[K11320](#) EP400; E1A-binding protein p400 [EC:3.6.4.-]
[K11548](#) NUF2; kinetochore protein Nuf2
[K11566](#) ASK1; DASH complex subunit ASK1
[K09888](#) zapA; cell division protein ZapA
[K15077](#) ELA1; elongin-A
[K17668](#) PET122; protein PET122, mitochondrial
[K17673](#) ATP22; mitochondrial translation factor ATP22

	<p>K13859 SLC4A8; solute carrier family 4 (sodium bicarbonate cotransporter), member 8</p> <p>K17471 SULTR3; sulfate transporter 3</p> <p>K03549 kup; KUP system potassium uptake protein</p> <p>K15547 mdtO; multidrug resistance protein MdtO</p> <p>K03832 tonB; periplasmic protein TonB</p> <p>K08470 OA1; ocular albinism type 1 protein</p> <p>K19069 CDH; cellobiose dehydrogenase (acceptor) [EC:1.1.99.18]</p> <p>K06871</p> <p>K01452 E3.5.1.41; chitin deacetylase [EC:3.5.1.41]</p> <p>K03881 ND4; NADH-ubiquinone oxidoreductase chain 4 [EC:7.1.1.2]</p> <p>K12861 BCAS2; pre-mRNA-splicing factor SPF27</p> <p>K13114 PNN; pinin</p> <p>K03660 OGG1; N-glycosylase/DNA lyase [EC:3.2.2.- 4.2.99.18]</p> <p>K10901 BLM; bloom syndrome protein [EC:3.6.4.12]</p> <p>K05746 ENAH; enabled</p> <p>K11246 SHO1; SHO1 osmosensor</p> <p>K06228 FU; fused [EC:2.7.11.1]</p> <p>K00476 ASPH; aspartate beta-hydroxylase [EC:1.14.11.16]</p> <p>K07877 RAB2A; Ras-related protein Rab-2A</p> <p>K10416 DYNC1LI; dynein light intermediate chain 1, cytosolic</p> <p>K08342 ATG4; cysteine protease ATG4 [EC:3.4.22.-]</p> <p>K09243 UME6; transcriptional regulatory protein UME6</p> <p>K02608 ORC6; origin recognition complex subunit 6</p> <p>K12577 FOB1; DNA replication fork-blocking protein FOB1</p> <p>K06663 DDC1; DNA damage checkpoint protein</p> <p>K13412 CPK; calcium-dependent protein kinase [EC:2.7.11.1]</p> <p>K17387 KIF23; kinesin family member 23</p> <p>K10955 MUC2; mucin-2</p> <p>K04573 NEF3; neurofilament medium polypeptide (neurofilament 3)</p> <p>K01377 PGC; gastricsin [EC:3.4.23.3]</p> <p>K09413 HCM1; forkhead transcription factor HCM1</p> <p>K13184 DHX9; ATP-dependent RNA helicase A [EC:3.6.4.13]</p> <p>K06178 rluB; 23S rRNA pseudouridine2605 synthase [EC:5.4.99.22]</p> <p>K15463 RIT1; tRNA A64-2'-O-ribosylphosphate transferase [EC:2.4.2.-]</p> <p>K01056 PTH1; peptidyl-tRNA hydrolase, PTH1 family [EC:3.1.1.29]</p> <p>K09512 DNAJB6; DnaJ homolog subfamily B member 6</p> <p>K17707 DOCK5; dedicator of cytokinesis protein 5</p> <p>K10734 GINS3; GINS complex subunit 3</p> <p>K11344 EAF6; chromatin modification-related protein EAF6</p> <p>K11515 INCENP; inner centromere protein</p> <p>K11557 SPC24; kinetochore protein Spc24, fungi type</p> <p>K17677 IRC3; ATP-dependent helicase IRC3 [EC:3.6.4.-]</p> <p>K17715 SAM35; sorting and assembly machinery component 35</p> <p>K15123 SLC25A45_47; solute carrier family 25, member 45/47</p> <p>K06221 dkgA; 2,5-diketo-D-gluconate reductase A [EC:1.1.1.346]</p> <p>K07401 selenoprotein W-related protein</p>
MKAA2	<p>ko00001 KEGG Orthology (KO) (291)</p> <p>K00689 E2.4.1.5; dextransucrase [EC:2.4.1.5]</p> <p>K03939 NDUFS6; NADH dehydrogenase (ubiquinone) Fe-S protein 6</p> <p>K03946 NDUF2; NADH dehydrogenase (ubiquinone) 1 alpha subcomplex subunit 2</p> <p>K00420 QCR10; ubiquinol-cytochrome c reductase subunit 10</p>

[K03661](#) ATPeV0B; V-type H⁺-transporting ATPase 21kDa proteolipid subunit
[K01674](#) cah; carbonic anhydrase [EC:4.2.1.1]
[K10246](#) ELO3; fatty acid elongase 3 [EC:2.3.1.199]
[K16368](#) DGK1; diacylglycerol kinase (CTP) [EC:2.7.1.174]
[K08726](#) EPHX2; soluble epoxide hydrolase / lipid-phosphate phosphatase [EC:3.3.2.10 3.1.3.76]
[K01424](#) E3.5.1.1; L-asparaginase [EC:3.5.1.1]
[K01826](#) hpaF; 5-carboxymethyl-2-hydroxy-muconate isomerase [EC:5.3.3.10]
[K03858](#) PIGH; phosphatidylinositol N-acetylglucosaminyltransferase subunit H
[K10524](#) NRK1_2; nicotinamide/nicotinate riboside kinase [EC:2.7.1.22 2.7.1.173]
[K00804](#) GGPS1; geranylgeranyl diphosphate synthase, type III [EC:2.5.1.1 2.5.1.10 2.5.1.29]
[K17842](#) carT; torulene dioxygenase [EC:1.13.11.59]
[K07824](#) CYP53A1; benzoate 4-monooxygenase [EC:1.14.14.92]
[K11092](#) SNRPA1; U2 small nuclear ribonucleoprotein A'
[K12833](#) SF3B14; pre-mRNA branch site protein p14
[K12627](#) LSM8; U6 snRNA-associated Sm-like protein LSM8
[K12741](#) HNRNPA1_3; heterogeneous nuclear ribonucleoprotein A1/A3
[K02982](#) RP-S3; small subunit ribosomal protein S3
[K02903](#) RP-L28e; large subunit ribosomal protein L28e
[K02908](#) RP-L30e; large subunit ribosomal protein L30e
[K12160](#) SUMO; small ubiquitin-related modifier
[K14321](#) NUPL2; nucleoporin-like protein 2
[K09521](#) DNAJC1; DnaJ homolog subfamily C member 1
[K14013](#) UBX2; UBX domain-containing protein 2
[K09562](#) HSPBP1; hsp70-interacting protein
[K08501](#) STX8; syntaxin 8
[K10570](#) ERCC8; DNA excision repair protein ERCC-8
[K03349](#) APC2; anaphase-promoting complex subunit 2
[K02740](#) PSMB8; 20S proteasome subunit beta 8 [EC:3.4.25.1]
[K12592](#) C1D; exosome complex protein LRP1
[K12593](#) MPHOSPH6; M-phase phosphoprotein 6, animal type
[K12574](#) mj; ribonuclease J [EC:3.1.-.-]
[K10840](#) CETN2; centrin-2
[K11084](#) phnT; 2-aminoethylphosphonate transport system ATP-binding protein
[K05669](#) ABCC6; ATP-binding cassette, subfamily C (CFTR/MRP), member 6
[K04771](#) degP; serine protease Do [EC:3.4.21.107]
[K03407](#) cheA; two-component system, chemotaxis family, sensor kinase CheA [EC:2.7.13.3]
[K17634](#) RASAL3; RAS protein activator-like 3
[K02649](#) PIK3R1_2_3; phosphoinositide-3-kinase regulatory subunit alpha/beta/delta
[K16197](#) YWHAB_Q_Z; 14-3-3 protein beta/theta/zeta
[K11213](#) STE2; pheromone alpha factor receptor
[K07756](#) IP6K; inositol-hexakisphosphate 5-kinase [EC:2.7.4.21]
[K07197](#) SREBP1; sterol regulatory element-binding transcription factor 1
[K18463](#) CCDC53; WASH complex subunit CCDC53
[K12183](#) TSG101; ESCRT-I complex subunit TSG101
[K12187](#) MVB12; ESCRT-I complex subunit MVB12
[K07898](#) RAB7B; Ras-related protein Rab-7B
[K15590](#) TFEB; transcription factor EB
[K17774](#) MDM10; mitochondrial distribution and morphology protein 10
[K06656](#) PCL1; G1/S-specific cyclin PLC1
[K18753](#) ZFP36L; butyrate response factor

[K08770](#) UBC; ubiquitin C
[K15008](#) DLGAP1; discs, large-associated protein 1
[K11126](#) TERT; telomerase reverse transcriptase [EC:2.7.7.49]
[K15042](#) KPNA1_5_6; importin subunit alpha-5/6/7
[K08855](#) GAK; cyclin G-associated kinase [EC:2.7.11.1]
[K08073](#) PNKP; bifunctional polynucleotide phosphatase/kinase [EC:3.1.3.32
 2.7.1.78]
[K09229](#) ZKSCAN; KRAB and SCAN domains-containing zinc finger protein
[K02529](#) lacI; LacI family transcriptional regulator
[K15145](#) MED1; mediator of RNA polymerase II transcription subunit 1, fungi type
[K15154](#) MED2; mediator of RNA polymerase II transcription subunit 2
[K11767](#) ARP7; actin-related protein 7
[K15220](#) RRN9; RNA polymerase I-specific transcription initiation factor RRN9
[K15223](#) UAF30; upstream activation factor subunit UAF30
[K18736](#) SHE2; SWI5-dependent HO expression protein 2
[K13122](#) FRG1; protein FRG1
[K17430](#) MRPL49; large subunit ribosomal protein L49
[K14814](#) ALB1; ribosome biogenesis protein ALB1
[K15902](#) PCC1; EKC/KEOPS complex subunit PCC1/LAGE3
[K11377](#) ELP6; elongator complex protein 6
[K15033](#) ICT1; peptidyl-tRNA hydrolase ICT1 [EC:3.1.1.29]
[K09537](#) DNAJC17; DnaJ homolog subfamily C member 17
[K07893](#) RAB6A; Ras-related protein Rab-6A
[K15690](#) RC3H; RING finger and CCCH-type zinc finger domain-containing
 protein
[K10694](#) ZNRF1_2; E3 ubiquitin-protein ligase ZNRF1/2 [EC:2.3.2.27]
[K11881](#) IRC25; proteasome chaperone 3
[K11346](#) ING4; inhibitor of growth protein 4
[K11403](#) SAS5; something about silencing protein 5
[K11484](#) HOS3; histone deacetylase HOS3 [EC:3.5.1.98]
[K11553](#) DAD1; DASH complex subunit DAD1
[K06024](#) scpB; segregation and condensation protein B
[K19027](#) ZFYVE26; zinc finger FYVE domain-containing protein 26
[K18155](#) AEP3; ATPase expression protein 3, mitochondrial
[K08188](#) SLC16A11; MFS transporter, MCT family, solute carrier family 16
 (monocarboxylic acid transporters), member 11
[K15119](#) SLC25A39_40; solute carrier family 25, member 39/40
[K18615](#) RCSD1; CapZ-interacting protein
[K17275](#) PLS1; plastin-1
[K17916](#) KIF16B; kinesin family member 16B
[K17292](#) TBCA; tubulin-specific chaperone A
[K07976](#) RAB; Rab family, other
[K11170](#) DHRSX; dehydrogenase/reductase SDR family member X [EC:1.1.-.-]
[K12260](#) SRX1; sulfiredoxin [EC:1.8.98.2]
[K08252](#) E2.7.10.1; receptor protein-tyrosine kinase [EC:2.7.10.1]
[K09456](#) aidB; putative acyl-CoA dehydrogenase
[K17338](#) REEP1_2_3_4; receptor expression-enhancing protein 1/2/3/4
[K07001](#) NTE family protein
[K15724](#) erpA; iron-sulfur cluster insertion protein
[K09705](#) uncharacterized protein
[K09780](#)
[K13954](#) yiaY; alcohol dehydrogenase [EC:1.1.1.1]
[K07248](#) aldA; lactaldehyde dehydrogenase/glycolaldehyde dehydrogenase
 [EC:1.2.1.22 1.2.1.21]

[K00123](#) fdoG; formate dehydrogenase major subunit [EC:1.17.1.9]
[K14263](#) BNA7; kynurenine formamidase [EC:3.5.1.9]
[K18369](#) adh2; alcohol dehydrogenase [EC:1.1.1.-]
[K18081](#) MTMR1_2; myotubularin-related protein 1/2 [EC:3.1.3.64 3.1.3.95]
[K00331](#) nuoB; NADH-quinone oxidoreductase subunit B [EC:7.1.1.2]
[K03937](#) NDUF54; NADH dehydrogenase (ubiquinone) Fe-S protein 4
[K03941](#) NDUF58; NADH dehydrogenase (ubiquinone) Fe-S protein 8 [EC:7.1.1.2
1.6.99.3]
[K03959](#) NDUFB3; NADH dehydrogenase (ubiquinone) 1 beta subcomplex
subunit 3
[K02152](#) ATPeV1G; V-type H⁺-transporting ATPase subunit G
[K13239](#) ECI2; Delta3-Delta2-enoyl-CoA isomerase [EC:5.3.3.8]
[K10526](#) OPCL1; OPC-8:0 CoA ligase 1 [EC:6.2.1.-]
[K00274](#) MAO; monoamine oxidase [EC:1.4.3.4]
[K00456](#) CDO1; cysteine dioxygenase [EC:1.13.11.20]
[K03859](#) PIGC; phosphatidylinositol N-acetylglucosaminyltransferase subunit C
[K01127](#) GPLD1; glycosylphosphatidylinositol phospholipase D [EC:3.1.4.50]
[K11151](#) RDH10; retinol dehydrogenase 10 [EC:1.1.1.-]
[K06998](#) phzF; trans-2,3-dihydro-3-hydroxyanthranilate isomerase [EC:5.3.3.17]
[K03016](#) RPB8; DNA-directed RNA polymerases I, II, and III subunit RPABC3
[K12846](#) SNRNP27; U4/U6.U5 tri-snRNP-associated protein 3
[K12847](#) USP39; U4/U6.U5 tri-snRNP-associated protein 2
[K12871](#) CCDC12; coiled-coil domain-containing protein 12
[K12877](#) MAGOH; protein mago nashi
[K14526](#) POP7; ribonuclease P/MRP protein subunit POP7 [EC:3.1.26.5]
[K03539](#) RPP1; ribonuclease P/MRP protein subunit RPP1 [EC:3.1.26.5]
[K14317](#) NUP214; nuclear pore complex protein Nup214
[K15543](#) REF2; RNA end formation protein 2
[K10080](#) LMAN1; lectin, mannose-binding 1
[K03868](#) RBX1; RING-box protein 1 [EC:2.3.2.32]
[K10587](#) UBE3A; ubiquitin-protein ligase E3 A [EC:2.3.2.26]
[K10144](#) RCHY1; RING finger and CHY zinc finger domain-containing protein 1
[EC:2.3.2.27]
[K03872](#) ELOC; elongin-C
[K12161](#) URM1; ubiquitin related modifier 1
[K10868](#) XRS2; DNA repair protein XRS2
[K04349](#) RASGRF1; Ras-specific guanine nucleotide-releasing factor 1
[K04392](#) RAC1; Ras-related C3 botulinum toxin substrate 1
[K04393](#) CDC42; cell division control protein 42
[K06683](#) CDC15; cell division control protein CDC15 [EC:2.7.11.1]
[K07198](#) PRKAA; 5'AMP-activated protein kinase, catalytic alpha subunit
[EC:2.7.11.11]
[K18441](#) CYTH; cytohesin
[K01379](#) CTSD; cathepsin D [EC:3.4.23.5]
[K12189](#) VPS25; ESCRT-II complex subunit VPS25
[K09105](#) TFE3; transcription factor E3
[K02365](#) ESP1; separase [EC:3.4.22.49]
[K06658](#) PHO4; phosphate system positive regulatory protein PHO4
[K06687](#) NET1; nucleolar protein involved in exit from mitosis
[K12578](#) LCD1; DNA damage checkpoint protein LCD1
[K07902](#) RAB8B; Ras-related protein Rab-8B
[K13867](#) SLC7A7; solute carrier family 7 (L-type amino acid transporter), member
7
[K10393](#) KIF2_24; kinesin family member 2/24

[K12035](#) TRIM71; tripartite motif-containing protein 71 [EC:2.3.2.27]
[K11647](#) SMARCA2_4; SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 2/4 [EC:3.6.4.-]
[K08805](#) DCLK1_2; doublecortin-like kinase 1/2 [EC:2.7.11.1]
[K17570](#) HYDIN; hydrocephalus-inducing protein
[K18084](#) MTMR9; myotubularin-related protein 9
[K15385](#) APDC; aspyridone synthetase trans-acting enoyl reductase
[K01894](#) gluQ; glutamyl-Q tRNA(Asp) synthetase [EC:6.1.1.-]
[K00517](#) CYP81F; indol-3-yl-methylglucosinolate hydroxylase [EC:1.14.-.-]
[K09238](#) ACE2; metallothionein expression activator
[K09249](#) ABF1; ARS-binding factor 1
[K11774](#) SNF11; SWI/SNF complex component SNF11
[K13102](#) KIN; DNA/RNA-binding protein KIN17
[K18720](#) NUP145; nucleoporin NUP145
[K18647](#) ANP32B; acidic leucine-rich nuclear phosphoprotein 32 family member B
[K11135](#) PINX1; Pin2-interacting protein X1
[K09506](#) DNAJA5; DnaJ homolog subfamily A member 5
[K19307](#) BMT5; 25S rRNA (uracil2634-N3)-methyltransferase [EC:2.1.1.313]
[K15453](#) PUS6; tRNA pseudouridine31 synthase [EC:5.4.99.42]
[K15901](#) CGI121; EKC/KEOPS complex subunit CGI121/TPRKB
[K17868](#) DPH7; diphthine methyl ester acylhydrolase [EC:3.1.1.97]
[K07890](#) RAB21; Ras-related protein Rab-21
[K06568](#) MUC1; mucin-1
[K11798](#) BRWD1_3; bromodomain and WD repeat domain containing protein 1/3
[K11887](#) PAAF1; proteasomal ATPase-associated factor 1
[K11378](#) SAS3; histone acetyltransferase SAS3 [EC:2.3.1.48]
[K11482](#) HOS1; histone deacetylase HOS1 [EC:3.5.1.98]
[K11678](#) IES4; Ino eighty subunit 4
[K14635](#) MPH1; ATP-dependent DNA helicase MPH1 [EC:3.6.4.12]
[K17336](#) PLS3; plastin-3
[K17661](#) CBP2; cytochrome b pre-mRNA-processing protein 2
[K17667](#) PET111; protein PET111, mitochondrial
[K17780](#) TIM8; mitochondrial import inner membrane translocase subunit TIM8
[K18170](#) LYRM7; complex III assembly factor LYRM7
[K13856](#) SLC4A3; solute carrier family 4 (anion exchanger), member 3
[K15108](#) SLC25A19; solute carrier family 25 (mitochondrial thiamine pyrophosphate transporter), member 19
[K03446](#) emrB; MFS transporter, DHA2 family, multidrug resistance protein
[K07114](#) yfbK; Ca-activated chloride channel homolog
[K10392](#) KIF1; kinesin family member 1
[K17914](#) KIF13; kinesin family member 13
[K18638](#) BNI4; protein BNI4
[K00062](#) E1.1.1.116; D-arabinose 1-dehydrogenase [EC:1.1.1.116]
[K03824](#) yhbS; putative acetyltransferase [EC:2.3.1.-]
[K05962](#) E2.7.13.1; protein-histidine pros-kinase [EC:2.7.13.1]
[K01175](#) ybfF; esterase [EC:3.1.-.-]
[K01185](#) E3.2.1.17; lysozyme [EC:3.2.1.17]
[K01534](#) zntA; Cd²⁺/Zn²⁺-exporting ATPase [EC:3.6.3.3 7.2.2.12]
[K04755](#) fdx; ferredoxin, 2Fe-2S
[K06999](#) phospholipase/carboxylesterase
[K18667](#) ASCC2; activating signal cointegrator complex subunit 2
[K07443](#) ybaZ; methylated-DNA-protein-cysteine methyltransferase related protein
[K03112](#)

[K00338](#) nuoI; NADH-quinone oxidoreductase subunit I [EC:7.1.1.2]
[K00412](#) CYTB; ubiquinol-cytochrome c reductase cytochrome b subunit
[K02143](#) ATPeFK; F-type H⁺-transporting ATPase subunit k
[K01673](#) cynT; carbonic anhydrase [EC:4.2.1.1]
[K12345](#) SRD5A3; 3-oxo-5-alpha-steroid 4-dehydrogenase 3 / polyprenol reductase [EC:1.3.1.22 1.3.1.94]
[K00038](#) E1.1.1.53; 3alpha(or 20beta)-hydroxysteroid dehydrogenase [EC:1.1.1.53]
[K06130](#) LYPLA2; lysophospholipase II [EC:3.1.1.5]
[K08966](#) mtnX; 2-hydroxy-3-keto-5-methylthiopentenyl-1-phosphate phosphatase [EC:3.1.3.87]
[K05528](#) OCH1; alpha 1,6-mannosyltransferase [EC:2.4.1.232]
[K10971](#) GMA12; alpha 1,2-galactosyltransferase [EC:2.4.1.-]
[K07541](#) PIGX; GPI mannosyltransferase 1 subunit X
[K14652](#) ribBA; 3,4-dihydroxy 2-butanone 4-phosphate synthase / GTP cyclohydrolase II [EC:4.1.99.12 3.5.4.25]
[K03012](#) RPB4; DNA-directed RNA polymerase II subunit RPB4
[K12824](#) TCERG1; transcription elongation regulator 1
[K12626](#) LSM7; U6 snRNA-associated Sm-like protein LSM7
[K02971](#) RP-S21e; small subunit ribosomal protein S21e
[K05019](#) CLNS1A; chloride channel, nucleotide-sensitive, 1A
[K13171](#) SRRM1; serine/arginine repetitive matrix protein 1
[K14543](#) MTR2; mRNA transport regulator MTR2
[K09648](#) IMP2; mitochondrial inner membrane protease subunit 2 [EC:3.4.21.-]
[K08509](#) SNAP29; synaptosomal-associated protein 29
[K12594](#) MPP6; M-phase phosphoprotein 6, fungi type
[K10739](#) RFA2; replication factor A2
[K10740](#) RPA3; replication factor A3
[K10802](#) HMGB1; high mobility group protein B1
[K06640](#) ATR; serine/threonine-protein kinase ATR [EC:2.7.11.1]
[K13924](#) cheBR; two-component system, chemotaxis family, CheB/CheR fusion protein [EC:2.1.1.80 3.1.1.61]
[K02678](#) ETS1; C-ets-1
[K04422](#) MAP3K13; mitogen-activated protein kinase kinase kinase 13 [EC:2.7.11.25]
[K01315](#) PLG; plasminogen [EC:3.4.21.7]
[K11247](#) SH3GL; endophilin-A
[K12478](#) EEA1; early endosome antigen 1
[K06546](#) CD164; CD164 antigen
[K12399](#) AP3S; AP-3 complex subunit sigma
[K14381](#) SQSTM1; sequestosome 1
[K06644](#) SFN; stratifin
[K12575](#) SLK19; kinetochore protein SLK19
[K12754](#) MYL7; myosin regulatory light chain 7
[K08762](#) DBI; diazepam-binding inhibitor (GABA receptor modulator, acyl-CoA-binding protein)
[K11651](#) SMARCE1; SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E, member 1
[K18177](#) COA4; cytochrome c oxidase assembly factor 4
[K15188](#) CCNT; cyclin T
[K15614](#) SIX1; homeobox protein SIX1
[K15593](#) ETV5; ets translocation variant 5
[K19202](#) SAP30; histone deacetylase complex subunit SAP30
[K11366](#) USP22_27_51; ubiquitin carboxyl-terminal hydrolase 22/27/51 [EC:3.4.19.12]

[K06836](#) ADAM15; disintegrin and metalloproteinase domain-containing protein 15 [EC:3.4.24.-]
[K01273](#) DPEP; membrane dipeptidase [EC:3.4.13.19]
[K18658](#) ASH1; transcriptional regulatory protein ASH1
[K15130](#) MED8; mediator of RNA polymerase II transcription subunit 8, fungi type
[K15153](#) MED31; mediator of RNA polymerase II transcription subunit 31
[K15181](#) TH1L; negative elongation factor C/D
[K15219](#) RRN7; RNA polymerase I-specific transcription initiation factor RRN7
[K13119](#) FAM50; protein FAM50
[K14853](#) RSA1; ribosome assembly protein 1
[K10669](#) TRPT1; 2'-phosphotransferase [EC:2.7.1.160]
[K05545](#) DUS4; tRNA-dihydrouridine synthase 4 [EC:1.3.1.90]
[K07055](#) TRM12; tRNA wybutosine-synthesizing protein 2 [EC:2.5.1.114]
[K15451](#) PPM2; tRNA wybutosine-synthesizing protein 4 [EC:2.1.1.290 2.3.1.231]
[K19371](#) DNAJC25; DnaJ homolog subfamily C member 25
[K09550](#) PFDN4; prefoldin subunit 4
[K10276](#) FBXL10_11; F-box and leucine-rich repeat protein 10/11 [EC:1.14.11.27]
[K10297](#) FBXO11; F-box protein 11
[K02621](#) parC; topoisomerase IV subunit A [EC:5.6.2.2]
[K11276](#) NPM1; nucleophosmin 1
[K10751](#) CHAF1B; chromatin assembly factor 1 subunit B
[K11399](#) EAF7; chromatin modification-related protein EAF7
[K11497](#) CENPC; centromere protein C
[K11558](#) SPC25; kinetochore protein Spc25, fungi type
[K16570](#) TUBGCP3; gamma-tubulin complex component 3
[K18188](#) PET117; protein PET117
[K13870](#) SLC7A13; solute carrier family 7 (L-type amino acid transporter), member 13
[K15278](#) SLC35B4; solute carrier family 35 (UDP-xylose/UDP-N-acetylglucosamine transporter), member B4
[K03284](#) corA; magnesium transporter
[K03498](#) trkH; trk system potassium uptake protein
[K18626](#) TCHH; trichohyalin
[K16946](#) SHS1; seventh homolog of septin 1
[K04882](#) KCNAB1; potassium voltage-gated channel Shaker-related subfamily A, beta member 1
[K00537](#) arsC1; arsenate reductase (glutaredoxin) [EC:1.20.4.1]
[K00661](#) maa; maltose O-acetyltransferase [EC:2.3.1.79]
[K08235](#) E2.4.1.207; xyloglucan:xyloglucosyl transferase [EC:2.4.1.207]
[K01250](#) rihA; pyrimidine-specific ribonucleoside hydrolase [EC:3.2.-.-]
[K01263](#) E3.4.11.14; cytosol alanyl aminopeptidase [EC:3.4.11.14]
[K19294](#) algI; alginate O-acetyltransferase complex protein AlgI
[K15977](#) putative oxidoreductase
[K12549](#) lapA; surface adhesion protein
[K07182](#) CBS domain-containing protein

Table S5. KEGG Orthologs (KO) of protein genes differentially expressed in MKAA1 and MKAA2 samples represented in Pearson's correlation plots.

KO	Protein gene
Metabolism (Bacteria)	
K00123	fdoG, fdhF, fdwA; formate dehydrogenase major subunit [EC:1.17.1.9]
K00133	asd; aspartate-semialdehyde dehydrogenase [EC:1.2.1.11]
K00432	gpx, btuE, bsaA; glutathione peroxidase [EC:1.11.1.9]

K00756	pdp; pyrimidine-nucleoside phosphorylase [EC:2.4.2.2]
K00793	ribE, RIB5; riboflavin synthase [EC:2.5.1.9]
K00841	patA; aminotransferase [EC:2.6.1.-]
K00950	folK; 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase [EC:2.7.6.3]
K00954	E2.7.7.3A, coaD, kdtB; pantetheine-phosphate adenylyltransferase [EC:2.7.7.3]
K01091	gph; phosphoglycolate phosphatase [EC:3.1.3.18]
K01452	E3.5.1.41; chitin deacetylase [EC:3.5.1.41]
K01515	nudF; ADP-ribose pyrophosphatase [EC:3.6.1.13]
K01595	ppc; phosphoenolpyruvate carboxylase [EC:4.1.1.31]
K01878	glyQ; glycyl-tRNA synthetase alpha chain [EC:6.1.1.14]
K02297	cyoA; cytochrome o ubiquinol oxidase subunit II [EC:7.1.1.3]
K02777	PTS-Glc-EIIA, crr; PTS system, sugar-specific IIA component [EC:2.7.1.-]
K03060	rpoZ; DNA-directed RNA polymerase subunit omega [EC:2.7.7.6]
K03101	lspA; signal peptidase II [EC:3.4.23.36]
K11936	pgaC, icaA; poly-beta-1,6-N-acetyl-D-glucosamine synthase [EC:2.4.1.-]
K14652	ribBA; 3,4-dihydroxy 2-butanone 4-phosphate synthase / GTP cyclohydrolase II [EC:4.1.99.12 3.5.4.25]
K19222	menI, DHNAT; 1,4-dihydroxy-2-naphthoyl-CoA hydrolase [EC:3.1.2.28]

Genetic Information Processing (Bacteria)

K02099	araC; AraC family transcriptional regulator, arabinose operon regulatory protein
K02881	RP-L18, MRPL18, rplR; large subunit ribosomal protein L18
K02892	RP-L23, MRPL23, rplW; large subunit ribosomal protein L23
K02895	RP-L24, MRPL24, rplX; large subunit ribosomal protein L24
K03088	rpoE; RNA polymerase sigma-70 factor, ECF subfamily
K03169	topB; DNA topoisomerase III [EC:5.6.2.1]
K03628	rho; transcription termination factor Rho
K03652	MPG; DNA-3-methyladenine glycosylase [EC:3.2.2.21]
K03671	trxA; thioredoxin 1
K03704	cspA; cold shock protein
K03973	pspC; phage shock protein C
K06204	dksA; DnaK suppressor protein
K07506	K07506; AraC family transcriptional regulator
K07560	dtd, DTD; D-aminoacyl-tRNA deacylase [EC:3.1.1.96]
K08300	rne; ribonuclease E [EC:3.1.26.12]
K09888	zapA; cell division protein ZapA
K14742	tsaB; tRNA threonylcarbamoyladenosine biosynthesis protein TsaB
K15192	BTAf1, MOT1; TATA-binding protein-associated factor [EC:3.6.4.-]
K16137	nemR; TetR/AcrR family transcriptional regulator, transcriptional repressor for nem operon
K17277	EPS8; epidermal growth factor receptor kinase substrate 8

Environmental Information Processing (Bacteria)

K02002	proX; glycine betaine/proline transport system substrate-binding protein
K02006	cbiO; cobalt/nickel transport system ATP-binding protein
K02041	phnC; phosphonate transport system ATP-binding protein [EC:7.3.2.2]
K02042	phnE; phosphonate transport system permease protein
K02406	fliC; flagellin
K02424	fliY, tcyA; L-cystine transport system substrate-binding protein
K03286	TC.OOP; OmpA-OmpF porin, OOP family
K03320	amt, AMT, MEP; ammonium transporter, Amt family
K03406	mcp; methyl-accepting chemotaxis protein
K03523	bioY; biotin transport system substrate-specific component
K03761	kgpT; MFS transporter, MHS family, alpha-ketoglutarate permease
K03811	pnuC; nicotinamide mononucleotide transporter
K06147	ABCB-BAC; ATP-binding cassette, subfamily B, bacterial

K06189	corC; magnesium and cobalt transporter
K07221	oprO_P; phosphate-selective porin OprO and OprP
K10823	oppF; oligopeptide transport system ATP-binding protein
K14205	mprF, fmtC; phosphatidylglycerol lysyltransferase [EC:2.3.2.3]
K14696	SLC30A9, ZNT9; solute carrier family 30 (zinc transporter), member 9
K16923	qrtT; energy-coupling factor transport system substrate-specific component
K17073	proX; glycine betaine/proline transport system substrate-binding protein

Metabolism (Yeast)

K00211	TYR1; prephenate dehydrogenase (NADP+) [EC:1.3.1.13]
K00272	DDO; D-aspartate oxidase [EC:1.4.3.1]
K00606	panB; 3-methyl-2-oxobutanoate hydroxymethyltransferase [EC:2.1.2.11]
K01048	pldB; lysophospholipase [EC:3.1.1.5]
K01190	lacZ; beta-galactosidase [EC:3.2.1.23]
K01225	CBH1; cellulose 1,4-beta-cellobiosidase [EC:3.2.1.91]
K01266	dmpA, dap; D-aminopeptidase [EC:3.4.11.19]
K01341	KEX2; kexin [EC:3.4.21.61]
K01487	E3.5.4.3, guaD; guanine deaminase [EC:3.5.4.3]
K02178	BUB1; checkpoint serine/threonine-protein kinase [EC:2.7.11.1]
K02266	COX6A; cytochrome c oxidase subunit 6a
K03083	GSK3B; glycogen synthase kinase 3 beta [EC:2.7.11.26]
K03146	THI4, THI1; cysteine-dependent adenosine diphosphate thiazole synthase [EC:2.4.2.60]
K03844	ALG11; alpha-1,2-mannosyltransferase [EC:2.4.1.131]
K04518	pheA2; prephenate dehydratase [EC:4.2.1.51]
K06237	COL4A; collagen, type IV, alpha
K07189	PPP1R3; protein phosphatase 1 regulatory subunit 3A/B/C/D/E
K07207	TSC2; tuberous sclerosis 2
K08793	STK32, YANK; serine/threonine kinase 32 [EC:2.7.11.1]
K15730	PTGES3; cytosolic prostaglandin-E synthase [EC:5.3.99.3]

Genetic Information Processing (Yeast)

K00555	TRMT1, trm1; tRNA (guanine26-N2/guanine27-N2)-dimethyltransferase [EC:2.1.1.215 2.1.1.216]
K00566	mnmA, trmU; tRNA-uridine 2-sulfurtransferase [EC:2.8.1.13]
K02213	CDC6; cell division control protein 6
K02953	RP-S13e, RPS13; small subunit ribosomal protein S13e
K02977	RP-S27Ae, RPS27A; small subunit ribosomal protein S27Ae
K03113	EIF1, SU1; translation initiation factor 1
K03260	EIF4G; translation initiation factor 4G
K04082	hscB, HSCB, HSC20; molecular chaperone HscB
K05747	WAS; Wiskott-Aldrich syndrome protein
K06654	PHO80; phosphate system cyclin PHO80
K06671	STAG1_2, SCC3, IRR1; cohesin complex subunit SA-1/2
K06679	MAD1; mitotic spindle assembly checkpoint protein MAD1
K08502	VAM7; regulator of vacuolar morphogenesis
K09235	RME1; zinc finger protein RME1
K10421	CLIP1, RSN; CAP-Gly domain-containing linker protein 1
K12857	SNRNP40, PRP8BP; Prp8 binding protein
K12878	THOC1; THO complex subunit 1
K14566	UTP24, FCF1; U3 small nucleolar RNA-associated protein 24
K14962	WDR82, SWD2, CPS35; COMPASS component SWD2
K17265	G3BP1; Ras GTPase-activating protein-binding protein 1 [EC:3.6.4.12 3.6.4.13]

Environmental Information Processing (Yeast)

K02013	ABC.FEV.A; iron complex transport system ATP-binding protein [EC:7.2.2.-]
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K03099	SOS; son of sevenless
K03320	amt, AMT, MEP; ammonium transporter, Amt family
K03450	SLC7A; solute carrier family 7 (L-type amino acid transporter), other
K05628	RERE; arginine-glutamic acid dipeptide repeats protein
K05667	ABCC3; ATP-binding cassette, subfamily C (CFTR/MRP), member 3
K05672	ABCC12; ATP-binding cassette, subfamily C (CFTR/MRP), member 12
K05673	ABCC4; ATP-binding cassette, subfamily C (CFTR/MRP), member 4
K08150	SLC2A13, ITR; MFS transporter, SP family, solute carrier family 2 (myo-inositol transporter), member 13
K08165	ATR1; MFS transporter, DHA2 family, multidrug resistance protein
K08192	DAL; MFS transporter, ACS family, allantoate permease
K12755	MYL9; myosin regulatory light chain 9
K13754	SLC24A6, NCKX6; solute carrier family 24 (sodium/potassium/calcium exchanger), member 6
K13781	SLC7A8, LAT2; solute carrier family 7 (L-type amino acid transporter), member 8
K14686	SLC31A1, CTR1; solute carrier family 31 (copper transporter), member 1
K14997	SLC38A11; solute carrier family 38 (sodium-coupled neutral amino acid transporter), member 11
K15280	SLC35C2; solute carrier family 35, member C2
K15377	SLC44A2_4_5; solute carrier family 44 (choline transporter-like protein), member 2/4/5
K18059	SULTR4; sulfate transporter 4
K19364	NIPA1, SLC57A1; magnesium transporter NIPA1
