

Supplementary materials

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Manuscript Title: Vanillin production by biotransformation of phenolic compounds in fungus, *Aspergillus luchuensis*

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Table S1. Candidate genes for vanillin production found in *Aspergillus luchuensis* genome

Accession number	Annotate description	E-value
BCWF01000001-111	sp Q5BB53 BGLI_EMENI Probable beta-glucosidase I OS= <i>Emericella nidulans</i> (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) GN=bglI PE=2 SV=2 (839)	2.00E-66
BCWF01000001-40	sp A2R0Z6 FAEB_ASPNC Probable feruloyl esterase B OS= <i>Aspergillus niger</i> (strain CBS 513.88 / FGSC A1513) GN=faeB PE=3 SV=1 (521)	0
BCWF01000006-16	sp Q05871 ECII_YEAST 3,2-trans-enoyl-CoA isomerase OS= <i>Saccharomyces cerevisiae</i> (strain ATCC 204508 / S288c) GN=ECII PE=1 SV=1 (280)	1.00E-36
BCWF01000006-226	sp Q4WGL5 SUN1_ASPFU Secreted beta-glucosidase sun1 OS= <i>Neosartorya fumigata</i> (strain ATCC MYA-4609 / Af293 / CBS 101355 / FGSC A1100) GN=sun1 PE=1 SV=1 (414)	0
BCWF01000006-280	sp G4MS28 CEGT_MAGO7 Ceramide glucosyltransferase OS= <i>Magnaporthe oryzae</i> (strain 70-15 / ATCC MYA-4617 / FGSC 8958) GN=MGG_10668 PE=1 SV=1 (494)	3.00E-158
BCWF01000006-381	sp A2QN74 BTGC_ASPNC Putative glucan endo-1,3-beta-glucosidase btgC OS= <i>Aspergillus niger</i> (strain CBS 513.88 / FGSC A1513) GN=btgC PE=3 SV=2 (684)	0
BCWF01000006-528	sp Q09140 UGGG_SCHPO UDP-glucose:glycoprotein glucosyltransferase OS= <i>Schizosaccharomyces pombe</i> (strain 972 / ATCC 24843) GN=gpt1 PE=1 SV=2 (1448)	0
BCWF01000006-535	sp P27034 BGLS_RHIRD Beta-glucosidase OS= <i>Rhizobium radiobacter</i> GN=cbg-1 PE=3 SV=1 (818)	7.00E-114
BCWF01000006-551	sp A2QNQ5 ATG26_ASPNC Sterol 3-beta-glucosyltransferase OS= <i>Aspergillus niger</i> (strain CBS 513.88 / FGSC A1513) GN=atg26 PE=3 SV=2 (1371)	0
BCWF01000006-829	sp A2QPK4 BGLD_ASPNC Probable beta-glucosidase D OS= <i>Aspergillus niger</i> (strain CBS 513.88 / FGSC A1513) GN=bglD PE=3 SV=2 (754)	0
BCWF01000006-97	sp P49426 EXG1_COCCA Glucan 1,3-beta-glucosidase OS= <i>Cochliobolus carbonum</i> GN=EXG1 PE=1 SV=1 (788)	4.00E-126
BCWF01000008-185	sp O35459 ECH1_MOUSE Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial OS= <i>Mus musculus</i> GN=Ech1 PE=1 SV=1 (327)	2.00E-74
BCWF01000008-195	sp Q9FZE0 BGL40_ARATH Beta-glucosidase 40 OS= <i>Arabidopsis thaliana</i> GN=BGLU40 PE=2 SV=1 (510)	3.00E-47
BCWF01000009-8	sp D4B0V1 E13B_ARTBC Probable glucan endo-1,3-beta-glucosidase ARB_02077 OS= <i>Arthroderma benhamiae</i> (strain ATCC MYA-4681 / CBS 112371) GN=ARB_02077 PE=1 SV=1 (878)	4.00E-102
BCWF01000009-95	sp D4AS70 FAE1_ARTBC Probable feruloyl esterase ARB_07085 OS= <i>Arthroderma benhamiae</i> (strain ATCC MYA-4681 / CBS 112371) GN=ARB_07085 PE=1 SV=1 (537)	4.00E-89
BCWF01000010-127	sp D4AS70 FAE1_ARTBC Probable feruloyl esterase ARB_07085 OS= <i>Arthroderma benhamiae</i> (strain ATCC MYA-4681 / CBS 112371) GN=ARB_07085 PE=1 SV=1 (537)	3.00E-122
BCWF01000010-325	sp O74799 EXG3_SCHPO Glucan 1,3-beta-glucosidase 3 OS= <i>Schizosaccharomyces pombe</i> (strain 972 / ATCC 24843) GN=exg3 PE=3 SV=1 (464)	9.00E-08
BCWF01000010-343	sp P87076 BGLA_ASPKW Beta-glucosidase A OS= <i>Aspergillus kawachii</i> (strain NBRC 4308) GN=bglA PE=1 SV=2 (860)	0
BCWF01000010-391	sp O05619 VDH_PSEUH Vanillin dehydrogenase OS= <i>Pseudomonas</i> sp. (strain HR199 / DSM 7063) GN=vdh PE=1 SV=1 (481)	2.00E-100
BCWF01000010-395	sp A2RAR6 EXGA_ASPNC Probable glucan 1,3-beta-glucosidase A OS= <i>Aspergillus niger</i> (strain CBS 513.88 / FGSC A1513) GN=exgA PE=3 SV=1 (416)	0
BCWF01000010-529	sp Q9F234 AGL2_BACTQ Alpha-glucosidase 2 OS= <i>Bacillus thermoamyloliquefaciens</i> PE=3 SV=1 (787)	2.00E-52
BCWF01000015-126	sp D4AS70 FAE1_ARTBC Probable feruloyl esterase ARB_07085 OS= <i>Arthroderma benhamiae</i> (strain ATCC MYA-4681 / CBS 112371) GN=ARB_07085 PE=1 SV=1 (537)	6.00E-96
BCWF01000015-37	sp A5ABF5 BGLM_ASPNC Probable beta-glucosidase M OS= <i>Aspergillus niger</i> (strain CBS 513.88 / FGSC A1513) GN=bglM PE=3 SV=1 (765)	0
BCWF01000015-401	sp Q05871 ECII_YEAST 3,2-trans-enoyl-CoA isomerase OS= <i>Saccharomyces cerevisiae</i> (strain ATCC 204508 / S288c) GN=ECII PE=1 SV=1 (280)	3.00E-40
BCWF01000015-590	sp Q2UN12 BGLF_ASPOR Probable beta-glucosidase F OS= <i>Aspergillus oryzae</i> (strain ATCC 42149 / RIB 40) GN=bglF PE=3 SV=1 (866)	0
BCWF01000015-77	sp Q9XIG1 U80B1_ARATH Sterol 3-beta-glucosyltransferase UGT80B1 OS= <i>Arabidopsis thaliana</i> GN=UGT80B1 PE=2 SV=1 (615)	2.00E-09
BCWF01000015-78	sp Q9XIG1 U80B1_ARATH Sterol 3-beta-glucosyltransferase UGT80B1 OS= <i>Arabidopsis thaliana</i> GN=UGT80B1 PE=2 SV=1 (615)	3.00E-77
BCWF01000016-15	sp P27034 BGLS_RHIRD Beta-glucosidase OS= <i>Rhizobium radiobacter</i> GN=cbg-1 PE=3 SV=1 (818)	1.00E-169
BCWF01000017-1081	sp O43053 ALG6_SCHPO Probable dolichyl pyrophosphate Man9GlcNAc2 alpha-1,3-glucosyltransferase OS= <i>Schizosaccharomyces pombe</i> (strain 972 / ATCC 24843) GN=alg6 PE=3 SV=1 (506)	5.00E-133
BCWF01000017-1129	sp P53626 E13B_TRIHA Glucan endo-1,3-beta-glucosidase BGN13.1 OS= <i>Trichoderma harzianum</i> GN=bgn13.1 PE=1 SV=1 (762)	1.00E-90
BCWF01000017-1136	sp Q9P6J3 MALT_SCHPO Alpha-glucosidase OS= <i>Schizosaccharomyces pombe</i> (strain 972 / ATCC 24843) GN=mal1 PE=2 SV=1 (579)	0
BCWF01000017-346	sp D4B0V1 E13B_ARTBC Probable glucan endo-1,3-beta-glucosidase ARB_02077 OS= <i>Arthroderma benhamiae</i> (strain ATCC MYA-4681 / CBS 112371) GN=ARB_02077 PE=1 SV=1 (878)	0
BCWF01000017-438	sp D4AS70 FAE1_ARTBC Probable feruloyl esterase ARB_07085 OS= <i>Arthroderma benhamiae</i> (strain ATCC MYA-4681 / CBS 112371) GN=ARB_07085 PE=1 SV=1 (537)	2.00E-93
BCWF01000017-501	sp Q4WRH9 AGDC_ASPFU Probable alpha/beta-glucosidase agdC OS= <i>Neosartorya fumigata</i> (strain ATCC MYA-4609 / Af293 / CBS 101355 / FGSC A1100) GN=agdC PE=3 SV=1 (881)	0
BCWF01000017-604	sp F4JML5 ECH2M_ARATH Probable enoyl-CoA hydratase 2, mitochondrial OS= <i>Arabidopsis thaliana</i> GN=At4g16800 PE=2 SV=1 (301)	2.00E-54
BCWF01000017-681	sp Q9XIG1 U80B1_ARATH Sterol 3-beta-glucosyltransferase UGT80B1 OS= <i>Arabidopsis thaliana</i> GN=UGT80B1 PE=2 SV=1 (615)	9.00E-13
BCWF01000017-880	sp G3V9D0 PGLT1_RAT Protein O-glucosyltransferase 1 OS= <i>Rattus norvegicus</i> GN=Poglut1 PE=3 SV=1 (392)	6.00E-09
BCWF01000018-649	sp A2QPK4 BGLD_ASPNC Probable beta-glucosidase D OS= <i>Aspergillus niger</i> (strain CBS 513.88 / FGSC A1513) GN=bglD PE=3 SV=2 (754)	8.00E-36
BCWF01000018-75	sp Q0CBM7 FAEA_ASPTN Probable feruloyl esterase A OS= <i>Aspergillus terreus</i> (strain NIH 2624 / FGSC A1156) GN=faeA PE=3 SV=1 (281)	2.00E-20
BCWF01000019-184	sp A5ABF5 BGLM_ASPNC Probable beta-glucosidase M OS= <i>Aspergillus niger</i> (strain CBS 513.88 / FGSC A1513) GN=bglM PE=3 SV=1 (765)	0
BCWF01000020-280	sp Q2UP89 FAEB1_ASPOR Probable feruloyl esterase B-1 OS= <i>Aspergillus oryzae</i> (strain ATCC 42149 / RIB 40) GN=faeB-1 PE=1 SV=1 (540)	6.00E-92
BCWF01000020-313	sp Q25BW5 BGL1A_PHACH Beta-glucosidase 1A OS= <i>Phanerochaete chrysosporium</i> GN=BGL1A PE=1 SV=1 (462)	1.00E-53

BCWF01000020-519	sp A2QPK4 BGLD_ASPNC Probable beta-glucosidase D OS=Aspergillus niger (strain CBS 513.88 / FGSC A1513) GN=bgID PE=3 SV=2 (754)	0
BCWF01000020-549	sp O94511 YN67_SCHPO Putative enoyl reductase C646.07c OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=SPBC646.07c PE=3 SV=1 (295)	3.00E-71
BCWF01000020-629	sp P56526 AGLU_ASPNG Alpha-glucosidase OS=Aspergillus niger GN=aglA PE=1 SV=1 (985)	0
BCWF01000020-760	sp Q2UB20 ALG8_ASPOR Dolichyl pyrophosphate Glc1Man9GlcNAc2 alpha-1,3-glucosyltransferase OS=Aspergillus oryzae (strain ATCC 42149 / RIB 40) GN=alg8 PE=3 SV=1 (504)	0
BCWF01000020-776	sp Q7D745 Y2525_MYCTO Putative trans-acting enoyl reductase MT2525 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=MT2525 PE=3 SV=2 (419)	1.00E-31
BCWF01000021-150	sp Q1ZXF1 ECHM_DICDI Probable enoyl-CoA hydratase, mitochondrial OS=Dictyostelium discoideum GN=echs1 PE=3 SV=1 (277)	3.00E-101
BCWF01000021-170	sp Q4X162 ALG10_ASPFU Dol-P-Glc:Glc(2)Man(9)GlcNAc(2)-PP-Dol alpha-1,2-glucosyltransferase OS=Neosartorya fumigata (strain ATCC MYA-4609 / Af293 / CBS 101355 / FGSC A1100) GN=alg10 PE=3 SV=1	0
BCWF01000021-231	sp P96559 GTFB_AMYOR Vancomycin aglycone glucosyltransferase OS=Amycolatopsis orientalis GN=gtfB PE=1 SV=1 (407)	1.00E-06
BCWF01000021-992	sp Q01336 YCR2_ESCVU Uncharacterized family 31 glucosidase ORF2 (Fragment) OS=Escherichia vulneris PE=3 SV=1 (529)	0
BCWF01000023-149	sp Q2UP89 FAEB1_ASPOR Probable feruloyl esterase B-1 OS=Aspergillus oryzae (strain ATCC 42149 / RIB 40) GN=faeB-1 PE=1 SV=1 (540)	7.00E-92
BCWF01000023-178	sp O05619 VDH_PSEUH Vanillin dehydrogenase OS=Pseudomonas sp. (strain HR199 / DSM 7063) GN=vdh PE=1 SV=1 (481)	5.00E-75
BCWF01000024-102	sp A2QX52 EXGD_ASPNC Probable glucan 1,3-beta-glucosidase D OS=Aspergillus niger (strain CBS 513.88 / FGSC A1513) GN=exgD PE=3 SV=1 (830)	0
BCWF01000025-366	sp Q2UP89 FAEB1_ASPOR Probable feruloyl esterase B-1 OS=Aspergillus oryzae (strain ATCC 42149 / RIB 40) GN=faeB-1 PE=1 SV=1 (540)	4.00E-67
BCWF01000026-16	sp O05619 VDH_PSEUH Vanillin dehydrogenase OS=Pseudomonas sp. (strain HR199 / DSM 7063) GN=vdh PE=1 SV=1 (481)	3.00E-108
BCWF01000026-7	sp Q2US39 BTGE_ASPOR Probable beta-glucosidase btgE OS=Aspergillus oryzae (strain ATCC 42149 / RIB 40) GN=btgE PE=3 SV=1 (602)	0
BCWF01000028-305	sp D4B2W4 BGL2_ARTBC Glucan 1,3-beta-glucosidase ARB_02797 OS=Arthroderma benhamiae (strain ATCC MYA-4681 / CBS 112371) GN=ARB_02797 PE=1 SV=1 (308)	5.00E-121
BCWF01000028-86	sp A2RAR6 EXGA_ASPNC Probable glucan 1,3-beta-glucosidase A OS=Aspergillus niger (strain CBS 513.88 / FGSC A1513) GN=exgA PE=3 SV=1 (416)	3.00E-25
BCWF01000029-114	sp Q2UP89 FAEB1_ASPOR Probable feruloyl esterase B-1 OS=Aspergillus oryzae (strain ATCC 42149 / RIB 40) GN=faeB-1 PE=1 SV=1 (540)	2.00E-19
BCWF01000029-134	sp Q2UTX5 BGLE_ASPOR Probable beta-glucosidase E OS=Aspergillus oryzae (strain ATCC 42149 / RIB 40) GN=bgIE PE=3 SV=2 (1048)	0
BCWF01000029-177	sp O14255 GCS1_SCHPO Probable mannosyl-oligosaccharide glucosidase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=SPAC6G10.09 PE=3 SV=1 (808)	0
BCWF01000029-193	sp Q05871 ECI1_YEAST 3,2-trans-enoyl-CoA isomerase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ECI1 PE=1 SV=1 (280)	9.00E-54
BCWF01000029-43	sp P32573 SPS19_YEAST Peroxisomal 2,4-dienoyl-CoA reductase SPS19 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SPS19 PE=1 SV=4 (292)	7.00E-84
BCWF01000030-146	sp A2QH21 EGLC_ASPNC Probable glucan endo-1,3-beta-glucosidase eglC OS=Aspergillus niger (strain CBS 513.88 / FGSC A1513) GN=eglC PE=3 SV=2 (460)	0
BCWF01000030-155	sp A1DFA8 BGLI_NEOFI Probable beta-glucosidase I OS=Neosartorya fischeri (strain ATCC 1020 / DSM 3700 / CBS 544.65 / FGSC A1164 / JCM 1740 / NRRL 181 / WB 181) GN=bgII PE=3 SV=1 (838)	0
BCWF01000030-3	sp Q25BW4 BGL1B_PHACH Beta-glucosidase 1B OS=Phanerochaete chrysosporium GN=BGL1B PE=1 SV=1 (540)	0
BCWF01000030-54	sp P40350 ALG5_YEAST Dolichyl-phosphate beta-glucosyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ALG5 PE=1 SV=1 (334)	2.00E-75
BCWF01000032-211	sp Q2UP89 FAEB1_ASPOR Probable feruloyl esterase B-1 OS=Aspergillus oryzae (strain ATCC 42149 / RIB 40) GN=faeB-1 PE=1 SV=1 (540)	1.00E-80
BCWF01000032-49	sp D4AS70 FAE1_ARTBC Probable feruloyl esterase ARB_07085 OS=Arthroderma benhamiae (strain ATCC MYA-4681 / CBS 112371) GN=ARB_07085 PE=1 SV=1 (537)	3.00E-33
BCWF01000033-14	sp Q6CBE4 ETR1_YARLI Probable trans-2-enoyl-CoA reductase, mitochondrial OS=Yarrowia lipolytica (strain CLIB 122 / E 150) GN=ETR1 PE=3 SV=1 (376)	7.00E-93
BCWF01000034-14	sp Q56078 BGLX_SALTY Periplasmic beta-glucosidase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) GN=bgIX PE=3 SV=2 (765)	3.00E-115
BCWF01000034-31	sp A2R989 BGLI_ASPNC Probable beta-glucosidase I OS=Aspergillus niger (strain CBS 513.88 / FGSC A1513) GN=bgII PE=3 SV=1 (818)	0
BCWF01000036-120	sp O13716 AGN1_SCHPO Glucan endo-1,3-alpha-glucosidase agn1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=agn1 PE=1 SV=2 (424)	1.00E-50
BCWF01000036-126	sp Q5B0F4 BGLG_EMENI Probable beta-glucosidase G OS=Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) GN=bgIG PE=3 SV=2 (819)	0
BCWF01000036-127	sp Q2U325 BGLG_ASPOR Probable beta-glucosidase G OS=Aspergillus oryzae (strain ATCC 42149 / RIB 40) GN=bgIG PE=3 SV=1 (815)	0
BCWF01000036-134	sp Q9XIG1 U80B1_ARATH Sterol 3-beta-glucosyltransferase UGT80B1 OS=Arabidopsis thaliana GN=UGT80B1 PE=2 SV=1 (615)	7.00E-126
BCWF01000036-145	sp D4AS70 FAE1_ARTBC Probable feruloyl esterase ARB_07085 OS=Arthroderma benhamiae (strain ATCC MYA-4681 / CBS 112371) GN=ARB_07085 PE=1 SV=1 (537)	7.00E-10
BCWF01000036-163	sp Q2UP89 FAEB1_ASPOR Probable feruloyl esterase B-1 OS=Aspergillus oryzae (strain ATCC 42149 / RIB 40) GN=faeB-1 PE=1 SV=1 (540)	1.00E-72
BCWF01000036-45	sp O05619 VDH_PSEUH Vanillin dehydrogenase OS=Pseudomonas sp. (strain HR199 / DSM 7063) GN=vdh PE=1 SV=1 (481)	2.00E-100
BCWF01000036-8	sp B0X1Q4 RUMI_CULQU O-glucosyltransferase rumi homolog OS=Culex quinquefasciatus GN=CPIJ013394 PE=3 SV=1 (403)	2.00E-11
BCWF01000040-41	sp Q9P6J3 MALT_SCHPO Alpha-glucosidase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=malI PE=2 SV=1 (579)	2.00E-149