

University of Groningen

Impact of Velvet Complex on Transcriptome and Penicillin G Production in Glucose-Limited Chemostat Cultures of a beta-Lactam High-Producing *Penicillium chrysogenum* Strain

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103 genes Upregulated in DS63171 relative to DS17690 in absence of PAA			Significance Analysis of Microarray (SAM) results						DS17690 -PAA			DS63171 -PAA		DS67261 -PAA		DS17690 + PAA		DS63171 +PAA		DS67261 +PAA		
Gene ID	Similar to		Score(d)	Numerator(r)	Denominator(s)	Fold Change	q-value(%)	1	2	3	1	2	1	2	1	2	1	2	1	2	1	2
Pc06g00230_at	hypothetical protein contig61.tfa_1250cg - A. fumigatus		12.37	178.80	14.45	12.04	0.00	19.8	12	16.8	211.4	178.6	157	151.1	12	12	16.3	106.3	130.4	12	12	
Pc06g02160_x_at	retrotransposon Tto1 - N. tabacum		6.85	429.70	62.76	3.45	0.00	83	204.2	238.4	606.4	603.4	12	12	28.8	34.9	33.3	12	12	76.9	82.6	
Pc12g00010_at	glucose oxidase GOD - P.amagasakiense		5.20	47.22	9.08	4.08	0.00	22	12	12	70.3	54.8	12	12	12	12	12	12	12	12	12	12
Pc12g01040_at	galactosyltransferase Bed1 - S.cerevisiae		6.69	31.88	4.77	3.25	0.00	18.4	12.1	12	47.3	44.8	12	12	12	12	12	12	12	12	12	12
Pc12g01280_at	RNA helicase GLH-2 - Caenorhabditis elegans		2.60	54.05	20.82	3.16	0.00	37.6	18.3	19.1	102	56.1	120.9	96.2	23.8	19	12	83.3	103.6	12.8	25.8	
Pc12g01540-3_s_at	sulfur permease SulB - P.chrysogenum		2.91	72.58	24.98	3.01	0.00	53.9	16.5	38.1	84.1	133.4	12	12	12	12	12	12	12	12	12	12
Pc12g02250_at	glucose dehydrogenase like protein An07g08190 - A. niger		2.87	35.37	12.32	3.94	0.00	12	12	12	61.4	33.4	12	12	12	12	12	12	13.8	12	12	12
Pc12g03130_at	acetyl-CoA hydrolase Ach1 - S.cerevisiae		3.97	32.22	8.12	3.20	0.00	19	12	12.9	54.3	39.4	12	12	12	12	12	12	12	12	12	12
Pc12g03260_at	hypothetical protein An16g07330 - A. niger		5.91	409.67	69.34	4.15	0.00	177.1	41.7	171	491.2	588	29.1	29	12	12	12	29.8	31.5	14.6	12	
Pc12g08750_at	polyamine oxidase PAO - Zea mays		6.42	30.02	4.68	3.49	0.00	12	12	12	38.3	45.8	12	12	12	12	12	12	12	12	12	12
Pc12g13160_at	hypothetical mixed-linked glucanase precursor MLG1 - N. crassa		6.09	141.23	23.18	3.03	0.00	81.2	38.2	89.6	203.4	218.4	12	12	14.3	12	12.5	12.2	12	12	16.4	
Pc12g13430_at	hypothetical protein B2J23.120 - N. crassa		4.55	107.42	23.60	3.32	0.00	73.2	27.9	37.6	170.4	136.9	99.8	104.1	17.6	16.9	15.3	126.2	85.8	12	19.2	
Pc12g13940_at	hypothetical protein contig_1..41_scaffold_2.tfa_160wg - A. nidulans		4.90	98.45	20.10	3.92	0.00	54	12	35.1	144.6	119.7	113.7	131.6	12	12	12	151.5	148.5	12	12	
Pc12g14380_at	ribonuclease T1 precursor rna1 - A. oryzae		9.54	215.35	22.59	3.80	0.00	73.3	88.5	69.2	266.5	318.2	1213.7	1361.4	21.7	25.1	18.6	1353.5	1515.1	30.6	23.5	
Pc12g14960_at	hypothetical protein An08g06730 - A. niger		6.14	512.53	83.54	4.58	0.00	247.3	31.2	151.3	639.1	672.5	12	12	12	12	12	12	12	12	12	12
Pc12g16280_at	multicopy suppressor Sur7 - S.cerevisiae		6.92	119.92	17.33	6.44	0.00	20.8	12	33.3	159.7	124.2	81.5	68.7	12	12	12	12.5	83.7	84.8	14	12
Pc13g00880_at	ceruloplasmin - Danio rerio		4.77	409.03	85.79	3.58	0.00	267.1	45.1	163.2	585.8	549.2	12	12	12	12	12	12	12	12	12	12
Pc13g03840_at	beta transducin-like protein het-e1 - Podospora anserina		7.42	28.62	3.86	3.38	0.00	12	12	12	43.3	38	12	12	12	12	12	12	12	12	12	12
Pc13g05340_at	cell wall synthesis protein KRE9 - Candida albicans		4.49	131.95	29.37	3.09	0.00	94.1	23	71.9	188.9	201	765.1	855.7	12	12	12	522.2	663.8	12	12	
Pc13g07280_at	hypothetical protein 1158_scaffold_2.tfa_100wg - F. graminearum		3.62	45.47	12.55	3.02	0.00	28.5	12.6	26.5	56.6	79.4	276.3	283.1	12	12	12	272.7	255.3	12	12	
Pc13g07820_at	serine protease SP1 like protein An07g0580 - A. niger		3.65	31.12	8.53	3.04	0.00	12	21.7	12	39.4	53.3	12	12	12	12	12	12	12	12	12	
Pc13g08210_at	hypothetical protein CC0533 - Caulobacter crescentus		8.65	39.45	4.56	4.01	0.00	15.3	12	12	49.5	55.6	272.1	349.0	12	12	12	2160.4	3166.9	12	12	
Pc13g11090_at	hypothetical protein		2.94	83.82	28.55	3.56	0.00	60.6	14.4	23.2	90.5	142.6	45.6	42.6	12	12	12	30.6	26.7	12	12	
Pc13g13450_at	purine-cytosine permease pcp13 - Kluyveromyces marxianus		3.74	123.17	32.91	4.08	0.00	76.1	17	26.7	136.1	190.1	56.2	61.6	12	12	12	103	50.7	12	16.3	
Pc13g13920_at	hypothetical protein		4.01	117.33	29.23	4.37	0.00	39.4	12	52.9	182.3	121.9	133.7	103.7	12	12	12	103.9	145	12	12	
Pc13g16010_at	spore-wall fungal hydrophobin dewA - A. nidulans		16.50	287.53	17.43	8.76	0.00	50.5	14	46.7	330.3	318.9	93.9	121.5	12	12	12	69	120.3	12.9	12	
Pc14g00110_at	hypothetical protein UNC-89 - Caenorhabditis elegans		6.70	79.95	11.93	3.89	0.00	30	18.4	34.7	118.2	97.1	12	12	12	12	12	12	12	12	12	
Pc14g00910_at	salicylate hydroxylase nahW - Pseudomonas stutzeri		5.86	268.93	45.92	3.29	0.00	76.1	144.1	132.2	339.8	433	12	12	12	12	12	12	12	14.2	22	
Pc16g00180_at	hypothetical protein contig10.tfa_220cg - A. fumigatus		5.73	248.88	43.46	4.51	0.00	125.2	15.8	71.6	330.7	308.8	64.2	72.3	12	12	12	85.1	111.4	12	12	
Pc16g04550_at	hypothetical protein		4.06	259.83	64.01	3.06	0.00	206.1	41.4	131.6	398.3	374.1	12	12	12	12	12	12	12	12	12	
Pc16g04840_at	hypothetical protein		3.91	332.08	84.97	3.29	0.00	259.6	37.4	137.9	470.2	483.9	12	12	12	12	12	12	12	12	12	
Pc16g06660_at	hypothetical protein encoded by CG4090 - Drosophila melanogaster		5.91	986.75	166.90	3.28	0.00	624.1	190	482.5	1421.6	1416.3	12	12	12	12	12	12	12	12	12	
Pc16g06690_at	spore-wall fungal hydrophobin dewA - A. nidulans		8.74	286.87	32.82	11.38	0.00	35.9	13.3	33.7	274.9	354.1	12	12	15.6	12	12	12	12	12	12	
Pc16g08980_at	1,3-beta-glucanosyltransferase gel1 - A. fumigatus		3.09	219.55	71.10	3.04	0.00	189.2	38.3	95.9	274.2	380.5	12	12	12	12	15.4	12	12	15.3	27.2	
Pc16g09610_at	protein abfA - A. nidulans		7.27	266.68	36.11	4.41	0.00	112.4	40.2	78.6	311.4	368.1	12	18	12	12	12	20.4	14	12	12	
Pc16g10180_at	fluconazole resistance transporter Flr1 - S.cerevisiae		10.59	57.63	5.44	3.05	0.00	24.8	27.1	32.6	83.2	88.4	292.2	363.2	19.5	14.6	14	501.9	390	12	15.3	
Pc16g10900_at	beta-fructofuranosidase precursor suc1 - A. niger		13.56	207.78	15.33	7.54	0.00	47.3	12	36	238.8	240.3	96.2	115.3	12	12	12	34.2	68.4	12	12	
Pc16g11130_at	allergen rAsp f4 - A. fumigatus		4.10	79.80	19.48	4.82	0.00	33.7	12	17	80	121.4	226.5	229.4	12	12	12	67	131.9	12	12	
Pc16g11480_at	lovastatin diketide synthase lovF - A. terreus		9.40	586.80	62.44	3.27	0.00	207.4	294.3	347	91.0	829.3	12	60.7	43.4	131.3	12	95	93.9	12		
Pc16g12580_at	hypothetical blue-light-inducible protein bli-3 - N. crassa		3.89	47.98	12.34	3.08	0.00	26.1	12.8	30.3	81.7	60.4	12	21.5	12.3	23.4	12	16.5	29.3	12		
Pc16g13260_at	hypothetical protein An01g10940 - A. niger		5.73	194.58	33.96	3.78	0.00	95.2	25.6	89.1	245.4	283.7	47.4	43.3	12	12	35	32.4	12	12	12	
Pc18g01150_at	polyamine transport protein Ptp1 - S.cerevisiae		4.87	78.88	16.20	3.88	0.00	41.1	13.3	27.7	119.5	93	12	12	12	12	12	12	12	12	12	
Pc18g02600_at	high affinity hexose transporter Hxt1 - S.cerevisiae		8.43	49.95	5.92	4.33	0.00	21	12	63.4	66.5	155	114.5	12	12	12	80.3	109.4	12	12		
Pc18g03170_at	43 kDa secreted glycoprotein precursor gp43 - P. brasiliensis		10.23	47.20	4.61	4.47	0.00	16.8	12	58.4	63.2	12	18.2	13.4	12	12	17.4	12	12	12		
Pc18g04570_at	phorbol activated nuclear factor-like protein An04g03830 - A. niger		4.70	71.20	15.15	3.56	0.00	21.1	40.5	21.8	85	113	459.8	464.6	12	12	482	395.3	12	12		
Pc20g01760_at	cercosporang transporter CFP - Cercospora kikuchi		4.27	120.32	28.16	4.05	0.00	68.5	12	37.8	138.7	180.8	83.6	69.3	12	12	45.7	58.9	12	12		
Pc20g02250_at	chitinase - <i>Chelonus</i> sp.		4.77	421.15	88.37	3.15	0.00	282.5	67.9	236.1	64.3	58.9	12	41.8	50.4	45.3	12	12	42.1	44.8		
Pc20g03190_at	hypothetical protein An11g09750 - A. niger		8.29	159.95	19.30	3.25	0.00	73.8	72.6	66.6	207.9	254	271.3	177.9	26.5	17.7	12	73.8	70.7	17.1	20.3	
Pc20g04600_at	DNA-directed RNA polymerase II largest chain - Mastigamoeba invertens		2.89	295.23	103.64	6.38	0.00	81.2	49.4	36.2	220.3	489.4	219.1	234.1	80.2	81.7	32	319.8	265.8	81.8	111	
Pc20g06260_at	hemolysin ASP-HS - A. fumigatus		8.60	44.62	5.19	4.07	0.00	19.6	12	59.8	58.5	12	12	12	12	12	12	12	12	12		
Pc20g06270_at	hypothetical protein An17g01885 - A. niger		7.66	51.22	6.69	5.																

Pc21g20790_at	hypothetical precursor of spore coat protein sp96 - N. crassa	8.00	252.02	31.49	5.02	0.00	95.2	21.2	71.5	302.4	326.9	194.7	182.4	12	12	12	306.3	349.9	12	12
Pc21g21440_at	hypothetical protein	5.10	759.18	148.81	3.84	0.00	306.4	55.1	441.8	1045.8	1008.1	12	12	64.7	23.7	101.1	14.3	12	43.1	29.9
Pc22g03220_at	regulator protein weIA - P.chrysogenum	3.82	32.60	8.53	3.51	0.00	12.3	12	14.7	36.8	54.4	118.8	162.3	17.6	20.8	29.1	426.1	487.2	45.3	25.5
Pc22g04080_at	glucan 1,3-beta-glucosidase Bgl2 - S.cerevisiae	5.01	80.25	16.01	5.25	0.00	22.8	17.3	16.6	80.5	117.8	114.5	139.7	12	12	12	230.1	150.1	12	12
Pc22g04640_at	high affinity glucose transporter HGT1 - Kluyveromyces lactis	6.66	175.22	26.29	4.45	0.00	81.2	17.8	53.2	233.9	218	923.4	769.8	12	12	12	408.9	393.4	12	12
Pc22g05480_at	hypothetical oxidoreductase PA0147 - Pseudomonas aeruginosa	10.16	59.65	5.87	4.75	0.00	12	14.3	21.4	73.4	77.7	192.1	134	12	12	12	174.7	210.2	12	12
Pc22g05490_at	2-haloacid halohydrolylase Iva - Burkholderia cepacia	4.96	58.55	11.80	3.69	0.00	22.7	22.4	20.3	67.1	93.6	12	12.6	15.5	12	12	15.6	14.4	12	12
Pc22g06430_at	hypothetical protein B6O22.140 - N. crassa	3.25	32.57	10.01	3.37	0.00	13.7	13.3	14.2	35.4	57.2	202.8	148.2	22.5	12	12	262.9	167.9	12	47.8
Pc22g06520_at	potassium transport protein Trk2 - S.cerevisiae	5.59	109.00	19.50	3.87	0.00	63.7	17.4	32.9	148.8	145.2	12	12	12	12	12	12	12	12	12
Pc22g07760_at	hypothetical protein 1194_scaffold_2.tfa_330wg - F. graminearum	7.16	124.23	17.36	4.68	0.00	53.6	14.9	32.8	165.5	150.5	12	12	12	12	12	13.4	16.7	12	12
Pc22g07910_at	hypothetical protein YGR086c - S.cerevisiae	8.72	67.42	7.73	5.54	0.00	16	12	16.5	89.7	74.8	1364.4	939.1	18.6	21.1	28.1	700.4	748.1	23.4	31.5
Pc22g08420_at	brown 2 protein abr2 - A. fumigatus	6.21	138.60	22.31	3.41	0.00	84.2	30.9	57.4	189.7	202.5	12	12	12	12	12	12	12	12	12
Pc22g08820_at	hypothetical protein	4.86	130.07	26.77	3.33	0.00	88.1	23.4	56	194.2	177.6	12	15.1	25.9	21.3	12	83.3	41.2	12	21.4
Pc22g13930_at	glutathione-dependent formaldehyde dehydrogenase FDH - M. marinus	10.48	70.58	6.73	4.95	0.00	23.8	12	17.8	91.2	85.7	683.8	831.2	26.2	16.4	34.5	1228.7	866.3	28.5	28.5
Pc22g14290_at	rodlesslet protein rodA - A. nidulans	9.16	215.70	23.55	3.74	0.00	96	48.7	91.1	281.3	307.3	81.5	85.1	23	23.5	12	108.4	112.6	14.4	12
Pc22g14300_at	hypothetical protein An02g09010 - A. niger	7.20	98.00	13.45	4.38	0.00	424	93.5	354.9	1320.8	1226.8	69.7	57.7	12	12	12	69.9	60	17.6	12
Pc22g17040_at	hypothetical protein	4.72	666.12	141.14	3.64	0.00	414.9	61.6	280.8	862.9	974.2	71.5	53.3	12	12	12	111.8	123.4	12	12
Pc22g19920_at	35.8K acid phosphatase - A. nidulans	5.70	335.37	58.82	3.02	0.00	116	185.9	196.2	438.7	564.1	12	12	12	12	12	12	12	16.4	13.8
Pc22g23660_at	Swe1 regulating protein kinase Hst1 - S.cerevisiae	3.50	436.28	124.55	4.10	0.00	149.8	52	220.2	435.7	718.2	19	26.9	12	12	12	47.7	45.9	12	12
Pc22g24580_at	thermostable alcohol dehydrogenase adhT - B. stearothermophilus	4.14	36.47	8.81	4.03	0.00	12	12	57.8	39.2	102.3	109.3	12	12	12	73.1	61.2	12	12	
Pc22g24750_at	hypothetical protein BBJ22.030 - N. crassa	10.67	166.08	15.57	4.73	0.00	59.8	30.9	43	199.4	221.9	12	12	12	12	12	12	12	12	
Pc22g26040_at	hypothetical protein	9.55	108.42	11.36	5.13	0.00	36.1	12	30.6	133.2	136.1	12	19.2	12	12	12	21.5	18.7	12	12
Pc22g26260_at	hypothetical protein	5.53	42.35	7.66	3.14	0.00	16.6	28.6	14.2	62.9	61.4	27.3	12	12	12	12	12	12	12	
Pc23g00530_at	ankyrin repeat protein E4 2 - Synthetic construct	9.52	122.80	12.89	3.32	0.00	53.1	39.9	65.7	168.5	182.9	13.9	36.1	71.9	57.8	72.7	602.8	506.8	127.1	48.5
Pc49g0070_at	hypothetical protein - P.mamelei	4.32	71.97	16.68	3.40	0.00	29.2	25.3	35.3	82.7	121.1	42.2	51.1	34.3	32	35.7	45.9	33.5	576.4	87

47 genes Downregulated in DS63171 relative to DS17690 in absence of PAA		Score(d)	Numerator(r)	Denominator(s)	Fold Change	q-value(%)	DS17690 -PAA			DS63171 -PAA			DS67261 -PAA			DS17690 + PAA			DS63171 +PAA		
Gene ID	Gene Name						1	2	3	1	2	1	2	1	2	3	1	2	3	1	2
Pc06g00210_at	secretory component IDGF - Sarcophaga peregrina	-20.10	-164.25	8.17	0.28	0.00	231.7	219.5	235.5	65.8	63.5	35	26	12	14.6	15.8	69.2	126.8	12.5	20.9	
Pc06g02040_at	hypothetical protein 15_scaffold_1.tfa_520cg - F. graminearum	-4.79	-77.05	160.93	0.28	0.00	1246.7	1116.4	834.6	261.5	329.8	12	12	77.6	69.3	74.5	12	17.6	37.8	47.9	
Pc06g02050_at	hypothetical protein An08g1190 - A. niger	-3.23	-846.95	262.12	0.16	0.53	1038.3	1331.6	650.2	88.5	231	148.5	165.8	64	44.4	22.2	107.2	120.8	12	27.7	
Pc06g02070_at	hypothetical protein contig46_part_iiffa_1990wg - A. fumigatus	-2.55	-578.38	226.89	0.09	0.53	782.5	837.5	291.4	31.8	85.7	469	470.6	28.3	20.5	12.5	327	342.1	12	12	
Pc06g02080_s_at	hypothetical protein contig46_part_iiffa_1990wg - A. fumigatus	-3.63	-754.60	207.61	0.12	0.00	97.24	1047.5	542.1	56.8	142	12	55.5	40.6	33.3	12	12	15.6	12	12	
Pc06g02080_S_at	hypothetical protein An06g02320 - A. niger	-3.45	-61.33	17.75	0.19	0.00	97	75.8	54.7	12	17	54.2	49	12	12	97	87.3	12	12		
Pc06g02090_s_at	hypothetical protein An06g02320 - A. niger	-2.47	-92.57	37.47	0.15	0.53	157	107.4	61.9	12	20.4	12	12	12	12	12	12	12	12	12	
Pc06g02090_S_at	hypothetical protein	-4.11	-74.45	18.11	0.17	0.00	102	101.9	64.6	12	18.1	908.3	982.9	12.4	12	949.3	1085.6	12	12		
Pc06g02100_s_at	hypothetical protein	-2.86	-473.68	165.38	0.16	0.53	746.6	621.3	320.6	75.5	102.8	247.96	3193.6	62.9	51.1	43	3606.1	3151	27.1	34.9	
Pc12g01130_at	aldehyde reductase II ARII - Sporidiobolus salmonicolor	-10.28	-1409.78	137.15	0.11	0.00	1497.9	1454	178.76	161.2	178.9	12	12	1460.7	1788	2153.3	35.9	21.4	2462.1	1844.6	
Pc12g02730_at	vegetative incompatibility factor het-1 - Podospora anserina	-4.89	-66.90	13.67	0.30	0.00	92.6	112.5	81.4	27.2	30	12	12	14.6	18.2	18.7	12	12	12	18.8	
Pc12g06310_at	aristolochene synthase Ar11 - P.roqueforti	-2.14	-77.55	36.18	0.13	0.95	141.3	53.1	74.4	12	2531.4	3234.8	12	12	12	12	2551	3325	12	12	
Pc12g06320_at	hydroquinone oxidase mcrA - Streptomyces lavendulae	-2.07	-45.62	22.00	0.21	0.95	88.3	37.4	47.3	12	75	85.2	12	12	28.8	25.1	12	12			
Pc12g06330_at	hypothetical short chain alcohol dehydrogenase cta - Cucumis sativus	-2.66	-56.95	21.43	0.17	0.53	97.3	45.5	64.2	12	302.5	283.5	12	12	349.4	382.9	12	12			
Pc12g06340_at	hypothetical cytochrome P450 monooxygenase p450-4 - Gibberella fujikuroi	-3.27	-30.18	9.23	0.29	0.00	52.3	32.6	41.8	12	629.3	609.6	12	12	1134.8	1064.5	12	12			
Pc12g06350_at	hypothetical cytochrome P450 protein 2E4.050 - N. crassa	-2.32	-57.52	24.82	0.31	0.53	118.5	67.7	63	25.5	347.6	278.6	26.1	24.5	320.2	206.8	18.9	17.2			
Pc12g06370_at	trichothecene 3-O-acetyltransferase TR1101 - Fusarium sporotrichoides	-2.71	-46.52	17.14	0.21	0.53	82.2	46.1	47.4	12	507	483.3	12	12	368.1	486.4	12	12			
Pc12g06450_at	hypothetical protein contig1_55_scaffold_3.tfa_110cg - A. nidulans	-5.20	-131.53	25.27	0.23	0.00	136.2	195.2	35.9	43.9	391.1	394.4	34.1	27.9	31.9	471.9	583.6	22.7	16.7		
Pc12g06460_at	hypothetical protein contig28.tfa_310cg - A. fumigatus	-2.97	-196.93	66.41	0.20	0.53	199.1	346.2	193.7	46.4	52.4	30.9	42.8	37.3	16.2	14.1	138.1	74.9	17.2	16.6	
Pc12g06880_at	hypothetical protein	-5.46	-190.10	34.84	0.24	0.00	201.5	262.8	286	53	67	12	12	110.5	115.1	63.6	12	79.6	84.6		
Pc12g08290_at	antifungal protein precursor pfaf - P.chrysogenum	-8.37	-338.55	40.46	0.19	0.00	366.8	414	465.7	61.7	92.2	302.3	143.8	31.3	41	43.6	12	13.6	25	16.2	
Pc12g15480_at	hypothetical protein contig1_93_6.tfa_720cg - A. nidulans	-3.02	-83.52	27.66	0.17	0.53	115.2	61.1	125.4	18.5	156	250.2	238.7	12	12	226.8	219.5	12	12		
Pc13g08150_at	hypothetical protein An04g03190 - A. niger	-2.71	-197.27	72.75	0.32	0.53	318.5	182.4	365.4	89.2	93.8	1275.3	1275.3	123.9	180.2	130.2	1318	1165.9	244.9	129.6	
Pc13g13200_at	dark repressor of condidin velvet veA - A. nidulans	-5.69</																			

62 genes Upregulated in DS63171 relative to DS17690 in presence of PAA		Significance Analysis of Microarray (SAM) results										DS17690 -PAA		DS63171 -PAA		DS67261 -PAA		DS17690 + PAA		DS63171 +PAA		DS67261 +PAA	
Gene ID	Similar to	Score(d)	Numerator(r)	Denominator(s+s0)	Fold Change	q-value(%)		1	2	3	1	2	1	2	1	2	3	1	2	1	2	1	2
Pc01g00030_s_at	hypothetical protein An12g08820 - A. niger	7.81463504	66.76666667	8.543798442	6.548476454	0	124	124.9	202.3	413	437.1	32	26.6	12	12	12	12	16.3	22.4	12	12	12	12
Pc06g00390_s_at	hypothetical protein An01g10620 - A. niger	8.62380958	32	3.710657073	3.273762238	0	69.3	103.5	60.6	104.9	113.2	12	12	12	16	14.9	12	12	25.5	17.5	12	25.3	17.5
Pc06g00400_at	hypothetical protein contig46_part_iIfa_580wg - A. fumigatus	6.90033739	112.5	16.30355063	4.90625	0	151	142	99.9	223.2	250.7	12	12	22.9	31	32.5	12	12	34.2	12	12	34.2	25.3
Pc06g00470_at	developmental regulatory protein brlA - A. nidulans	11.3724264	171.1	15.0451622	5.33164557	0	119.7	122.3	149.9	321	324.4	84.9	84.1	45.7	34	38.8	101.8	78.4	95.4	64.5	1773.6	1474.4	
Pc06g00650_at	retrotransposon Tnt1 - Nicotiana tabacum	3.04996843	129.8166667	42.56328212	5.014948454	0	83	204.2	238.4	606.4	603.4	12	12	28.8	34.9	33.3	12	12	76.9	82.6	12	76.9	71
Pc12g00650_at	hypothetical protein CC3092 - Caulobacter crescentus	5.87207735	204.5166667	34.82867379	4.518061927	0	210	131.2	171.2	465.4	427.7	12	12	58.1	59.3	57	12	12	79.9	79.9	12	40.5	33.5
Pc12g03690_at	hypothetical protein contig_1_128_scaffold_8.ifa_30wg - A. nidulans	2.3582876	328.65	124.60075054	3.368888889	0.57585	22.2	36.4	23.7	44.2	62.1	12	12	27.3	22.9	17.3	12	12	40.5	33.5	12	40.5	33.5
Pc12g04120_at	hypothetical protein contig_1_116_scaffold_8.ifa_30wg - A. nidulans	2.63513896	124.7182804	3.436249073	0.57585	0	262.6	177.5	198.9	150.3	131.8	281.5	272.8	169.4	130.1	105.2	225.6	201.9	169.8	218.5	12	21.1	
Pc12g09090_at	hypothetical protein SPAC1420.1c - S.pombe	12.3298047	169.333333	13.733659	4.178973717	0	47	66.1	109.3	130	193.3	14.6	22.6	57.6	37.4	64.8	22.9	21.1	201.9	104.5	12	20.1	
Pc12g09570_at	integral membrane protein PTH11 - grisea	9.45836602	145.9166667	15.42725946	3.154281496	0	60	54.1	65.4	77.4	62.6	450.5	471.7	75.6	67.6	60	369.9	370.2	83.2	72.3	12	72.3	
Pc12g10800_at	endo_1,5-alpha-D-arabinanase abna - A. niger	4.23132021	61.06666667	14.43204283	6.074792244	0	171.3	69.7	138.1	276.8	311.9	18	15	12	12	19.5	18.6	16.6	12	12	16.6	12	
Pc12g12710_at	multidrug resistance ABC transporter like protein An02g04910 - A. niger	6.14054032	52.91666667	8.617591272	3.32771261	0	37.2	32.6	53.2	69.3	71.7	22.3	28.7	17.2	45.5	46.6	34.2	36.2	12	12	12	12	
Pc12g14960_at	hypothetical protein An08g06730 - A. niger	3.39308856	26.96666667	7.94728107	3.24097923	0	247.3	31.2	151.3	639.1	672.5	12	12	12	12	12	12	12	12	12	12	12	
Pc13g00880_at	ceruloplasmin - Danio rerio	6.76432327	30.31666667	4.4818477	3.519399582	0	267.1	45.1	163.2	585.8	549.2	12	12	12	12	12	12	12	12	12	12	12	
Pc13g02150_at	hypothetical protein An11g05870 - A. niger	8.23181366	36.15	4.391498826	3.177710843	0	82.7	91.2	49.1	193.9	220.2	12	12	16.2	19.9	13.7	12	12	21.2	12	21.2	12	
Pc13g02910_at	transcription factor Sp7 - S.cerevisiae	12.1282562	35.3333333	2.912342125	3.683544304	0	15.5	12.5	12	52.7	81.9	86.2	13.3	14.2	12	97.9	111	46.1	16.5	12	16.5		
Pc13g10790_at	hypothetical protein An16g03760 - A. niger	1.96804125	69.5	35.31430303	3.43006993	1.109819	26.6	35.3	46.5	86.4	106.7	76.2	76.8	26.4	27.1	32.3	64.3	68.4	117.9	81.9	12	81.9	
Pc13g12780_at	regulator protein Rph1 - S.cerevisiae	2.3522061	30.96666667	13.16494618	3.573470202	0.57585	12	12	12	32.8	12	12	12	12	12	12	12	12	12	12	12		
Pc13g12950_at	transcription regulator of maltose utilization amyR - A. oryzae	3.57261809	29.7333333	8.32241426	3.08411215	0	16.2	23.8	28.2	31.6	35.6	33.4	27.6	18.4	12	12	45.7	31	13.5	12			
Pc14g01940_at	hypothetical protein 1424_scaffold_7.tfa_400w - F. graminearum	8.16183239	44.86666667	7.258061274	3.888412017	0	16.6	24.8	20.5	35.1	75.6	1053.9	12	20.8	13.8	668.3	792.4	48	22.9	12	22.9		
Pc16g00830_at	hypothetical protein contig_1_108_scaffold_7.tfa_310cg - A. nidulans	7.34682822	52.35	7.123778541	3.17219917	0	71.1	51	55.2	61.1	69.9	12	24.3	22.2	25.8	12	12	16.3	12	16.3	12		
Pc16g00840_at	O-methyltransferase A omta - A. parasiticus	17.1389571	160.75	9.37921714	3.1751236806	0	189.6	63.9	137.2	148.6	216.6	12	12	84.4	66.4	70.9	15.6	12	101	57.5	12	57.5	
Pc16g02980_at	hypothetical protein contig_1_65_scaffold_4.tfa_330wg - A. nidulans	9.0392295	925.16666667	10.35017198	4.303737336	0	349.5	256.5	509.1	424.4	413.1	203.4	191.9	353.8	257.9	228.4	191.7	229.2	332.3	367	12	367	
Pc16g06660_at	hypothetical protein encoded by CG4090 - D. melanogaster	15.2734039	72.26666667	5.1898449451	5.7852756718	0	624.1	190	482.5	142.6	141.6	12	12	12	12	12	12	12	12	12	12	12	
Pc16g08700_at	Pcl-like cyclin pCa1 - A. nidulans	4.49288839	43.56666667	9.69860591	5.3528046422	0	80	67.7	106.2	229.7	240.6	74	63.7	24	15.7	12	73.8	57.8	23.5	17.1	12	23.5	
Pc16g09610_at	protein abaa - A. nidulans	3.6170156	25.01666667	3.960203	3.078947368	0	112.4	40.2	78.6	311.4	368.1	12	18	12	12	20.4	12	14	12	12	14	12	
Pc16g11480_at	lovastatin diketide synthase lovF - A. terreus	4.48698964	167.0333333	23.22614643	3.128170707	0	207.4	294.3	347	91.0	829.3	12	12	60.7	43.4	131.3	12	95	93.9	12	93.9	12	
Pc16g13800_at	large subunit TFIIB like protein An01g12770 - A. niger	5.78220921	76.16666667	13.16375806	3.1514254583	0	29.1	53.2	83.3	89.5	118.4	30.9	37	24.6	43.7	37	137	175.3	81.1	67.4	12	67.4	
Pc16g14610_at	hypothetical protein 66B2.10 - N. crassa	2.75638883	23.21666667	26.21674241	3.407880133	0	40.8	78.7	74.1	80	114.5	252.2	191	23.4	29.7	37	206.5	182.8	114.4	63.6	12	63.6	
Pc16g15190_at	hypothetical protein	5.76959705	212.5323233	28.11277795	3.6372893	0	97.1	77.8	82.6	111.4	118.0	12	12	82.6	81.5	78.8	12	12	110	12	12	12	
Pc18g03030_at	integral membrane protein PTH11 - grisea	17.627974	98.8333333	5.606618976	4.865710561	0	270.2	268.7	238.2	397.7	368.2	493.7	624.2	238	30.7	22.2	259.7	406.9	50.2	38.7	12	38.7	
Pc18g04570_at	hypothetical protein C039w0 - Plasmodium falciparum	8.41823964	99.35	11.62828601	5.31596491	0	821.5	206.5	88.1	2565.3	2150.8	43.3	43.2	29.1	24.5	23	39.4	37.5	40.7	12	40.7		
Pc20g02040_at	methicillin resistance gene HmrA - Staphylococcus aureus	9.58679265	52.61666667	57.64245489	3.304169562	0	347.9	156.9	413.8	627.2	502.1	26.7	20.5	17.1	24.4	15.6	48.8	28.3	36.4	51	12	202.8	
Pc20g02640_at	integral membrane protein PTH11 - grisea	3.72948648	107.6833333	28.87350149	5.493045897	0	17.2	22	36.3	28.9	12	12	35.1	19.2	17.6	12	12	38.3	26.7	12	38.3	26.7	
Pc20g02640_at	serine-type carboxypeptidase precursor cpdS - <i>A. phoenicis</i>	5.0482431	134.61666667	8.945673288	0.87267951	0	36	22.9	54.8	102.5	91.7	308	346.7	12	17	12	278	352.1	30.3	13	13		
Pc20g13450_at	integral membrane protein PTH11 from patient WO9/13094-A2 - grisea	2.808699877	47.38333333	7.789379153	3.511484099	0	52.3	24.5	69.9	29.7	39.8	266.1	301.9	21.8	17.7	18.6	227.4	23.1	31.5	14.5	12		
Pc20g15050_at	hypothetical protein Chol esterase I - <i>B. cephalosporinaceae</i>	8.1381995	311.15	38.23237048	3.277818484	0	626.8	441.5	675.5	764.8	824.5	62.5	65	110.5	135.5	163.8	95.9	85.3	320.3	325	12	325	
Pc20g15090_at	hypothetical protein B2E1.75 - N. crassa	6.69028922	40.85	4.58238575	3.475757576	0	12	12	15.6	12	30.3	365.6	273.4	12	20.8	16.7	222.2	413.6	59.7	18.8	12		
Pc21g03010_at	molasses resistance protein Rtm1 - S.cerevisiae	4.11109948	51.96666667	12.6405763	3.019430052	0	322.9	360.9	256.6	609.1	685.9	105.9	105.6	14.5	40.4	22.3	76.2	64.1	40.3	36.9	12		
Pc21g05120_at	poly(A)-specific ribonuclease Pan1 - S.cerevisiae	4.30579735	189.4833333	46.092542501	3.500879894	0	50.6	81.6	59.7	88.8	145	48.5	37	71.7	68.6	37.2	36.5	296.6	76.4	12	76.4		
Pc21g05380_at	hypothetical protein	14.7666818	118.7	8.027494012	3.35049505	0	89.5	86.2	79.5	114.0	106.8	67.4	67.4	12	12	12	12	12	12	12	12		
Pc21g06230_at	hypothetical protein contig_1_5_scaffold_1.tfa_170cg - A. nidulans	1.94388896	43.85	22.55787289	3.139024399	1.109819	19.7	30.9	33.4	22	60.2	185.6	220.8	67.7	57.7	12	12	69.9	60	17.6	12		
Pc22g04990_at	hypothetical protein An02g09010 - A. niger	11.7002012	102.41666667	8.753401756	0.234961289	0																	

Pc20g11120_at	hypothetical protein	-4.48256668	-35.2333333	7.860080142	0.317624274	0	65.7	63.3	49.4	33.4	51.9	12	12	58.7	44.7	51.5	12	12	24.6	30.3	
Pc21g08480_at	hypothetical protein	-3.31950981	-104.416667	31.4554475	0.311084231	0	169.5	151.4	125.6	101.8	124.2	69.9	65.9	196	132.5	126.2	35.8	25.3	99.2	278	
Pc21g10690_at	hypothetical protein contig1488_2.tfa_1690cg - A. fumigatus	-2.91723759	-52.0166667	17.83079543	0.256669834	0	74	77.4	54.4	48.9	59.5	12	12	74.5	88.6	47.4	12	12	30.9	51.5	
Pc21g10880_at	7-aminocholesterol resistance protein Rta1 - S.cerevisiae	-3.79252385	-333.783333	88.01087265	0.327501679	0	1038.3	827.3	769.2	693.8	946.5	12	12	12.3	435.1	629.1	424.8	30.1	12	209.9	230.3
Pc21g12470_at	heterokaryon incompatibility protein het-6 - N. crassa	-4.48310611	-39.4833333	8.807137803	0.263823465	0	29.7	56.4	35.1	27.1	19.5	82.5	66.4	63.2	45.9	51.8	43	66.2	37.1	65.7	
Pc21g12590_at	6-hydroxy-D-nicotine oxidase 6-HDNO - Arthrobacter oxidans	-4.47094319	-1360.75	304.3541245	0.311814109	0	1748.6	1442.3	2403	1698.7	1513.2	481.3	307.3	1769.2	1724	2438.7	128.7	135.5	1354.1	1479.9	
Pc21g12610_at	7alpha-cephem-methoxykase subunit cmcJ - Streptomyces lactamdurans	-5.06037908	-368.416667	72.8041637	0.266345835	0	811.7	479.2	665.9	451.6	582.1	74.7	59.8	440.9	454.2	611.4	156.7	159.6	336.9	286.3	
Pc21g12620_at	asparagine synthase asnB - Bacillus subtilis	-3.51220767	-1256.8	357.8376101	0.245119827	0	1652.4	1382.1	2088.4	1378.6	1234.2	44.9	44.7	1379.7	1403.9	2211.1	67.9	56.1	1285.5	1088.8	
Pc21g12630_at	peptide synthase pesA - Metarhizium anisopliae	-5.56511953	-873.133333	156.8939048	0.170445908	0	1276.3	1133.9	1333.2	1047.3	1291.8	142.4	105.4	1021.4	864.9	1271.3	114.6	66.8	587.5	653.3	
Pc21g12820_at	3-dehydroshikimate dehydratase qa-4 - N. crassa	-2.94492879	-197.916667	67.20592607	0.331513173	0	1109	1097.5	729.5	559.8	484.6	12	12	331.9	359.4	196.9	12	12	191.3	167.3	
Pc21g14970_at	protein D-lactate dehydrogenase YEL071w - S.cerevisiae	-4.72345787	-161.366667	34.16282546	0.286198761	0	248.9	270.9	226.7	232.5	99.7	530.4	570.5	243.5	253.5	181.2	415	449.1	120.9	133.7	
Pc21g17030_at	hypothetical protein An04g08060 - A. niger	-5.20428437	-44.9666667	8.640316984	0.271991365	0	23.2	35.1	13.8	12	12	12	12	69.4	54.6	61.3	36.7	14.8	34	43.8	
Pc21g17040_at	beta transducin-like protein het-e1 - Podospora anserina	-8.5485196	-269.283333	31.50058091	0.04824581	0	37.8	151.7	57.5	19.4	12	18.6	20.6	291.1	240	317.7	12	12	175.3	284.7	
Pc21g17620_at	hypothetical conserved protein TM1177 - Thermotoga maritima	-4.43574703	-159.583333	35.97665334	0.323034502	0	107.9	105.7	81.1	75.7	87.9	76.8	84.6	282.9	210.1	214.2	45.2	63.2	126.5	234.7	
Pc21g22120_at	hypothetical protein 1316_scaffold_4.tfa_360cg - F. graminearum	-8.78022105	-115.766667	13.1849376	0.159690298	0	39.7	33.6	44	44	14.1	15.9	12	12	123.1	137.3	152.9	12	12	103.5	44.8
Pc21g22230_at	hypothetical protein 1158_scaffold_2.tfa_20wg - F. graminearum	-3.7552336	-189.9	50.56942396	0.165641476	0	173.9	78.9	144.8	55.8	78	55.2	94.3	157.7	238.8	286.3	60.9	81.5	235.4	148.3	
Pc21g22240_at	cholesterol 7alpha-monoxygenase CYP7 - Oryctolagus cuniculus	-8.61030778	-80.6666667	9.368615937	0.189008043	0	115.8	63.7	92.9	27.3	32.5	18.1	19	88.6	102.9	106.9	13.7	23.5	77.6	47.6	
Pc21g22260_at	T-2 toxin biosynthesis protein TR17 - F. sporotrichoides	-9.76492319	-401.416667	41.15016175	0.159220237	0	232.3	144.6	139.3	56	67.7	12	12	447.6	527.3	445.7	12	12	310.2	301.2	
Pc21g22260_at	cholesterol 7alpha-monoxygenase CYP7 - Oryctolagus cuniculus	-6.71753106	-446.116667	66.41080819	0.129981148	0	160.4	107.2	151.2	55.4	59.2	306.1	306.7	432.1	506	600.2	270.8	342.8	460.9	282.2	
Pc21g22270_at	cytochrome P450 monooxygenase P450l - Gibberella fujikuroi	-16.9921585	-132.166667	7.778097549	0.259846929	0	57.5	52	57.5	34.6	25	157.6	123.4	162.8	183.1	169.8	107.5	139.8	209.1	109.5	
Pc21g23590_at	cyanamide hydratase - Myrothecium verrucaria	-5.10701372	-483.366667	94.64761473	0.297908395	0	237.5	400.2	302.6	228.5	266.7	12	12	827.7	634.7	603	12	12	581.1	744.3	
Pc22g13600_at	hypothetical protein SPAC922.05c - Schizosaccharomyces pombe	-16.6418178	-195.216667	11.73048934	0.325132519	0	31	21.7	18.5	33.8	13	21.6	12	295.3	281.2	291.3	22.4	27.5	212.4	64	
Pc22g14570_at	protein disulfide isomerase A pdia - A. niger	-5.37965771	-531.95	98.88175587	0.219442406	0	952.4	788.6	782.2	500.9	471	54.9	60.1	541.3	710.5	792.7	62.3	64.1	520.6	453.7	
Pc22g15510_at	ATP-dependent DNA helicase II subunit Ku70 - Mus musculus	-6.10940884	-80.4166667	13.16275744	0.130317231	0	117.1	110.4	89.5	12	99	92.2	100.1	102	75.3	73.3	76.6	12	12	43.4	66.8
Pc22g25460_at	hypothetical protein	-3.37651862	-701.833333	207.8570897	0.036648975	0	2483.3	739.5	2367.2	1368	1475.2	12	12	1032.8	658.4	494.4	12	12	117.5	76.8	
Pc24g00370_at	hypothetical protein 1196_scaffold_3.tfa_500cg - F. graminearum	-5.11530826	-140.416667	27.4502844	0.293560288	0	777.4	558.3	805.8	837.5	913	141.6	157.4	163.1	213.6	219.6	80.9	69.1	117.5	76.8	

182 genes Upregulated in DS67261 relative to DS17690 in absence of PAA		Significance Analysis of Microarray (SAM) results											
Gene ID	Similar to	Score(d)	Numerator(r)	Denominator(s+d)	Fold Change	q-value(%)	DS17690 -PAA	DS63171 -PAA	DS67261 -PAA	DS17690 + PAA	DS63171 +PAA	DS67261 +PAA	
		1	2	3	1	2	1	2	1	2	1	2	1
Pc06g00170_at	gentisate 1,2-dioxygenases GDO - <i>Pseudomonas alcaligenes</i>	2.83	94.97	33.60	3.67	0.30	46.3	12	48.6	38.9	62.5	82.8	68.3
Pc06g00230_at	hypothetical protein contig61.tfa_1250cg - <i>A. fumigatus</i>	8.17	50.15	6.14	4.10	0.00	19.8	12	16.8	211.4	178.6	157	151.1
Pc06g00280_at	enoyl reductase of the lovastatin biosynthesis lovC - <i>A. terreus</i>	3.84	166.63	43.42	3.33	0.00	68.4	27	119.3	64.6	61	12	12
Pc06g00390_at	heat shock protein hsp30 - <i>A. nidulans</i>	5.72	160.42	260.23	5.56	0.00	24.4	92	751.6	246.8	340	134.5	176.8
Pc06g00492_at	heat shock protein hsp104 - <i>S. cerevisiae</i>	3.32	466.65	140.79	3.77	0.00	9.7	117	293.1	214.1	249.1	733.5	293
Pc06g1300_at	thioredoxin - <i>A. nidulans</i>	2.06	230.37	112.08	7.58	0.79	30.3	19.8	55	40.5	49.2	19.6	20.3
Pc06g1800_at	quinone oxidoreductase P1 - <i>Arabidopsis thaliana</i>	2.91	289.77	99.55	4.04	0.30	87.6	86.3	111.8	94	111.3	112	101.8
Pc06g2020_at	hypothetical protein At1g20250 - <i>A. niger</i>	2.93	42.30	14.42	4.20	0.30	15.1	12	12.5	19.3	36.4	12	12
Pc12g00730_at	hypothetical protein contig1492_tfa_2140cg - <i>A. fumigatus</i>	7.32	53.65	7.33	4.83	0.00	12	12	18	33.3	30.5	32.9	31.3
Pc12g00750_at	hypothetical protein An09g3050 - <i>A. niger</i>	3.49	120.88	34.62	7.08	0.30	17.8	15.8	26	37.2	44.9	36.8	42.8
Pc12g00830_at	sorbitol utilization protein sou2 - <i>Candida albicans</i>	3.54	159.02	449.25	5.65	0.30	363.8	302	360.7	433.3	546.3	15.5	12
Pc12g2180_at	hypothetical protein contig11.tfa_2280cg - <i>A. fumigatus</i>	1.69	35.87	21.22	3.98	0.91	12	12	12	12	12	12	12
Pc12g2290_at	hypothetical protein An15g04670 - <i>A. niger</i>	2.30	35.07	15.25	3.91	0.79	12	12	21.3	19.8	12	12	12
Pc12g2300_at	hypothetical protein ncu7485.1 - <i>N. crassa</i>	2.97	74.57	25.10	5.83	0.30	15.1	19.2	12	12	370.9	426.3	12
Pc12g3140_at	hypothetical protein An16g07080 - <i>A. niger</i>	1.70	85.80	50.53	5.64	0.91	25	12	18.5	15.1	18	259.5	282.4
Pc12g3550_at	p-nitrobenzyl esterase pnbA - <i>Bacillus subtilis</i>	3.38	111.25	32.91	6.01	0.30	21.4	21.1	54.7	41.9	12	12	12
Pc12g4310_at	acetate-inducible gene acA - <i>A. nidulans</i>	7.65	175.65	22.96	3.41	0.00	45.7	93.8	79.5	105.6	84.1	44.3	38.6
Pc12g6200_at	hypothetical glutathione S-transferase CA1906.1 - SchizoS.pombe	7.50	151.72	20.24	4.04	0.00	45.8	39.9	64.1	53.7	50.1	49	61.9
Pc12g6960_at	hypothetical protein contig1477_tfa_810wg - <i>A. fumigatus</i>	4.72	277.17	58.75	3.13	0.00	139.3	123.1	127.7	110	160.8	12	217.9
Pc12g7010_at	hypothetical protein An12g1650 - <i>A. niger</i>	2.54	241.23	95.15	7.96	0.53	30.3	31	42.7	31.1	28	23	28.2
Pc12g7920_at	hypothetical protein SPCC757.02c - SchizoS.pombe	3.32	204.52	61.52	12.04	0.30	13.5	14.1	28	32.1	41.8	12	27.8
Pc12g8490_at	hypothetical protein An19g06690 - <i>A. niger</i>	3.50	66.90	19.12	4.43	0.30	17.9	17.7	22.9	42.1	38.5	42.2	24
Pc12g8790_at	branched-chain alpha-keto acid dehydrogenase E1 alpha subunit BCHE1 - H.sapiens	2.03	82.33	40.52	3.20	0.79	38.1	34	40.3	32.8	59.9	80.2	76.1
Pc12g9570_at	integral membrane protein PTTH1 - Magnaporthe grisea	3.61	142.47	39.49	3.38	0.30	60	54.1	65.4	77.4	62.6	450.5	471.7
Pc12g1040_at	alternative oxidase axo1 - <i>A. niger</i>	3.16	124.33	39.45	5.46	0.00	26	14.8	42.8	23.8	32.5	12	22.4
Pc12g10870_at	L-proline analogue resistance gene Mpr1 - <i>S.cerevisiae</i>	6.39	145.65	22.79	3.31	0.00	56.4	46.9	52.1	47.7	19.4	30.1	88.3
Pc12g10920_at	secretory lipoprotein LP2 - <i>Candida albicans</i>	3.67	30.62	95.08	4.98	0.30	89.7	63.7	82	216.6	242.1	22	23.5
Pc12g1250_at	hypothetical protein Mch2 - <i>S.cerevisiae</i>	2.89	127.89	42.98	3.34	0.30	50.9	35.1	76.5	94.4	85.4	12	14.5
Pc12g1260_at	branched-chain amino acid aminotransferase Bat2 - <i>S.cerevisiae</i>	4.58	827.37	180.52	4.73	0.00	211.7	105.2	348.9	268.5	276	12	22.9
Pc12g13120_at	the transcription factor Pip2 - <i>S.cerevisiae</i>	2.38	77.68	32.59	3.04	0.79	43.8	35.1	35.3	52.8	52.8	116.4	112.7
Pc12g13130_at	hypothetical protein SPAC869.06c - SchizoS.pombe	5.77	129.12	36.53	5.34	0.30	22.4	35.7	31.1	29.4	34.9	12	13.9
Pc12g14560_at	hypothetical protein	5.10	434.27	85.15	3.34	0.00	129.7	186.4	240.2	127.7	128.6	12	12
Pc12g15670_at	hypothetical protein An16g03500 - <i>A. niger</i>	3.41	689.78	202.15	4.24	0.30	224.9	200	213.7	313.4	336.8	22.9	21.7
Pc13g00300_at	hypothetical protein contig127.tfa_340wg - <i>A. fumigatus</i>	2.18	268.25	102.5	0.79	18.1	40.4	28.5	12	14.2	100	128.4	21.4
Pc13g00700_at	hypothetical protein	2.99	32.38	10.83	3.18	0.30	12	20.6	12	12	14	25.1	21.7
Pc13g07690_at	3-oxoadipate enol-lactone hydrolase part of the dual specificity protein pcaL - <i>R. opacus</i>	5.60	245.42	43.86	5.69	0.00	54.5	41.3	61.2	112.8	117.2	160.4	198.1
Pc13g07770_at	transcription factor atf21p - SchizoS.pombe	1.91	30.63	16.02	3.31	0.79	15.8	12	35.9	32.4	75.3	78.9	12
Pc13g08820_at	mitochondrial heat shock protein Hsp70 - <i>S.cerevisiae</i>	3.04	442.37	145.70	4.00	0.30	78.6	68.3	296	109.8	154.7	40	39.2
Pc13g08950_at	hypothetical protein contig_1_172_scaffold_16.tfa_410cg - <i>A. nidulans</i>	5.77	3255.85	564.49	3.47	0.00	988.7	975.6	1991.8	1843.9	1861.4	12	12
Pc13g09300_at	pyruvate decarboxylase pdcA - <i>A. oryzae</i>	2.09	398.37	190.80	6.27	0.79	64.7	76.8	85.4	183.8	152.5	20.1	12
Pc13g09910_at	hypothetical protein An22g07350 - <i>A. niger</i>	2.02	184.58	91.34	6.72	0.79	26	35.3	35.5	48	66.5	12.5	23.9
Pc13g10400_at	meiotic sister-chromatid recombination protein Msc1 - <i>S.cerevisiae</i>	1.89	530.53	280.41	11.17	0.79	40.6	33.3	82.6	112.8	169.7	151.9	35.1
Pc13g10910_at	hypothetical protein An08g04015 - <i>A. niger</i>	3.18	84.72	26.62	3.50	0.30	28.8	25	48	25.1	40.6	12	12
Pc13g12490_at	sugar transporter Sut2 - <i>Pichia stipitis</i>	2.34	55.37	23.68	5.60	0.79	12	12	29.8	27.5	521.6	387	17.2
Pc13g12530_at	hypothetical protein An08g06600 - <i>A. niger</i>	2.82	32.07	11.38	3.68	0.30	12	12	18	16.1	46.7	51.2	22.45
Pc13g13750_at	steric C24(28) reductase stp1 - SchizoS.pombe	2.44	57.85	23.72	5.70	0.79	12	12.9	12	12	521	446.7	12
Pc13g13870_at	hypothetical acetyltransferase 2SCG4.07c - Streptomyces coelicolor	5.33	129.97	42.65	8.35	0.35	68.5	58.5	369.2	194.9	170.3	20.6	58.8
Pc13g14030_at	phenolic acid esterase AfaE - <i>A. niger</i>	4.21	510.82	121.25	3.02	0.00	244.6	140	374.5	186.8	183.3	21	22.1
Pc13g14310_at	methyl chloride transferase AAC72357.1 - <i>Batis maritima</i>	2.77	102.46	413.70	8.41	0.79	74.6	132.6	111.5	166.8	25.3	326.4	31
Pc13g14940_at	hypothetical short chain dehydrogenase SPCC736.13 - SchizoS.pombe	3.65	28.47	7.80	3.37	0.00	12	12	12	12	20.1	31.5	38.0
Pc13g15670_at	hypothetical protein CAD7005.1 - <i>N. crassa</i>	2.23	800.68	351.16	6.87	0.79	119.6	86.7	202.8	257.8	282	12	105.8
Pc14g00150_at	lysine permease LysP1 - <i>S.cerevisiae</i>	5.31	95.42	17.96	3.21	0.00	49.2	22.5	57.7	54.7	36	323	40.4
Pc14g1290_at	heat shock protein hsp30 - <i>A. nidulans</i>	4.63	1291.80	279.00	4.66	0.00	196.7	105.6	751.8	334.7	410.7	29.7	28.8
Pc15g14940_at	copper resistance-associated P-type ATPase CRP1 - <i>Candida albicans</i>	2.16	58.72	27.24	3.26	0.79	20.1	19.8	37.9	25.2	27.5	12	12
Pc15g1500_at	hemolysin AspH - <i>A. fumigatus</i>	4.22	58.92	13.96	5.78	0.00	13	12	12	12.3	48.9	67.8	26.5
Pc15g1550_at	hypothetical protein contig46_part_ii.tfa_1990wg - <i>A. fumigatus</i>	5.71	2458.50	430.62	34.86	0.00	44.6	12	161.2	12	12	12	12
Pc15g1570_at	hypothetical protein 2D9-9 - <i>A. fumigatus</i>	9.89	1914.75	193.62	20.88	0.00	48.9	41.2	198.8	24	20.1	12	46.3
Pc15g1590_at	hypothetical protein 2D9-9 - <i>A. fumigatus</i>	8.47	378.12	64.3	0.00	67.69	51.75	893.7	452.2	12	12	519.3	426
Pc15g1590_at	hypothetical protein 1141_scaffold_2.tfa_260cg - <i>Fusarium graminearum</i>	6.16	3693.40	599.24	4.96	0.00	743	536.5	151.6	786.1	794	12	49.9
Pc16g02750_at	hypothetical protein contig50.tfa_250wg - <i>A. fumigatus</i>	9.77	223.30	22.86	4.73	0.00	61.3	84.7	33.7	43	46	1169.7	1231.4
Pc16g03830_at	hypothetical protein An12g0250 - <i>A. niger</i>	1.66	29.62	17.82	3.17	0.91	12	16.9	12	12	601.2	422.3	58
Pc16g05570_at	hypothetical protein PA2915 - <i>Pseudomonas aeruginosa</i>	2.83	328.88	116.12	3.73	0.30	89.1	78.3	194.3	125.2	123.8	83.8	95.2
Pc16g05690_at	protease inhibitor like protein An08g01700 - <i>A. niger</i>	2.16	264.37	122.58	3.18	0.79	123.9	99.1	141.3	80.7	102.7	12	12
Pc16g06110_at	hypothetical protein contig41_part_ii.tfa_930cg - <i>A. fumigatus</i>	3.85	72.72	18.87	7.04	0.00	12	12	29.7	23.2	12	12	17.5
Pc16g07430_at	hypothetical protein contig31_part_ii.tfa_2900wg - <i>A. fumigatus</i>	4.51	99.63	22.10	4.03	0.00	41.6	15.9	41.1	29.2	26.1	61.9	25.8
Pc16g08930_at	hypothetical protein contig497_2.tfa_1060cg - <i>A. fumigatus</i>	2.28	317.70	44.87	6.70	0.00	34.3	24.2	108.6	44.8	52.7	844.6	599.3
Pc16g09940_at	hypothetical protein PA4177 - <i>Pseudomonas aeruginosa</i>	1.78	80.63	45.31	5.37	0.79	15.1	14.8	25.5	12	12	253.7	247.6
Pc16g12620_at	hypothetical protein 1324_scaffold_5.tfa_120cg - <i>Fusarium graminearum</i>	8.35	900.39	107.39	3.19	0.00	265.6	419.9	545.7	381.9	31.9	12	12
Pc16g12													

Pc18g02950_at	hypothetical protein An04g03610 - A. niger	2.80	388.93	137.37	3.54	0.30	149.6	116.8	204.8	118.4	119.2	12	12	121.1	92.1	126	12	12	87.4	159.3	
Pc18g03680_at	hypothetical arylanthene N-hydroxycinnamoyl benzoyltransferase At2g19070 - A. thaliana	8.83	28.73	3.26	3.25	0.00	14.3	12	12	12	12	12	12	12	12	12	12	12	12		
Pc18g04600_at	high-affinity zinc transport protein Zn11 - S.cerevisiae	3.57	31.27	8.76	3.40	0.30	12	15.1	12	15.8	17.8	12	12	14.8	39.5	24.4	12	12	16.7	12.3	
Pc18g04700_at	hypothetical protein An08g07900 - A. niger	9.55	44.13	4.62	4.60	0.00	12.8	12	12	12	13	12	12	16.3	13.2	22.3	12	12	16.3	55.4	
Pc20g00340_at	hypothetical protein SPA15E1.02c - Schizosaccharomyces pombe	2.27	1597.05	704.16	5.15	0.79	403.9	318	433.4	666.2	835.3	36.1	28.1	848.6	282	405.4	38.1	31.8	359.9	897.3	
Pc20g01520_at	hypothetical protein mg07210.1 - Magnaporthe grisea	10.44	1759.18	168.44	5.89	0.00	337.7	367.1	94.2	123.3	244.9	160.7	167.0	85.6	92.3	59.8	231.4	220.1	17.4	29.5	
Pc20g01260_at	lipase LipP - Pseudomonas sp.	4.90	56.10	11.44	4.08	0.00	24.5	14.3	15.8	14.9	20.7	177.4	209.6	46	58.9	68.4	176.9	150.2	40.1	59.9	
Pc20g03240_at	ACC synthase acs - P. putrefaciens	3.93	201.98	51.34	3.02	0.00	113.9	78.8	106.9	84	80	51.1	81.9	122.7	117.8	151.2	125.9	122.9	100.4	163.7	
Pc20g03620_at	integral membrane protein PTH11 - Magnaporthe grisea	3.54	41.43	11.69	3.43	0.30	17.2	12	22	36.3	28.9	12	12	35.1	19.2	17.6	12	12	38.3	26.7	
Pc20g04680_at	hypothetical protein	2.85	51.47	18.09	5.28	0.30	12	12	12	12	12	12	12	12	12	12	12	12	12		
Pc20g05830_at	enoyl reductase of the lovastatin biosynthesis lovC - A. terreus	8.89	196.52	22.10	3.07	0.00	92	77	116.4	140	125.8	63.4	70.2	276.3	246	381.1	58.9	87.1	345.2	554.5	
Pc20g06310_at	hypothetical protein contig42.tfa_1610cg - A. fumigatus	2.33	115.67	49.59	4.74	0.79	32.8	27.5	32.5	57.5	49	12	12	30.6	21.2	15.9	12	12	18.3	39.3	
Pc20g06390_at	hypothetical protein An08g06620 - A. niger	2.06	196.00	95.17	8.81	0.79	23.2	24.3	27.8	58.3	59.9	313.75	4015.3	19.2	12	3115.7	3886.1	19	12		
Pc20g11010_at	hypothetical protein contig_1_169_scaffold_15.tfa_910wg - A. nidulans	2.79	81.23	29.16	5.15	0.30	25.2	12.7	20.8	24.3	38.3	30.7	21.5	12	12	18.8	25.5	12	12	12.3	
Pc20g13600_at	hypothetical protein contig_1_104_scaffold_7.tfa_590cg - A. nidulans	2.88	539.88	187.75	3.71	0.30	228.3	51.1	319	74.5	68.2	23.8	17.3	60.9	62.3	72	33.3	15.6	21.7	37.8	
Pc20g13670_at	hypothetical exported protein YPO0987 - Yersinia pestis	7.90	126.92	16.07	7.81	0.00	19.3	20.5	16.1	24.3	23.7	111.5	113.5	23.4	20.6	13.4	104.3	107.7	16.2	22.3	
Pc20g14390_at	mitochondrial phosphate transport protein G7 - Glycine max	2.33	73.77	31.64	5.69	0.79	15.7	12	19.5	33.4	34.5	125.4	130.1	161.3	117.7	137.9	79.5	151.9	137.8	102.9	
Pc20g15670_at	NAD-GSH-dependent formaldehyde dehydrogenase fthA - Paracoccus denitrificans	10.68	88.57	8.30	3.40	0.00	40.2	30.4	39.9	22.2	32	61.2	310.3	84.4	97.5	106.8	384	339.2	58	152.9	
Pc20g15860_at	hypothetical protein An13g01790 - A. niger	2.18	38.52	17.68	4.20	0.79	12	12	12	12	101.3	89.7	24.8	17.7	15.3	72.7	70.3	13.7	29.8		
Pc21g00040_at	histidine kinase like protein An10g0250 - A. niger	4.31	55.42	12.87	4.92	0.00	12	17.1	13.3	15.6	17.5	12	12	12	12	12	12	12	12		
Pc21g01000_at	hypothetical protein	6.70	33.15	4.94	3.08	0.00	12	16.2	19.5	20.7	21.8	101.4	13.5	19.1	26.4	109.5	108.3	25	45.8		
Pc21g01220_at	alcohol dehydrogenase (NADH) ALR - S. cerevisiae	2.89	210.22	70.28	6.30	0.00	32.8	25.4	48.7	22.3	22.3	40.5	38.7	16.5	26.6	10.5	13.6	12.2	24.2	18.9	
Pc21g01370_at	trehalose-6-phosphate synthase subunit tpsA - A. niger	1.89	166.72	88.19	14.74	0.79	12	12.4	51.8	51.7	55.6	30.3	297.5	69.5	103.6	232.2	259.4	84.1	186.9		
Pc21g01400_at	hemolysin ASP-HS - A. fumigatus	2.17	59.05	27.24	4.17	0.79	19.4	19.4	17	17.9	26.6	78.2	105.8	16.5	17.2	12	143.3	136.9	13.1	15.1	
Pc21g01620_at	hypothetical protein contig1_spart_1.tfa_2160wg - A. fumigatus	2.67	70.10	26.25	5.05	0.53	13.2	12	26.7	29.5	41.8	12	12	23.7	23.8	25.0	12	12	18.7	24.3	
Pc21g02140_at	hypothetical protein contig1_spart_1.tfa_2160wg - A. fumigatus	4.34	298.10	68.66	4.10	0.00	112.2	73.9	102.5	143.9	145.6	18	12	119.1	89.1	145.4	23.6	12	171.7	231.8	
Pc21g03190_at	hydroxypruvrate dehydrogenase HPRA - Methyllobacter extorquens	4.50	78.33	17.41	3.38	0.00	32.2	15.1	51.6	37.5	39.6	12	15.1	84.9	70.4	103.9	12.8	12	70.3	107.7	
Pc21g03410_at	hypothetical protein An14g04910 - A. niger	2.60	47.62	18.35	4.96	0.53	12	12	12	12	18.1	181.1	131.5	12	12	11.2	12	12	12	12	
Pc21g03870_at	ankyrin 3 (splice form 3) - Mus musculus	2.74	370.02	135.24	4.38	0.30	98.3	122.7	107.3	87.1	83.3	85.3	81.4	48.7	39.5	94.7	49.9	41.6	52.7		
Pc21g04250_at	protein Ao23.3 - oryzate	1.92	103.58	53.88	4.12	0.79	29.1	27	43.4	64.6	71.7	12	12	35.8	21.8	38.5	12	12	36.7	27.6	
Pc21g05360_at	hypothetical protein An16g08650 - A. niger	2.53	130.23	51.45	6.09	0.53	29.7	16.6	30.4	54.3	54.3	12	12	18.1	23.9	13.8	12	12	22.8	47.7	
Pc21g06080_at	hypothetical protein YOL032w - S.cerevisiae	5.23	82.60	15.80	3.10	0.00	38.4	28.7	50.8	41	38.5	12	12	44.3	43.7	52.9	12	12	47.1	275.3	
Pc21g08220_at	hypothetical protein B10H18.060 - N. crassa	1.77	55.42	31.32	5.61	0.79	12	12	12	14.6	12	55.7	58	12	12	92.4	79.7	12	12		
Pc21g08440_at	hypothetical protein An14g06330 - A. niger	1.61	28.97	18.01	3.41	0.91	12	12	12	12.8	14.1	171.1	214.4	12	12	12	177.8	118.9	12	12	
Pc21g09230_at	hypothetical protein 118s_scaffold_2.tfa_130cg - Fusarium graminearum	7.31	468.85	64.17	3.11	0.00	237.2	144.5	283.7	214.3	228.9	12	12	19.7	205.7	207.2	250.9	12	12	182.9	142
Pc21g09240_at	signal peptidase subunit like protein An10g0560 - A. niger	4.96	197.42	39.82	3.92	0.00	88.8	34.2	79.6	46.7	53.1	12	12	61.8	61.4	92.5	12	12	32	42.8	
Pc21g09250_at	T-2 toxic biosynthesis protein TRIT7 - Fusarium sporotrichoides	12.79	42.12	3.29	4.50	0.00	12	12	12	13.4	19.9	12	12	12	12	26.6	12	12	12	12	
Pc21g09260_at	hypothetical protein mg05764.1 - Magnaporthe grisea	5.20	1194.42	229.85	5.40	0.00	325.3	19.2	470.1	339.3	387.8	12	12	125.8	42	122.9	12	12	15	31.3	
Pc21g09270_at	hypothetical protein B11B22.80 - N. crassa	5.34	460.27	86.18	3.75	0.00	165.9	127.7	207.8	115.4	125.3	12	12	265.5	306.2	327.1	12	12	295.5	273.5	
Pc21g09730_at	hypothetical protein nc09821.1 - N. crassa	2.08	113.75	54.67	6.86	0.79	21.5	19.6	17.1	30.9	41	12	12	27.2	16.6	12	12	12	15.7	22.3	
Pc21g09850_at	peptidase pePA - A. niger	2.69	288.62	107.36	12.22	0.53	20.1	25.5	31.6	20.2	20.2	12	12	14.7	13.3	18.3	12	12	17.3	15.1	
Pc21g13700_at	opsin opn-1 - N. crassa	2.26	155.87	69.02	6.35	0.79	27.3	17.9	42.2	72.2	91.4	82.4	93.3	19.2	13.3	16.3	68.8	66.3	23.6	28.8	
Pc21g14100_at	hypothetical protein An02g0280 - A. niger	2.00	61.62	30.63	6.12	0.79	12	12	12	20.8	28.1	41.68	56.3	12	12	45.4	521.8	12	12		
Pc21g14100_at	hypothetical protein contig1_gm0330 - A. niger	2.00	25.97	6.15	0.00	12	12	12	12	12	12	12	12	12	12	24.1	192.3	234.2	12	12	
Pc21g14240_at	hypothetical protein contig1_gm0330 - A. niger	4.79	30.42	18.65	3.47	0.91	12	12	12	12	15.4	58.4	34.2	12.7	12	26.1	16.9	12	12		
Pc21g14400_at	hypothetical protein C-8,7 sterol isomerase - Arabidopsis thaliana	2.31	97.83	405.89	4.50	0.79	306.4	55.1	441.8	104.8	108.1	12	12	64.7	23.7	101.1	14.3	12	42.1	29.9	
Pc21g15200_at	alcohol dehydrogenase alca - A. nidulans	2.35	108.05	46.01	3.08	0.79	58.1	32.3	65.3	40.7	48	125.9	146.3	114.5	109.3	185.1	89.6	103.3	123.6	63.6	
Pc21g18280_at	flavin-containing monooxygenase like protein An08g08060 - A. niger	2.37	325.87	137.26	3.00	0.79	279.2	103.9	105.4	115.7	135.2	56.2	53.6	111	138.1	146.6	70.4	86	144.3	70.3	
Pc22g00360_at	hypothetical protein contig12.tfa_360cg - A. fumigatus	3.63	115.77	31.87	8.04	0.00	12.6	14.9	21.8	39.1	48.4	162.9	162.9	27.5	16.3	29.8	114.9	103.8	24.5	18.7	
Pc22g06430_at	hypothetical protein B5022.140 - N. crassa	2.27	75.02	33.03	6.46	0.79	13.7	13.3	14.2	25.5	30.7	149.6	87.2	33.6	13.6	21.9	92.8	134.3	23.4	27.4	
Pc22g06540_at	hypothetical protein contig1_128_scaffold_9.tfa_720cg - A. nidulans	2.81	80.37	28.60	7.68	0.30	12	12	12	12	12	55.6	33.3	21.3	12.9	26.3	44.7	46.4	12	12.7	
Pc22g06650_at	acetylomithine deacetylase like protein An12g10510 - A. niger	4.70	105.03	22.33	3.22	0.00	43.7	43.1	55.3	49.5	43.8	12	12	88.9	70.1	106.2	12	12	75.8	76.2	
Pc22g06660_at	N-carbamyl-L-amino acid amidohydrolase like protein An12g10500 - A. niger	13.68	90.38	6.61	4.90	0.00															

Pc22g00060_at	hypothetical protein An12g05030 - A. niger	1.93	70.97	36.72	6.90	0.79	12	12	12	25	39.2	12	12	12	12	12	12	12	12	12	12	12	
Pc22g1240_at	catelase etpA - Schizosaccharomyces pombe	3.18	128.50	40.42	4.98	0.30	30.4	31.4	35.1	37.9	18.5	12	12	28.9	37.1	26	12	12	58.4	55.5			
Pc22g3100_at	aspartate transaminase - <i>Sus scrofa</i>	2.74	139.50	50.96	5.96	0.30	24.6	18.3	41.4	34.2	27.7	12	12	13.4	13.4	29.4	12	12	17	14.3			
Pc22g3390_at	hypothetical protein contig1497_1.tfa_610cg - <i>A. fumigatus</i>	2.16	38.80	17.94	4.15	0.79	12.3	12	12.6	23.1	16.1	12	12	12	12	12	12	12	12	12	12	12	
Pc22g3500_at	bifunctional cytochrome P450monooxygenase - <i>Rhodotorula minuta</i>	3.28	75.52	23.02	3.19	0.30	37	37.9	28.7	43.2	53.5	12	12	117	135.6	72.4	12.8	12	77.4	136			
Pc22g3890_at	hypothetical protein An12g07920 - A. niger	2.78	496.45	178.58	3.55	0.30	148.6	230.7	205.7	386.5	466.9	425.4	414.9	114.4	86.7	101.2	686.1	489.7	157.8	321.6			
Pc22g4170_at	hypothetical protein An12g19130 - A. niger	3.31	60.20	18.17	3.03	0.30	21.5	33.9	33.7	37.5	51.9	355.9	300.4	30.4	24.6	17	324.4	403.5	12.8	15.4			
Pc22g4430_at	biotin biosynthesis gene bioS1 like protein An12g08940 - A. niger	3.63	72.37	19.93	3.96	0.00	22.9	19.3	31.1	19.6	20.3	106	118.8	31.7	33.8	52.3	178.8	185.2	35	26.1			
Pc22g4990_at	hypothetical protein An12g00810 - A. niger	1.76	90.17	51.17	5.39	0.79	17.5	17.8	26.3	32.3	32.1	310.8	463.2	20.4	14.4	21.5	182.8	172.2	19.2	12			
Pc22g5060_at	hypothetical protein contig589.tfa_1960wg - <i>A. fumigatus</i>	3.54	448.67	126.79	5.13	0.30	113.4	84	128.5	76.1	85.8	12	12	95.7	95.2	110.6	12	12	93.6	75.4			
Pc22g5240_at	ACC deaminase - <i>P. citrinum</i>	11.22	59.62	5.31	3.03	0.00	27.7	30.9	29.4	57.2	71.1	12	12	37.5	40.8	44.2	20.4	12	29	49.6			
Pc23g00530_at	ankyrin repeat protein E4_2 - Synthetic construct	1.64	50.75	30.94	4.76	0.91	12	12	16.5	24.3	29.7	12	12	12	12	15	12	12	15.3	18.7			
Pc23g00540_at	hypothetical protein	13.35	163.80	12.27	4.10	0.00	53.1	39.9	65.7	165.5	182.9	13.9	36.1	71.9	57.8	72.7	602.8	506.8	127.1	48.5			
Pc24g1640_s_at	hypothetical protein BAC82546 - <i>P. chrysogenum</i>	1.74	46.80	26.96	3.89	0.79	24.6	12	12	12	148.3	122.4	77.3	90.8	73.4	199.5	224	91.8	99				
Pc24g2760_at	hypothetical membrane protein YIL151c - <i>S.cerevisiae</i>	5.95	135.72	22.83	4.96	0.00	41.3	34.2	27.2	39.9	37	292.6	218.5	21.2	23.4	27.7	221.3	271.9	34.8	83.7			
Pc49g00020_s_at	NADH2 dehydrogenase (ubiquinone) chain 6 - <i>A. nidulans</i>	5.26	41.85	7.95	3.65	0.00	12.7	18.4	16.3	26.9	16.5	106.9	95.8	13	12	24.3	43.2	63.9	26.1	12			
Pc49g00030_s_at	H+ transporting two-sector ATPase proteine 6 - <i>P. chrysogenum</i>	4.66	140.50	30.14	3.34	0.00	44.1	70	65.9	294.9	407	829.4	855.8	70.9	63.9	78.3	781.6	673.5	841.2	69.4			
Pc49g00070_at	hypothetical protein - <i>P. marneffei</i>	7.46	597.12	80.08	20.95	0.00	29.2	25.3	35.3	82.7	121.1	42.2	51.1	34.3	32	35.7	45.9	33.5	576.4	87			
Pc49g00110_at	NADH2 dehydrogenase (ubiquinone) chain 3 - <i>A. nidulans</i>	14.46	216.68	14.99	6.38	0.00	43.4	40.3	37.1	77.2	46.6	169.5	133.8	66.1	43.7	48.4	78.4	98.4	97.9	34.6			
Pc49g00120_at	hypothetical protein contig1480_2.tfa_70wg - <i>A. fumigatus</i>	3.16	46.55	14.74	3.41	0.30	19.3	24.9	13.7	33.7	18.2	840.2	813.9	19.2	23	13.7	837.7	994.3	26.1	12			
Pc49g00150_at	ribosomal protein var1 - <i>P. chrysogenum</i>	6.05	283.35	46.81	8.91	0.00	29.2	37.6	40.6	81.7	21.1	40.5	43.6	27.9	23.2	16.7	215.6	31.1					

140 genes Downregulated in DS67261 relative to DS17690 in absence of PAA		Significance Analysis of Microarray (SAM) results										DS17690 -PAA												
Gene ID	Gene Name	Score(d)	Numerator(r)	Denominator(s=0)	Fold Change	q-value(%)	1	2	3	1	2	3	1	2	3	1	2	3	1	2	3			
Pc01g00030_s_at	hypothetical protein An12g08820 - A. niger	-2.97	-106.50	35.92	0.29	0.38	124	124.9	202.3	413	437.1	32	26.6	12	12	12	16.3	22.4	12	12				
Pc06g0320_s_at	hypothetical protein contig1493_1.tfa_303wg - <i>A. fumigatus</i>	-2.23	-45.08	20.20	0.21	0.98	67.1	29.5	74.8	54.1	49.5	12	12	12	12	12	12	12	12	12	12	12		
Pc06g0150_at	hypothetical protein An12g02740 - A. niger	-4.36	-61.88	14.20	0.23	0.00	96.2	64.1	80.4	35.9	41.8	325.5	297.8	39.4	29.1	32.4	204.2	275.7	17.2	35.6				
Pc06g0150_s_at	hypothetical protein 4 - <i>Streptomyces coelicolor</i>	-5.78	-58.75	10.17	0.17	0.00	74.8	58.6	73	38.5	38.5	25.1	51.4	12	12	12	360.3	472.5	12	12				
Pc06g02050_at	hypothetical protein An12g11990 - A. niger	-6.02	-99.90	159.18	0.18	0.00	124.6	118.4	84.6	261.5	299.8	12	77.8	69.3	74.5	17.6	37.2	47.9						
Pc06g02050_at	hypothetical protein An12g11990 - A. niger	-3.69	-94.79	257.38	0.06	0.00	1038.3	1331.6	650.2	88.5	88.5	231	148.5	165.8	64	44.4	22.2	107.2	120.6	12	27.7			
Pc06g02070_at	hypothetical protein contig468_part_itfa_1990wg - <i>A. fumigatus</i>	-2.57	-581.23	226.34	0.09	0.53	79.5	83.75	85.5	281.4	31.6	469	470.6	28.3	20.5	32.7	342.1	12						
Pc06g02080_at	hypothetical protein An06g02320 - A. niger	-3.56	-63.78	17.90	0.16	0.00	97	75.8	54.7	17	54.2	49	12	12	97	87.3	12	12	12	12	12	12		
Pc06g02080_s_at	hypothetical protein An06g02320 - A. niger	-2.45	-92.37	37.73	0.15	0.53	157	107.4	61.9	12	12	12	12	12	12	12	12	12	12	12	12	12		
Pc06g02090_s_at	hypothetical protein	-4.09	-74.50	18.21	0.17	0.00	102	101.9	64.6	12	18.1	908.3	982.9	12.4	12	12	949.3	1085.6	12	12				
Pc06g02100_s_at	ribonuclease H 3'-5' exonuclease like protein An11g03420 - A. niger	-2.33	-384.83	165.37	0.32	0.53	74.66	62.13	320.6	75.5	102.8	247.9	319.6	62.9	51.1	43	3606.1	3151	27.1	34.9				
Pc12g0560_at	hypothetical protein	-3.74	-341.53	46.54	0.31	0.00	431.9	523.3	520.3	413.8	415.4	358.2	891.2	281.4	338	261.2	77.8	633.9	607.1	490.4				
Pc12g0900_at	nuclear migration factor nudF - <i>A. nidulans</i>	-3.76	-100.30	26.69	0.11	0.00	110.8	146.4	80.6	63.6	62.2	12	101.4	72.5	61.3	12	103.6	57.3						
Pc12g09270_at	vegetative incompatibility factor hetE1 - <i>Podospora anserina</i>	-5.29	-74.75	14.14	0.22	0.00	92.6	112.5	81.4	27.2	30	12	12	14.6	18.2	18.7	12	12	12	18.8				
Pc12g09290_at	hypothetical protein	-2.85	-273.45	95.81	0.12	0.38	436.7	185.4	313.6	250	256.7	570.4	602.7	27.5	27.4	26.5	473.3	329.5	16.9	29.8				
Pc12g09300_at	hypothetical protein An16g07260 - A. niger	-7.33	-103.45	14.12	0.25	0.00	132.6	156.5	126.4	110.5	147.4	12	12	116.5	104.5	99.4	12	12	167	127.6				
Pc12g09360_at	hypothetical protein An16g07330 - A. niger	-1.74	-102.88	59.24	0.21	0.98	177.1	41.7	491.2	58.8	29.1	29	12	12	29.8	31.5	14.6	12						
Pc12g09370_at	hypothetical protein contig_1_116_scaffold_8.tfa_30wg - <i>A. nidulans</i>	-3.87	-143.25	37.01	0.33	0.00	262.6	177.5	198.9	150.3	131.8	281.5	272.8	169.4	130.1	105.2	225.6	201.9	169.8	218.5				
Pc12g09370_at	Wilms tumor susceptibility protein WT1 - Homo sapiens	-4.00	-61.62	15.41	0.20	0.00	74.1	95.9	60.6	42.4	54.7	80.6	68.6	26.9	18.2	16.1	82.4	50.4	20.2	29.4				
Pc12g09380_at	hypothetical protein	-2.92	-33.88	19.03	0.27	0.00	73.2	37.9	170.4	136.9	99.8	104.1	176.8	16.9	15.3	126.2	85.8	12.2	19.2					
Pc13g09460_at	hypothetical protein	-1.58	-131.22	82.84	0.08	0.98	247.3	31.2	151.3	63.0	67.2	12	12	12	12	12	12	12	12	12	12	12		
Pc13g09460_at	hypothetical protein An04g03190 - A. niger	-2.22	-36.75	16.59	0.25	0.98	39.4	71.1	35.9	19.5	27.4	16.1	17.6	12	12	24	16.5	12						
Pc13g09808_at	ceruloplasmin - <i>Danio rerio</i>	-1.57	-133.57	84.94	0.16	0.98	267.1	45.1	163.2	58.5	549.2	12	12	12	12	12	12	12	12	12	12	12		
Pc13g1150_at	hypothetical protein	-1.74	-98.85	55.71	0.23	0.98	204.4	65.4	105.2	54	68.4	12	12	12.8	43.6	46.2	12	12	58	62				
Pc13g16420_at	cell wall synthesis protein KRE9 - <i>Candida albicans</i>	-1.70	-49.75	29.27	0.21	0.98	94.1	23	71.9	188.9	201	765.1	855.7	12										

Pc16g08990_at	hypothetical protein	-2.19	-64.52	29.46	0.30	0.98	133.2	64.7	77.4	52.4	51.1	12	12	34.1	19.1	18	12	12	21.9	12		
Pc16g08990_at	cDNA O-methyltransferase mt-I - A. parasiticus	-1.75	-109.37	62.50	0.27	0.98	240.7	92.9	115.4	75.3	193.9	218	66	17.9	21.3	100.9	130	14.9	18			
Pc16g08910_at	cDNA O-methyltransferase mt-I - A. parasiticus	-2.56	-138.02	53.85	0.32	0.53	281.9	169.5	161.7	108.9	98.9	104.6	99.1	108.9	126.5	91.6	91.1	71	66.4	76.9		
Pc16g09920_at	cytochrome P450 monooxygenase P4501 - Gibberella fujikuroi	-5.38	-324.77	60.38	0.28	0.00	537.9	391.3	431.2	262.5	250.9	12	12	379.7	244.7	236	25.6	12	204.9	144.4		
Pc16g13260_at	hypothetical protein An01g10940 - A. niger	-1.88	-57.92	30.87	0.17	0.98	95.2	25.6	89.1	245.4	283.9	47.4	43.3	12	12	35	32.4	12	12			
Pc16g14010_at	hypothetical methyltransferase AAO34671.1 - Gibberella zaeae	-15.79	-506.55	32.07	0.02	0.00	535.8	547.3	312.5	323.3	12	12	465.6	529.6	452	16.9	12	12				
Pc16g14270_at	heterokaryon incompatibility protein het-6 - N. crassa	-6.83	-175.08	25.64	0.28	0.00	225.8	274.3	232.9	201.5	266.2	37.9	51.2	80.5	177.5	139.7	73.2	54.1	128.4	150.5		
Pc16g15440_at	ankyrin Ank2 - Homo sapiens	-1.97	-570.93	290.40	0.06	0.98	314.9	1044.5	458.1	173.6	203.7	135.2	139.6	52.6	37.6	32.8	209.8	182.5	74.1	70.6		
Pc17g00320_at	hypothetical protein	-2.12	-1112.58	525.25	0.06	0.98	831.6	1987	719.4	184.8	243.2	186.7	138.7	75.2	70.4	75.3	256.2	269	51.1	118.2		
Pc18g00150_at	high affinity glucose transporter HGT1 - Kluyveromyces lactis	-3.12	-145.12	46.55	0.30	0.38	171.6	276.9	176	137.7	194	213.4	215.4	31	26.1	12	341.4	431.1	20.8	23.8		
Pc18g00350_at	hypothetical protein	-7.92	-173.90	21.97	0.25	0.00	243	200.7	249.6	87.1	101.5	12	12	90.2	132.8	131.5	12	12	158.6	91.2		
Pc18g02200_at	hypothetical protein contig_1_66_scaffold_4.tfa_140cg - A. nidulans	-4.75	-71.28	15.01	0.26	0.00	76.9	106.6	107	61.4	122.6	60.6	38.2	82.7	68.2	51.6	51.2	41.1	139.2	85.4		
Pc18g03030_at	integral membrane protein PTTH11 - Magnaporthe grisea	-10.17	-190.03	18.68	0.27	0.00	270.2	268.7	238.7	397.7	368.2	493.7	624.2	23.8	30.7	22.2	259.7	406.9	50.2	38.7		
Pc18g04450_at	hypothetical protein contig1492_2.tfa_580wg - A. fumigatus	-4.00	-800.02	200.07	0.29	0.00	913.2	1056.3	1397	972.3	807.3	12	12	658.6	851	610.2	15.8	12	1156.2	931.6		
Pc18g04570_at	hypothetical protein C0390v - Plasmodium falciparum	-2.03	-573.30	282.32	0.10	0.98	821.5	206.5	888.1	2565.3	2150.8	43.3	43.2	29.1	24.5	14.8	23	39.4	37.5	40.7		
Pc18g04580_at	hypothetical protein An04g07540 - A. niger	-1.87	-324.18	173.45	0.13	0.98	603.3	145.4	364.4	723.1	739.6	12	12	14	13.1	12	12	12	12			
Pc20g00950_at	hypothetical protein 15_scaffold_1.tfa_30wg - Fusarium graminearum	-2.49	-43.80	17.58	0.28	0.53	83.3	43.4	56.6	43.4	48.8	287.4	237	58	72	91.1	308	352.9	63.1	42.3		
Pc20g02640_at	glutaminase A gtaA - A. oryzae	-2.17	-232.50	107.07	0.24	0.98	347.9	156.9	413.8	627.2	502.1	26.7	20.5	17.1	24.4	15.6	48.8	28.3	36.4	51		
Pc20g03030_at	hypothetical protein contig1487_1.tfa_1020wg - A. fumigatus	-2.31	-219.35	95.14	0.33	0.53	249.9	314.4	421.5	391.3	394.4	136.4	187.1	208.7	267.8	323.5	119.7	125.5	478.1	372.6		
Pc20g03770_at	hypothetical protein	-6.70	-197.08	291.97	0.22	0.00	2149.4	260.9	2923.6	2157.6	199.1	264.6	196	553.1	461.1	326.7	299.1	161.2	360.6	310.2		
Pc20g07770_at	hypothetical protein An1g05770 - A. niger	-7.33	-115.12	15.71	0.23	0.00	170.5	144.6	130.1	52.6	32.2	12	12	16.6	17.6	150.2	12	12	195.8	99.9		
Pc20g12800_at	hypothetical protein P450 alk2A - Candida malosa	-2.13	-59.50	27.90	0.20	0.98	101.8	20.9	45.3	20.9	35.7	100.3	62.0	59	54	41.1	59	40.0	49.0	6.6		
Pc20g14940_at	hypothetical protein	-4.83	-215.08	44.53	0.27	0.00	349.8	253	280.2	179.1	170.9	12	12	22	219.4	165.1	12	12	237.7	159.8		
Pc20g15160_at	hypothetical protein An1g07720 - A. niger	-3.92	-840.18	214.42	0.33	0.00	1072.9	1498.1	1166.3	649.4	912.7	12	12	177	163.1	145.5	12	12	151.5	87		
Pc20g15280_at	hypothetical protein An08g12140 - A. niger	-2.03	-191.20	94.22	0.27	0.98	198	402.9	185.7	180.5	184.4	12	12	173.6	236.7	131.6	12	12	159.3	192.3		
Pc20g15310_at	sterol C24(28) reductase stp1 - Schizosaccharomyces pombe	-4.15	-81.40	19.62	0.25	0.00	134.4	90.7	101.9	145.1	154.2	26.2	20.4	16.8	12.2	12	15.7	18.9	12	16.7		
Pc20g15730_at	hypothetical protein An01g11500 - A. niger	-10.59	-76.72	7.25	0.27	0.00	108.4	101.2	106.5	81.3	84.3	29.8	16.6	63.2	50.2	48.7	24.9	68.4	72.1			
Pc20g15740_at	hypothetical protein BAB55393.1 - Homo sapiens	-4.36	-226.08	51.88	0.05	0.00	283.5	161.5	269.4	61.1	52.8	12	12	109.3	163.2	91.1	12	12	169.8	153.3		
Pc20g15750_at	hypothetical protein contig1474.1 - Magnaporthe grisea	-7.76	-132.98	17.14	0.09	0.00	163.5	149.8	123.9	67.8	37.3	90.9	76.7	57.3	60.7	24.4	36.5	63	62.3	52.9		
Pc20g15820_at	hypothetical protein An07g04620 - A. niger	-7.51	-1173.38	156.29	0.29	0.00	1656.7	1462.8	1805.4	1159.7	1109.7	143.3	155.1	820.8	1105.8	761.6	139	120.9	1261.1	907.8		
Pc20g15950_at	hypothetical protein contig_1_168_scaffold_14.tfa_260wg - A. nidulans	-6.42	-634.67	98.89	0.23	0.00	814.8	794.4	860.6	311.7	302	28.6	30.3	327	454	401.9	32.7	41.9	400.7	375.9		
Pc20g16060_at	lovastatin didehydratase qd4 - N. crassa	-2.92	-166.95	57.15	0.28	0.38	175.8	289.7	231.7	105.8	112.8	12	12	90.4	130.3	95.4	16	12	175.6	94.2		
Pc20g16120_at	hypothetical amine transporter SPCC18.02 - Schizosaccharomyces pombe	-4.92	-210.30	42.72	0.08	0.00	270.8	247.8	167.8	48.8	16.6	12	12	119	198.5	13.6	24.2					
Pc20g16250_at	nitrate reductase (NADPH) niaD - A. niger	-5.57	-41.40	7.44	0.29	0.00	62.1	62.9	50.2	63.5	62.9	12	12	14.7	12.3	12	15.3	13.6				
Pc20g16310_at	hypothetical protein CAD21189.1 - N. crassa	-5.15	-287.42	55.86	0.31	0.00	339.8	481.2	423	356.3	265.9	12	12	22.8	281.7	135.4	12	12	281.6	277.6		
Pc20g16320_at	hypothetical protein contig_1_187_scaffold_29.tfa_20cg - A. nidulans	-2.77	-72.70	26.27	0.33	0.00	79.8	102.4	143.3	89.1	109.2	12	12	74.1	71.2	61	12	12	205.7	93.5		
Pc20g16380_at	hypothetical protein	-7.17	-618.85	86.33	0.27	0.00	894	668.2	795.2	1140.8	1068.4	677.4	515.1	45.1	58.8	47.6	448.9	380.7	93.8	43.8		
Pc21g06640_at	hypothetical transcription regulator SPCC4F11.01 - Schizosaccharomyces pombe	-16.91	-437.33	25.86	0.22	0.00	537.7	593.9	553	669.4	570.5	12	12	104.9	110.3	50.5	12	12	97	137.2		
Pc21g11170_at	triacylglycerol lipase lpl - Geotrichum candidum	-15.45	-246.63	15.97	0.22	0.00	312.7	300.9	336.3	341.8	364.6	69.9	65.8	13.7	24.1	12	114.5	122	40.8	31.5		
Pc21g12820_at	3-dehydroshikimate dehydratase qd4 - N. crassa	-5.06	-826.32	163.39	0.16	0.00	1109.5	729.5	559.8	484.6	12	12	331.9	359.4	196.9	12	12	191.3	167.3			
Pc21g12840_at	hypothetical amine transporter SPCC18.02 - Schizosaccharomyces pombe	-5.66	-217.22	38.36	0.22	0.00	327.1	230.2	273.9	103.1	110	149.7	86.2	97.1	123.7	113.6	1406	1338.3	86.8	74.1		
Pc21g12849_at	hypothetical protein contig_1_153_scaffold_12.tfa_20wg - A. nidulans	-5.00	-291.15	51.41	0.20	0.00	374.4	344.1	248.2	175.5	152.1	12	12	76	67	58.2	12	12	76.7	48		
Pc21g14950_at	hypothetical protein contig1495_1.tfa_120wg - A. fumigatus	-2.62	-79.35	30.55	0.25	0.00	152.1	152.7	48.1	45.3	45.3	12	12	63.2	59.2	31.4	12	12	23	26		
Pc21g16130_at	hypothetical protein F3E22.6 - Arabidopsis thaliana	-5.32	-468.05	32.04	0.16	0.00	609.9	544.3	280.7	299.1	789.5	178.4	237.9	166	105.2	819.5	748.9	184.7	112.9			
Pc21g16160_at	hypothetical protein contig1495_1.tfa_120wg - A. fumigatus	-2.47	-241.67	97.68	0.14	0.00	232.3	144.6	139.3	58	67.7	12	12	44.6	53.7	445.7	12	12	310.2	391.2		
Pc21g22260_at	cholesterol 7alpha-monooxygenase CYP7 - Oryctolagus cuniculus	-5.25	-233.65	23.53	0.11	0.00	160.4	107.2	152.1	55.2	59.2	306.7	432.1	50	600.2	270.8	342.8	460.9	282.2			
Pc21g22270_at	cholesterol 7alpha-monooxygenase P45051 - Gibberella fujikuroi	-9.17	-41.67	4.55	0.25	0.00	57.5	57.5	46.6	30.4	38.6	48.9	46.2	115	112.5	13.2	12	96.8	214.1	13.1	12.5	
Pc21g23660_at	phosphatidylinositol(3)-phosphate binding protein Ptb1 - S. cerevisiae	-4.42	-140.32	31.74	0.32	0.00	195.9	174.2	247.8	181.3	202.6	12	12	207.5	205.9	217.8	15	12	441.9	208.7		
Pc21g23770_at	rodlettose protein rod4 - A. nidulans	-1.83	-40.80	22.26	0.29	0.98	84.2	30.9	57.4	187.7	202.5	12	12	12	12	12	12	12	12	12		
Pc22g02202_at	hypothetical protein	-1.67	-43.78	26.25	0.22	0.98	85.1	23.4	56	194.2	177.6	12	12	15.1	25.9	21.3	12	12	83.4	41.2		
Pc22g08920_at	hypothetical protein contig2.tfa_104cg - A. fumigatus	-4.15	-26.54	6.34</																		

Pc22g24760_at	hypothetical protein B8J22.030 - N. crassa	-2.44	-31.67	12.97	0.29	0.53	59.8	30.9	43	199.4	221.9	12	12	12	12	12	12	12	12	
Pc22g5460_at	hypothetical protein	-2.11	-1544.43	702.12	0.17	0.98	2483.3	730.5	2367.2	1365	1475.2	12	12	1032.8	658.4	494.4	12	12	43.4	66.8
Pc24g00370_at	hypothetical protein 1196_scaffold_3.tfa_500cg - Fusarium graminearum	-4.13	-493.08	119.29	0.31	0.00	777.4	558.3	805.8	837.5	913	141.6	157.4	163.1	213.6	219.6	80.9	69.1	117.5	76.8
Pc24g01580_at	polycystic kidney disease 1-like 3 - Mus musculus	-2.76	-36.37	13.16	0.29	0.38	36.3	65.5	52.9	39.1	37.2	18.4	13.9	15.5	21.1	19.9	17.7	13.7	23	20

4 genes Upregulated in DS67261 relative to DS17690 in presence of PAA				Significance Analysis of Microarray (SAM) results					DS17690 -PAA			DS63171 -PAA		DS67261 -PAA		DS17690 + PAA			DS63171 +PAA		DS67261 +PAA	
Gene ID	Similar to	Score(d) Numerator(r) Denominator(s+s0)			Fold Change	q-value(%)	1	2	3	1	2	1	2	1	2	3	1	2	1	2	1	2
		Score(d)	Numerator(r)	Denominator(s+s0)																		
Pc06g00720_at	cellulosomal scaffoldin anchoring protein C - <i>Acetivibrio cellulolyticus</i>	6.80	1184.37	174.17	3.69	0.00	135.1	698.6	566.2	612.4	822.4	70.2	75.4	237.3	526.8	554.8	109.5	89.1	1773.6	1474.4		
Pc13g10790_at	hypothetical protein An16g03760 - <i>Aspergillus niger</i>	4.53	71.30	15.75	3.49	9.68	26.6	35.3	46.5	86.4	106.7	76.2	76.8	26.4	27.1	32.3	64.3	68.4	117.9	81.9		
Pc21g08860_at	acvA gene expression regulator Pc804 like protein An13g01050 - <i>A. niger</i>	5.28	76.27	14.46	2.92	0.00	17.2	49.1	77.8	77.9	134.8	12	12	48.2	30.3	40.4	12	12	129.8	102		
Pc22g11800_at	hypothetical protein	4.47	62.95	14.10	2.52	9.68	51.1	118.2	88.3	85.8	135.4	12	12	45.3	50.3	28.6	12	12	115.7	93		

7 genes Downregulated in DS67261 relative to DS17690 in presence of PAA				Significance Analysis of Microarray (SAM) results					DS17690 -PAA			DS63171 -PAA		DS67261 -PAA		DS17690 + PAA			DS63171 +PAA		DS67261 +PAA		
Gene ID	Similar to	Score(d) Numerator(r) Denominator(s+s0)			Fold Change	q-value(%)	1	2	3	1	2	1	2	1	2	3	1	2	1	2	1	2	
		Score(d)	Numerator(r)	Denominator(s+s0)																			
Pc13g15370_at	hypothetical protein contig61_ifa_1360wg - <i>A.fumigatus</i>	-3.32	-27.03	8.15	0.33	12.91	1	2	3	1	2	1	2	1	2	3	1	2	1	2	1	2	
Pc16g03870_at	multidrug resistance protein atrD - <i>A. nidulans</i>	-3.69	-38.72	10.50	0.37	12.91	55.3	26.8	34.1	42.7	27.9	1961.6	3100.6	63.5	61	61.1	12	12	34.3	12			
Pc16g03890_at	hypothetical protein SPAC56E4.07 - <i>S. pombe</i>	-3.44	-101.67	29.52	0.36	12.91	152.8	58.9	88.9	80.7	66.8	3912.5	5043	147	160.5	167.9	366.2	315.9	92	21.6			
Pc16g14010_at	hypothetical methyltransferase AAO34671.1 - <i>Gibberella zaeae</i>	-14.25	-470.35	33.01	0.02	0.00	535.8	547.3	472.7	312.5	323.3	12	12	465.6	529.6	452	16.9	12	12	12	12		
Pc20g01520_at	hypothetical protein mg07210.1 - <i>Magnaporthe grisea</i>	-3.56	-55.78	15.69	0.30	12.91	337.7	367.1	375.1	94.2	123.3	244.9	160.7	85.6	92.3	59.8	231.4	220.1	17.4	29.5			
Pc22g15510_at	ATP-dependent DNA helicase II subunit Ku70 - <i>Mus musculus</i>	-6.08	-80.42	13.23	0.13	0.00	117.1	110.4	89.5	12	12	99	92.2	100.1	102	75.3	73.3	76.6	12	12			
Pc22g18080_at	amino acid transporter ATA1 - <i>Homo sapiens</i>	-4.24	-50.25	11.84	0.34	12.91	92.8	68.4	29.7	48.4	59.2	164.6	169	77.7	88.1	62.2	235.7	354.2	25.8	25.7			

Hoff B, Kamerewerd J, Sigl C, Mitterbauer R, Zadra I, Kumsteiner H, Kuck U: Two components of a velvet-like complex control hyphal morphogenesis, conidiophore development, and penicillin biosynthesis in *Penicillium chrysogenum*. *Eukaryotic Cell* 2010, 9:1236-1255.

This study

Gene name	Description	DS17690 Sample1	DS17690 Sample2	DS17690 Sample3	DS17690 Sample1	DS63171 Sample2	DS17690 Average	Fold-change DS63171 vs DS17690
Pc12g03690_at	strong similarity to hypothetical protein contig_1_116_scaffold_8.tfa_30wg - Aspergillus nidulans	169.4	624.9	105.2	624.9	302.2	134.90	463.55
Pc12g12710_at	strong similarity to multidrug resistance ABC transporter like protein An02g04910 - Aspergillus nidulans	22.3	17.2	82.3	69	22.73	75.65	3.0
Pc16g00830_at	similarity to hypothetical protein contig_1_108_scaffold_7.tfa_310cg - Aspergillus nidulans	24.3	83	25.8	83	69.9	24.89	76.45
Pc16g00840_at	similarly to O-methyltransferase A omta - Aspergillus phoenicis	84.4	237.6	70.9	237.6	231.7	73.89	234.65
Pc16g02890_at	strong similarity to hypothetical protein contig_1_65_scaffold_4.tfa_330wg - Aspergillus nidulans	353.8	1322.7	228.4	1322.7	1087.7	280.03	1205.20
Pc20g02040_at	strong similarity to methicillin resistance gene Hmra - Staphylococcus aureus	173.2	833.9	295.8	833.9	751	239.83	792.45
Pc20g03620_at	similarity to integral membrane protein PTTH11 - Magnaporthe grisea	35.1	166.3	17.6	166.3	97	23.97	131.65
Pc20g10240_at	strong similarity to Serine-type carboxypeptidase precursor cpds - Aspergillus phoenicis	4	51.9	9.6	51.9	66.7	10.20	59.30
Pc20g13450_at	similarity to integral membrane protein PTTH11 from patent WO200913094-A2 - Magnaporthe grisea	21.8	73.5	17.1	73.5	59	18.87	66.25
Pc21g13140_at	strong similarity to cholinesterase 1 ChE1 - Branchiostoma floridae	19	77.4	21.2	77.4	60.1	21.57	68.75
Pc06g02070_at	weak similarity to hypothetical protein contig46_part_iifaa_1990wg - Aspergillus fumigatus	28.3	4.3	12.5	4.3	2.4	20.43	3.35
Pc12g06880_at	hypothetical protein	110.5	32.9	63.6	32.9	17	96.40	24.95
Pc13g13200_at	strong similarity to dark repressor of conidiation velvet veA - Aspergillus nidulans	631.9	49.8	596.1	49.8	60.6	569.93	55.20
Pc18g01840_at	strong similarity to hypothetical methyltransferase AAQ30615 - Gibberella zeae	1753.7	331.8	2168.5	331.8	288.8	1917.77	310.30
Pc21g12610_at	weak similarity to 7alpha-cephem-methoxylose subunit cmcJ - Streptomyces lactamidans	440.9	137.7	611.4	137.7	129.8	502.17	133.75
Pc21g12630_at	similarity to peptide synthase pesA - Metarhizium anisopliae	1021.4	145.7	1271.3	145.7	213.1	1052.53	179.40
Pc21g12820_at	strong similarity to 3-dehydroshikimate dehydratase qac4 - Neurospora crassa	331.9	106.8	196.9	106.8	89.5	296.07	98.15