Supplementary Table 19 Secondary metabolism genes and gene clusters			
Gene	**Function**	**Description**	**Remark**
An01g01130	PKS	strong similarity to polyketide synthase FUM5 - Gibberella moniliformis	
An01g02030	PKS	similarity to polyketide synthase FUM5 - Gibberella moniliformis	
Fumonisin cluster		Similarity+C40 to Gibberella moniliformis cluster	
An01g06820		strong similarity to fatty acid omega-hydroxylase (P450foxy) CYP505 - Fusarium oxysporum	fum6
An01g06830		similarity to 3-ketosphinganine reductase Tsc10 - Saccharomyces cerevisiae	
An01g06840		strong similarity to acid-CoA ligase Fat2 - Saccharomyces cerevisiae	fum10
An01g06850		similarity to 4-hydroxybutyrate dehydrogenase - Alcaligenes eutrophus	
An01g06860		strong similarity to hypothetical protein Fum9p - Gibberella moniliformis	fum3
An01g06870		strong similarity to hypothetical protein Fum8p - Gibberella moniliformis	fum8
An01g06880		similarity to dihydroflavonol 4-reductase BAA12723.1 - Rosa hybrid cultivar	fum13
An01g06890	NRPS	similarity to peptide synthase pesA - Metarhizium anisopliae	fum14 - not a complete NRPS
An01g06900		weak similarity to transcription regulator of maltose utilization amyR - Aspergillus oryzae	
An01g06910		strong similarity to cytochrome P450 CYP94A5 - Nicotiana tabacum	fum15
An01g06920		strong similarity to multidrug resistance protein ABCC2 - Homo sapiens	fum19
An01g06930	PKS	strong similarity to polyketide synthase FUM5 - Gibberella moniliformis	fum1 (previous fum5)
An01g06940		strong similarity to hypothetical transmembrane transport protein SCC30.17c - Streptomyces coelicolor	
An01g06950	PKS	strong similarity to polyketide synthase FUM5 - Gibberella moniliformis	
An01g11770	NRPS	similarity to peptide synthase enniatin synthase esyn1 - Fusarium scirpi	
An01g12040		similarity to polyketide synthase FUM5 - Gibberella moniliformis	
An01g13170		strong similarity to hypothetical peptide synthase-like protein CPS1 - Cochliobolus heterostrophus	
An02g00210		strong similarity to nonribosomal peptide synthase MxaA - Stigmatella aurantiaca	
An02g00450	PKS	strong similarity to lovastatin diketide synthase lovF - Aspergillus terreus [putative sequencing error]	
An02g00840		similarity to nonribosomal peptide synthase MxcG - Stigmatella aurantiaca	
An02g02300		weak similarity to nonribosomal peptide synthetase tex1 - Hypocrea virens	
An02g05070	NRPS	strong similarity to d-lysergyl-peptide-synthase PS1 - Claviceps purpurea	
An02g05080		strong similarity to maackiain detoxification protein MAK1 - Nectria haematococca	

An02g05090		strong similarity to cytochrome P450 monooxygenase P450I - Gibberella fujikuroi	
An02g08290	PKS-NRPS	strong similarity to lovastatin nonaketide synthase lovB - Aspergillus terreus	
An02g09420		strong similarity to cytochrome P450 trichodiene oxygenase TRI4 - Fusarium sporotrichioides	
An02g09430	PKS	strong similarity to polyketide synthase FUM5 - Gibberella moniliformis [putative frameshift]	
An02g10140		strong similarity to o peptide-polyketide synthase McyG - Microcystis aeruginosa	
An02g13080		similarity to N epsilon-(indole-3-acetyl)-L-lysine synthase iaaL - Pseudomonas syringae	
An02g13090		strong similarity to alanine racemase TOXG - Cochliobolus carbonum	
An03g00650	NRPS	similarity to cyclic peptide AM-toxin synthase AMT - Alternaria alternata	
An03g00660		similarity to taurine dioxygenase tauD - Escherichia coli	
An03g00670		similarity to D-nopaline dehydrogenase nos - Agrobacterium tumefaciens	
An03g00680		strong similarity to multidrug resistance protein fnx1p - Schizosaccharomyces pombe	
An03g01820	PKS	strong similarity to melanin polyketide synthase PKS - Nodulisporium sp.	
Siderophore cluster		Similarity+C467 to Sid2/SidD siderophore cluster of other filamentous fungi	
An03g03520	NRPS	similarity to cyclic peptide AM-toxin synthase AMT - Alternaria alternata	NRPS Sid2/sidD orthologue
An03g03530		similarity to protein fragment SEQ ID NO:9681 from patent EP1033405-A2 - Arabidopsis thaliana	acyltransferase/hydrolase
An03g03540		similarity to aerobactin biosynthesis protein iucB - Escherichia coli	acetyl transferase
An03g03550		strong similarity to carnitine racemase caiD - Escherichia coli	enoyl-CoA hydratase
An03g03560		strong similarity to ferrichrome-type siderophore transporter Arn1 - Saccharomyces cerevisiae	siderophore transporter
An03g03620		strong similarity to multidrug resistance protein atrD - Aspergillus nidulans	ABC transporter
An03g05130		similarity to hypothetical dihydrofolate reductase CAB16576.1 - Schizosaccharomyces pombe	
An03g05140	PKS	strong similarity to polyketide synthase PKS1 - Cochliobolus heterostrophus	
An03g05150		strong similarity to D-mandelate dehydrogenase - Rhodotorula graminis	
An03g05160		similarity to ferric/cupric reductase Fre2 - Saccharomyces cerevisiae	
An03g05420		strong similarity to nitrogen metabolic repression regulator protein hNmrr from patent CN1269419-A - Homo sapiens	
An03g05430		strong similarity to O-methyltransferase A omtA - Aspergillus parasiticus	
An03g05440	PKS	strong similarity to polyketide synthase alb1 - Aspergillus fumigatus	
An03g05450		similarity to zeaxanthin epoxidase ABA2 - Nicotiana plumbaginifolia	
An03g05460		strong similarity to cytochrome P450 monooxygenase avnA - Aspergillus parasiticus	
An03g05470		strong similarity to hypothetical protein SCD69.03 - Streptomyces coelicolor	
An03g05480		similarity to O-methyltransferase omtA - Aspergillus parasiticus	

An03g05490		strong similarity to maleylacetate reductase macA - Rhodococcus opacus	
An03g05660		strong similarity to catalase C catC - Aspergillus nidulans	
An03g05670		strong similarity to aryl-alcohol oxidase precursor aao - Pleurotus pulmonarius	
An03g05680		strong similarity to peptide synthase mps - Mycobacterium smegmatis	
An03g05990		strong similarity to O-methyltransferase B omtB - Aspergillus parasiticus	
An03g06000		similarity to 6-Hydroxy-D-nicotine oxidase 6-HDNO - Arthrobacter oxidans	
An03g06010	NRPS	strong similarity to cyclic peptide AM-toxin synthase AMT - Alternaria alternata	
An03g06370		weak similarity to transcription activator Cha4 - Saccharomyces cerevisiae	
An03g06380	PKS	strong similarity to polyketide synthase FUM5 - Gibberella moniliformis	
An03g06390		strong similarity to 3-(3-hydroxyphenyl)propionate hydroxylase MhpA - Comamonas testosteroni	
An03g06400		similarity to zinc-finger transcription factor amdA - Aspergillus nidulans	
An03g06410		strong similarity to methyl sterol oxidase Erg25 - Saccharomyces cerevisiae	
An03g06420		similarity to hypothetical protein encoded by An08g08870 - Aspergillus niger	
An03g06430		strong similarity to cinnamyl-alcohol dehydrogenase MsaCAD1 - Medicago sativa	
An03g06440		strong similarity to hypothetical protein EAA64120.1 - Aspergillus nidulans	
An03g06450		weak similarity to protein SEQ ID NO: 2310 from patent US6562958-B1 - Acinetobacter baumannii	
An03g06460		strong similarity to hypothetical sterigmatocystin biosynthesis p450 monooxygenase stcB - Aspergillus nidulans	
An03g06470		weak similarity to MigA - Dictyostelium discoideum	
An03g06480		strong similarity to Steroid monooxygenase smo - Rhodococcus rhodochrous	
An03g06490		similarity to heroin esterase her - Rhodococcus sp.	
An03g06500		strong similarity to zeaxanthin epoxidase ABA2 - Nicotiana plumbaginifolia	
An03g06510		weak similarity to regulator protein Uga3 - Saccharomyces cerevisiae	
An04g01140		strong similarity to 8-amino-7-oxononanoate synthase/KAPA synthase BioF - Kurthia sp.	
An04g01150		strong similarity to nonribosomal peptide synthase MxaA - Stigmatella aurantiaca	
An04g01160		strong similarity to hypothetical ABC transporter SPBC15C4.02 - Schizosaccharomyces pombe	
An04g04330		strong similarity to 4-coumarate-CoA ligase 4 4CL4 - Glycine max	
An04g04340	PKS	strong similarity to nonaketide synthase lovB - Aspergillus terreus	
An04g04350		similarity to hypothetical protein encoded by prophage CP-933X Z1925 - Escherichia coli	
An04g04360		similarity to hypothetical protein 104H10.250 - Neurospora crassa	
An04g04370		strong similarity to phenylalanine ammonia-lyase Pal - Rhodosporidium toruloides	
An04g04380		strong similarity to nonribosomal peptide synthase MxaA - Stigmatella aurantiaca	
An04g04390		similarity to phthalate ester hydrolase pehA - Arthrobacter keyseri	

An04g05420		strong similarity to alpha-aminoadipate reductase large subunit lys2 - Penicillium chrysogenum	lys2 orthologue - resembles NRPS
An04g06240		similarity to transcription regulator TRI10 - Fusarium sporotrichioides	
An04g06250		strong similarity to HC-toxin efflux pump TOXA - Cochliobolus carbonum	
An04g06260	NRPS	strong similarity to peptide synthase TycC - Bacillus brevis	
An04g06270		similarity to hypothetical methyltransferase AAO27746.2 - Fusarium sporotrichioides	
An04g09500		strong similarity to hypothetical aldehyde reductase 6 alr6 - Colletotrichum gloeosporioides	
An04g09510		similarity to hypothetical UbiE/COQ5 family methlytransferase - Caulobacter crescentus	
An04g09520		strong similarity to O-methyltransferase omtB - Aspergillus flavus	
An04g09530	PKS	strong similarity to melanin polyketide synthase PKS - Nodulisporium sp.	
An04g09540		similarity to fatty acid omega-hydroxylase cytochrome P-450 CYP4A4 - Oryctolagus cuniculus	
An04g09550		strong similarity to 4-Hydroxyacetophenone monooxygenase hapE - Pseudomonas fluorescens	
An04g10030	PKS	strong similarity to polyketide synthase PKS1 - Cochliobolus heterostrophus	
An04g10100		similarity to polyketide synthase PKS17 - Botryotinia fuckeliana	
An05g01060	NRPS	strong similarity to HC-toxin synthase HTS1 - Cochliobolus carbonum	
An05g01070		strong similarity to 7-aminocholesterol resistance protein Rta1 - Saccharomyces cerevisiae	
An05g01080		weak similarity to potassium channel protein AKT1 - Arabidopsis thaliana	
An05g01090		questionable ORF	
An05g01100		strong similarity to HC-toxin biosynthesis protein TOXF - Cochliobolus carbonum	
An05g01110		strong similarity to cadmium resistance protein Ycf1 - Saccharomyces cerevisiae	
An05g01120		strong similarity to hypothetical cytochrome P450 monooxygenase TRI11 - Fusarium sporotrichioides	
An05g00220		strong similarity to L-ornithine N5-hydroxylase psbA - Pseudomonas sp.	sidA orthologue - ornithine hydroxylase
An06g01300	NRPS	strong similarity to cyclic peptide AM-toxin synthase AMT - Alternaria alternata	sidC orthologue
An06g01310		hypothetical protein	
An06g01320		strong similarity to feruloyl-CoA synthase fcs - Amycolatopsis sp.	adjacent in A. fumigatus
An07g01030	PKS	strong similarity to polyketide synthase FUM5 - Gibberella moniliformis	
An07g01040		weak similarity to polyketide synthase Fum5 - Gibberella moniliformis	
An08g02290		strong similarity to fluconazole resistance protein FLU1 - Candida albicans	
An08g02300	NRPS	weak similarity to enniatin synthase - Fusarium scirpi [truncated ORF]	truncated NRPS C-term?

An08g02310	NRPS	similarity to HC-toxin non-ribosomal peptide synthase HTS1 - Cochliobolus carbonum [truncated ORF]	truncated NRPS N-term?
An08g02320		questionable ORF	
An08g02330		strong similarity to multidrug resistance protein MLP-2 - Rattus norvegicus	
An08g03730		similarity to gibberellin 7-oxidase - Cucurbita maxima	
An08g03740		strong similarity to enoyl reductase of the lovastatin biosynthesis lovC - Aspergillus terreus	
An08g03750		strong similarity to fluconazole resistance protein FLU1 - Candida albicans	
An08g03760		similarity to hypothetical protein Rv3472 - Mycobacterium tuberculosis	
An08g03770		weak similarity to mucin MUC5AC - Homo sapiens	
An08g03780		strong similarity to cytochrome P450 monooxygenase TRI11 - Fusarium sporotrichioides	
An08g03790	PKS-NRPS	strong similarity to lovastatin nonaketide synthase lovB - Aspergillus terreus	
An08g03800		similarity to saframycin Mx1 synthase safA - Myxococcus xanthus [truncated ORF]	
An08g03810		similarity to hypothetical protein encoded by An02g00870 - Aspergillus niger	
An08g03820		strong similarity to enoyl reductase of the lovastatin biosynthesis lovC - Aspergillus terreus	
An08g04820		similarity to saframycin Mx1 synthase safA - Myxococcus xanthus	
An08g09220	NRPS	similarity to multifunctional peptide synthetase of the nostopeptolide biosynthetis NosD - Nostoc sp.	
An08g09230		strong similarity to isotrichodermin C-15 hydroxylase Tri11 - Fusarium sporotrichioides	
An08g10860		strong similarity to fatty acid synthase beta subunit fasB - Aspergillus nidulans	
An08g10870		strong similarity to 2-methylcitrate dehydratase PrpD - Salmonella typhimurium	
An08g10880		strong similarity to regulator protein of lovastatin biosynthesis gene cluster encoded by ORF13 - Aspergillus terreus	
An08g10890		questionable ORF	
An08g10900		hypothetical protein	
An08g10910		questionable ORF	
An08g10920		strong similarity to citrate synthase YKPSCA - Pseudomonas aeruginosa	
An08g10930		strong similarity to fatty acid synthase alpha subunit Fas2 - Saccharomyces cerevisiae	
An09g00520	NRPS	similarity to tyrocidine synthase 2 tycB - Brevibacillus brevis	

An09g00530		similarity to salicylate hydroxylase nahW - Pseudomonas stutzeri	
An09g00540		hypothetical protein	
An09g00550		similarity to multidrug resistance protein fnx1p - Schizosaccharomyces pombe	
An09g00560		similarity to mitochondrial 25-hydroxyvitamin D3 24-hydroxylase cP450cc24 - Gallus gallus	
An09g01260		similarity to oxidoreductase OXRD-1 from patent WO200071679-A2 - Homo sapiens	
An09g01270		strong similarity to n-alkane inducible cytochrome P450 protein ALK1 - Yarrowia lipolytica	
An09g01280		questionable ORF	
An09g01290	PKS	strong similarity to polyketide synthase FUM5 - Gibberella moniliformis	
An09g01300		weak similarity to protein fragment SEQ ID NO:2141 from patent EP1033405-A2 - Arabidopsis thaliana	
An09g01310		hypothetical protein	
An09g01320		strong similarity to isoamyl alcohol oxidase mreA - Aspergillus oryzae	
An09g01330		strong similarity to lanosterol synthase Erg7 - Saccharomyces cerevisiae	
An09g01340		similarity to leukotriene B(4) omega-hydroxylase cytochrome P450 4F2 CYP4F2 - Homo sapiens	
An09g01350		questionable ORF	
An09g01370		strong similarity to lignostilbene-alpha,beta-dioxygenase LSD - Pseudomonas paucimobilis	
An09g01380		strong similarity to vanillyl-alcohol oxidase vaoA - Penicillium simplicissimum	
An09g01690	NRPS	strong similarity to HC-toxin synthase HTS1 - Cochliobolus carbonum	
An09g01700		strong similarity to multidrug resistance protein MRP1 - Homo sapiens	
An09g01710		similarity to epoxide hydrolase from patent EP879890-A - grobacterium radiobacter	
An09g01730		hypothetical protein	
An09g01740		strong similarity to beta chain of fatty-acyl-CoA synthase Fas1 - Saccharomyces cerevisiae [truncated ORF]	
An09g01750		strong similarity to fatty acid synthase beta subunit fasB - Aspergillus nidulans [truncated ORF]	
An09g01800		strong similarity to trichothecene 3-O-acetyltransferase TRI101 - Fusarium sporotrichioides	
An09g01810		strong similarity to ketoreductase from patent EP918090-A - Saccharomyces cerevisiae	
An09g01820		strong similarity to 4-coumarate-CoA ligase 4CL - Arabidopsis thaliana	
An09g01830		similarity to 6-hydroxy-D-nicotine oxidase 6-HDNO - Arthrobacter oxidans	
An09g01840		strong similarity to salicylate hydroxylase nahG - Pseudomonas putida	
An09g01850		strong similarity to benzoate 4-monooxygenase cytochrome P450 53 bphA - Aspergillus niger	
An09g01860	PKS	strong similarity to polyketide synthase wA - Aspergillus nidulans	
An09g01870		similarity to hypothetical binuclear zinc transcription factor PRF - Nectria haematococca	
An09g01880		strong similarity to enoyl reductase of the lovastatin biosynthesis lovC - Aspergillus terreus	
An09g01910		similarity to tetracyclin resistance protein tetA - Agrobacterium tumefaciens	
An09g01920		similarity to 6-hydroxy-D-nicotine oxidase 6-HDNO - Arthrobacter oxidans	

An09g01930	PKS	strong similarity to lovastatin diketide synthase lovF - Aspergillus terreus	
An09g01940		strong similarity to 7-aminocholesterol resistance protein Rta1 - Saccharomyces cerevisiae	
An09g01950		strong similarity to cytochrome P450 monooxygenase TRI11 - Fusarium sporotrichioides	
An09g01960		hypothetical protein	
An09g01970		similarity to oxidoreductase from patent WO0100844 - Corynebacterium glutamicum	
An09g01980		hypothetical protein	
An09g01990		strong similarity to branched-chain amino acid aminotransferase bcaT - Lactococcus lactis	
An09g02000		strong similarity to cytochrome P450 - Rhodotorula minuta	
An09g02010		strong similarity to fatty acid synthase alpha subunit fasA - Aspergillus nidulans	
An09g02590		strong similarity to cytochrome P450 monooxygenase stcS - Aspergillus nidulans	
An09g02600		hypothetical protein	
An09g02610		similarity to trichodiene synthase - Gibberella pulicaris	
An09g02620		similarity to transcription factor ntf1p - Schizosaccharomyces pombe	
An09g05060		strong similarity to transcription repressor Rdr1 - Saccharomyces cerevisiae	
An09g05070		strong similarity to fluconazole resistance protein FLU1 - Candida albicans	
An09g05080		similarity to aromatic aminotransferase I Aro8 - Saccharomyces cerevisiae	
An09g05100		similarity to Impact - Mus musculus	
An09g05110		strong similarity to peptide-polyketide synthase McyG - Microcystis aeruginosa	
An09g05120		similarity to lipase lip1 - Geotrichum candidum	
An09g05130		similarity to monophenol monooxygenase melC2 - Streptomyces antibioticus	
An09g05340	PKS	strong similarity to polyketide synthase FUM5 - Gibberella moniliformis	
An09g05350		strong similarity to mature penicillin V amidohydrolase PVA from patent US5516679-A - Fusarium oxysporum	
An09g05720		hypothetical protein	
An09g05730	PKS	strong similarity to polyketide synthase alb1 - Aspergillus fumigatus	wA/alb1 orthologue
An09g05740		hypothetical protein	no adjacent pigment
An09g05750		hypothetical protein	genes detected
An10g00110		strong similarity to O-methylsterigmatocystin oxidoreductase ordA - Aspergillus parasiticus	
An10g00120		similarity to 2,3-dihydroxybenzoic acid decarboxylase from patent WO9909048-A1 - Aspergillus niger	
An10g00130		strong similarity to para-hydroxybenzoate--polyprenyltransferase ppt1p - Schizosaccharomyces pombe	
An10g00140	PKS	strong similarity to 6-methylsalicylic acid synthase atX - Aspergillus terreus	resembles PKS for 6-MSA
An10g00150		strong similarity to cytochrome P450 monooxygenase TRI4 - Myrothecium roridum	

An10g00620		strong similarity to hypothetical branched-chain amino acid aminotransferase ToxF - Cochliobolus carbonum	
An10g00630		strong similarity to alpha subunit of the fatty acid synthase fasA - Aspergillus nidulans	
An10g00640		hypothetical protein	
An10g00650		strong similarity to fatty acid synthase beta subunit fasB - Aspergillus nidulans	
An10g00660		strong similarity to cytochrome P450 monooxygenase TRI11 - Fusarium sporotrichioides	
An11g00050	NRPS	strong similarity to enniatin synthase esyn1 - Fusarium scirpi	
An11g00060		similarity to integral membrane protein PTH11 - Magnaporthe grisea	
An11g00070		strong similarity to O-methyltransferase B omtB - Aspergillus parasiticus	
An11g00080		weak similarity to integral membrane protein PTH11 - Magnaporthe grisea	
An11g00090		similarity to hypothetical membrane protein pth - Blumeria graminis	
An11g00230		strong similarity to 6-hydroxy-d-nicotine oxidase 6-HDNO - Arthrobacter oxidans	
An11g00240		weak similarity to 2-hydroxyisoflavone reductase IRL - Zea mays	
An11g00250	PKS-NRPS	strong similarity to lovastatin diketide synthase lovF - Aspergillus terreus	
An11g00260		strong similarity to monocarboxylate transporter MCT3 - Homo sapiens	
An11g00270		strong similarity to lanosterol 14 alpha-demethylase CYP51 - Homo sapiens	
An11g00280		strong similarity to O-methyltransferase omtB - Aspergillus flavus	
An11g00320		similarity to pristinamycin I synthase 3 SnbDE - Streptomyces pristinaespiralis	
An11g00330		strong similarity to hypothetical protein encoded by An07g00480 - Aspergillus niger	
An11g00340		questionable ORF	
An11g00350		strong similarity to berberine bridge enzyme BBE - Papaver somniferum	
An11g03920	PKS	strong similarity to lovastatin diketide synthase lovF - Aspergillus terreus	
An11g03930		similarity to hypothetical protein encoded by An15g02140 - Aspergillus niger	
An11g03940		strong similarity to bifunctional cytochrome P450rm - Rhodotorula minuta	
An11g03950		similarity to hypothetical protein required for biosynthesis of the host-specific AK-toxin Akt2 - Alternaria alternata	
An11g03960		similarity to integral membrane protein PTH11 - Magnaporthe grisea	
An11g04250		similarity to aminoadipate reductase enzyme lys2 - Acremonium chrysogenum	
An11g04260		weak similarity to dihydrofolate reductase dfr1p - Schizosaccharomyces pombe	
An11g04270		strong similarity to enoyl reductase of the lovastatin biosynthesis lovC - Aspergillus terreus	
An11g04280	PKS	strong similarity to polyketide synthase PKS1 - Cochliobolus heterostrophus	

An11g05550		similarity to hypothetical major facilitator transporter Mfs1.1 - Coprinus cinereus	
An11g05560		similarity to 8-amino-7-oxononanoate synthase bioF - Bacillus sphaericus	
An11g05570	PKS	strong similarity to polyketide synthase FUM5 - Gibberella moniliformis	
An11g05930		strong similarity to allantoate permease Dal5 - Saccharomyces cerevisiae	
An11g05940	PKS	strong similarity to polyketide synthase PKS1 - Cochliobolus heterostrophus	
An11g05950		weak similarity to dihydrofolate reductase dfr1p - Schizosaccharomyces pombe	
An11g05960		strong similarity to lovastatin diketide synthase lovF - Aspergillus terreus	
An11g06430		similarity to integral membrane protein PTH11 - Magnaporthe grisea	
An11g06440		strong similarity to enoyl reductase of the lovastatin biosynthesis lovC - Aspergillus terreus	
An11g06450		strong similarity to hypothetical protein encoded by An02g08300 - Aspergillus niger	
An11g06460	PKS-NRPS	strong similarity to lovastatin nonaketide synthase lovB - Aspergillus terreus	
An11g07290		similarity to spectinomycin adenylyltransferase spc - Staphylococcus aureus	
An11g07300		similarity to fluconazole resistance protein FLU1 - Candida albicans [truncated ORF]	
An11g07310	PKS	strong similarity to polyketide synthase PKS1 - Colletotrichum lagenarium	
An11g07320		similarity to glyoxalase II Glo2 - Saccharomyces cerevisiae	
An11g07330		similarity to 6-hydroxynicotinic acid mono-oxygenase 6-HNAMO from patent JP09121864-A - Pseudomonas fluorescens	
An11g07340		strong similarity to hypothetical O-methyl transferase EncK - Streptomyces maritimus	
An11g07350		similarity to transcription regulator amdR - Aspergillus oryzae	
An11g07360		hypothetical protein	
An11g07370		questionable ORF	
An11g07380		similarity to phenazine biosynthesis oxidoreductase phzF - Pseudomonas fluorescens	
An11g09710		strong similarity to 4-coumarate-CoA ligase - Populus tremuloides	
An11g09720	PKS	strong similarity to polyketide synthase PKS1 - Cochliobolus heterostrophus	
An12g01980		strong similarity to fatty acid synthase alpha subunit Fas2 - Saccharomyces cerevisiae	
An12g01990		strong similarity to fatty-acyl-CoA synthase beta chain fas1p - Schizosaccharomyces pombe	
An12g02000		strong similarity to salicylate hydroxylase nahG - Pseudomonas putida [putative frameshift]	
An12g02010		weak similarity to hypothetical protein At2g22660 - Arabidopsis thaliana	
An12g02020		strong similarity to trichothecene 3-O-acetyltransferase TRI101 - Fusarium sporotrichioides	
An12g02030		weak similarity to hypothetical ATP-binding ABC transporter protein - Deinococcus radiodurans	
An12g02040		similarity to acetate regulatory DNA binding protein facB - Aspergillus niger	
An12g02050	PKS	strong similarity to polyketide synthase wA - Aspergillus nidulans [putative frameshift]	
An12g02060		strong similarity to hypothetical protein encoded by An03g02680 - Aspergillus niger	
An12g02070		similarity to ribonuclease T1 precursor rntA - Aspergillus oryzae	

An12g02080		strong similarity to cytochrome P450 monooxygenase stcS - Aspergillus nidulans [putative frameshift]	
An12g02640		strong similarity to clavin biosynthesis gene orfup1 from patent WO9833896-A2 - Streptomyces clavuligerus	
An12g02650		similarity to 24-sterol C-methyltransferase ESMT1 - Zea mays	
An12g02660		hypothetical protein	
An12g02670	PKS	strong similarity to polyketide synthase FUM5 - Gibberella fujikuroi	
An12g02680		weak similarity to hypothetical protein encoded by An02g12900 - Aspergillus niger	
An12g02690		weak similarity to cytochrome b5 CB5 - Oryza sativa	
An12g02700		strong similarity to gluconate 5-dehydrogenase GNO - Gluconobacter oxydans	
An12g02710		similarity to cercosporin transporter CFP - Cercospora kikuchii	
An12g02720		similarity to hypothetical protein C25G4.2 - Caenorhabditis elegans	
An12g02730	PKS	strong similarity to polyketide synthase PKS1 - Cochliobolus heterostrophus	
An12g02740		weak similarity to ATP-dependent proteinase Clp from patent WO9743303-A1 - Streptococcus pneumoniae	
An12g02750		similarity to FK520 biosynthetic gene cluster polyketide synthase fkbB - Streptomyces hygroscopicus	
An12g02760		similarity to hypothetical protein BAB49075.1 - Mesorhizobium loti	
An12g02770		similarity to beta transducin-like protein het-e1 - Podospora anserina	
An12g02780		strong similarity to hypothetical protein AAO55050.1 - Pseudomonas syringae	
An12g02790		strong similarity to phenylcoumaran benzylic ether reductase pcbera - Populus trichocarpa	
An12g02800		strong similarity to polyamine transport protein Tpo1 - Saccharomyces cerevisiae	
An12g02810		strong similarity to O-methyltransferase omtB - Aspergillus flavus	
An12g02820		strong similarity to fluconazole resistance protein FLU1 - Candida albicans	
An12g02830		weak similarity to hypothetical methyltransferase adpE - Anabaena sp.	
An12g02840	NRPS	strong similarity to d-lysergyl-peptide-synthase PS1 - Claviceps purpurea	
An12g02850		strong similarity to sulphydryl oxidase Sox from patent EP565172-A1 - Aspergillus niger	
An12g02860		strong similarity to hypothetical protein of the lovastatin biosynthesis gene cluster - Aspergillus terreus	
An12g03950		strong similarity to hypothetical protein npgA - Aspergillus nidulans	npgA/pptA (phosphopantetheine tranferase
An12g07050		weak similarity to dihydrofolate reductase dfr1p - Schizosaccharomyces pombe	
An12g07060		similarity to hypothetical protein YMR222c - Saccharomyces cerevisiae	
An12g07070	PKS	strong similarity to polyketide synthase PKS1 - Cochliobolus heterostrophus	
An12g07090		similarity to 6-hydroxy-D-nicotine oxidase 6-HDNO - Arthrobacter oxidans [putative sequencing error]	
An12g07100		strong similarity to cucumopine synthase cus - Agrobacterium rhizogenes	
An12g07110		strong similarity to anthranilate synthase component I ybtS - Yersinia pestis	
An12g07120		similarity to cytochrome P450 monooxygenase P450II - Gibberella fujikuroi	

An12g07230	NRPS	strong similarity to enniatin synthase esyn1 - Fusarium scirpi	
An13g02380		weak similarity to hypothetical NADH dehydrogenase subunit 2 ND2 - Lophognathus longirostris	
An13g02390		similarity to fluconazole resistance protein FLU1 - Candida albicans	
An13g02400		similarity to nitrate assimilation regulatory protein nirA - Aspergillus nidulans	
An13g02410		weak similarity to hypothetical cation transporter DRA0361 - Deinococcus radiodurans	
An13g02420		strong similarity to hypothetical protein EAA54802.1 - Magnaporthe grisea	
An13g02430	PKS	strong similarity to polyketide synthase PKS1 - Cochliobolus heterostrophus	
An13g02450		strong similarity to hypothetical protein AAO76127.1 - Bacteroides thetaiotaomicron	
An13g02460		similarity to nonribosomal peptide synthase MxcG - Stigmatella aurantiaca	
An13g02470		hypothetical protein	
An13g02480		strong similarity to polyamine oxidase PAO - Zea mays	
An13g02920		similarity to polyketide synthase lovF - Aspergillus terreus	
An13g02930		questionable ORF	
An13g02940		strong similarity to enoyl reductase of the lovastatin biosynthesis lovC - Aspergillus terreus	
An13g02950		hypothetical protein	
An13g02960	PKS	strong similarity to lovastatin nonaketide synthase lovB - Aspergillus terreus [truncated ORF]	
An13g02970		weak similarity to hypothetical protein encoded by An08g03800 - Aspergillus niger	
An13g02980		similarity to hypothetical protein encoded by An01g08440 - Aspergillus niger	
An13g02990		similarity to hypothetical protein EAA71271.1 - Gibberella zeae	
An13g03000		strong similarity to n-alkane-inducible cytochrome P450 protein ALK1 - Yarrowia lipolytica	
An13g03010		hypothetical protein	
An13g03020		questionable ORF	
An13g03030		similarity to hypothetical protein CAB91400.2 - Neurospora crassa [putative sequencing error]	
An13g03040	NRPS	strong similarity to enniatin synthase esyn1 - Fusarium scirpi	
An13g03050		weak similarity to hypothetical protein encoded by An04g04070 - Aspergillus niger	
An13g03060		strong similarity to ATP-binding cassette multidrug transport protein atrB - Aspergillus nidulans	
An14g01910	PKS-NRPS	strong similarity to lovastatin nonaketide synthase lovB - Aspergillus terreus [truncated ORF]	
An14g01920		questionable ORF	
An14g01930		questionable ORF	
An14g01940		strong similarity to enoyl reductase of the lovastatin biosynthesis lovC - Aspergillus terreus	
An14g01950		similarity to hypothetical protein SPAC18B11.03c - Schizosaccharomyces pombe	
An14g01960		strong similarity to aberrant X segregation Axs - Drosophila melanogaster	
An14g01970		similarity to aflatoxin biosynthesis regulatory protein aflR - Aspergillus parasiticus	
An14g01980		similarity to 2-heptaprenyl-1,4-naphthoquinone methyltransferase menG - Bacillus stearothermophilus	
An14g04840		similarity to hypothetical O-methyl transferase EncK - Streptomyces maritimus	

An14g04850	PKS-NRPS	strong similarity to pimaricin polyketide synthase pimS2 - Streptomyces natalensis	
An15g04140	PKS	strong similarity to polyketide synthase PKS1 - Cochliobolus heterostrophus	
An15g04150		strong similarity to oxidoreductase involved in actinorhodin production encoded by Orf11 - Streptomyces lividans	
An15g05060		strong similarity to protein involved in cercosporin production CFP - Cercospora kikuchii	
An15g05070		similarity to cytochrome P-450 protein Cyp3a-13 - Mus musculus	
An15g05080		weak similarity to hypothetical protein CAD21084.1 - Neurospora crassa	
An15g05090	PKS	strong similarity to polyketide synthase FUM5 - Gibberella moniliformis	
An15g05100		similarity to transcription activator Upc2 - Saccharomyces cerevisiae	
An15g05110		strong similarity to cytochrome P450 monooxygenase P450I - Gibberella fujikuroi	
An15g07510		strong similarity to peptide transport gene CaPTR2 - Candida albicans	
An15g07520		similarity to hypothetical protein mlr2143 - Mesorhizobium loti	
An15g07530	NRPS	strong similarity to cyclic peptide AM-toxin synthase AMT - Alternaria alternata	
An15g07540		hypothetical protein [truncated ORF]	
An15g07550		strong similarity to neutral amino acid permease mtr - Neurospora crassa	
Putative ochratoxin cluster		Based on similarity to PKS fragment for A. ochraceus ochratoxin biosynthesis	
An15g07860		strong similarity to hypothetical short chain dehydrogenase SPCC736.13 - Schizosaccharomyces pombe	
An15g07870		strong similarity to alcohol dehydrogenase adhT - Bacillus stearothermophilus	
An15g07880		strong similarity to hypothetical hydroxylase A - Amycolatopsis orientalis	
An15g07890		resembles bZIP transcription factor	
An15g07900		strong similarity to cytochrome P450 - Myrothecium roridum	
An15g07910	NRPS	strong similarity to cyclic peptide AM-toxin synthase AMT - Alternaria alternata	
An15g07920	PKS	strong similarity to PKS of A. ochraceus fragment involved in ochratoxin biosynthesis	PKS - A. ochraceus ochratoxin
An15g07930		strong similarity to nitric-oxide synthase - Manduca sexta [truncated ORF]	
An16g00010		similarity to alcohol dehydrogenase orfB from patent WO9807867-A2 - Lactococcus lactis	
An16g00600		similarity to saframycin Mx1 synthase safA - Myxococcus xanthus	
An16g01630		strong similarity to enoyl reductase of the lovastatin biosynthesis lovC - Aspergillus terreus	
An16g01640		similarity to transcription factor Gal4 - Saccharomyces cerevisiae	
An16g01650		strong similarity to 1,3,6,8-tetrahydroxynaphthalene reductase arp2 - Aspergillus fumigatus	
An16g01660		strong similarity to multidrug resistance protein MDR1 - Candida dubliniensis	
An16g06720	NRPS	strong similarity to HC-toxin peptide synthase HTS - Cochliobolus carbonum	

An16g07170		similarity to polyketide synthase FUM5 - Gibberella moniliformis [putative frameshift]	
An16g07180		strong similarity to vanillin dehydrogenase VDH from patent EP0845532 - Unclassified organism	
An17g00120		strong similarity to major facilitator superfamily transporter protein mfs1 - Botrytis cinerea	
An17g00130		weak similarity to cercosporin resistance protein crg1 - Cercospora nictotianae	
An17g00140		strong similarity to lovastatin nonaketide synthase lovB - Aspergillus terreus [putative frameshift]	
An18g00480		strong similarity to cycloheximide resistance protein CYHR - Candida maltosa	
An18g00490		similarity to salicylate hydroxylase nahW - Pseudomonas stutzeri	
An18g00500		strong similarity to obtusifoliol 14-alpha demethylase CYP51 - Sorghum bicolor	
An18g00510		similarity to 6-hydroxy-d-nicotine oxidase 6-HDNO - Arthrobacter oxidans	
An18g00520	PKS-NRPS	strong similarity to polyketide synthase PKS1 - Cochliobolus heterostrophus	
An18g00530		strong similarity to versicolorin B synthase vbs - Aspergillus parasiticus	
An18g00540		similarity to precursor of alpha-latrotoxin - Latrodectus tredecimguttatus	
An18g00550		strong similarity to O-methyltransferase B omtB - Aspergillus parasiticus	
Fatty acid synthetases		Primary metabolism (others are associated with secondary metabolism clusters above)	
An01g00050		similarity to fatty-acyl-CoA synthase beta chain Fas1 - Saccharomyces cerevisiae [truncated ORF]+C32	fasB orthologue
An01g00060		strong similarity to fatty acid synthase alpha subunit fas2p - Schizosaccharomyces pombe	fasA orthologue