

**Table S4. Putative essential genes in the *A. fumigatus* genome.**

<i>A. fumigatus</i> pub_locus	Query protein (yeast)	KOG ID	(predicted) KOG function	Multiprotein complex	Functional category <sup>a</sup>	Yeast knockout <sup>b</sup>	Worm knockout <sup>b</sup>
Afu3g02320	YOR077W	KOG2837	Protein involved in rRNA processing and ribosomal assembly	?	A	0	1
Afu3g04310	YLR409C	KOG1539	DNA polymerase ? processivity subunit, inactivated phosphatase	DNA polymerase ? holoenzyme	L	0	0
Afu6g05090	YGR200C	KOG1063	RNA polymerase II elongator complex, subunit ELP2, WD repeat protein	RNA polymerase II elongator complex	K	1	X
Afu6g04870	YGL095C	KOG1299	Vacuolar sorting protein VPS45/Stt10 (Sec1 family)	t-SNARE complex	O	1	X
Afu6g04810	YHR058C	KOG3169	RNA polymerase II transcriptional regulation mediator	Mediator complex [120]	K	0	X
Afu6g04610	YNL113W	KOG3438	Subunit common to RNA polymerases I (A) and III (C); Rpc19p	RNAP I and III holoenzymes	K	0	1
Afu6g04510	YKR038C	KOG2708	tRNA-specific adenosine-34 deaminase subunit Tad3p	Heterodimeric RNA-specific deaminase	A	0	X
Afu6g04400	YNL039W	KOG2009	NEDD8-activating complex, UBA3 subunit	NEDD8-activating complex	O	1	1
Afu6g04290	YLL031C	KOG2126	DNA primase, large subunit	DNA polymerase ? :primase complex	L	0	0
Afu6g04260	YAL025C	KOG3064	RNA-binding nuclear protein containing a distinct C4 Zn-finger; implicated in the biogenesis of 60S ribosomal subunits [111]	Processosome	A	0	0
Afu6g04010	YGL238W	KOG1992	Transcription initiation factor TFIIIB, Bdp1 subunit (Myb domain)	TFIIIB	K	0	0
Afu6g02700	YOL034W	KOG0979	Structural maintenance of chromosome protein 5 (cohesin subunit SMC5)	Sister chromatid cohesion complex	L	0	X
Afu6g02270	YNL221C	KOG3322	RNase P/MRP subunit, involved in processing of pre-tRNAs and the 5.8S rRNA	RNase P/MRP holoenzyme	A	0	1
Afu7g01850	YNR003C	KOG3233	RNA polymerase III subunit C34	RNAP III holoenzyme	K	0	1
Afu5g04335	YLR005W	KOG2807	RNA polymerase II transcription initiation/nucleotide excision repair factor TFIIH, subunit SSL1	TFIIH	K, I	0	0
Afu7g02620	YOR210W	KOG3497	RNA polymerase II subunit; Rpb10p	RNAP II holoenzyme	K	0	X
Afu4g04360	YPL122C	KOG3471	RNA polymerase II transcription initiation/nucleotide excision repair factor TFIIH, subunit TFB2	TFIIH	K	0	X
Afu6g06430	YOR145C	KOG3273	Predicted RNA-binding protein containing KH domain, interacts with Nob1p	26S proteasome, pre-40S subunit	A, O	0	0
Afu6g06440	YBL041W	KOG0179	20S proteasome, regulatory subunit beta type PSMB1/PRE7 (paralog of KOG0185)	20S proteasome	O	0	0
Afu6g06450	YFR050C	KOG0185	20S proteasome, regulatory subunit beta type PSMB4/PRE4 (paralog of KOG0179)	20S proteasome	O	0	0
Afu6g07690	YBR236C	KOG1975	DNA mismatch repair ATPase, MLH1	Mismatch repair complex	L	1	1
Afu6g07760	YPR108W	KOG0687	26S proteasome regulatory complex, subunit RPN7/PSMD6	26S proteasome	O	0	0

Afu6g08100	YML038C	KOG1443	Multitransmembrane protein, predicted drug/metabolite transporter	?	R	1	X
Afu6g08210	YDR489W	KOG3176	Predicted $\alpha$ -helical protein, possibly involved in replication/repair; paralog of KOG3636	A novel complex with PCNA involved in replication?	L?	0	X
Afu6g08300	YPR010C	KOG0216	RNA polymerase I, second largest subunit	RNAPI holoenzyme	K	0	X
Afu6g10320	YMR131C	KOG0302	RNA helicase involved in 28S rRNA processing	Processosome	A	0	X
Afu6g10630	YOR262W	KOG1533	Predicted GTPase of the XAB1 family (paralog of KOG1757) [122]	TBP-free TAF(II) complex?	L	0	X
Afu6g11070	YJL033W	KOG0343	RNA helicase involved in 28S rRNA processing	Processosome	A	0	X
Afu6g11120	YDL031W	KOG0337	RNA helicase involved in 28S rRNA processing	Processosome	A	0	X
Afu6g11410	YMR224C	KOG2310	PP-loop family ATP pyrophosphatase domain, which in fungi, plants and insects is fused to a duplicated translation inhibitor domain.	?	A	1	X
Afu6g12390	YMR296C	KOG1358	Serine palmitoyltransferase	?	I	0	0
Afu6g12770	YDR427W	KOG2908	Membrane component of ER protein translocation apparatus (Sec62)	Sec complex	U	0	1
Afu5g04000	YOR056C	KOG2463	RNA polymerase II transcription initiation/nucleotide excision repair factor TFIIH, subunit TFB4	TFIIH	K	0	1
Afu5g03560	YGL245W	KOG1147	Glutamyl-tRNA synthetase	Multispecificity aminoacyl-tRNA synthetase complex	J	0	X
Afu5g03090	YCR057C	KOG0291	Protein required for normal rates of ubiquitin-dependent proteolysis, contains WD40 repeats	Proteasome?	O	1	X
Afu5g02590	YKL022C	KOG1173	Anaphase-promoting complex (APC), Cdc16 subunit (TPR-repeat protein)	APC	D	0	0
Afu5g02520	YLR274W	KOG0481	DNA replication licensing factor MCM5	Pre-replication complex	L	0	X
Afu8g04790	YKR081C	KOG3031	Protein involved in large ribosome subunit assembly and 28S rRNA processing (Rrf2)	Processosome	A	0	X
Afu8g04950	YCR042C	KOG1932	TBP-interacting protein TIP49 (DNA helicase)	chromatin remodeling complex	L	0	0
Afu8g04350	YKL144C	KOG3297	RNA polymerase III subunit C25	RNAP III holoenzyme	K	0	0
Afu2g01330	YGR095C	KOG1069	3'-5' exoribonuclease (RNase PH), exosome subunit Rrp46	Exosome	A	0	1
Afu2g01780	YMR093W	KOG0310	Chaperonin complex component, TCP-1 beta subunit (CCT2)	TCP-1	O	0	0
Afu2g03580	YFL022C	KOG2784	Protein containing a U1-type, RNA-binding C2H2 Zn-finger. Probable role in RNA splicing/processing	Spliceosome?	A	0	0
Afu2g04780	YGR145W	KOG2321	Predicted RNA-binding protein, consisting of a PIN domain and a Zn-ribbon. Involved in 26S proteasome assembly	26S proteasome, pre-40S subunit	A, O	0	X
Afu2g05420	YDR365C	KOG2318	Nucleolar protein, contains WD40 repeats	rRNA processosome?	A	0	1
Afu2g05480	YJR063W	KOG2907	26S proteasome regulatory complex, subunit RPN9/PSMD13	26S proteasome regulatory complex	O	0	0
Afu2g08390	YNL317W	KOG0284	Polyadenylation factor I complex, subunit PFS2, WD40-repeat protein	Poly-adenylation complex	A	0	X

Afu2g08570	YPL178W	KOG0121	Nuclear cap-binding protein complex, subunit CBP20 (RRM-domain-containing RNA-binding protein)	Cap-binding complex	A	1	X
Afu2g10140	YBR202W	KOG0482	DNA replication licensing factor MCM7	Pre-replication complex	L	0	0
Afu2g11380	YCL059C	KOG2874	26S proteasome regulatory complex, subunit RPN10/PSMD4	26S proteasome regulatory complex	O	1	1
Afu2g11450	YDR083W	KOG3045	Predicted RNA methylase involved in rRNA processing	Processosome?	A	1	1
Afu2g12580	YPL094C	KOG2927	Origin recognition complex, subunit 2 (ORC2)	ORC	L	1	1
Afu2g12610	YDR376W	KOG1800	Deadenylating 3'-5' exonuclease, negative regulator of PolII transcription	CCR4-NOT core complex	A, K	0	0
Afu2g12890	YER082C	KOG1272	WD40-repeat proteins, subunits of rRNA processing complexes [69,70]	Processosome	A	0	1
Afu2g13730	YPR066W	KOG2015	Nonsense-mediated mRNA decay complex, subunit 2	NMD complex	A	1	X
Afu2g13780	YMR288W	KOG0213	U2-snRNP associated splicing factor 3b, subunit 1	Spliceosome	A	0	0
Afu2g14080	YJL074C	KOG0964	Structural maintenance of chromosome protein 3 (cohesin subunit SMC3)	Sister chromatid cohesion complex	L	0	X
Afu2g15070	YHR200W	KOG2884	RNA polymerase I transcription factor TFIIIS, subunit A12.2/RPA12	TFIIIS	K	1	0
Afu2g15080	YDR246W	KOG3369	Subunit of the targeting complex (TRAPP) involved in ER to Golgi trafficking	TRAPP	U	0	X
Afu2g15210	YBL026W	KOG3448	Predicted snRNP core protein	Spliceosome	A	0	1
Afu2g16040	YMR229C	KOG1070	Exosome subunit Rrp5 (RNA-binding S1 domain fused to TPR repeats)	Exosome	A	0	1
Afu2g16750	YHR170W	KOG2613	Coatamer (COPI) complex delta subunit	COPI complex	U	0	0
Afu2g10120	YKL151C	KOG3974	Predicted sugar kinase	Putative novel complex with KOG2585 proteins	R	1	1
Afu2g15500	YPR182W	KOG3482	Small nuclear ribonucleoprotein (snRNP) SMF subunit	Spliceosome	A	0	0
Afu2g08540	YGL070C	KOG2691	Predicted metalloprotease with chaperone activity (RNase H/HSP70 fold) [124]	Putative complex involved in translation regulation [125]	O	0	X
Afu2g11700	YDR305C	KOG3379	Uncharacterized member of the histidine triad superfamily of nucleotide hydrolases	?	R	1	X
Afu3g14370	YOR116C	KOG0261	RNA polymerase III, largest subunit	RNAPIII holoenzyme	K	0	X
Afu3g14040	YGL127C	KOG4086	SOH1 protein potentially involved in Pol II transcription regulation and repair	SMCC complex [121]	K	1	X
Afu3g13790	YEL031W	KOG0209	Endoplasmic reticulum membrane P-type ATPase	?	P	1	X
Afu3g13350	YFL001W	KOG2554	Upflp-interacting protein, NMD complex subunit Nmd3p	NMD complex	A	0	X
Afu3g11020	YMR061W	KOG1914	RNA polymerase II Elongator subunit	RNAP II elongator complex	K	1	X
Afu3g10400	YPR183W	KOG2978	Exosome subunit Rrp4	Exosome	A	0	X
Afu3g10240	YCR093W	KOG1831	mRNA cleavage and polyadenylation factor I complex, subunit RNA14	Cleavage and polyadenylation complex	A	0	X

Afu3g09720	YLR115W	KOG1135	mRNA cleavage and polyadenylation complex subunit CFT2 (CPSF)	Cleavage and polyadenylation complex	A	0	0
Afu3g07830	YDL143W	KOG0358	Chaperonin complex component, TCP-1 delta subunit (CCT4)	TCP-1	O	0	0
Afu3g07170	YPL076W	KOG3059	N-acetylglucosaminyltransferase complex, subunit PIG-C/GPI2, involved in phosphatidylinositol biosynthesis	N-acetylglucos-aminyltransferase complex	I	0	1
Afu3g06010	YLR186W	KOG3073	Predicted RNA-binding protein containing PIN domain and involved in 18S rRNA processing	Pre-40S subunit	A	0	1
Afu3g05860	YHR069C	KOG3013	Protein required for 60S ribosomal subunit biogenesis; [107] contains the IMP4 domain, which is involved in rRNA processing [108]	Processosome	A	0	X
Afu5g13930	YOR091W	KOG1763	Ferredoxin/adrenodoxin reductase	?	C	0	X
Afu5g13520	YNL163C	KOG0467	Translation elongation factor 2 paralog (GTPase)	?	J	0	X
Afu5g13020	YBL035C	KOG1625	Uncharacterized conserved protein containing a CCCH Zn-finger; possible role in RNA processing or splicing	?	A	1	1
Afu5g12880	YDR472W	KOG3315	Subunit of the targeting complex (TRAPP) involved in ER to Golgi trafficking	TRAPP	U	0	X
Afu5g12430	YJR122W	KOG2929	Dolichol-phosphate mannosyltransferase	?	U	0	X
Afu5g11730	YNL207W	KOG2268	Ribonuclease HI	Replisome	L	1	X
Afu5g11700	YMR167W	KOG1979	Nuclear export receptor CSE1/CAS (importin beta)	?	U, Y	0	X
Afu5g11580	YPR056W	KOG2487	Predicted N-acetyltransferase	?	R	1	X
Afu5g11130	YPL101W	KOG3949	RNA polymerase II elongator complex, subunit ELP4	RNAP II elongator complex	K	1	1
Afu5g08370	YKL213C	KOG0301	RNA helicase involved in 28S rRNA processing	Processosome	A	0	X
Afu5g07290	YPR048W	KOG1159	NADP-dependent flavoprotein reductase, probably sulfite reductase subunit	?	C, L	0	X
Afu5g06690	YGR063C	KOG3490	Transcription elongation factor SPT4, Zn-ribbon protein	Chromatin-associated transcription complexes	K	1	1
Afu5g05930	YHR088W	KOG2780	Subunit of the small (ribosomal) subunit (SSU) processosome (snoRNP), IMP4	Processosome	A	0	1
Afu5g05720	YIL097W	KOG0396	Predicted E3 ubiquitin ligase	Ub ligase	O	1	1
Afu5g05570	YDL166C	KOG3347	Predicted nucleotide kinase; nuclear protein (Fap7p)	?	R	0	1
Afu5g11940	YOR349W	KOG1943	RNA (guanine-7-) methyltransferase (capping enzyme subunit)	Capping enzyme	A	0	1
Afu1g09200	YMR049C	KOG0650	WD40-repeat proteins, subunits of rRNA processing complexes [69,70]	Processosome	A	0	1
Afu1g09350	YML098W	KOG3901	Transcription initiation factor IID subunit (Taf13p)	TFIID	K	0	X
Afu1g09810	YER007C-A	KOG2523	Pseudouridylylase synthase	?	A	1	1
Afu1g13070	YNL075W	KOG2781	Phenylalanyl-tRNA synthetase, beta subunit	Heterodimeric phenylalanyl-tRNA synthetase	J	0	X
Afu1g13900	YOR341W	KOG0262	RNA polymerase I, largest subunit	RNAPI holoenzyme	K	0	X
Afu1g14020	YLR172C	KOG3123	Diphtamide synthase (methyltransferase)	?	J	1	1

Afu1g14580	YKL099C	KOG3237	Uncharacterized conserved protein containing coiled-coil domain	?	S	0	1
Afu1g15130	YDR331W	KOG1349	GPI-anchor transamidase complex, GPI8 subunit	GPI-anchor transamidase complex	O	0	1
Afu1g15770	YGL240W	KOG3437	Anaphase-promoting complex (APC), subunit 10	APC	D	1	1
Afu1g15860	YFR051C	KOG2635	Multitransmembrane protein, potential transporter	?	R	0	1
Afu1g16820	YML105C	KOG3198	Signal recognition particle, subunit Srp19	Signal recognition particle	U	0	X
Afu1g13910	YER171W	KOG1131	RNA polymerase II transcription initiation/nucleotide excision repair factor TFIIH, 5'-3' helicase subunit RAD3	RNAPII holoenzyme	K	0	X
Afu4g12430	YDR013W	KOG3303	Predicted ?-helical protein, possibly involved in replication/repair transcription; paralog of KOG3508	A novel complex with PCNA involved in replication?	L?	0	0
Afu4g11880	YDL043C	KOG0227	snRNA-associated protein, splicing factor 3a, subunit b (Prp11p)	Spliceosome	A	0	0
Afu4g11820	YJR072C	KOG1532	Predicted GTPase of the XAB1 family [122]	TBP-free TAF(II) complex	L	0	0
Afu4g10730	YDR190C	KOG1942	Beta-tubulin folding cofactor D, involved in chromosome segregation	?	O	1	1
Afu4g09070	YLR143W	KOG2316	Uncharacterized conserved protein	?	S	0	1
Afu4g08900	YDR460W	KOG3800	Predicted E3 ubiquitin ligase containing RING finger, subunit of transcription/repair factor TFIIH and CDK-activating kinase assembly factor	TFIIH	K, O	0	X
Afu4g08210	YMR069W	KOG2488	Predicted RNA-binding protein containing a PUA domain, probable role in RNA modification [129]	Putative novel RNA modification complex	A	1	X
Afu4g07780	YMR208W	KOG1511	Mevalonate kinase	?	I	0	X
Afu4g07540	YLR222C	KOG0319	WD40-repeat proteins, subunits of rRNA processing complexes	Processosome	A	0	1
Afu4g07140	YLR384C	KOG1920	TBP-associated factor (Taf2p)	TFIID complex	K	0	X
Afu4g11280	YBR004C	KOG2647	RNA polymerase II subunit 9	RNAP II holoenzyme	K	1	X
Afu1g01740	YIL142W	KOG0363	Chaperonin complex component, TCP-1 beta subunit (CCT2)	TCP-1	O	0	0
Afu1g01990	YCR072C	KOG0271	Notchless-like WD40 repeat-containing protein		S	0	1
Afu1g02630	YLR196W	KOG0270	WD40 repeat-containing protein	Processosome	A	0	X
Afu1g02680	YLR129W	KOG0306	Chaperonin complex component, TCP-1 delta subunit (CCT4)	TCP-1	O	0	0
Afu1g03410	YKL045W	KOG2267	Predicted nucleic-acid-binding protein kinase of the RIO1 family; 40S ribosomal subunit biogenesis/18S rRNA processing	Pre-40S subunit	A	0	X
Afu1g03920	YEL032W	KOG0479	DNA replication licensing factor MCM3	Pre-replication complex	L	0	X
Afu1g04980	YGR047C	KOG2076	Phosphoethanolamine N-methyltransferase involved in GPI-anchor biosynthesis	?	O	0	X
Afu1g05830	YPL082C	KOG0392	SNF2 family DNA-dependent ATPase	TBP-DNA complex	K	0	1
Afu1g06690	YOR006C	KOG3154	Uncharacterized protein with potential function in translation or ribosomal biogenesis	Pre-40S subunit?	A?	1	X

Afu1g07080	YLR316C	KOG2771	Protein involved in ribosomal large subunit assembly (RPF1), contains IMP4 domain	Processosome	A	0	1
Afu1g07600	YNL072W	KOG2299	DNA repair exonuclease MRE11	MRN complex involved in double-strand break repair	L	1	1
Afu1g02460	YOR207C	KOG0215	RNA polymerase III, second largest subunit	RNAPIII holoenzyme	K	0	X
Afu7g05430	YHR077C	KOG2051	RNA polymerase III transcription factor TFIIC, TPR-repeat-containing protein	TFIIC	K	0	X

**<sup>a</sup>Functional categories:**

INFORMATION STORAGE AND PROCESSING

[A] RNA processing and modification

[J] Translation, ribosomal structure and biogenesis

[K] Transcription

[L] Replication, recombination and repair

CELLULAR PROCESSES AND SIGNALING

[D] Cell cycle control, cell division, chromosome partitioning

[O] Posttranslational modification, protein turnover, chaperones

[U] Intracellular trafficking, secretion, and vesicular transport

[Y] Nuclear structure

METABOLISM

[C] Energy production and conversion

[I] Lipid transport and metabolism

POORLY CHARACTERIZED

[R] General function prediction only

[S] Function unknown

**<sup>b</sup>Knockouts:**

0: essential gene (lethal knockout)

1: non-essential gene (non-lethal knockout)

X: no data available