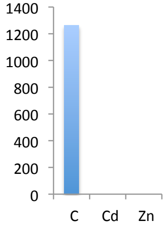
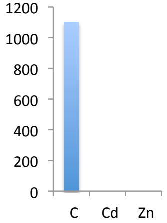
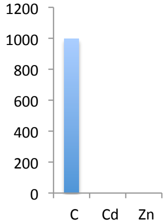
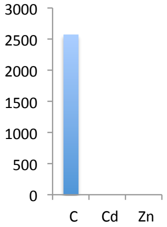
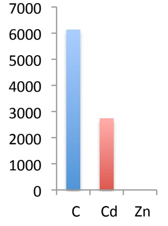
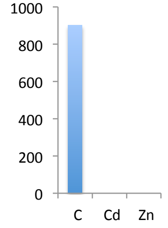
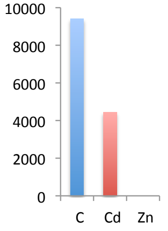
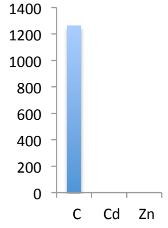
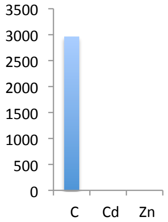
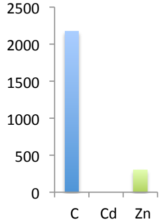
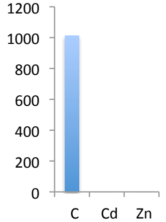
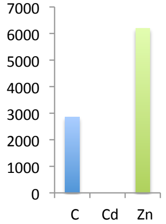
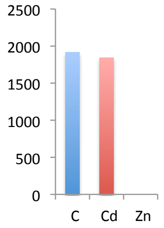
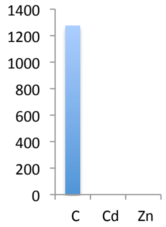
Table S1. Identification of 2-DE protein spots visualised by SYPRO-Ruby. The protein spots excised from 2-DE gels (Fig.2) were analysed by mass spectrometry and identified by MASCOTon the NCBInr database, as well as on a translated EST database of *O. maius* Zn .

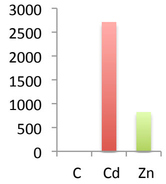
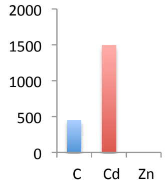
SPOTS FROM 2-DE GEL OF CONTROL SAMPLES												
Spot number (a)	MASCOT ID (b)				*O. maius* DB ID (c)			*PFAM* (d)				
	Accession number	Description	Organism	Score	Accession number	% identity	e-value	Accession number	Description	e-value	Peptides (e)	Graph (f)
3705	gi|145608376	heat shock protein 60, mitochondrial precursor	*Magnaporthe oryzae*	485	jgi|Oidma1|181472|estExt_Genemark1.C_10_t10207	87%	0.00E+00	pfam00118	Cpn60_TCP1, TCP-1/cpn60 chaperonin family	4.00E-108	FGVEGR EGVITVK APGFGDNR FVDALNATR VGGSSEVEVGEK NVLIESSYGSPK GFVSPYFITDAK AAVEEGILPGGGTALLK	
3703	gi|4164594	heat shock protein 70	*Paracoccidioides brasiliensis*	57	jgi|Oidma1|52231|gm1.5561_g	90%	0.00E+00	pfam00012	HSP70, Hsp70 protein	0.00E+00	DAGLIAGLNVLR LVNHFVNEFK	
2504	gi|70992763	carboxypeptidase CpyA/Prc1	*Aspergillus fumigatus*	149	jgi|Oidma1|189905|estExt_Genewise1.C_2_t30270	70%	0.00E+00	pfam00450	Peptidase_S10, Serine carboxypeptidase	5.00E-157	TGQNVYDIR DVYALLTLFFK	
1604	gi|46128691	hypothetical protein FG08723.1	*Gibberella zeae*	213	jgi|Oidma1|187123|estExt_Genewise1.C_1_t50474	80%	0.00E+00	pfam00923	Transaldolase	2.00E-85	VSTEVDAR FAADAVTLK ATGTTVVSDSGDFASIGK	

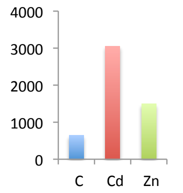
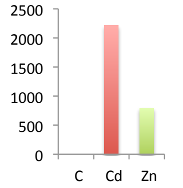
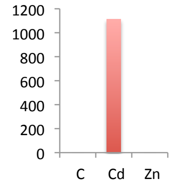
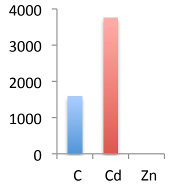
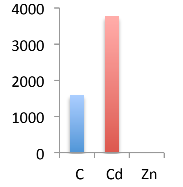
1505	gi|70992763	carboxypeptidase CpyA/Prc1	*Aspergillus fumigatus Af293*	198	jgi|Oidma1|189905|estExt_Genewise1.C_2_t30270	70%	0.00E+00	pfam00450	Peptidase_S10, Serine carboxypeptidase	5.00E-157	QFPEYAK TGQNVYDIR DVYALLTLFFK	
2501	gi|74612186	RecName: Full=Enolase; AltName: Full=2-phosphoglycerate dehydratase; AltName: Full=2-phospho-D-glycerate hydro-lyase	*Tuber borchii*	175	jgi|Oidma1|194545|estExt_Genewise1.C_4_t40282	85%	0.00E+00	pfam00113	Enolase_C, Enolase, C-terminal TIM barrel domain	0.00E+00	LGANAILGVSLAVAK SGETEDVTIADIVVGLR	
1504	gi|70992763	carboxypeptidase CpyA/Prc1	*Aspergillus fumigatus Af293*	201	jgi|Oidma1|189905|estExt_Genewise1.C_2_t30270	70%	0.00E+00	pfam00450	Peptidase_S10, Serine carboxypeptidase	5.00E-157	QFPEYAK DVYALLTLF TGQNVYDIR DVYALLTLFFK	
0403	gi|258574925	heat shock protein 70	*Uncinocarpus reesii 1704*	73	jgi|Oidma1|198916|estExt_Genewise1.C_7_t30365	80%	0.00E+00	pfam00012	HSP70, Hsp70 protein	0.00E+00	LSNVAYPITSK IDEDDKETILEAVK	

1502	gi|154315635	dnaK-type molecular chaperone BiP	*Botryotinia fuckeliana B05.10*	661	jgi|Oidma1|198916|estExt_Genewise1.C_7_t30365	91%	0.00E+00	pfam00012	HSP70, Hsp70 protein	0.00E+00	VINYFAK TLKPVEQVLK LSNVAYPITSK FELTGIPPAPR NGLENYAFSLK FEELNIDLFK VQELIEEYFGGK AKFEELNIDLFK MVQEAEKYADEDK IDEDDKETILDAVK GVPQIEVSFELDANGILK SQIFSTAADNQPVVLIQVYEGER	
4203	gi|154301061	hypothetical protein BC1G_10503	*Botryotinia fuckeliana B05.10*	132	jgi|Oidma1|84080|gw1.4.1094.1	73%	0.00E+00	pfam00326	Peptidase_S9, Prolyl oligopeptidase family	6.00E-66	NGIVFVAK TDLYYIPLK	
6104	gi|154300849	conserved hypothetical protein	*Botryotinia fuckeliana B05.10*	416	jgi|Oidma1|59014|gm1.12344_g	86%	0.00E+00	pfam00056	Ldh_1_N, lactate/malate dehydrogenase, NAD binding domain	2.00E-48	VQFGGDEVVK LFGVTTLDVVR GLIEIIAEVAPK NADIIVIPAGIPR DGAGSATLSMAYAGFR AVVAGASGGIGQPLSLLLK AYILIISNPVNSTVPIAAEVLK	
7306	gi|121705810	fructose-bisphosphate aldolase, class II	*Aspergillus clavatus NRRL 1*	80	jgi|Oidma1|196444|estExt_Genewise1.C_6_t20073	85%	0.00E+00	pfam01116	F_bP_aldolase, Fructose-bisphosphate aldolase class-II	3.00E-115	DYLMTPVGNPDGEDKPNKK GVSNDGQNASIAGGIAAAHYIR	

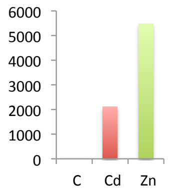
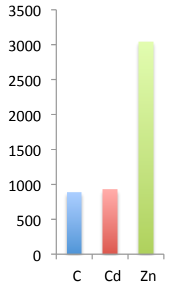
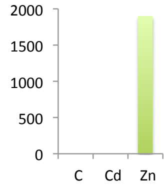
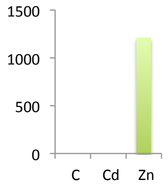
8402	gi|116201625	hypothetical protein CHGG_08697	*Chaetomium globosum CBS 148.51*	91	jgi|Oidma1|96668|gw1.2.2487.1	70%	2.00E-176	pfam00160	Pro_isomerase, Cyclophilin type peptidyl-prolyl cis-trans isomerase/CL	2.00E-50	HVVFGEVLSGK QIENLRTQSDKPIK	
8603	gi|116179598	conserved hypothetical protein	*Chaetomium globosum CBS 148.51*	214	jgi|Oidma1|197945|estExt_Genewise1.C_7_t10331	75%	0.00E+00	pfam07992	Pyr_redox_2, Pyridine nucleotide-disulphide oxidoreductase	5.00E-53	LNLAQLMK TNLDTEGMVK AEEEAVAAVEYIK	

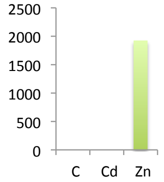
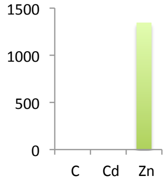
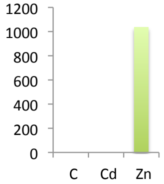
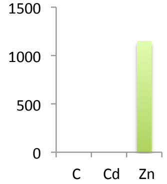
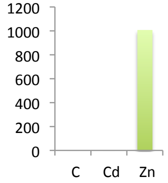
SPOTS FROM 2-DE GEL OF CADMIUM TREATED SAMPLES

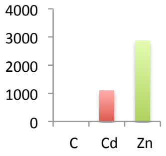
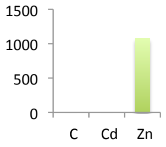
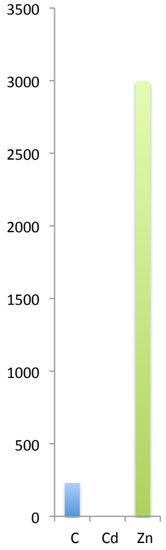
Spot number (a)	MASCOT ID (b)				*O. maius* DB ID (c)			*PFAM* (d)				
	Accession number	Description	Organism	Score	Accession number	% identity	e-value	Accession number	Description	e-value	Peptides (e)	Graph (f)
1301	gi|156055864	hypothetical protein SS1G_05284	*Sclerotinia sclerotiorum 1980*	204	jgi|Oidma1|199231|estExt_Genewise1.C_7_t40191	92%	9.00E-115	---	---	---	VQELIEEYFGGK ITPSYVAFTDEER QIIVYDLGGGTFDVSLLSIDR GVFEVLSTAGDTHLGGEDFDQR	
1802	gi|156060255	hypothetical protein SS1G_02266	*Sclerotinia sclerotiorum 1980*	230	jgi|Oidma1|198916|estExt_Genewise1.C_7_t30365	89%	0.00E+00	pfam00012	HSP70, Hsp70 protein	*0*	VQELIEEYFGGK ITPSYVAFTDEER QIIVYDLGGGTFDVSLLSIDR GVFEVLSTAGDTHLGGEDFDQR	

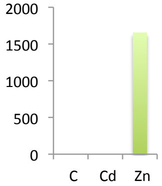
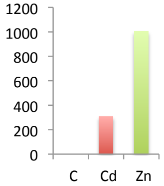
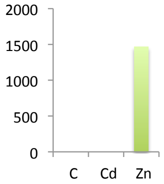
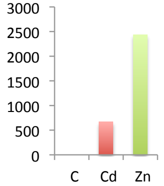
1804	gi|156060255	hypothetical protein SS1G_02266	*Sclerotinia sclerotiorum 1980*	284	jgi|Oidma1|198916|estExt_Genewise1.C_7_t30365	89%	0.00E+00	pfam00012	HSP70, Hsp70 protein	*0*	TLKPVEQVLK LSNVAYPITSK FEELNMDLFK VQELIEEYFGGK ITPSYVAFTDEER IEIEAFHNGNDFSETLTR QIIVYDLGGGTFDVSLLSIDR GVFEVLSTAGDTHLGGEDFDQR	
4206	gi|154323902	enolase	*Botryotinia fuckeliana B05.10*	101	jgi|Oidma1|194545|estExt_Genewise1.C_4_t40282	94%	0.00E+00	pfam00113	Enolase_C, Enolase, C-terminal TIM barrel domain	*0*	SGETEDVTIADIVVGLR YGQSAGNVGDEGGVAPDIQTAEEALELITE SIEAAGYTGK	
6604	gi|74612186	RecName: Full=Enolase; AltName: Full=2-phosphoglycerate dehydratase; AltName: Full=2-phospho-D-glycerate hydro-lyase	*Tuber borchii*	90	jgi|Oidma1|194545|estExt_Genewise1.C_4_t40282	85%	0.00E+00	pfam00113	Enolase_C, Enolase, C-terminal TIM barrel domain	*0*	LGANAILGVSLAVAK SGETEDVTIADIVVGLR	
6404	gi|46128691	hypothetical protein FG08723.1	*Gibberella zeae PH-1*	267	jgi|Oidma1|187123|estExt_Genewise1.C_1_t50474	79%	0.00E+00	pfam00923	Transaldolase	*2.00E-85*	LLVEFGK VSTEVDAR FAADAVTLK ATGTTVVSDSGDFASIGK YKPQDATTNPSLILAASK	
6407	gi|46126317	hypothetical protein FG07536.1	*Gibberella zeae PH-1]*	84	jgi|Oidma1|191617|estExt_Genewise1.C_3_t10358	87%	2.00E-141	pfam00578	AhpC-TSA, AhpC/TSA family	*8.00E-35*	SVFIIDPK LGSTAPNFQAETTK	

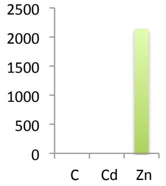
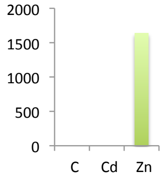
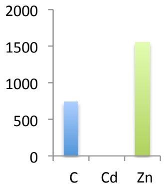
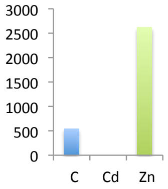
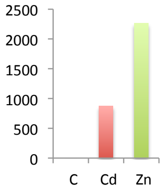
SPOTS FROM 2-DE GEL OF ZINC TREATED SAMPLES												
Spot	MASCOT ID (b)				*O. maius* DB ID (c)			*PFAM* (d)				

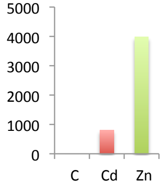
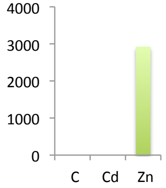
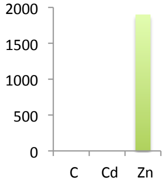
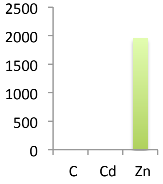
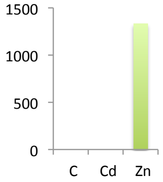
number (a)	Accession number	Description	Organism	Score	Accession number	% identity	e-value	Accession number	Description	e-value	Peptides (e)	Graph (f)
0101	gi|50550179	YALI0D08184p	*Yarrowia lipolytica*	204	jgi|Oidma1|52231|gm1.5561_g	82%	0.0	pfam00012	HSP70, Hsp70 protein	*0*	LSKEDIER FELTGIPPAPR NGLESYAYSLK SETFSTYADNQPGVLIQVFEGER	
1101	gi|154294634	20S proteasome alpha subunit E	*Botryotinia fuckeliana B05.10*	663	jgi|Oidma1|187708|estExt_Genewise1.C_1_t70156	99%	6.00E-179	pfam00227	Proteasome, Proteasome subunit	*2.00E-50*	SLTIEEAETLVLK IVEIDR SMVEHAR NVQLASVTK GINTFSPEGR VTSTLLETSSVEK LFQVEYSLEAIK LFQVEYSLEAIK SLTIEEAETLVLK HIGCAMSGLQADAR RVTSTLLETSSVEK LGSTAIGVATGGGVVLGVEK AIGSGSEGAQAELQNEFHK FGEGADGEESIMSR	
1404	gi|169622210	hypothetical protein SNOG_14322	*Phaeosphaeria nodorum SN15*	460	jgi|Oidma1|52231|gm1.5561_g	80%	0.0	pfam00012	HSP70, Hsp70 protein	*2.00E-151*	NVLIFDLGGGTFDVSLLTIEEGIFEVK FADAEVQADMK KFADAEVQADMK TTPSFVAFTDTER DDRIEIIANDQGNR NQVAMNPSNTVFDAK IINEPTAAAIAYGLDK STAGDTHLGGEDFDNR	
1408	gi|39964999	F-actin capping protein subunit beta, putative	*Magnaporthe grisea 70-15*	137	jgi|Oidma1|192203|estExt_Genewise1.C_3_t20478	70%	2.00E-138	pfam01115	F_actin_cap_B, F-actin capping protein, beta subunit	*1.00E-128*	DVVGDLR LVEDMELK ANEAFDVYR	

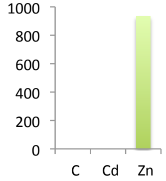
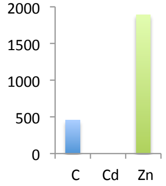
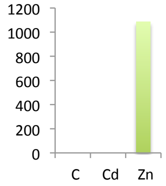
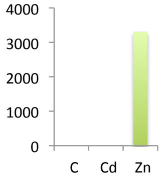
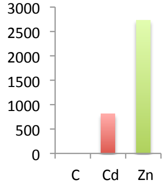
1706	gi|154323902	enolase	*Botryotinia fuckeliana B05.10*	113	jgi|Oidma1|194545|estExt_Genewise1.C_4_t40282	93%	0.0	pfam00113	Enolase_C, Enolase, C-terminal TIM barrel domain	*0*	AVANVNDIIGPALIK SGETEDVTIADIVVGLR	
2101	gi|154296240	hypothetical protein BC1G_12947	*Botryotinia fuckeliana B05.10*	585	jgi|Oidma1|194528|estExt_Genewise1.C_4_t40265	100%	5.00E-171	pfam00244	14-3-3, 14-3-3 protein	*7.00E-152*	SLEAYK HLIPSAK IVTSIEQK QKIEAELAK YLAEFAIGDK IVTSIEQKEESK SVASEDQELSVEER NATEVAQTDLAPTHPIR LAEQAERYEEMVENMK QAFDDAIAELDTLSEESYK	
2403	gi|154276988	ATP synthase beta chain, mitochondrial precursor	*Ajellomyces capsulatus NAm1*	238	jgi|Oidma1|127197|e_gw1.10.740.1	89%	0.0	pfam00006	ATP-synt_ab, ATP synthase alpha/beta family, nucleotide-binding domain	*6.00E-75*	VIQLDGESK VQQMLQEYK IMNVTGDPIDER FTQAGSEVSALLGR SLQDIIAILGMDELSEADKLTVER	
3104	gi|6320801	Hyp2p	*Saccharomyces cerevisiae*	207	jgi|Oidma1|187775|estExt_Genewise1.C_1_t70224	76%	1.00E-79	pfam01287	eIF-5a, Eukaryotic elongation factor 5A hypusine, DNA-binding OB fold	*2.00E-29*	HGHAKVHLVAIDIFTGK NGFVVIK IVDMSTSK VHLVAIDIFTGK	
3205	gi|156051562	hypothetical protein SS1G_07188	*Sclerotinia sclerotiorum 1980*	131	jgi|Oidma1|89238|gw1.2.1486.1	78%	4.00E-140	pfam01182	Glucosamine_iso, Glucosamine-6-phosphate isomerases/6-phosphogluconolactonase	*3.00E-66*	IAFVATGGGK IAVSGGSLPK IAFVATGGGKK	

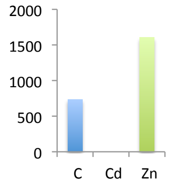
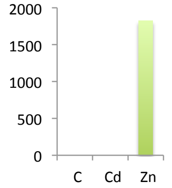
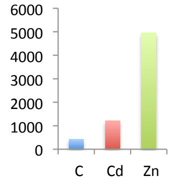
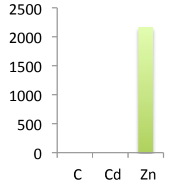
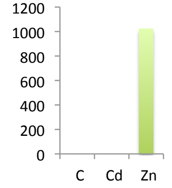
3402	gi|154312262	heat shock 70 kDa protein 2	*Botryotinia fuckeliana B05.10]*	98	jgi|Oidma1|52231|gm1.5561_g	88%	0.0	pfam00012	HSP70, Hsp70 protein	*5.00E-126*	DDRIEIIANDQGNR GVPQIEVTFDLDANGIMNVSALEK SEVFSTFSDNQPGVLIQVFEGER STNEILLLDVAPLSLGIETAGGQMTK TLSSSAQTSIEIDSLFEGIDFYTSITR NVLIFDLGGGTFDVSLLTIEEGIFEVK DDRIEIIANDQGNR STNEILLLDVAPLSLGIETAGGQMTK TLSSSAQTSIEIDSLFEGIDFYTSITR	
3506	gi|154276988	ATP synthase beta chain, mitochondrial precursor	*Ajellomyces capsulatus NAm1]*	954	jgi|Oidma1|127197|e_gw1.10.740.1	89%	0.0	pfam00006	ATP-synt_ab, ATP synthase alpha/beta family, nucleotide-binding domain	*6.00E-75*	IGLFGGAGVGK VIQLDGESK VQQMLQEYK TIAMDGTEGLVR IMNVTGDPIDER FTQAGSEVSALLGR VALTGLTVAEYFR TVFIQELINNIAK IPSAVGYQPTLAVDMGGMQER VALVFGQMNEPPGAR LVLEVAQHLGENVVR GISELGIYPAVDPLDSK DEEGQDVLLFIDNIFR APIHAEAPEYVEQATSAEVLVTGIK SLQDIIAILGMDELSEADKLTVER	
3808	gi|156064253	heat shock 70 kDa protein	*Sclerotinia sclerotiorum 1980*	1101	jgi|Oidma1|194758|estExt_Genewise1.C_4_t50002	92%	0.0	pfam00012	HSP70, Hsp70 protein	*0*	VLADAK LIGDAAK DNNLLGK NTTIPTK GVPQIEVTFDLDANGIMNVSALEK STNEILLLDVAPLSLGIETAGGQMTK NTTIPTKK NVLIFDLGGGTFDVSLLTIEEGIFEVK LSKEDIER TKDNNLLGK FELTGIPPAPR DAGLIAGLNVLR FADAEVQADMK IEIIANDQGNR VHEIVLVGGSTR KFADAEVQADMK TTPSFVAFTDTER LITDYFNGKEPNK QFTPEEISSMILVK DDRIEIIANDQGNR IINEPTAAAIAYGLDK STAGDTHLGGEDFDNR IINEPTAAAIAYGLDKK ETAEAYLGGTVNNAVVTVPAYFTDSQR SEVFSTFSDNQPGVLIQVFEGER KSEVFSTFSDNQPGVLIQVFEGER TLSSSAQTSIEIDSLFEGIDFYTSITR	

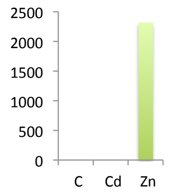
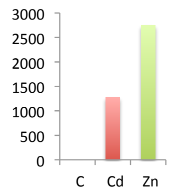
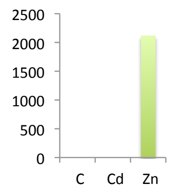
3904	gi|154309232	hypothetical protein BC1G_07510	*Botryotinia fuckeliana B05.10*	832	jgi|Oidma1|192450|estExt_Genewise1.C_3_t30227	94%	0.0	pfam00004	AAA, ATPase family associated with various cellular activities (AAA)	*4.00E-55*	HPQLFK SVSDVEIR QGDLFTVR RSVSDVEIR ESISLDIER LEILQIHTK EVAVVEVPNVR FALGVSNPSALR EVDIGIPDPTGR VVSQLLTLMDGMK THGFSGADLGFITQR VVNQLLTEMDGMTSK AAAPCVVFLDELDSIAK VVNQLLTEMDGMTSKK NSPAIIFIDEIDSIAPK DTVLIVLADDDLDDGSAR	
4005	gi|154305175	hypothetical protein BC1G_08882	*Botryotinia fuckeliana B05.10*	154	jgi|Oidma1|192399|estExt_Genewise1.C_3_t30176	89%	2.00E-165	pfam00121	TIM, Triosephosphate isomerase	*4.00E-180*	VASTEQAQEVHAAIR IVIAYEPIWAIGTGK	
5413	gi|156065173	hypothetical protein SS1G_00597	*Sclerotinia sclerotiorum 1980*	146	jgi|Oidma1|134854|e_gw1.19.291.1	89%	0.0	pfam00294	PfkB, pfkB family carbohydrate kinase	*2.00E-43*	LIAGGGAQNTAR YGLKPNDAILAEEK	
5302	gi|71000118	inorganic diphosphatase	*Aspergillus fumigatus Af293*	224	jgi|Oidma1|194204|estExt_Genewise1.C_4_t30432	85%	0.0	pfam00719	Pyrophosphatase, Inorganic pyrophosphatase	*2.00E-62*	HLPGLLR ATNEWFR IDINDPLAPK VIVIDINDPLAPK VLGVMALLDEEETDWK	

5104	gi|154305175	hypothetical protein BC1G_08882	*Botryotinia fuckeliana B05.10*	303	jgi|Oidma1|192399|estExt_Genewise1.C_3_t30176	89%	2.00E-165	pfam00121	TIM, Triosephosphate isomerase	*4.00E-108*	IIYGGSVSEK VASTEQAQEVHAAIR DSNITWTLLGHSER IVIAYEPIWAIGTGK	
4903	gi|156063540	hypothetical protein SS1G_01888	*Sclerotinia sclerotiorum 1980*	350	jgi|Oidma1|187496|estExt_Genewise1.C_1_t60355	87%	0.0	pfam00012	HSP70, Hsp70 protein	*2.00E-176*	NTVGSLK ATPSLVGFGPK YFDKVEAER SLMDAAEIAGVK GVDVITNEVSNR NLSFTLNQDEAIAR KNELETYIYEMR LMNDTTAAALGYGITK LPVSDMVMSVPAWFTDVQR	
4401	gi|156065173	hypothetical protein SS1G_00597	*Sclerotinia sclerotiorum 1980*	105	jgi|Oidma1|134854|e_gw1.19.291.1	89%	0.0	pfam00294	PfkB, pfkB family carbohydrate kinase	*2.00E-43*	LIAGGGAQNTAR YGLKPNDAILAEEK	
4305	gi|116193369	hypothetical protein CHGG_06402	*Chaetomium globosum CBS 148.51*	115	jgi|Oidma1|37331|fgenesh1_pm.1_#_780	80%	0.0	pfam00923	Transaldolase	*7.00E-73*	FAADAVTLK YKPQDATTNPSLILAATK	
4304	gi|67539246	hypothetical protein AN5793.2	*Aspergillus nidulans FGSC A4*	198	jgi|Oidma1|194011|estExt_Genewise1.C_4_t30232	83%	3.00E-176	pfam00227	Proteasome, Proteasome subunit	*5.00E-45*	HFVSR LLKPGANK NFQVEYAVK AVENGGTSIGIR GRHEEVPKELLEEAER HEEVPKELLEEAER	

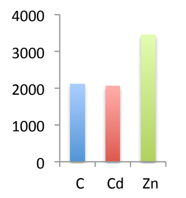
4108	gi|389624992	agmatinase 1 (MGG_10533)	*[Magnaporthe grisea 70-15]*	78	jgi|Oidma1|104689|estExt_fgenesh1_pm.C_90246	83%	0.0	pfam00491	Arginase, Arginase family	*4.00E-96*	EIDTIGTTGIIK VITLGGDHTITLPLLR AYGPVSVIHFDSHLDTWKPK	
4107	gi|156047535	hypothetical protein SS1G_09508	*Sclerotinia sclerotiorum 1980*	57	jgi|Oidma1|137902|e_gw1.26.110.1	67%	3.00E-94	---	---	---	AFVPSR WQNQFTWELAR	
8206	gi|156036416	hypothetical protein SS1G_12897	*Sclerotinia sclerotiorum 1980*	122	jgi|Oidma1|192127|estExt_Genewise1.C_3_t20398	59%	2.00E-75	---	---	---	SVGEFSR EAGEVYELQGELPGIEQK NGILSIIVPK ASMKNGILSIIVPK	
7802	gi|156042500	hypothetical protein SS1G_11047	*Sclerotinia sclerotiorum 1980*	427	jgi|Oidma1|28690|fgenesh1_pg.7_#_166	87%	0.0	pfam00330	Aconitase, Aconitase family (aconitate hydratase)	*0*	GVSYLK FSEAVK VAGILTVK EHAALEPR NGSALNTMAK SLFTVTPGSEQIR KGEANSIISSYNR TTTDHISMAGPWLK QGMLPLTFINPEDYDK	
7707	gi|154292650	phosphoenolpyruvate carboxykinase	*Botryotinia fuckeliana B05.10*	305	jgi|Oidma1|198578|estExt_Genewise1.C_7_t30005	92%	0.0	pfam01293	PEPCK_ATP, Phosphoenolpyruvate carboxykinase	*0*	SPLDKR AIDYLNTR TTLSADPNR DGDVTVFFGLSGTGK GVFTVLFYEMPVK LVDYDDSTLTENTR DLEHFHPDYTIYNAGSFPANR	

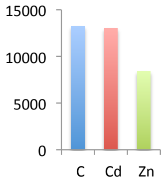
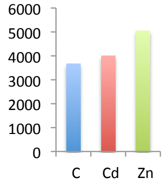
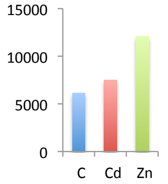
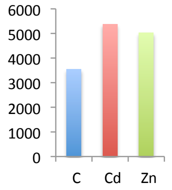
6802	gi|156042500	hypothetical protein SS1G_11047	*Sclerotinia sclerotiorum 1980*	246	jgi|Oidma1|28690|fgenesh1_pg.7_#_166	87%	0.0	pfam00330	Aconitase, Aconitase family (aconitate hydratase)	*0*	GVSYLK FSEAVK NGSALNTMAK SLFTVTPGSEQIR KGEANSIISSYNR	
6503	gi|261359650	L-galactonate dehydratase	*Verticillium albo-atrum VaMs.102*	208	jgi|Oidma1|121181|e_gw1.6.1583.1	87%	0.0	pfam13378	MR_MLE_C, Enolase C-terminal domain-like	*3.00E-21*	SEEARPIIEGVK MGGVNEVLAVLLMAK	
5706	gi|154300406	hypothetical protein BC1G_11392	*Botryotinia fuckeliana B05.10*	249	jgi|Oidma1|197740|estExt_Genewise1.C_7_t10114	85%	0.0	pfam01676	Metalloenzyme, Metalloenzyme superfamily	*3.00E-96*	IDQTIK EITQLLGDVDRSPKPDFAYPK VVWQDVVR APEMSAAGVAK EITQLLGDVDR NITLTTMTQYK	
5705	gi|154300406	hypothetical protein BC1G_11392	*Botryotinia fuckeliana B05.10*	356	jgi|Oidma1|197740|estExt_Genewise1.C_7_t10114	85%	0.0	pfam01677	Metalloenzyme, Metalloenzyme superfamily	*3.00E-96*	VVWQDVVR APEMSAAGVAK QDHLYALLK EITQLLGDVDR EIGIGEVATVVGR NITLTTMTQYK IKEIGIGEVATVVGR YAHVTFFFNGGVEK EITQLLGDVDRSPKPDFAYPK	
6210	gi|74612186	Full=Enolase; AltName: Full=2-phosphoglycerate dehydratase; AltName: Full=2-phospho-D-glycerate hydro-lyase	*Tuber borchii*	171	jgi|Oidma1|194545|estExt_Genewise1.C_4_t40282	85%	0.0	pfam00113	Enolase_C, Enolase, C-terminal TIM barrel domain	*0*	SGETEDVTIADIVVGLR TSDFQIVGDDLTVTNPIR	

6302	gi|46128691	hypothetical protein FG08723.1	*Gibberella zeae PH-1*	160	jgi|Oidma1|187123|estExt_Genewise1.C_1_t50474	79%	0.0	pfam00923	Transaldolase	*2.00E-85*	FAADAVTLK ATGTTVVSDSGDFASIGK	
6502	gi|154308516	conserved hypothetical protein	*Botryotinia fuckeliana B05.10*	129	jgi|Oidma1|121181|e_gw1.6.1583.1	88%	0.0	pfam13378	MR_MLE_C, Enolase C-terminal domain-like	*7.00E-22*	TLSSLVSNWGQTWR YLVSDSQLR MGGVNEVLAVLLMAK YITDAITPEEAIAMLK EALKPYGIGVATGEMCQNR GNILMVDANQVWSVPEAIEYMQ	
7206	gi|156048488	hypothetical protein SS1G_08975	*Sclerotinia sclerotiorum 1980*	588	jgi|Oidma1|59014|gm1.12344_g	86%	0.0	pfam00056	Ldh_1_N, lactate/malate dehydrogenase, NAD binding domain	*6.00E-46*	VQFGGDEVVK LFGVTTLDVVR RVQFGGDEVVK SGGIGQPLSLLLK GASGGIGQPLSLLLK DGAGSATLSMAYAGFR AVVAGASGGIGQPLSLLLK AKDGAGSATLSMAYAGFR ILIISNPVNSTVPIAAEVLK AGASGGIGQPLSLLLK AYILIISNPVNSTVPIAAEVLK	
7408	gi|154315742	ketol-acid reductoisomerase, mitochondrial precursor	*Botryotinia fuckeliana B05.10*	243	jgi|Oidma1|184925|estExt_Genemark1.C_320056	90%	0.0	pfam01450	Acetohydroxy acid isomeroreductase, catalytic domain	*5.00E-58*	EVYSDLYGER VDVPTDVDVILVAPK AIALGVGVGSGYLYETTFEK NDTMAIIGYGSQGHAQSLNMR	
7709	gi|74612186	RecName: Full=Enolase; AltName: Full=2-phosphoglycerate dehydratase; AltName: Full=2-phospho-D-glycerate hydro-lyase	*Tuber borchii*	166	jgi|Oidma1|194545|estExt_Genewise1.C_4_t40282	85%	0.0	pfam00113	Enolase_C, Enolase, C-terminal TIM barrel domain	*0*	SGETEDVTIADIVVGLR TSDFQIVGDDLTVTNPIR	

7801	gi|255946954	Pc22g02000	*Penicillium chrysogenum Wisconsin 54-1255*	97	jgi|Oidma1|28690|fgenesh1_pg.7_#_166	81%	0.0	pfam00330	Aconitase, Aconitase family (aconitate hydratase)	*0*	MSENLAIVR SLFTVTPGSEQIR	
8412	gi|154315742	ketol-acid reductoisomerase, mitochondrial precursor	*Botryotinia fuckeliana B05.10*	276	jgi|Oidma1|184925|estExt_Genemark1.C_320056	90%	0.0	pfam01450	Acetohydroxy acid isomeroreductase, catalytic domain	*5.00E-58*	EVYSDLYGER TLYFSHGFSPVFK VDVPTDVDVILVAPK AIALGVGVGSGYLYETTFEK	
9406	gi|258676930	glyceraldehyde-3-phosphate dehydrogenase	*Bryoria fremontii*	79	jgi|Oidma1|127805|e_gw1.10.403.1	75%	5.00E-140	pfam02800	Glyceraldehyde 3-phosphate dehydrogenase, C-terminal domain	*7.00E-77*	DPANIPWKDTGAYYGVESTGVFTTTEK	

SPOTS EXCISED FROM 2-DE GELS OF ALL TREATMENTS

Spot number (a)	MASCOT ID (b)				*O. maius* DB ID (c)			*PFAM* (d)				
	Accession number	Description	Organism	Score	Accession number	% identity	e-value	Accession number	Description	e-value	Peptides (e)	Graph (f)
3404	gi|154289586	phosphatidylinositol/phosphatidylcholine transfer protein	*Botryotinia fuckeliana B05.10*	115	jgi|Oidma1|197782|estExt_Genewise1.C_7_t10159	71%	1.00E-139	pfam00650	CRAL_TRIO, CRAL/TRIO domain	*5.00E-39*	VPSVYAYVK MLQNLAVEYEK	

5006	gi|154312864	hypothetical protein BC1G_05133	*Botryotinia fuckeliana B05.10*	109	jgi|Oidma1|191404|estExt_Genewise1.C_3_t10134	77%	6.00E-89	---	---	---	YAIVIEGGK RYAIVIEGGK	
5603	gi|154323902	enolase	*Botryotinia fuckeliana B05.10*	511	jgi|Oidma1|194545|estExt_Genewise1.C_4_t40282	93%	0.00E+00	pfam00113	Enolase_C, Enolase, C-terminal TIM barrel domain	*0*	LGANAILGVSLAVAK AVANVNDIIGPALIK DSFAAGWGVMVSHR IDEFLISLDGTPNK VNQIGTLTESIQAAK SGETEDVTIADIVVGLR GNPTVEVDVVTETGLHR SSDFQIVGDDLTVTNPIR TAEEALELITESIEAAGYTGK	
6601	gi|154323902	enolase	*Botryotinia fuckeliana B05.10*	512	jgi|Oidma1|194545|estExt_Genewise1.C_4_t40282	93%	0.00E+00	pfam00113	Enolase_C, Enolase, C-terminal TIM barrel domain	*0*	LGANAILGVSLAVAK AVANVNDIIGPALIK IDEFLISLDGTPNK VNQIGTLTESIQAAK SGETEDVTIADIVVGLR AIVPSGASTGQHEAVELR GNPTVEVDVVTETGLHR SSDFQIVGDDLTVTNPIR MNIAMDVASSEFYKEDAK	
7701	gi|154310767	hypothetical protein BC1G_06362	*Botryotinia fuckeliana B05.10*	277	jgi|Oidma1|180344|estExt_Genemark1.C_7_t20217	83%	0.00E+00	pfam00171	Aldedh, Aldehyde dehydrogenase family	*0*	VTLELGGK KVTLELGGK DVDIAVAAAR ELGEAALSNYTQTK	

(a) Spot number: protein ID from 2DE gel

(b) Mascot ID: shows protein ID, protein description, source organism and score after MASCOT analysis on NCBInr limited to fungi

(c) *O.maius* DB ID: shows the proteins identified in a translated ESTdatabase of *O. maius* Zn (O.maius DB) using the same peptides used for MASCOT identifications. % identity and e-value refer to the match between NCBI ID and O.maius DB ID

(d) PFAM: shows the protein family based on O.maius sequence

(e) Peptides: shows the peptide sequences used for protein identification

(f) Graph: shows the protein expressionlevel in the three samples, as evaluated by SYPRO-Ruby staining and PDQuest analysis