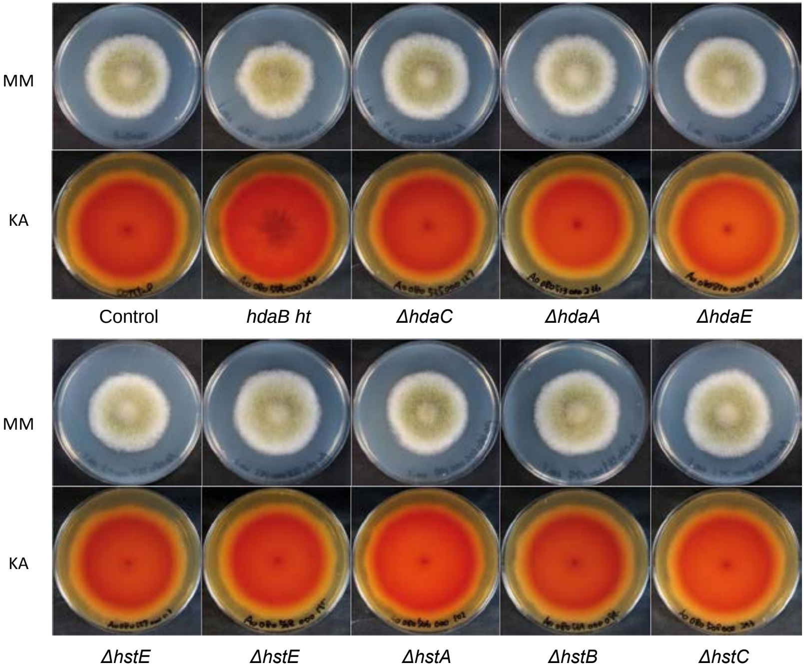
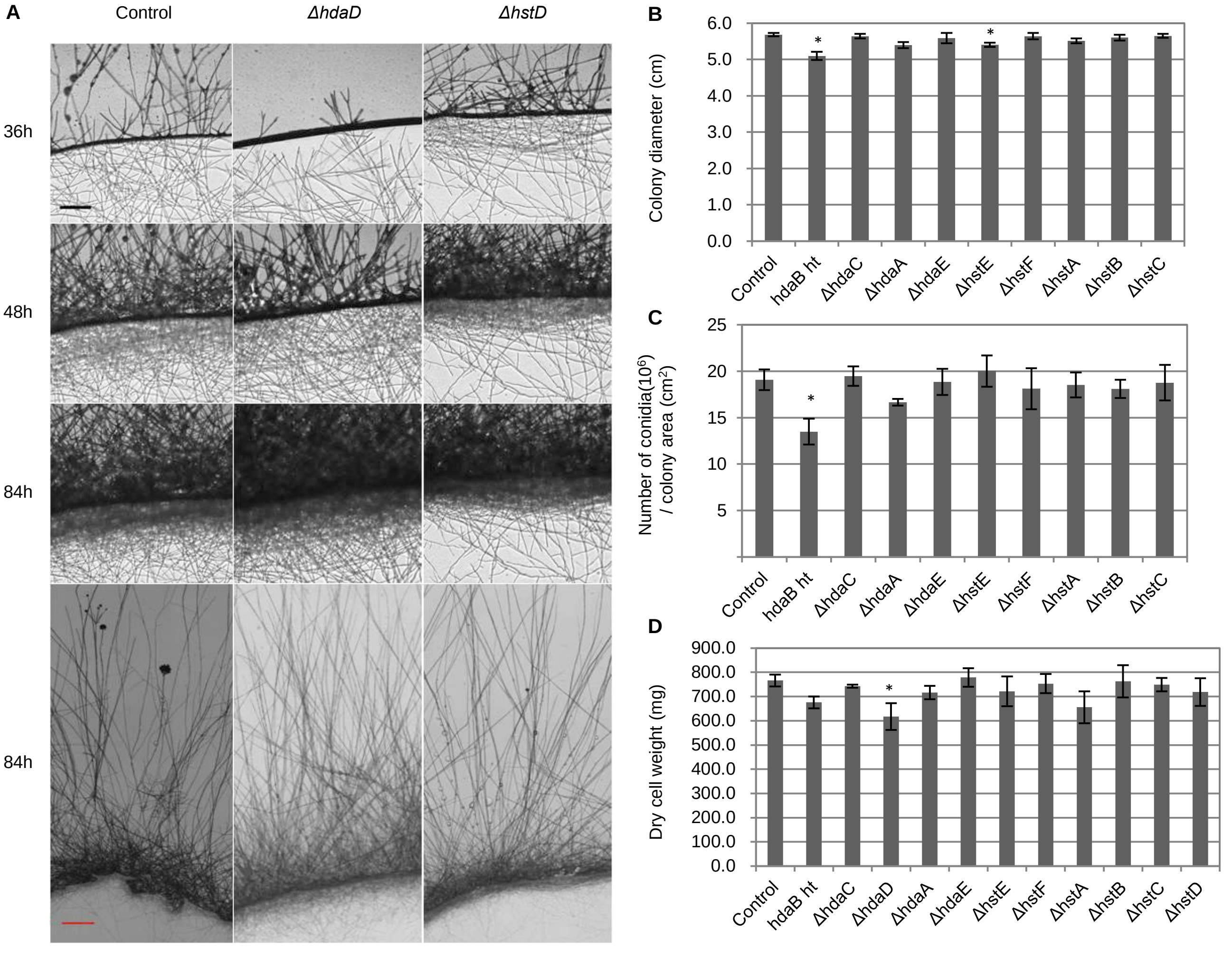
Figure S1. Kojic acid production and developmental phenotype of AoHDACs disruptants and heterokaryon strain



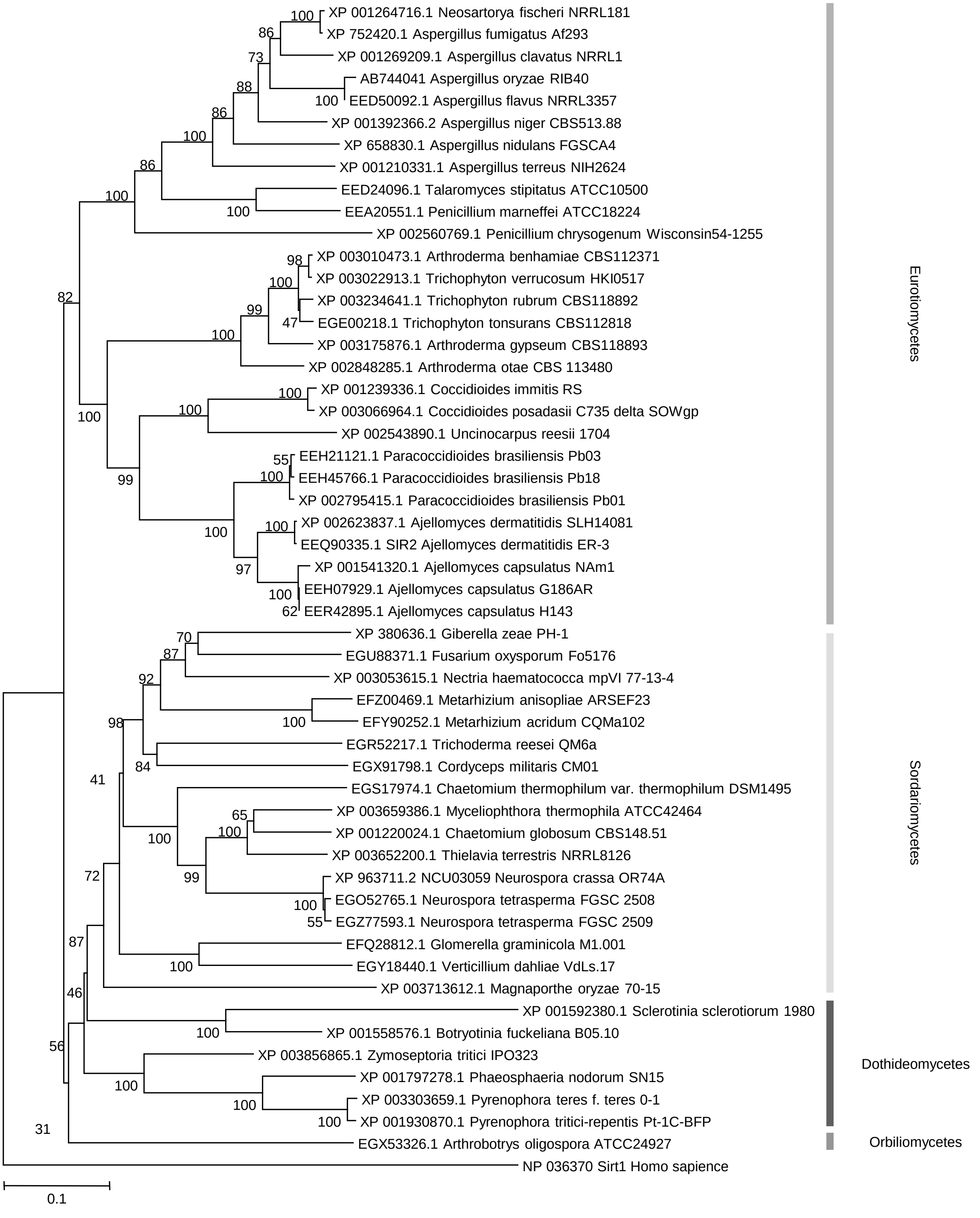
MM and KA show the morphological phenotype and kojic acid production plate assays of the indicated strains, respectively.

Figure S2. Phenotypic analysis of AoHDACs disruptants and hetrokaryon strain on plates and submerged cultures.



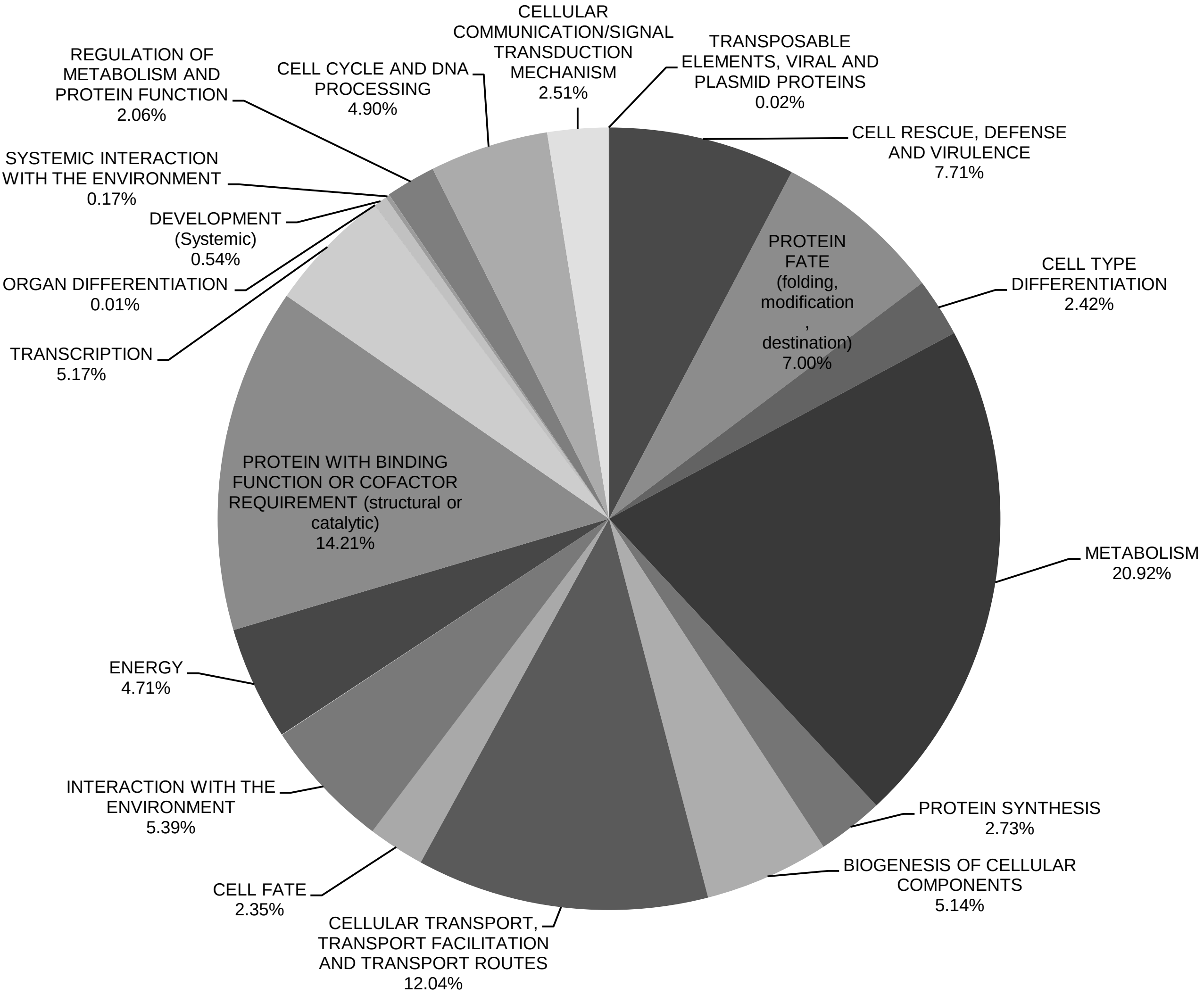
(A) Time-lapse microscopic analysis of *ΔhstD* and *ΔhdaD*. The pictures were taken at 36, 48, and 84 hr of incubation (black scale bar, 200 μm; red scale bar, 500 μm). **(B-D)** Quantification of colony diameter, conidiation rate, and mycelial dry cell weight of AoHDACs disruptants or the heterokaryon strain, respectively. The colony diameter and conidiation rates were measured on plate cultures. Dry cell weight was measured on submerged cultures. All data are represented as means ± s.d. (n=3); $*p < 0.01$, t-test

Figure S3. Phylogenetic analysis of *hstD* in filamentous fungi



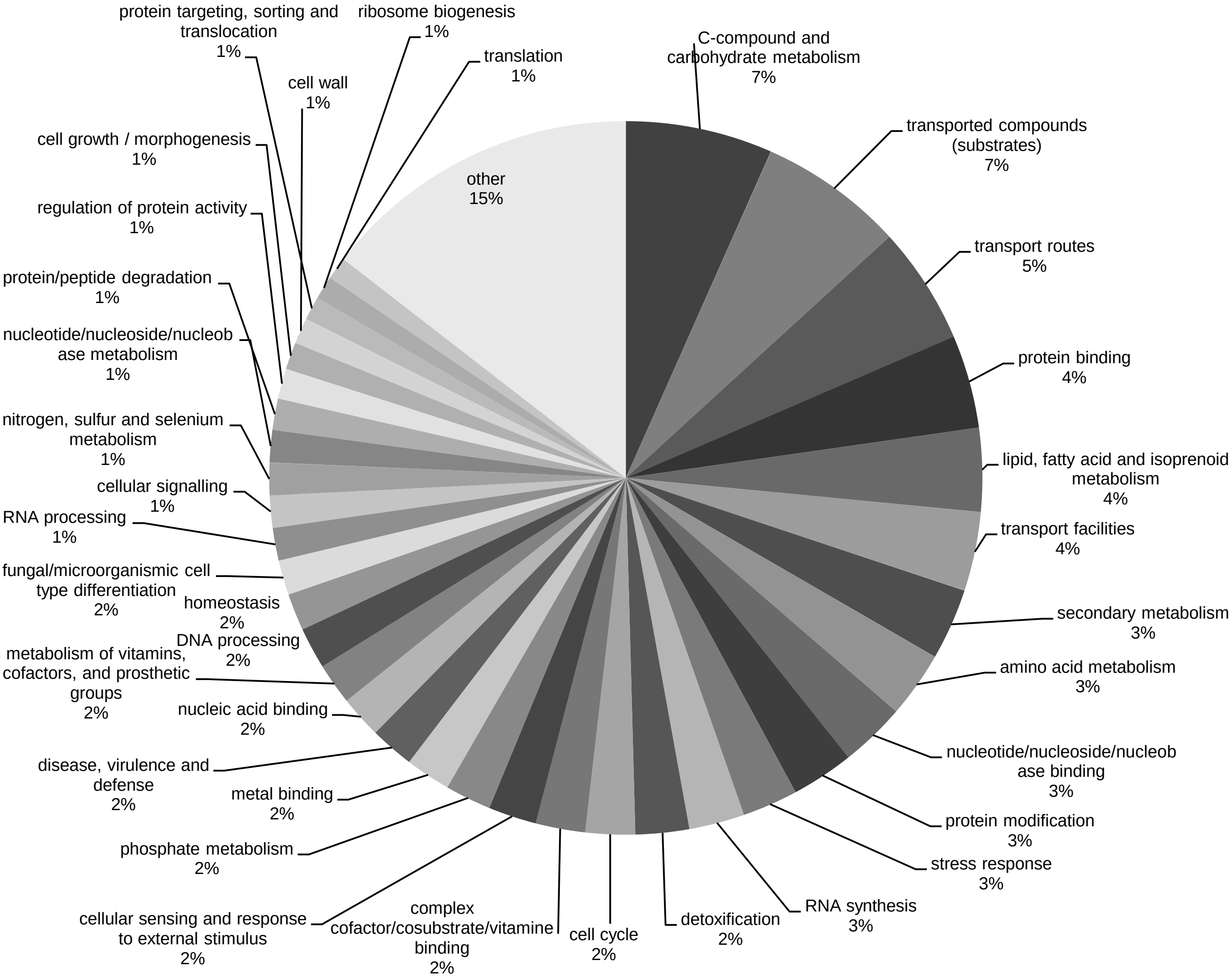
The Genebank accession numbers and species names are indicated for each branch. The numbers at the nodes are bootstrap values obtained from 1000 replicates and are indicated as percentages. The scale bar indicates a distance corresponding to 0.1 amino acid substitutions per site. Each class of ascomycetes is shown at the right. *Sirt1* is used as the out-group in this phylogenetic analysis.

Figure S4. Whole genome distribution of FunCat level 1 categories



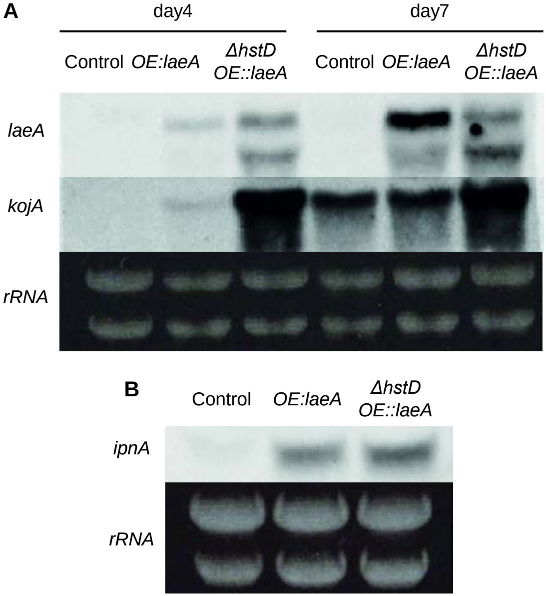
This pie-chart indicates the distribution of all mapped genes of *A. oryzae* RIB40 genome in the categories of FunCat level 1. Percentages of each category was calculated against all mapped genes. This result was imported from FungiFun software (https://sbi.hki-jena.de/FungiFun/FungiFun.cgi) and used as a reference to analyzed FunCat level 1 enrichment analysis . Details of each category are available at the FunCat Database (http://mips.helmholtzmuenchen.de/proj/funcatDB/search_main_frame.html).

Figure S5. Whole genome distribution of FunCat level 2 categories



This pie-chart indicates the distribution of all mapped genes of *A. oryzae* RIB40 genome in the categories of FunCat level 2. Percentages of each category was calculated against all mapped genes. Miner categories(< 1%) were indicated as “other” in this pie chart. This result was imported from FungiFun software (https://sbi.hki-jena.de/FungiFun/FungiFun.cgi) and used as a reference for the analysis of FunCat level 2 enrichment analysis. Details of each category are available at the FunCat Database (http://mips.helmholtzmuenchen.de/proj/funcatDB/search_main_frame.html).

Figure S6. Expression profiling of *laeA*, *kojA*, and *ipnA* in *OE::laeA* and *ΔhstD OE::laeA* strains, respectively



(A) Northern hybridization of *laeA and kojA*, respectively. The culture time of the indicated strain is shown at the top of the panel. *rRNA* is shown as the loading control. The analyzed gene is indicated on the left side of each blot **(B)** Northern hybridization of the penicillin biosynthetic gene *ipnA*. *rRNA* is shown as the loading control. The *adeA*$^+$ *pUSA*$^+$ strain was used as the control, and the *OE:laeA adeA*$^+$strain represents *OE::laeA* in this figure.

Table S1. Strain used in this study

Name	Parental strain	Genotype[b]	Reference
RIB40		wild type	NRIB[a]
NSR-ΔLD2	*RIB40*	*niaD*$^-$ *sC*$^-$ *adeA*$^-$ *argB::adeA*$^-$ *ΔligD::argB*	(25)
adeA$^+$	*NSR-ΔLD2*	*niaD*$^-$ *sC*$^-$ *adeA*$^-$ *argB::adeA*$^-$ *ΔligD::argB adeA*$^+$	this study
pUSA$^+$	*NSR-ΔLD2*	*niaD*$^-$ *sC*$^-$ *adeA*$^-$ *argB::adeA*$^-$ *ΔligD::argB pUSA*$^+$	this study
adeA$^+$ *sC*$^+$	*adeA*$^+$	*niaD*$^-$ *sC*$^-$ *adeA*$^-$ *argB::adeA*$^-$ *ΔligD::argB adeA*$^+$ *AnsC*$^+$	this study
adeA$^+$ *pUSA*$^+$	*adeA*$^+$	*niaD*$^-$ *sC*$^-$ *adeA*$^-$ *argB::adeA*$^-$ *ΔligD::argB adeA*$^+$ *pUSA*$^+$	this study
hdaB *ht*[c]	*NSR-ΔLD2*	*niaD*$^-$ *sC*$^-$ *adeA*$^-$ *argB::adeA*$^-$ *ΔligD::argB ΔhdaB::adeA hdaB*	this study
ΔhdaC	*NSR-ΔLD2*	*niaD*$^-$ *sC*$^-$ *adeA*$^-$ *argB::adeA*$^-$ *ΔligD::argB ΔhdaC::adeA*	this study
ΔhdaD	*NSR-ΔLD2*	*niaD*$^-$ *sC*$^-$ *adeA*$^-$ *argB::adeA*$^-$ *ΔligD::argB ΔhdaD::adeA*	this study
ΔhdaA	*NSR-ΔLD2*	*niaD*$^-$ *sC*$^-$ *adeA*$^-$ *argB::adeA*$^-$ *ΔligD::argB ΔhdaA::adeA*	this study
ΔhdaE	*NSR-ΔLD2*	*niaD*$^-$ *sC*$^-$ *adeA*$^-$ *argB::adeA*$^-$ *ΔligD::argB ΔhdaE::adeA*	this study
ΔhstA	*NSR-ΔLD2*	*niaD*$^-$ *sC*$^-$ *adeA*$^-$ *argB::adeA*$^-$ *ΔligD::argB ΔhstA::adeA*	this study
ΔhstB	*NSR-ΔLD2*	*niaD*$^-$ *sC*$^-$ *adeA*$^-$ *argB::adeA*$^-$ *ΔligD::argB ΔhstB::adeA*	this study
ΔhstC	*NSR-ΔLD2*	*niaD*$^-$ *sC*$^-$ *adeA*$^-$ *argB::adeA*$^-$ *ΔligD::argB ΔhstC::adeA*	this study
ΔhstD	*NSR-ΔLD2*	*niaD*$^-$ *sC*$^-$ *adeA*$^-$ *argB::adeA*$^-$ *ΔligD::argB ΔhstD::adeA*	this study
ΔhstE	*NSR-ΔLD2*	*niaD*$^-$ *sC*$^-$ *adeA*$^-$ *argB::adeA*$^-$ *ΔligD::argB ΔhstE::adeA*	this study
ΔhstF	*NSR-ΔLD2*	*niaD*$^-$ *sC*$^-$ *adeA*$^-$ *argB::adeA*$^-$ *ΔligD::argB ΔhstF::adeA*	this study
ΔlaeA	*NSR-ΔLD2*	*niaD*$^-$ *sC*$^-$ *adeA*$^-$ *argB::adeA*$^-$ *ΔligD::argB ΔlaeA::adeA*	this study
ΔhstD sC$^+$	*ΔhstD*	*niaD*$^-$ *sC*$^-$ *adeA*$^-$ *argB::adeA*$^-$ *ΔligD::argB ΔhstD::adeA AnsC*$^+$	this study
ΔhstD pUSA$^+$	*ΔhstD*	*niaD*$^-$ *sC*$^-$ *adeA*$^-$ *argB::adeA*$^-$ *ΔligD::argB ΔhstD::adeA pUSA*$^+$	this study
ΔhstD OE::laeA	*ΔhstD*	*niaD*$^-$ *sC*$^-$ *adeA*$^-$ *argB::adeA*$^-$ *ΔligD::argB ΔhstD::adeA pUSlaeA*$^+$	this study
ΔlaeA sC$^+$	*ΔlaeA*	*niaD*$^-$ *sC*$^-$ *adeA*$^-$ *argB::adeA*$^-$ *ΔligD::argB ΔlaeA::adeA AnsC*$^+$	this study
ΔlaeA pUSA$^+$	*ΔlaeA*	*niaD*$^-$ *sC*$^-$ *adeA*$^-$ *argB::adeA*$^-$ *ΔligD::argB ΔlaeA::adeA pUSA*$^+$	this study
ΔlaeA OE::hstD	*ΔlaeA*	*niaD*$^-$ *sC*$^-$ *adeA*$^-$ *argB::adeA*$^-$ *ΔligD::argB ΔlaeA::adeA pUShstD*$^+$	this study
OE::laeA	*NSR-ΔLD2*	*niaD*$^-$ *sC*$^-$ *adeA*$^-$ *argB::adeA*$^-$ *ΔligD::argB pUSlaeA*$^+$	this study
OE::hstD	*NSR-ΔLD2*	*niaD*$^-$ *sC*$^-$ *adeA*$^-$ *argB::adeA*$^-$ *ΔligD::argB pUShstD*$^+$	this study
ΔhstD ΔlaeA	*ΔhstD*	*niaD*$^-$ *sC*$^-$ *adeA*$^-$ *argB::adeA*$^-$ *ΔligD::argB ΔhstD::adeA ΔlaeA::AnsC*	this study
hstD$^+$	*ΔhstD*	*niaD*$^-$ *sC*$^-$ *adeA*$^-$ *argB::adeA*$^-$ *ΔligD::argB ΔhstD::adeA::hstD::AnsC*	this study
OE::laeA adeA$^+$	*OE::laeA*	*niaD*$^-$ *sC*$^-$ *adeA*$^-$ *argB::adeA*$^-$ *ΔligD::argB pUSlaeA*$^+$ *adeA*$^+$	this study
OE::hstD adeA$^+$	*OE::hstD*	*niaD*$^-$ *sC*$^-$ *adeA*$^-$ *argB::adeA*$^-$ *ΔligD::argB pUShstD*$^+$ *adeA*$^+$	this study

[a] National Research institute of Brewing

[b] *AnsC: Aspergillus nidulans sC*

[c] *ht:* heterokaryon

Table S2. List of sequence accession numbers used in this study

Saccharomyces cerviciae		***Homo sapience***		***Neurospora crassa***		***Aspergillus nidulans***		***Aspergillus oryzae***	
Gene[a]	Accession number	Gene[a]	Accession number	Gene[a]	Accession number	Gene[a]	Accession number	Gene[a]	Accession number
Classical HDACs familly									
rpd3	YNL330C	*hdac1 / Hsrpd3*	NP_004955	*hda3 / Ncrpd3*	NCU00824	*rpdA / Anrpd3*	AN4493	*hdaB / Aorpd3*	AB744040
		hdac2 / Hsrpd3	NP_001518					*hdaC / Aorpd3*	AO080525000127
		hdac3 / Hsrpd3	NP_003874						
hos2	YGL194C			*hda2 / Nchos2*	NCU02795	*hosA / Anhos2*	AN3806	*hdaD / Aohos2*	AO080511000459
hos1	YPR068C								
hda1	YRL021W	*hdac6 / Hshda1*	NP_006035	*hda1 / Nchda1*	NCU01525	*hdaA / Anhda1*	AN8024	*hdaA / Aohda1*	AO080513000236
		hdac10 / Hshda1	NP_114408						
hos3	YPL116W			*hda4 / Nchos3*	NCU07018	*hosB / Anhos3*	AN7019	*hdaE / Aohos3*	AO080570000061
		hdac4	NP_006028						
		hdac5	NP_001015053						
		hdac7	NP_056216						
		hdac8	NP_060956						
		hdac9	NP_055522						
		hdac11	NP_079103						
TheSirtuin familly									
sir2	YDL042C	*sirt1 / Hssir2*	NP_036370	*nst1 / Ncsir2*	NCU04737	*sirA / Ansir2*	AN10449	*hstA / Aosir2*	AO080506000102
hst1	YOL068C								
hst2	YPL015C	*sirt2 / Hshst2*	NP_036369	*nst2 / Nchst2*	NCU00523	*AN7461/ Anhst2*	AN7461	*hstB / Aohst2*	AO080569000094
		sirt3 / Hshst2	NP_036371			*AN11873/ Anhst2*	AN11873	*hstC / Aohst2*	AO080508000293
hst3	YOR025W			*nst4 / Nchst3*	NCU04859				
hst4	YDR191W			*nst3 / Nchst4*	NCU03059	*AN1226 / Anhst4*	AN1226	*hstD / Aohst4*	AB744041
		sirt4	NP_036372	*nst5 / Ncsirt4*	NCU00203	*hstA / Ansirt4*	AN11067	*hstE / Aosirt4*	AO080559000113
		sirt5	NP_036373	*nst6 / Ncsirt5*	NCU05973	*AN1782 / Ansirt5*	AN1782	*hstF / Aosirt5*	AO080568000195
		sirt6	NP_057623	*nst7 / Ncsirt6*	NCU07624				
		sirt7	NP_057622						

[a] HDAC names of *Saccharomyces cerevisiae* or *Homo Sapiens* with the species name indicated followed by a slash.

[b] Hda : Histone DeAcetylase

[c] Hst : Homolog of SirTuins

Table S3. PCR primers used in this study

Primer name	Sequence(5' to 3')^{a,b}	Region or purpose
adeA-F	CCGTCATGTCCAGGAAGATAGGTCAG	*adeA* amplification
adeA-R	CTGCGCAACAGCATACGAGTCCACAG	
hdaB-A	CAATGGCATGACAAAGAACC	5' flanking region of *hdaB*
hdaB-B	CTGACCTATCTTCCTGGACATGACGGCTGTTCCTGCAACATGAGATACA	
hdaB-C	CTGTGGACTCGTATGCTGTTGCGCAGAAGATCCGTGCGCAAGTT	3'flanking region of *hdaB*
hdaB-D	CCATGGTGAATTAGGGCTCA	
hdaB-A2	CAATAGAATATTCCCCGCGT	fusion PCR for *hdaB*
hdaB-D2	CCCTTGGGATTAGAGTGCTT	
hdaB-F	GTTGATCGGGATGTCAAAGG	*hdaB* ORF
hdaB-G	AATTCTCGGTTCTGCTGGTG	
hdaC-A	TCTGTGCAAGCCTTATGTGC	5' flanking region of *hdaC*
hdaC-B	CTGACCTATCTTCCTGGACATGACGGTCCGTCGAGGTTAGTGACAA	
hdaC-C	CTGTGGACTCGTATGCTGTTGCGCAGTCACTTTGACTACGGAGGGCT	3'flanking region of *hdaC*
hdaC-D	GCCTCGAAATCATGGTCCTA	
hdaC-F	TGAGTGCCTCGTAATGCTTG	*hdaC* ORF
hdaC-G	GTGGGCAGGTTGAAACTCTT	
hdaD-A	TAACTGGCGCAGACCCATAA	5' flanking region of *hdaD*
hdaD-B	CTGACCTATCTTCCTGGACATGACGGCCCTTCTTCTCTTTCCTTATTGC	
hdaD-C	CTGTGGACTCGTATGCTGTTGCGCAGCTGTACGGTAAATGAAGGTCAGC	3'flanking region of *hdaD*
hdaD-D	AAGGGGTCAGATCCACAATG	
hdaD-A2	CGCAGACCCATAAGAAGGAA	fusion PCR for *hdaD*
hdaD-D2	CTGTGTCCACAACTGCCATT	
hdaD-F	GTTGTTTGGTCAGCGTCAGA	*hdaD* ORF
hdaD-G	CCCAAAGGTGACAAGACGAT	
hdaA-A	AACAAAGTGCCCTGTTGACC	5'flanking region of *hdaA*
hdaA-B	CTGACCTATCTTCCTGGACATGACGGCATTGCTATGGCTAGCACCA	
hdaA-C	CTGTGGACTCGTATGCTGTTGCGCAGTTTAGGACGTTCAGATGGGG	3'flanking region of *hdaA*
hdaA-D	TAGGTTTTCTGATGGCCCAG	
hdaA-F	GTGATGCCTATTGCACAGGA	*hdaA* ORF
hdaA-G	GCTTTCGGGTACATGCAACT	

hdaE-A	TCCGAAGTCCACTTTCTTGC	5' flanking region of *hdaE*
hdaE-B	CTGACCTATCTTCCTGGACATGACGGCAAATAGTAGGTTCATTTGGGGG	
hdaE-C	CTGTGGACTCGTATGCTGTTGCGCAGAGTCTATCGGACTTTTGGTCG	3'flanking region of *hdaE*
hdaE-D	AGATCCGGAGTCGTTCCTTT	
hdaE-A2	AGTCTCTTTTCTTTGGCCGC	fusion PCR for *hdaE*
hdaE-D2	ATTGTTCACGTTCTCCACCC	
hdaE-F	GGACCTTTACGCATCCAAGT	*hdaE* ORF
hdaE-G	GATGCGTGTTGGACATTAGC	
hstA-A	ATTACCTGGCGTTCTTGTGG	5'flanking region of *hst A*
hstA-B	CTGACCTATCTTCCTGGACATGACGGGGTTCTTGTTTGGAGGGTT	
hstA-C	CTGTGGACTCGTATGCTGTTGCGCAGCGGATTCTTCAACGAAGAGC	3'flanking region of *hstA*
hstA-D	ACAGCTGCGAACTGATGATG	
hstA-F	GATTTCCGGCTCTTGTGTGT	*hstA* ORF
hstA-G	GGTATTCCCGATTTTCGGTC	
hstB-A	CTTTGCTTTGAGTTCCTGCC	5'flanking region of *hstB*
hstB-B	CTGACCTATCTTCCTGGACATGACGGTCTAACCTGGCGGAGAGAAA	
hstB-C	CTGTGGACTCGTATGCTGTTGCGCAGTACCGCGAAAAGGAGAGAGA	3'flanking region of *hstB*
hstB-D	AACAGTCGGCGATGTATTCC	
hstB-F	CTTTTTCAGGGAGAATCCGC	*hstB* ORF
hstB-G	CGCTCCATGTTAATGAGCAC	
hstC-A	AGTCATGGAAAAGACTGCGG	5'flanking region of *hstC*
hstC-B	CTGACCTATCTTCCTGGACATGACGGATTGGACTCAGCCTGATTGG	
hstC-C	CTGTGGACTCGTATGCTGTTGCGCAGAGTGCCCGAATAGGTTTCTG	3'flanking region of *hstC*
hstC-D	AGCCATCGCTGTCAGTTTCT	
hstC-F	GCCTTGCTGGCTAAGAAGAA	*hstC* ORF
hstC-G	TCACACGACCCAAGGATACA	
hstD-A	TGCGGAAATGGGTTGTTT	5'flanking region of *hstD*
hstD-B	CTGACCTATCTTCCTGGACATGACGGATGGCACTTGTCGCATGTC	
hstD-C	CTGTGGACTCGTATGCTGTTGCGCAGGGCGTGGTGTAATTCTTCGT	3'flanking region of *hstD*
hstD-D	TAACCGTGACATGACCCTTG	
hstD-A2	TGAAAGGATTACCTCCTCCC	fusion PCR for *hstD*
hstD-D2	ACGTCCGGGATATTATGGGT	
hstD-F	ACCATCAAGTCCCAGCAATC	*hstD* ORF
hstD-G	AGACATCCATGCCTCCCTTA	

hstE-A	TCCATCTGATAAGGTTCGGC	5'flanking region of *hstE*
hstE-B	CTGACCTATCTTCCTGGACATGACGGAGATAATGGGTACGGCGAGA	
hstE-C	CTGTGGACTCGTATGCTGTTGCGCAGGGCGCTGTCCGAATGTATTA	3'flanking region of *hstE*
hstE-D	CCAGTGTACAATTCCGCCAT	
hstE-A2	ATAAGGTTCGGCATGAGTGG	fusion PCR for *hstE*
hstE-D2	GCCATGATACATCCAGCAGA	
hstE-F	AATATCTGGGGCAGACGAGA	*hstE* ORF
hstE-G	GGCACATTCTCAAGAGCACA	
hstF-A	ATTGACGAACCCTTGGACTG	5'flanking region of *hstF*
hstF-B	CTGACCTATCTTCCTGGACATGACGGGCGGGGTGTTGATAATGACT	
hstF-C	CTGTGGACTCGTATGCTGTTGCGCAGGGTATTATGGGGATTGTCGG	3'flanking region of *hstF*
hstF-D	TCTTCGTCTTCAAAGGCTCC	
hstF-A2	CGTCAGCTCACGGATTATGA	fusion PCR for *hstF*
hstF-D2	TCTCGTTTGCCTTAGCTGTG	
hstF-F	AGACATATGGCGCTGAAAGC	*hstF* ORF
hstF-G	GCAATGTGGAAGGACATCAG	
Fusion-hstD-F	tcgagctcggtacccATGGTGCGGTCGCTGTCCGAAGAGG	vector construction for *pUShstD*
Fusion-hstD-R	ctctagaggatccccTCATGCGGCCGGCTGATTTAACAAC	
Fusion-laeA-F	tcgagctcggtacccATGTTTGGAAACGGCCAGACTGGAC	vector construction for *pUSlaeA*
Fusion-laeA-R	ctctagaggatccccTCAGTTCGCAGGTTTCCGTGCTTGG	
laeA-A	CCGGCTGTTCAAGATCCATGGATAG	5'flanking region of *laeA*
laeA(adeA)-B	CTGACCTATCTTCCTGGACATGACGGTCGATGGCGACAGGCTGATG	
laeA(adeA)-C	CTGTGGACTCGTATGCTGTTGCGCAGAGAGCTCCATTACTGGGTATTCGG	3'flanking region of *laeA*
laeA-D	GAACCCGCCAACATCAAGCTTC	
laeA-A2	GGGATACCAACCACAACACCT	fusion PCR for *laeA*
laeA-D2	TTACGTTTGGGAACGGAGTCA	
laeA-F	CAGCCCTCAAACCACCCAAA	*laeA* ORF
laeA-G	TTGAACGCCTCCGACTTGAC	
laeA(sC)-B	GAACGAGACGAACGAGGAGCCATATTCGATGGCGACAGGCTGATG	disruption casette for *laeA* in *Δ hstD* background
laeA(sC)-C	CATACGGGCAGCTATTGCCAAGAGAAGAGCTCCATTACTGGGTATTCGG	
sC-F	ATATGGCTCCTCGTTCGTCTCGTTC	*sC* amplification
sC-R	TCTCTTGGCAATAGCTGCCCGTATG	

P-amyB-F	GGCAACTCGCTTACCGATTAC	confirmation of transformation of over expression construct
hstD-comp-B	GAACGAGACGAACGAGGAGCCATATTAACCGTGACATGACCCTTG	Complementation of *hstD*
adeA fusion sC-F	CATACGGGCAGCTATTGCCAAGAGACCGTCATGTCCAGGAAGATAGGTCA	
nested adeA-R	GCCTTGGTCTGGGAGTGT	
kojA-F	GGTTTCCAGGGCCTCATCAG	probe for *kojA*
kojA-R	GAGAAATCCGGGCCAGAACC	
kojR-F	CGGCCAGCTATGACCCCATT	probe for *kojR*
kojR-R	GGCGTCATGGGAGAGTGTGA	
kojT-F	CGAGGTGTCTCTTGCAAACC	probe for *kojT*
kojT-R	GTTCTGGGATAGGCGAACCA	
ipnA-F	CACCTACTCACGAGGTCAAC	probe for *ipnA*
ipnA-R	GTTGACCTCGTGAGTAGGTG	
laeA-F	AGCCCTCAAACCACCCAAAG	probe for *laeA*
laeA-R	TTGAACGCCTCCGACTTGAC	

[a] Additional nucleotides for fusion PCR are indicated by underlines

[b] Additional nucleotides for In-Fusion reaction are indicated in small letters

Table S4. Significantly changed genes in *ΔhstD*

Gene ID	Description	Fold change	FunCat categorization[a,b]	
		(*ΔhstD* / Control)	level 1	level 2
AO080553000121	KojT, putative transporter; present in the kojic acid biosynthetic gene cluster	105.5	[20][32]	[20.01][20.03][20.09][32.05][32.07]
AO080550000061	Hydroxyindole-O-methyltransferase and related SAM-dependent methyltransferases	102.5	[01]	[01.05][01.20]
AO080501000196	fleA fucose-specific lectin	61.82	#	#
AO080563000007	CpaD, O-dimethylallyltransferase (DMAT); dimethylallylates cAATrp to form beta-cyclopiazonic acid	49.39	#	#
AO080554000441	Uncharacterized membrane protein, predicted efflux pump	38.39	[20][32]	[20.01][32.07]
AO080563000004	Predicted protein	32.27	[20][32][34]	[20.01][20.03][20.09][32.05][32.07][34.11]
AO080525000393	Predicted protein	29.96	[01][11]	[01.02][11.02]
AO080563000005	Cytochrome P450 CYP3 CYP5 CYP6 CYP9 subfamilies	27.59	[01]	[01.06][01.20]
AO080563000006	Predicted protein	25.97	#	#
AO080508000254	Predicted protein	24.93	[01]	[01.05]
AO080511000457	Predicted protein	21.4	#	#
AO080522000026	Catalase (peroxidase I)	20.19	[32]	[32.07]
AO080536000097	Predicted protein	19.6	#	#
AO080542000015	Predicted protein	19.4	[32]	[32.05]
AO080515000039	Predicted protein	17.93	#	#
AO080550000056	Proteins containing the FAD binding domain	14.42	[01]	[01.05][01.20]
AO080508000512	mleA lectin	12.87	#	#
AO080515000015	Uncharacterized protein, possibly involved in utilization of glycolate and propanediol	12.31	#	#
AO080513000111	Predicted protein	11.85	#	#
AO080529000071	Predicted protein	10.43	#	#
AO080508000290	Predicted protein	10.11	#	#
AO080523000388	Predicted protein	9.984	#	#
AO080554000006	Predicted protein	9.951	#	#
AO080550000062	Dehydrogenases (flavoproteins)	9.86	#	#
AO080525000250	Predicted protein	9.747	#	#
AO080553000119	KojA, FAD-dependent oxidoreductase; present in the kojic acid biosynthetic gene cluster	9.711	#	#
AO080541000467	Predicted protein	9.668	#	#
AO080550000076	Predicted protein	9.323	#	#
AO080539000068	Predicted protein	9.028	#	#
AO080510000132	Predicted protein	8.772	#	#
AO080529000068	Predicted protein	8.053	#	#
AO080554000051	Predicted protein	7.73	#	#
AO080550000193	RNA 3 -terminal phosphate cyclase	7.67	#	#
AO080551000140	Polyketide synthase modules and related proteins	7.028	[01][32]	[01.20][32.05]
AO080511000259	Predicted protein	6.937	#	#
AO080523000239	TPR repeat	6.617	#	#
AO080537000053	Predicted hydrolases or acyltransferases (alpha beta hydrolase superfamily)	6.315	#	#
AO080527000194	Predicted xylanase chitin deacetylase	6.251	[01][16]	[01.05][01.25][16.05]
AO080551000190	Beta-lactamase class C and other penicillin binding proteins	6.175	#	#
AO080508000358	Predicted protein	5.923	#	#
AO080515000064	Multicopper oxidases	5.855	[01][32]	[01.05][01.07][01.25][32.07]
AO080527000284	Predicted protein	5.77	#	#

AO080549000421	Predicted protein	5.727	#	#
AO080550000107	Predicted protein	5.723	#	#
AO080523000444	Predicted protein	5.71	#	#
AO080567000074	Predicted protein	5.689	#	#
AO080541000077	Predicted protein	5.673	#	#
AO080523000389	Cytochrome P450 CYP4 CYP19 CYP26 subfamilies	5.589	[32]	[32.07]
AO080521000213	Predicted protein	5.575	#	#
AO080547000015	Predicted protein	5.394	#	#
AO080523000405	Predicted protein	5.171	[32][42]	[32.01][42.01][42.04]
AO080527000412	Predicted protein	5.107	#	#
AO080525000701	Alkaline phosphatase	5.07	[01]	[01.04][01.06][01.07]
AO080523000550	Predicted protein	4.932	#	#
AO080562000080	aflJ Predicted protein	4.922	#	#
AO080554000398	Predicted protein	4.746	#	#
AO080525000625	Predicted protein	4.693	#	#
AO080541000440	Predicted protein	4.676	#	#
AO080530000095	Predicted protein	4.602	#	#
AO080554000103	Cytochrome P450 CYP3 CYP5 CYP6 CYP9 subfamilies	4.597	[01][20][32]	[01.01][01.02][01.06][01.20][20.01][32.07]
AO080547000014	Ankyrin	4.512	#	#
AO080549000406	Predicted dehydrogenases and related proteins	4.472	[01][11]	[01.05][11.02]
AO080508000357	Chitin synthase hyaluronan synthase (glycosyltransferases)	4.45	#	#
AO080523000006	Predicted protein	4.401	#	#
AO080525000059	Cytochrome P450 CYP2 subfamily	4.37	[01][16][20][32]	[01.06][01.07][01.20][16.17][16.21][20.01][32.07]
AO080523000500	Predicted protein	4.32	#	#
AO080527000186	Oxidosqualene-lanosterol cyclase and related proteins	4.272	[01]	[01.06][01.20]
AO080523000718	Carboxylesterase type B	4.266	#	#
AO080529000067	Cytochrome P450 CYP11 CYP12 CYP24 CYP27 subfamilies	4.247	[01][32]	[01.01][01.20][32.07]
AO080515000065	Predicted protein	4.223	#	#
AO080532000090	Predicted protein	4.183	#	#
AO080508000361	Predicted protein	4.159	#	#
AO080551000170	Predicted protein	4.114	[01][16]	[01.01][01.20][16.17]
AO080525000706	Predicted protein	4.098	#	#
AO080532000546	Cytochrome P450 CYP2 subfamily	4.046	[01][16][20]	[01.20][16.17][16.21][20.01]
AO080508000305	Vesicular amine transporter	4.008	#	#
AO080527000377	Glucose dehydrogenase choline dehydrogenase mandelonitrile lyase (GMC oxidoreductase family)	4.008	[01][16][20]	[01.01][01.05][01.20][16.21][20.01]
AO080531000104	Predicted protein	3.951	#	#
AO080525000269	Predicted protein	3.848	#	#
AO080557000082	Cofilin; actin depolymerisation factor	3.847	#	#
AO080532000337	Chaperone-dependent E3 ubiquitin protein ligase (contains TPR repeats)	3.838	#	#
AO080523000512	Predicted protein	3.774	#	#
AO080523000573	Predicted protein	3.77	#	#
AO080536000086	ATPases of the AAA$^+$ class	3.719	#	#
AO080515000151	Predicted protein	3.707	[43]	[43.01]
AO080525000687	Predicted transporter (major facilitator superfamily)	3.648	#	#
AO080557000045	Predicted protein	3.624	[32]	[32.05]

AO080515000071	Predicted protein	3.604	#	#
AO080501000080	Predicted protein	3.559	#	#
AO080566000093	Ankyrin	3.555	#	#
AO080525000026	SAM-dependent methyltransferases	3.536	#	#
AO080515000098	Predicted protein	3.503	#	#
AO080554000362	Predicted protein	3.493	#	#
AO080503000171	Phosphoenolpyruvate carboxykinase (ATP)	3.468	[01][02]	[01.04][01.05][02.01]
AO080523000572	Predicted protein	3.423	#	#
AO080533000376	Multidrug resistance-associated protein mitoxantrone resistance protein, ABC superfamily	3.391	[01][16][20][32]	[01.04][16.19][20.03][32.07]
AO080508000531	Predicted protein	3.39	#	#
AO080549000304	Carboxylesterase type B	3.38	[01]	[01.06]
AO080506000286	Predicted protein	3.315	#	#
AO080523000216	Predicted protein	3.303	#	#
AO080538000066	Acyl-CoA synthetase	3.298	[01]	[01.01][01.05][01.20]
AO080523000032	Amino acid transporters	3.296	[01][20][32][34]	[01.06][20.01][20.03][20.09[32.01][34.01][34.11]
AO080510000108	ATPases of the AAA$^+$ class	3.199	#	#
AO080513000093	Jacalin-like lectin domain-containing protein	3.158	#	#
AO080525000640	Predicted protein	3.156	#	#
AO080527000200	Chitinase	3.085	[01]	[01.05][01.25]
AO080553000120	KojR, Zn(II)2Cys6 transcription factor; induced by kojic acid; present in the kojic acid biosynthetic gene cl	3.083	[11][34]	[11.02][34.11]
AO080525000062	Acetylcholinesterase Butyrylcholinesterase	3.076	[01][32]	[01.05][01.06][01.20][01.25][32.05][32.07][32.10]
AO080541000359	Integral membrane ankyrin-repeat protein Kidins220 (protein kinase D substrate)	3.076	#	#
AO080541000097	Predicted transporter (major facilitator superfamily)	3.063	[20][32]	[20.01][32.07]
AO080546000223	Predicted protein	3.039	#	#
AO080542000014	Cytochrome P450 CYP4 CYP19 CYP26 subfamilies	3.037	[01][32]	[01.01][32.05][32.07]
AO080539000029	Predicted protein	3.016	[11]	[11.02]
AO080547000070	Predicted protein	2.985	#	#
AO080523000242	Predicted protein	2.977	#	#
AO080502000014	Uncharacterized conserved protein	2.976	#	#
AO080503000338	NAD$^+$ ADP-ribosyltransferase Parp, required for poly-ADP ribosylation of nuclear proteins	2.959	[01][10][14][16]	[01.05][10.01][14.07][16.01][16.03]
AO080506000124	Predicted protein	2.951	#	#
AO080542000029	Conserved protein domain typically associated with flavoprotein oxygenases, DIM6 NTAB family	2.943	#	#
AO080521000317	Predicted protein	2.904	#	#
AO080536000058	Predicted protein	2.901	#	#
AO080518000104	Predicted protein	2.888	#	#
AO080551000149	Predicted protein	2.88	#	#
AO080550000101	Predicted protein	2.853	#	#
AO080501000088	3-polyprenyl-4-hydroxybenzoate decarboxylase and related decarboxylases	2.843	#	#
AO080509000188	Predicted aminoglycoside phosphotransferase	2.835	#	#
AO080554000077	Monodehydroascorbate ferredoxin reductase	2.835	[02]	[02.11]
AO080536000060	Predicted protein	2.826	#	#
AO080506000051	Predicted short chain-type dehydrogenase	2.821	[01][32]	[01.05][01.20][32.05]
AO080549000353	ATP adenylyltransferase (5 ,5 -P-1, P-4-tetraphosphate phosphorylase II)	2.812	[01][11][16][20]	[01.04][01.06][11.04][16.17][16.19][20.01][20.03][20.09]

AO080523000207	Predicted protein	2.766	#	#
AO080536000143	Tellurite resistance protein and related permeases	2.743	#	#
AO080505000118	Predicted protein	2.726	#	#
AO080546000372	Ornithine aminotransferase	2.705	[01][16]	[01.01][01.02][01.20][16.21]
AO080505000202	Methionyl-tRNA formyltransferase	2.701	#	#
AO080522000033	Predicted protein	2.694	#	#
AO080509000132	Predicted protein	2.686	#	#
AO080546000363	Predicted protein	2.676	#	#
AO080534000002	Non-ribosomal peptide synthetase modules and related proteins	2.663	#	#
AO080561000015	Predicted protein	2.659	#	#
AO080532000416	Threonine dehydrogenase and related Zn-dependent dehydrogenases	2.657	[01][02][16]	[01.01][01.05][02.16][16.17]
AO080515000061	Uncharacterized conserved protein	2.644	#	#
AO080503000025	Predicted protein	2.631	#	#
AO080525000209	Dihydrolipoamide succinyltransferase (2-oxoglutarate dehydrogenase, E2 subunit)	2.617	#	#
AO080541000475	Glutathione S-transferase	2.593	[32][40]	[32.01][32.07][40.10]
AO080512000001	Transposon-encoded proteins with TYA, reverse transcriptase, integrase domains in various combinations	2.561	#	#
AO080523000247	Predicted acyl-CoA transferases carnitine dehydratase	2.553	#	#
AO080508000270	RNA polymerase II transcription termination factor TTF2 lodestar, DEAD-box superfamily	2.541	#	#
AO080523000391	Cytochrome P450 CYP3 CYP5 CYP6 CYP9 subfamilies	2.519	[16][32]	[16.21][32.05][32.07]
AO080527000504	Predicted protein	2.503	#	#
AO080525000318	Predicted protein	2.501	#	#
AO080566000091	Predicted protein	2.493	#	#
AO080503000216	Predicted protein	2.492	#	#
AO080523000079	Beta-lactamase class C and other penicillin binding proteins	2.491	#	#
AO080532000061	Uncharacterized conserved protein	2.483	[20]	[20.01][20.03][20.09]
AO080505000203	Nucleoside-diphosphate-sugar epimerases	2.467	[01][11][42]	[01.05][11.02][42.10]
AO080513000020	Predicted protein	2.459	#	#
AO080505000159	Alcohol dehydrogenase, class V	2.446	[01][02][16][42]	[01.05][01.20][02.01][02.16][16.17][42.01]
AO080546000050	Protein tyrosine serine phosphatase	2.442	[14]	[14.07]
AO080531000027	Dimethylglycine dehydrogenase precursor	2.426	[01][16][20]	[01.01][01.02][01.05][16.21][20.01]
AO080501000014	wykB, FAD-dependent oxidoreductase	2.412	[14]	[14.07]
AO080567000034	Predicted protein	2.409	#	#
AO080536000139	7-keto-8-aminopelargonate synthetase and related enzymes	2.406	#	#
AO080523000390	Cytochrome P450 CYP4 CYP19 CYP26 subfamilies	2.401	[01]	[01.01]
AO080563000003	Synaptic vesicle transporter SVOP and related transporters (major facilitator superfamily)	2.394	[20][32][34]	[20.01][20.03][20.09][32.05][32.07][34.11]
AO080520000010	Reverse transcriptase	2.393	#	#
AO080527000001	Predicted protein	2.392	#	#
AO080546000314	Predicted protein	2.368	#	#
AO080537000005	Predicted flavin-nucleotide-binding protein structurally related to pyridoxine 5 -phosphate oxidase	2.363	#	#
AO080568000203	Predicted protein	2.359	#	#
AO080521000212	Predicted protein	2.35	#	#
AO080515000262	ATP-dependent RNA helicase	2.337	#	#
AO080506000125	ADP-ribose pyrophosphatase	2.331	[01][16][32]	[01.03][16.17][32.01]
AO080548000022	Zn-finger	2.326	#	#
AO080533000254	Inositol monophosphatase	2.32	[01][30]	[01.04][01.05][01.06][01.20][30.01]

AO080554000301	Predicted protein	2.319	#	#
AO080509000068	Predicted protein	2.315	#	#
AO080521000046	Putative dehydrogenase domain of multifunctional non-ribosomal peptide synthetases and related enzymes	2.299	[01][20][34]	[01.20][20.01][34.01]
AO080561000093	Predicted protein	2.298	#	#
AO080503000246	Predicted transporter (major facilitator superfamily)	2.293	[01][20][34]	[01.05][20.01][20.03][20.09][34.01][34.11]
AO080523000538	Predicted glutamine synthetase	2.287	#	#
AO080528000042	Permease of the major facilitator superfamily	2.284	[20]	[20.01][20.03][20.09]
AO080523000723	Acetyltransferases, including N-acetylases of ribosomal proteins	2.282	#	#
AO080570000066	Permease of the major facilitator superfamily	2.263	[20]	[20.01][20.03][20.09]
AO080569000133	Predicted protein	2.255	[10][11][42]	[10.03][11.04][11.06][42.16]
AO080523000499	Predicted protein	2.238	#	#
AO080527000070	Lactoylglutathione lyase and related lyases	2.231	#	#
AO080553000127	Predicted protein	2.231	#	#
AO080567000088	Predicted protein	2.219	#	#
AO080551000005	Spt6 ortholog, DNA-binding subunit of a DNA-dependent protein kinase (Ku70 autoantigen)	2.214	[10][11]	[10.01][11.02]
AO080515000013	Predicted protein	2.212	#	#
AO080537000052	Predicted protein	2.212	#	#
AO080550000146	Exopolyphosphatase	2.207	[01][11][30]	[01.05][11.02][30.01]
AO080527000050	Predicted protein	2.19	#	#
AO080511000186	Predicted protein	2.175	#	#
AO080509000038	Predicted protein	2.172	[43]	[43.01]
AO080515000014	Predicted protein	2.168	#	#
AO080532000091	Cysteine desulfurase NFS1	2.162	[01]	[01.20]
AO080511000049	Predicted protein	2.161	#	#
AO080511000294	Predicted protein	2.16	#	#
AO080523000130	Predicted protein	2.157	#	#
AO080536000059	Predicted protein	2.152	#	#
AO080508000090	Predicted protein	2.151	#	#
AO080527000162	Predicted protein	2.147	[30][34][43]	[30.01][34.11][43.01]
AO080501000155	Predicted transporter (major facilitator superfamily)	2.145	[01][20]	[01.05][20.01][20.03][20.09]
AO080505000279	Predicted protein	2.142	#	#
AO080508000097	3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase	2.139	[01]	[01.01][01.05][01.20]
AO080523000024	Glycerol uptake facilitator and related permeases (Major Intrinsic Protein Family)	2.129	#	#
AO080501000008	wykN, Non-ribosomal peptide synthetase modules and related proteins	2.117	#	#
AO080539000074	Predicted protein	2.097	#	#
AO080518000037	Predicted transporter (major facilitator superfamily)	2.073	[20][32]	[20.01][20.03][20.09][32.05][32.07]
AO080541000154	Carboxypeptidase C (cathepsin A)	2.062	[14]	[14.13]
AO080567000053	Predicted protein	2.062	#	#
AO080550000102	Predicted acyl esterases	2.055	#	#
AO080505000097	Transthyretin and related proteins	2.053	[01]	[01.02][01.03]
AO080546000347	Catalase (peroxidase I)	2.051	[20][32][42]	[20.01][32.01][32.07][42.16]
AO080533000188	Predicted protein	2.046	#	#
AO080551000123	Predicted protein	2.039	#	#
AO080562000073	Predicted protein	2.036	#	#
AO080551000142	Predicted protein	2.034	#	#
AO080532000609	Predicted protein	2.032	#	#

AO080527000203	Isocitrate isopropylmalate dehydrogenase	2.021	[01][02][16][20]	[01.01][01.05][02.01][02.10][16.21][20.01]
AO080525000648	Predicted protein	2.02	#	#
AO080571000012	Molecular chaperone (DnaJ superfamily)	2.014	#	#
AO080523000419	Predicted protein	2.007	#	#
AO080531000318	2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases	2.004	[01]	[01.05][01.20]
AO080504000029	Phospholipase C	2.002	#	#
AO080533000108	Protein kinase PCTAIRE and related kinases	2.001	[01][02][10][11][14][16][18][30][34][40]	[01.04][01.05][02.19][10.01][10.03][11.02][14.07][16.01][16.03][16.19][18.01][18.02][30.01][30.05][34.05][34.11][40.01][42.10][43.01]
AO080505000181	Glycosyltransferase	0.498	[01][02][32][34][43	[01.05][02.19][32.01][34.11][43.01]
AO080503000128	Predicted protein	0.496	#	#
AO080521000172	Predicted membrane protein	0.496	#	#
AO080514000015	Transcription factor PRD and related proteins, contain PAX and HOX domains	0.495	#	#
AO080531000179	Predicted protein	0.494	#	#
AO080503000252	Predicted protein	0.492	#	#
AO080546000219	Predicted protein	0.492	#	#
AO080560000080	Predicted protein	0.492	#	#
AO080513000270	Predicted protein	0.491	#	#
AO080508000004	Predicted protein	0.487	#	#
AO080503000123	Predicted protein	0.486	#	#
AO080513000060	Alpha-amylase	0.485	[01]	[01.05]
AO080532000307	Predicted protein	0.481	#	#
AO080554000482	NADPH:quinone reductase and related Zn-dependent oxidoreductases	0.481	[01][16]	[01.05][01.20][16.17]
AO080523000408	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	0.48	#	#
AO080550000156	Predicted protein	0.479	#	#
AO080513000204	Predicted protein	0.478	#	#
AO080560000087	Predicted protein	0.478	#	#
AO080505000104	Predicted protein	0.476	#	#
AO080568000096	Cytochrome P450 CYP4 CYP19 CYP26 subfamilies	0.474	[01][02]	[01.06][01.20][02.45]
AO080523000182	Acetylcholinesterase Butyrylcholinesterase	0.47	#	#
AO080532000189	Predicted protein	0.469	[11][14]	[11.06][14.07][14.13]
AO080570000072	Cytochrome P450 CYP4 CYP19 CYP26 subfamilies	0.469	[01][32]	[01.01][32.05][32.07]
AO080561000074	Endopolygalacturonase	0.468	#	#
AO080511000067	Predicted protein	0.466	#	#
AO080533000118	Predicted protein	0.464	#	#
AO080508000310	Ketopantoate hydroxymethyltransferase	0.463	[01][42]	[01.07][42.01]
AO080523000640	Sorbin and SH3 domain-containing protein	0.463	[10]	[10.03]
AO080536000108	Predicted protein	0.459	#	#
AO080508000430	Predicted protein	0.457	#	#
AO080521000200	Predicted protein	0.456	[20][34]	[20.01][34.11]
AO080522000004	Cytochrome P450	0.456	#	#
AO080506000272	Predicted protein	0.455	#	#
AO080557000027	Predicted protein	0.455	#	#
AO080555000231	Predicted protein	0.454	#	#
AO080523000128	Predicted protein	0.453	#	#

AO080533000173	Predicted protein	0.453	#	#
AO080508000082	Predicted protein	0.451	#	#
AO080515000125	Permeases of the major facilitator superfamily	0.449	[20]	[20.01][20.03][20.09]
AO080542000184	Cytochrome P450 CYP4 CYP19 CYP26 subfamilies	0.448	#	#
AO080533000250	Predicted protein	0.447	#	#
AO080549000362	Endonuclease III	0.447	[01][10][16][32]	[01.03][10.01][16.03][16.17][16.21][32.01]
AO080523000306	Predicted protein	0.442	#	#
AO080532000098	beta-1,6-N-acetylglucosaminyltransferase, contains WSC domain	0.442	#	#
AO080536000028	Predicted protein	0.442	#	#
AO080550000149	Predicted protein	0.441	#	#
AO080513000148	Amidases	0.44	[01]	[01.02]
AO080508000396	Acetylornithine aminotransferase	0.438	[01]	[01.07][01.20]
AO080501000092	Nucleoside phosphorylase	0.437	#	#
AO080521000357	Predicted protein	0.437	#	#
AO080536000070	Predicted transporter (major facilitator superfamily)	0.437	[01][20][32][34]	[01.07][20.01][20.09][32.07][34.01]
AO080532000519	Predicted protein	0.435	#	#
AO080503000049	Serine threonine protein kinase	0.434	#	#
AO080508000367	Predicted protein	0.433	[01]	[01.04]
AO080541000303	Predicted protein	0.433	#	#
AO080525000618	Predicted protein	0.432	#	#
AO080529000044	Predicted Zn-dependent hydrolases of the beta-lactamase fold	0.432	#	#
AO080550000111	Predicted protein	0.432	#	#
AO080508000204	Predicted dehydrogenase	0.431	#	#
AO080523000678	Predicted protein	0.431	[10][16]	[10.01][16.03]
AO080515000221	Aspartyl protease	0.43	[01][14]	[01.25][14.13]
AO080521000254	1-Acyl dihydroxyacetone phosphate reductase and related dehydrogenases	0.427	[01][43]	[01.05][01.06][43.01]
AO080523000411	Predicted protein	0.426	#	#
AO080541000075	Predicted protein	0.426	#	#
AO080501000186	Predicted protein	0.424	#	#
AO080538000052	Uncharacterized conserved protein	0.419	#	#
AO080508000165	FAD FMN-containing dehydrogenases	0.418	[01]	[01.20]
AO080501000074	nucS nuclease S1 precursor	0.416	[01]	[01.03]
AO080523000712	Permeases of the major facilitator superfamily	0.416	[01][20]	[01.05][20.01][20.03]
AO080530000037	Signal transduction histidine kinase	0.413	#	#
AO080515000068	Carboxylesterase and related proteins	0.412	#	#
AO080515000315	Fructose tagatose bisphosphate aldolase	0.412	[01][02]	[01.05][02.01][02.07]
AO080539000047	Predicted protein	0.412	#	#
AO080558000032	Permeases of the major facilitator superfamily	0.41	#	#
AO080550000154	Amino acid transporters	0.409	#	#
AO080531000003	SAM-dependent methyltransferases	0.402	#	#
AO080502000037	NADPH:quinone reductase and related Zn-dependent oxidoreductases	0.399	#	#
AO080523000067	Predicted metal-dependent hydrolase with the TIM-barrel fold	0.399	#	#
AO080525000576	Predicted protein	0.398	#	#
AO080515000209	Uncharacterized protein conserved in bacteria	0.395	#	#
AO080553000093	Predicted protein	0.394	#	#
AO080549000130	Predicted transporter (major facilitator superfamily)	0.393	[01][20][34]	[01.05][20.01][20.03][20.09][34.01]

AO080530000032	Predicted protein	0.385	#	#
AO080533000073	Predicted protein	0.379	#	#
AO080503000122	Predicted protein	0.371	#	#
AO080513000198	Cytochrome P450 CYP2 subfamily	0.369	#	#
AO080521000073	Aldo keto reductase family proteins	0.369	[01][02][16][32][34]	[01.01][01.05][01.06][01.07][01.20][02.01][02.16][16.21][32.01][32.10][34.11]
AO080521000107	Flavonol reductase cinnamoyl-CoA reductase	0.369	[01][02][32][42]	[01.05][01.07][01.20][02.01][32.01][32.07][42.01]
AO080567000015	Predicted protein	0.369	#	#
AO080505000144	Predicted protein	0.368	#	#
AO080503000326	Predicted protein	0.367	#	#
AO080508000394	Predicted protein	0.366	#	#
AO080515000088	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	0.366	[01][02][43]	[01.05][01.06][01.20][02.25][43.01]
AO080508000236	Predicted protein	0.363	#	#
AO080531000178	Predicted protein	0.362	#	#
AO080522000018	Fatty acid desaturase	0.356	[01]	[01.06]
AO080533000203	Cytochrome P450 CYP3 CYP5 CYP6 CYP9 subfamilies	0.355	[01][20][32]	[01.06][01.20][20.01][32.05][32.07]
AO080508000166	Synaptic vesicle transporter SVOP and related transporters (major facilitator superfamily)	0.354	[20]	[20.01]
AO080541000328	1-aminocyclopropane-1-carboxylate synthase, and related proteins	0.353	[01][36][40]	[01.02][01.05][01.20][36.02][40.02]
AO080610000005	Predicted protein	0.343	#	#
AO080502000006	Endo-1,4-beta-glucanase IV	0.34	[01]	[01.05][01.25]
AO080554000005	Predicted protein	0.338	#	#
AO080539000025	Predicted protein	0.332	[10][14][20][32][42	[10.01][10.03][14.07][20.01][32.01][32.07][42.25]
AO080515000066	Permease of the major facilitator superfamily	0.331	[20]	[20.01][20.03][20.09]
AO080523000164	Predicted protein	0.328	[32]	[32.07]
AO080525000600	Mg^{2+} and Co^{2+} transporters	0.325	#	#
AO080530000035	Predicted protein	0.325	#	#
AO080536000027	manD, Endo-beta-mannanase	0.319	[01]	[01.05]
AO080541000084	Predicted protein	0.316	[01]	[01.05]
AO080521000262	Predicted protein	0.314	#	#
AO080525000417	Predicted protein	0.314	#	#
AO080551000032	Predicted protein	0.314	#	#
AO080541000430	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	0.309	#	#
AO080503000237	Predicted protein	0.308	#	#
AO080525000729	Probable taurine catabolism dioxygenase	0.308	[01]	[01.02]
AO080521000084	2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase	0.302	[01]	[01.20]
AO080513000199	Predicted protein	0.299	#	#
AO080523000583	Predicted protein	0.299	#	#
AO080523000582	Predicted transporter (major facilitator superfamily)	0.289	[01][20][34][41]	[01.05][20.01][20.03][20.09][34.01][34.11][41.01]
AO080523000410	Predicted protein	0.288	#	#
AO080528000012	Predicted protein	0.283	#	#
AO080532000211	Ca^{2+} Na^{+} antiporter	0.28	#	#
AO080503000406	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	0.276	[01][16]	[01.05][01.20][16.21]
AO080513000058	Predicted protein	0.275	#	#

AO080562000011	Amino acid transporters	0.274	[20]	[20.01][20.03][20.09]
AO080525000086	Predicted protein	0.271	[01]	[01.05][01.25]
AO080508000345	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	0.269	[01][02][10][16][20][30][32][34]	[01.05][01.06][01.07][01.20][02.07][10.03][16.01][16.21][20.01][30.05][32.05][34.01]
AO080549000389	Sorbitol dehydrogenase	0.269	[01][02][16]	[01.01][01.05][01.07][01.20][02.16][16.17][16.21]
AO080536000095	Predicted protein	0.266	#	#
AO080532000017	Phenylpropionate dioxygenase and related ring-hydroxylating dioxygenases, large terminal subunit	0.263	#	#
AO080554000001	H^+ oligopeptide symporter	0.259	[20]	[20.01][20.03][20.09]
AO080532000023	Predicted protein	0.258	#	#
AO080525000588	1-aminocyclopropane-1-carboxylate synthase, and related proteins	0.251	[01]	[01.02][01.05][01.20]
AO080510000163	Predicted protein	0.244	#	#
AO080541000142	WD40 repeat	0.243	#	#
AO080513000202	Chitinase	0.24	#	#
AO080531000064	Predicted protein	0.24	#	#
AO080531000061	Predicted protein	0.238	#	#
AO080541000150	Predicted protein	0.228	#	#
AO080549000322	Protocatechuate 3,4-dioxygenase beta subunit	0.225	#	#
AO080525000018	Predicted protein	0.224	#	#
AO080532000465	Predicted protein	0.221	#	#
AO080532000197	Synaptic vesicle transporter SVOP and related transporters (major facilitator superfamily)	0.216	[20][32][34]	[20.01][20.03][20.09][32.05][32.07][34.11]
AO080530000022	Predicted protein	0.208	#	#
AO080523000427	Permease of the major facilitator superfamily	0.193	#	#
AO080513000203	Predicted protein	0.19	#	#
AO080521000112	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	0.172	[01]	[01.05][01.06][01.20]
AO080501000148	Hydroxyindole-O-methyltransferase and related SAM-dependent methyltransferases	0.162	[01]	[01.05][01.20]
AO080501000144	Glutaminyl cyclase	0.155	[01][14]	[01.01][14.07][14.13]
AO080501000147	Predicted protein	0.151	#	#
AO080532000466	Predicted protein	0.142	#	#
AO080554000025	Amino acid transporters	0.14	[20]	[20.01][20.09]
AO080501000146	Predicted protein	0.136	#	#
AO080501000145	Predicted protein	0.135	#	#
AO080561000089	Endo-1,4-beta-xylanase G2	0.111	[01]	[01.05]
AO080536000049	Predicted protein	0.0778	#	#
AO080508000347	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	0.0748	#	#
AO080522000002	Predicted protein	0.0479	#	#
AO080513000200	Predicted protein	0.0336	#	#
AO080501000141	Predicted protein	0.0322	#	#

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[a] FunCat (http://www.webcitation.org/getfile?fileid=be4936ae25ebb5dfb89b687842ea640f8acf7790) is the organism independent functional description of proteins. FunCat consists of 28 main functional categories (level 1). The level 1 is the most general one, whereas level 2 shows much more detail.

[b] #: Unclassified gene

[c] Detailed descriptions of each category are available at the MIPS Functional Catalogue Database (http://mips.helmholtz-muenchen.de/proj/funcatDB/)