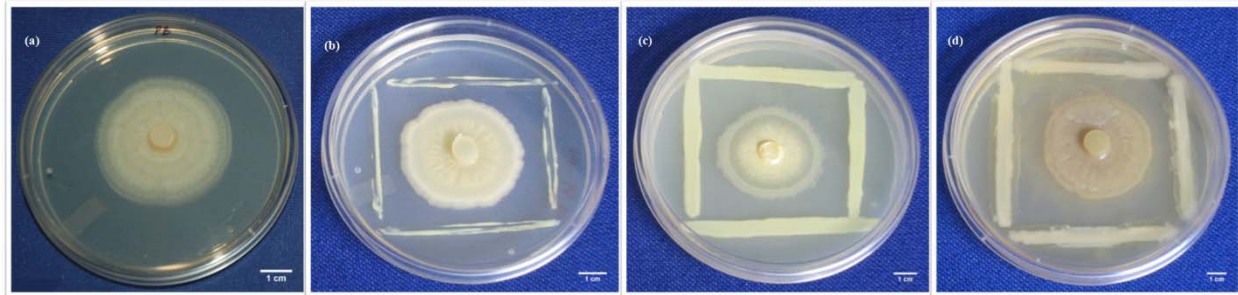


## Interaction of *Piriformospora indica* with *Azotobacter chroococcum*

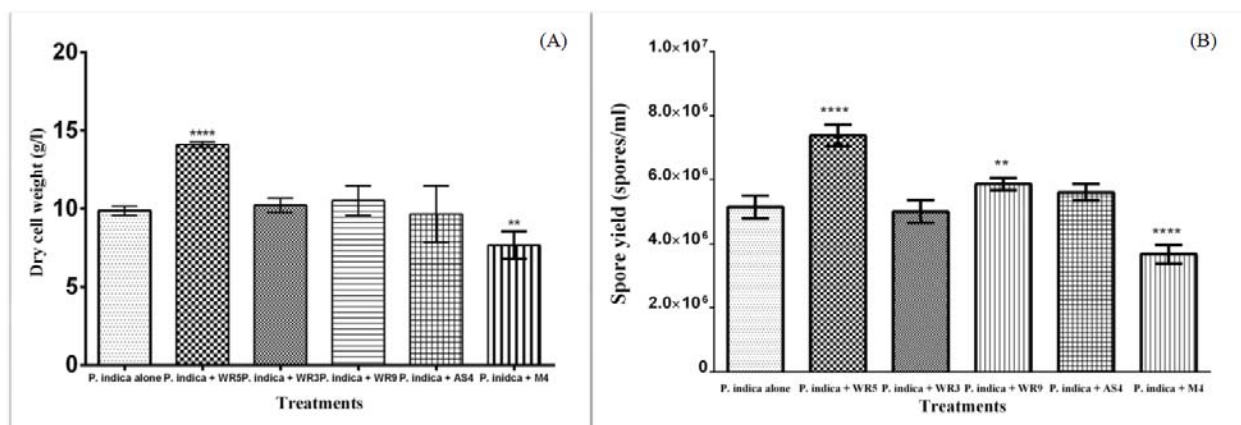
Soubhagya Kumar Bhuyan<sup>1</sup>, Prasun Bandyopadhyay<sup>2</sup>, Pramod Kumar<sup>1</sup>, Deepak Kumar Mishra<sup>1</sup>, Ramraj Prasad<sup>1</sup>, Abha Kumari<sup>1</sup>, Kailash Chandra Upadhyaya<sup>3</sup>, Ajit Varma<sup>2</sup> & Pramod Kumar Yadava<sup>1\*</sup>

### Supplimentary data

**Figure S1.** Visualization of the *A. chroococcum* – *P. indica* interaction in Hill and Kaeyer agar plates in the presence and absence of *A. chroococcum* strains. (A) control plate. (B) interaction of *P. indica* with WR3. (C) interaction of *P. indica* with WR9. (D) interaction of *P. indica* with AS4.



**Figure S 2.** Influence of *A. chroococcum* strains on the (A) dry cell weight and (B) spore yield of *P. indica* in Hill and Kaeyer liquid medium. Statistical analysis was performed using GraphPad Prism software by one way analysis of variance (ANOVA), followed by Dunnett's multiple comparison test. Values represented as mean  $\pm$ sd, n=3. \*\* $P \leq 0.01$ , \*\*\*\* $P \leq 0.01$  compared with *P. indica* alone. Error bar represents standard deviation (SD).

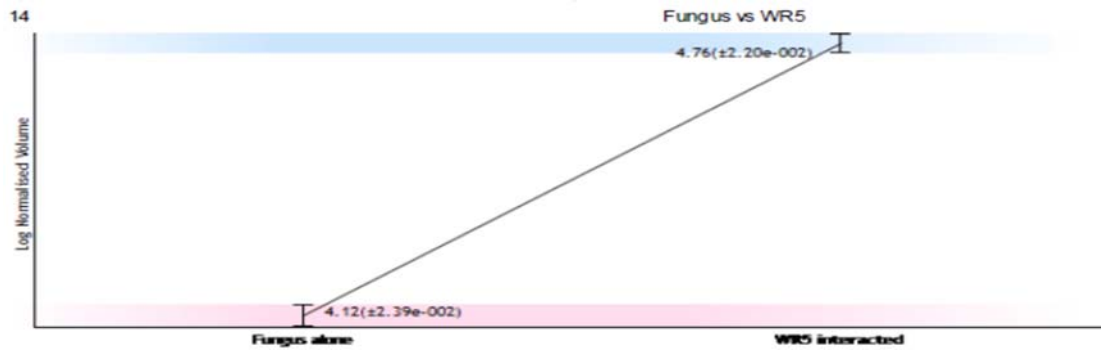
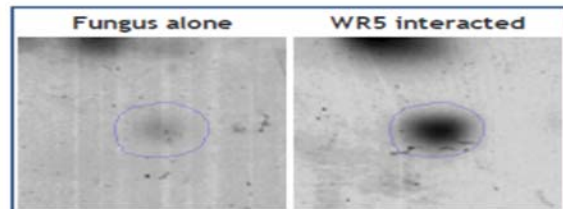


**Figure S3.** A list of protein spots identifier number, that exhibit change in expression fold level was analyzed pairwise between control and WR5-treated *P. indica* using Progenesis SameSpots analysis software.

Identifier 457

Position (740, 1256)

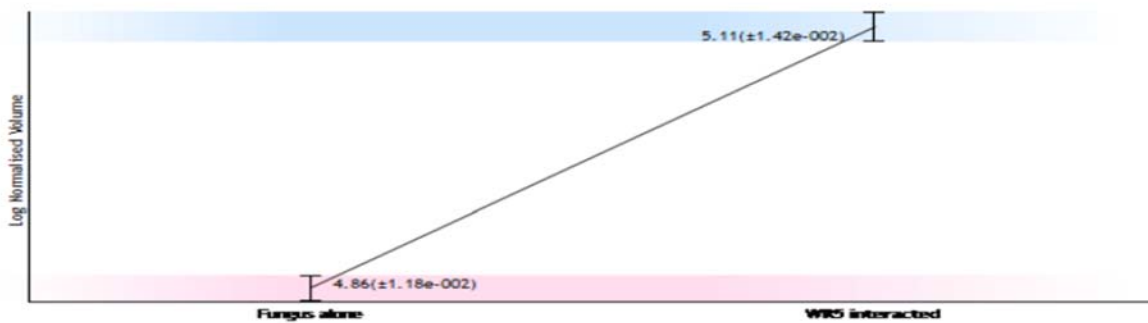
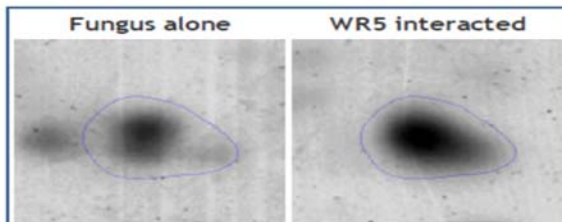
Notes



Identifier 444

Position (709, 1178)

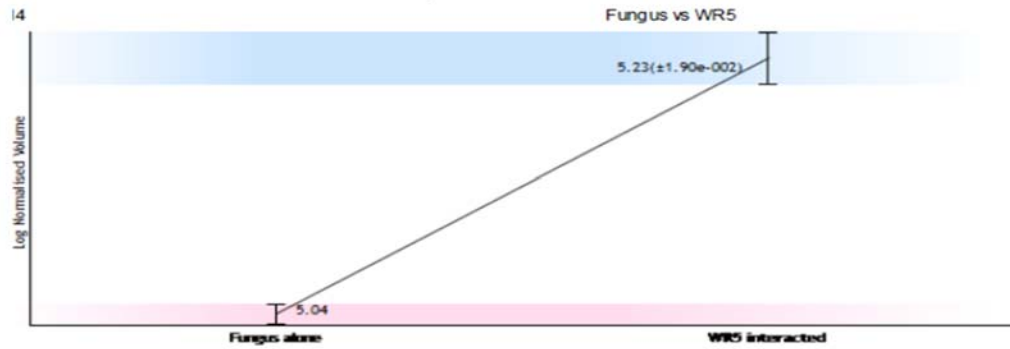
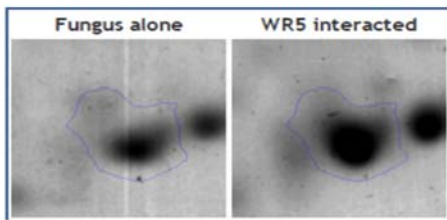
Notes



Identifier 443

Position (395, 1177)

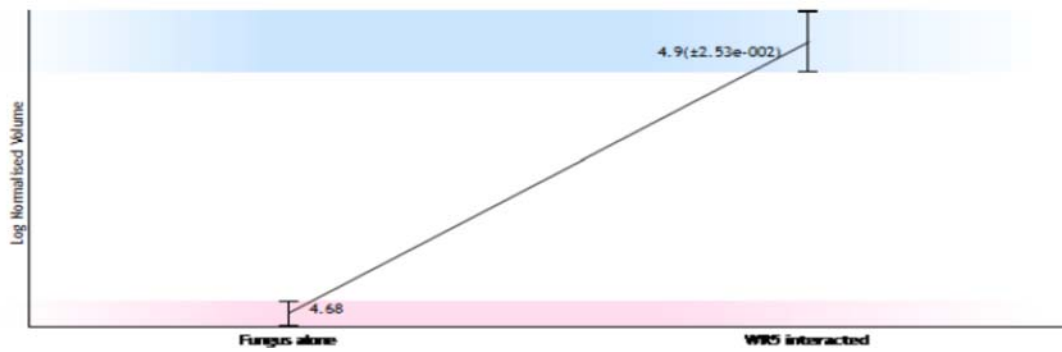
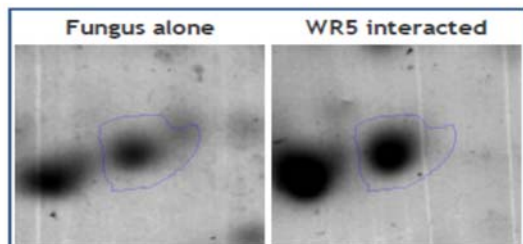
Notes



Identifier 440

Position (439, 1160)

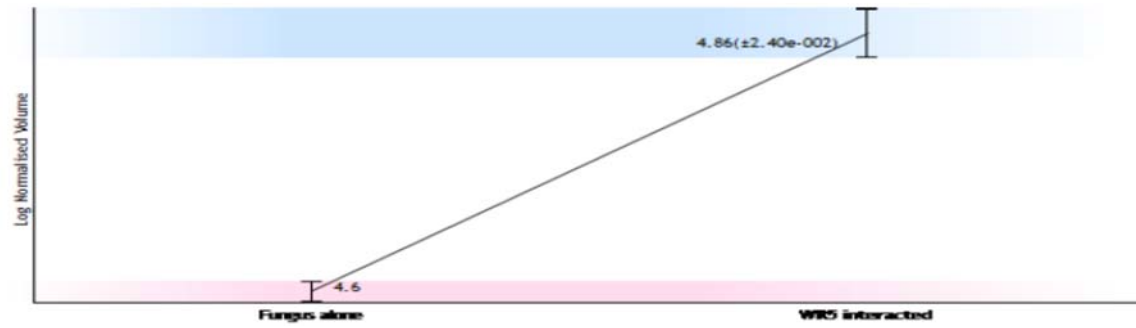
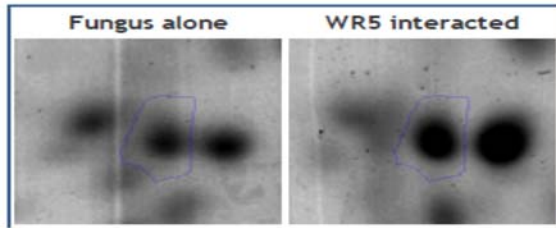
Notes



Identifier 406

Position (287, 999)

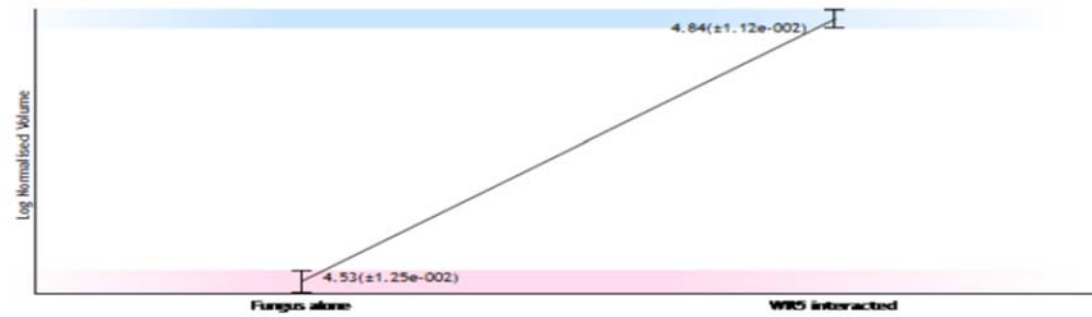
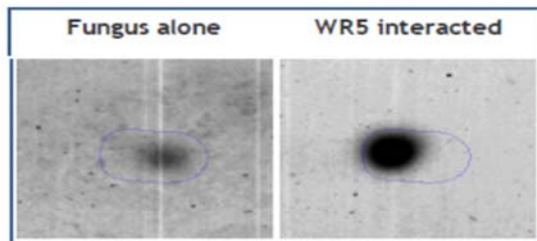
Notes



Identifier 416

Position (927, 1037)

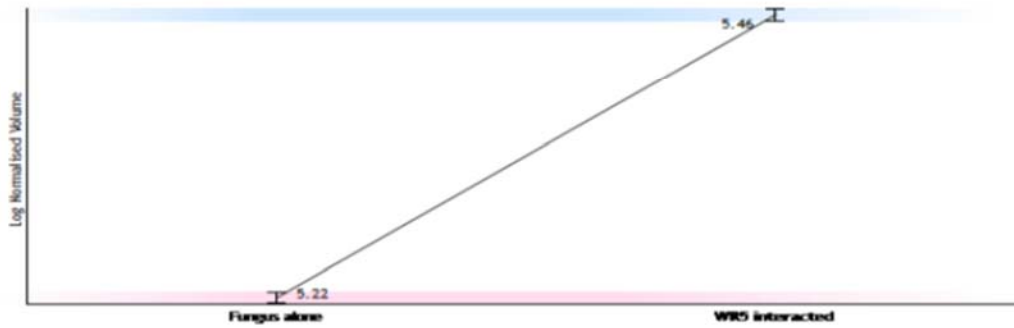
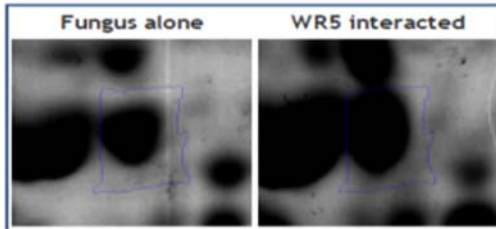
Notes



# Identifier 332

Position (368, 710)

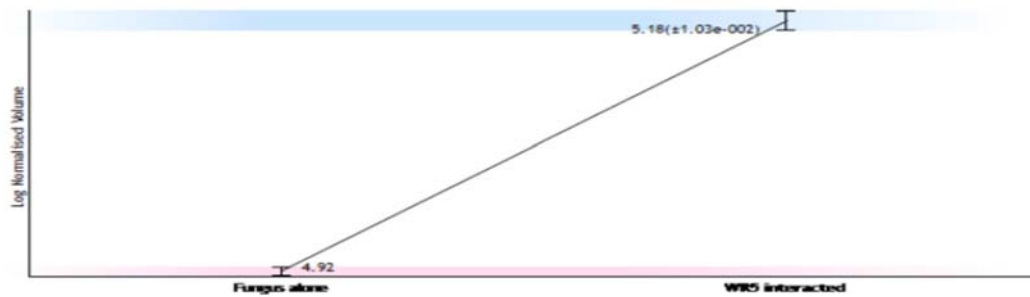
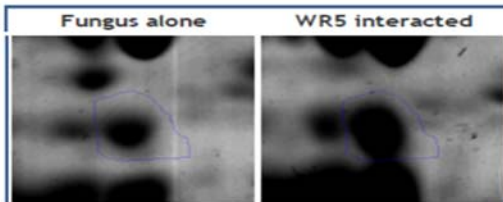
Notes



# Identifier 320

Position (363, 651)

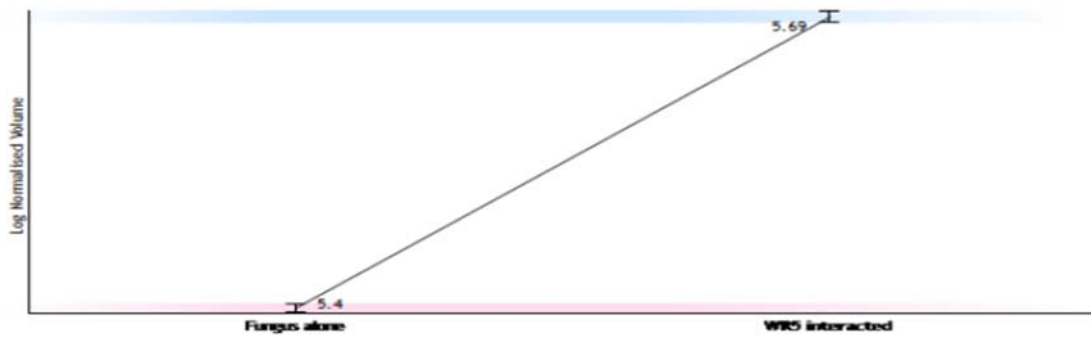
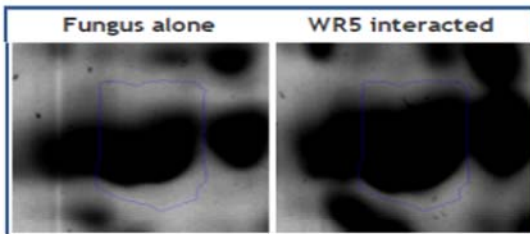
Notes



Identifier 342

Position (319, 724)

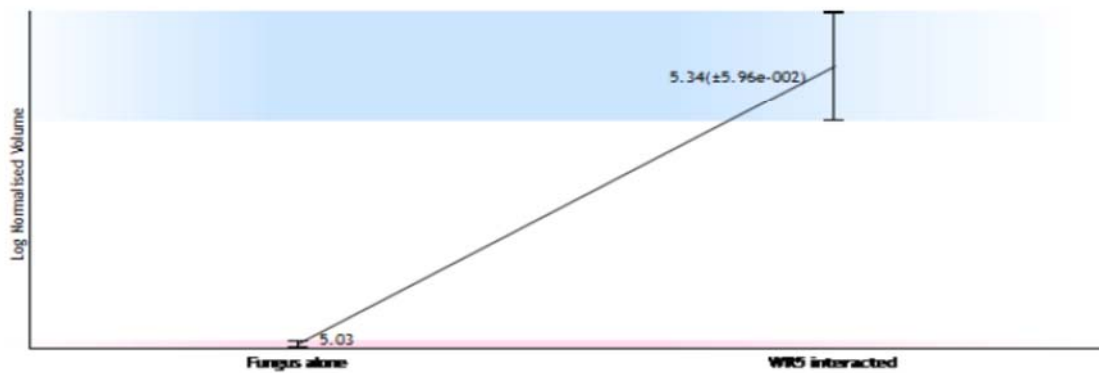
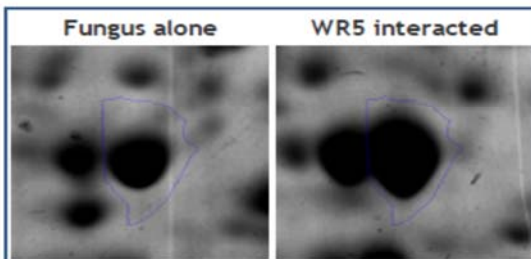
Notes



Identifier 287

Position (373, 583)

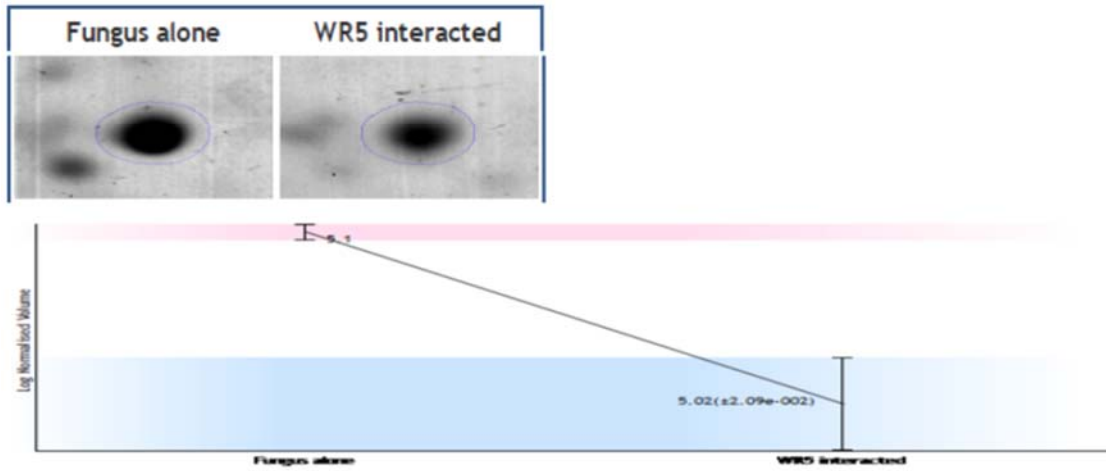
Notes



Identifier 428

Position (613, 1084)

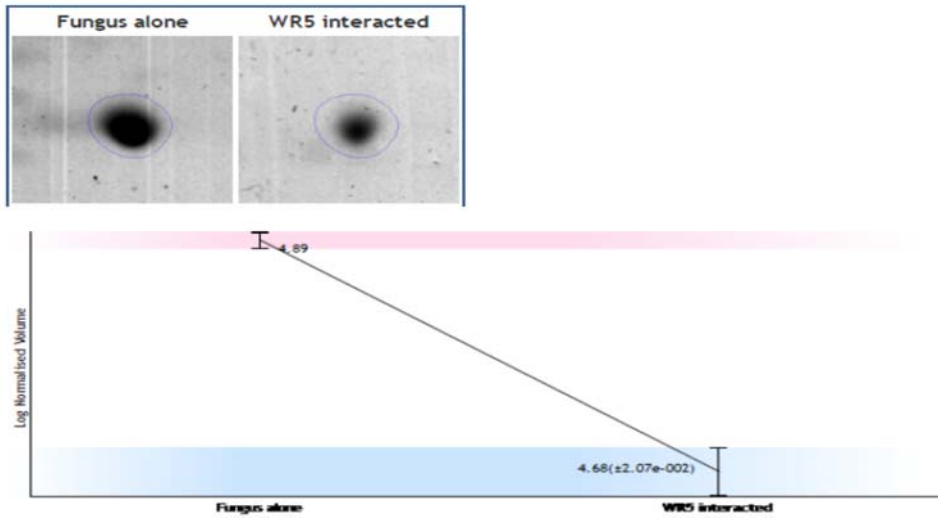
Notes



Identifier 330

Position (965, 701)

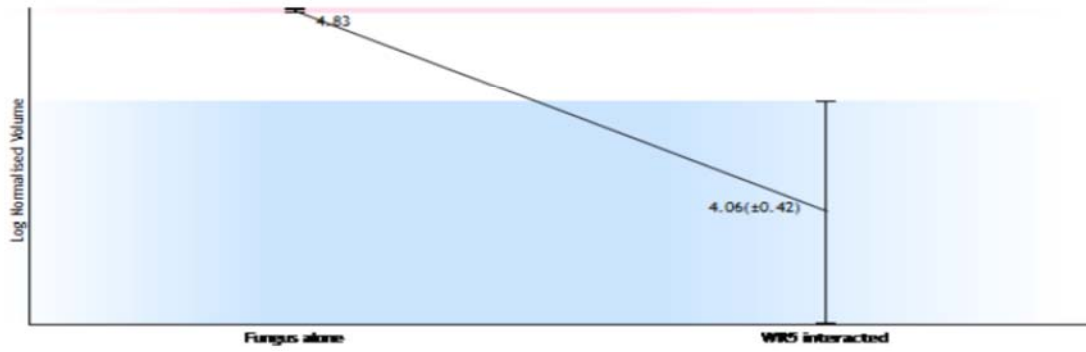
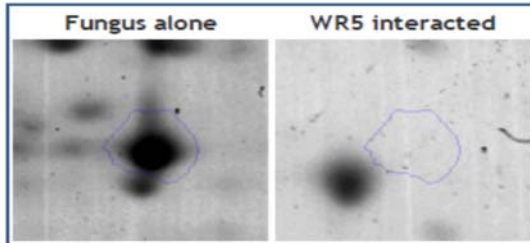
Notes



Identifier 305

Position (858, 623)

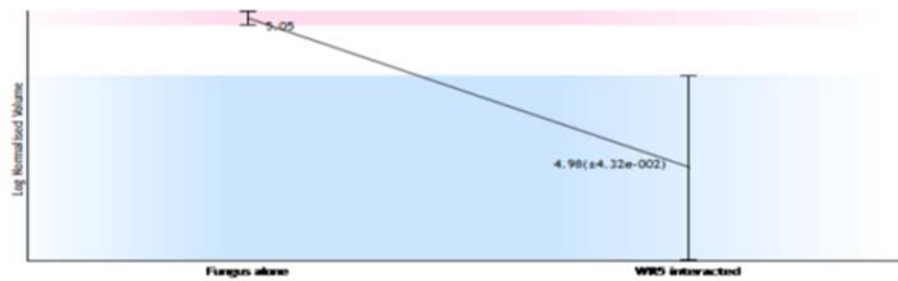
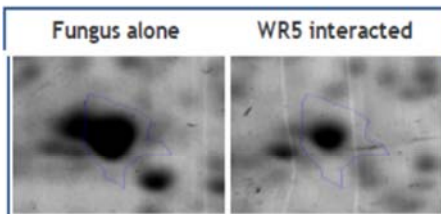
Notes



Identifier 296

Position (481, 606)

Notes

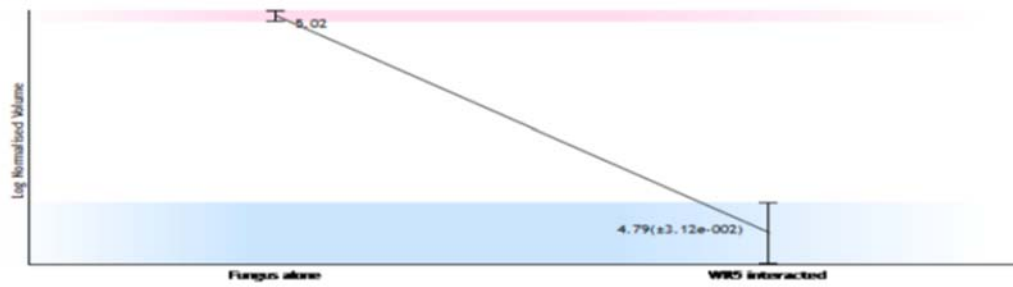
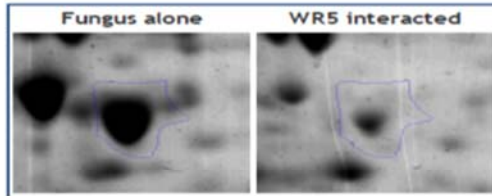




# Identifier 207

Position (442, 427)

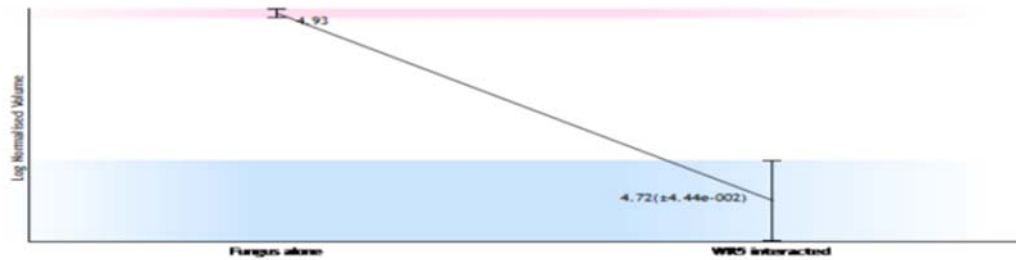
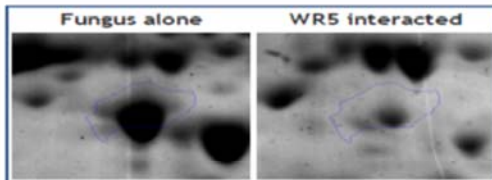
Notes



# Identifier 198

Position (398, 406)

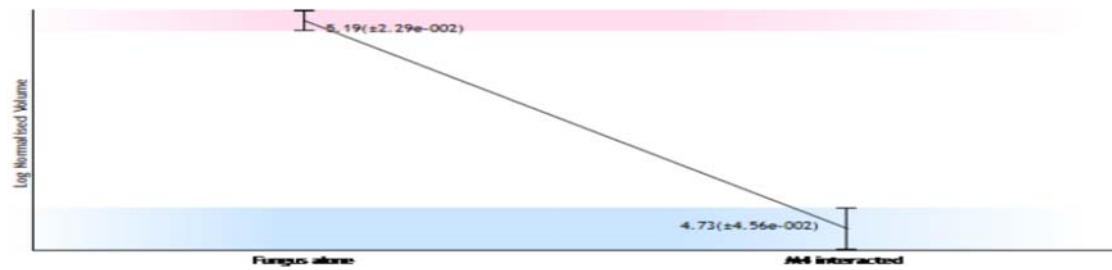
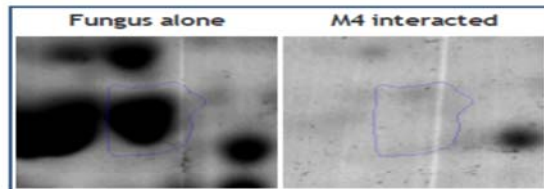
Notes



**Figure S4.** A list of protein spots identifier number, that exhibit a drastic change in expression fold level in M4-treated fungus analyzed pairwise between control and M4-treated *P. indica* using Progenesis SameSpots analysis software.

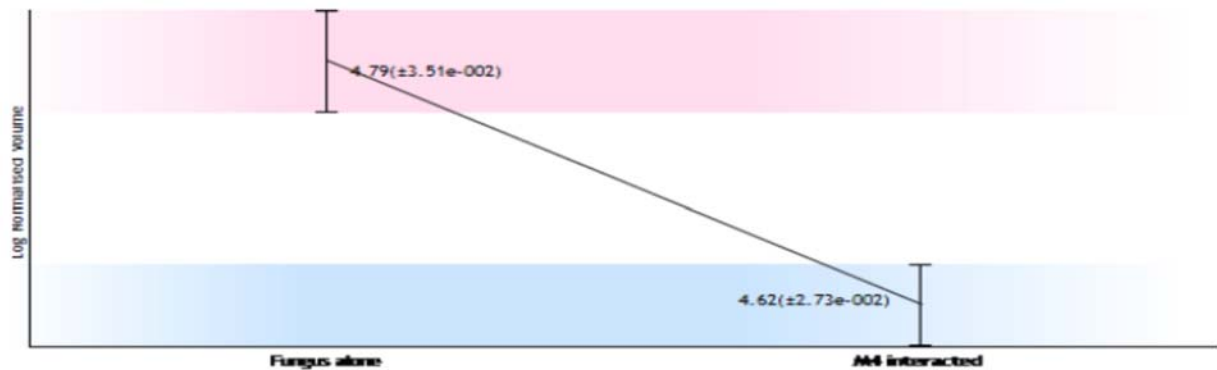
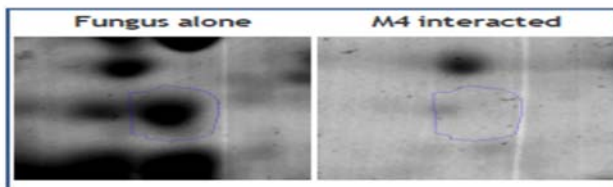
Identifier 334

Position (344, 700)  
Notes



Identifier 320

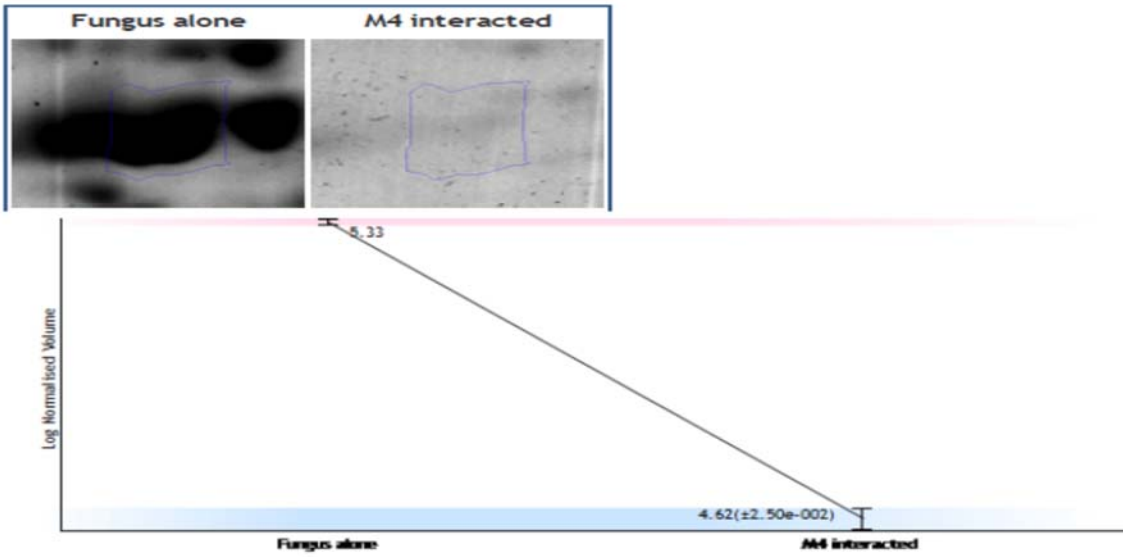
Position (339, 642)  
Notes



Identifier 341

Position (295, 716)

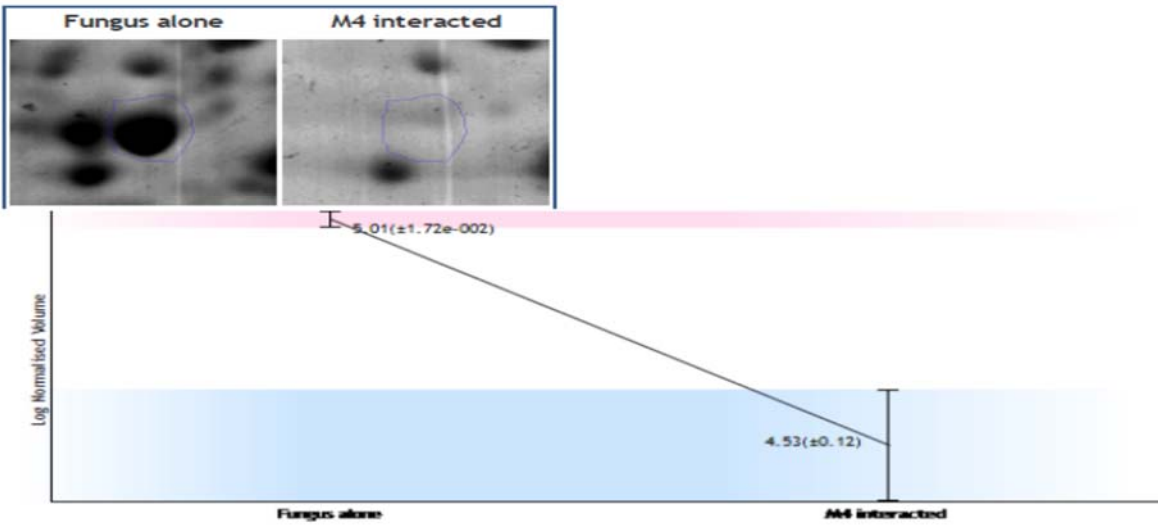
Notes



Identifier 292

Position (349, 574)

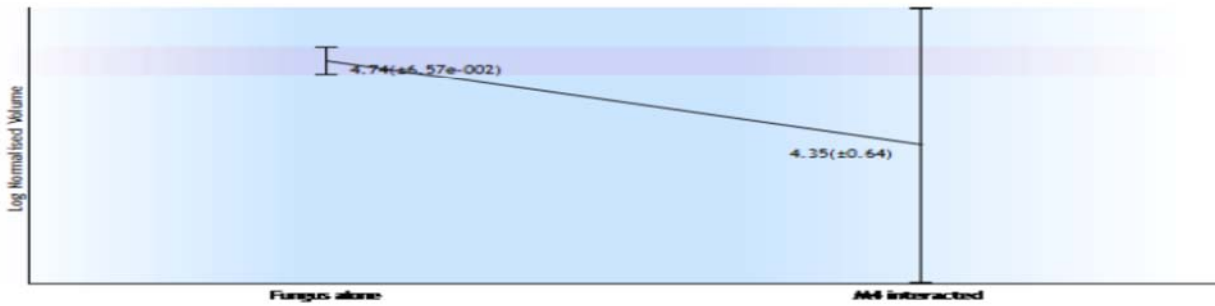
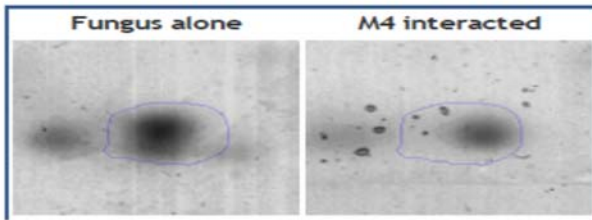
Notes



Identifier 452

Position (690, 1166)

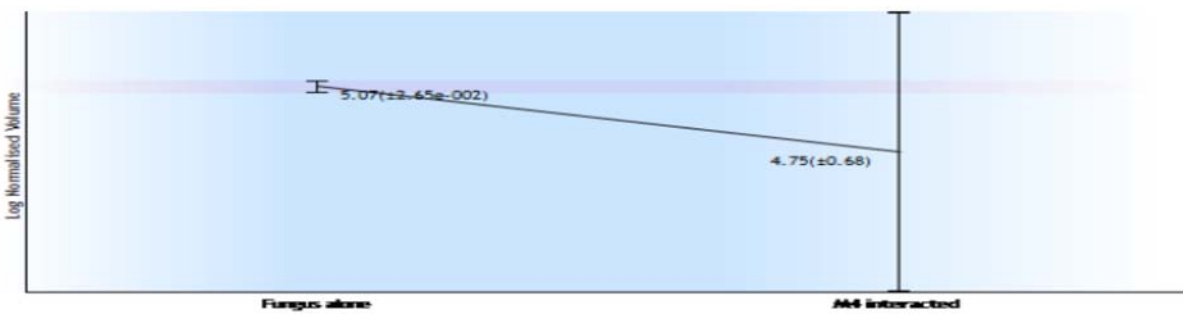
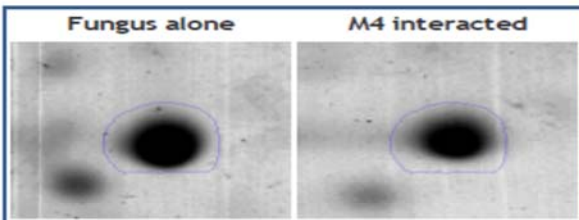
Notes



Identifier 422

Position (588, 1076)

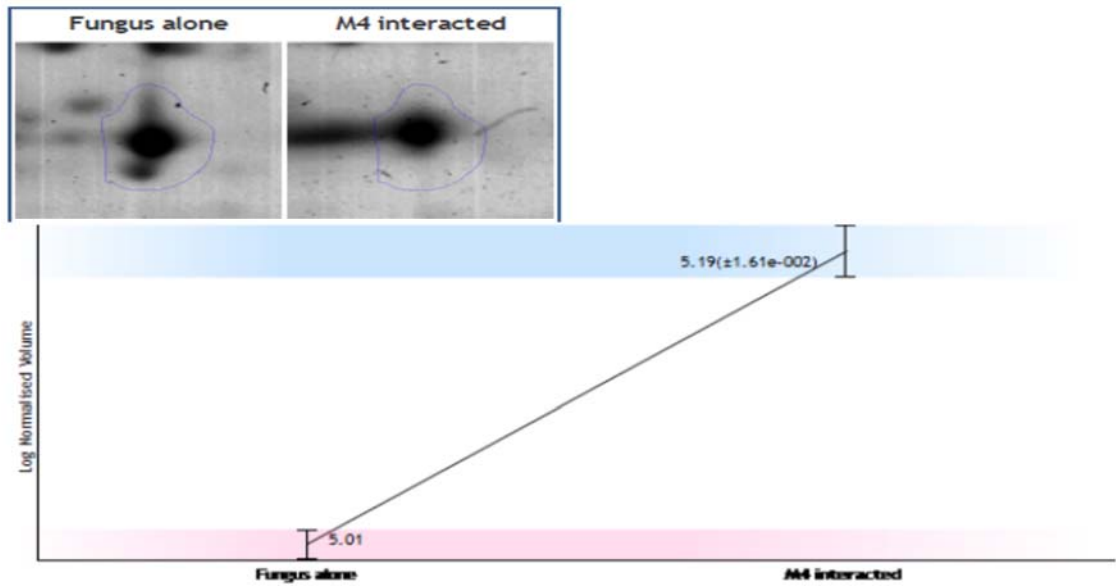
Notes



Identifier 309

Position (833, 614)

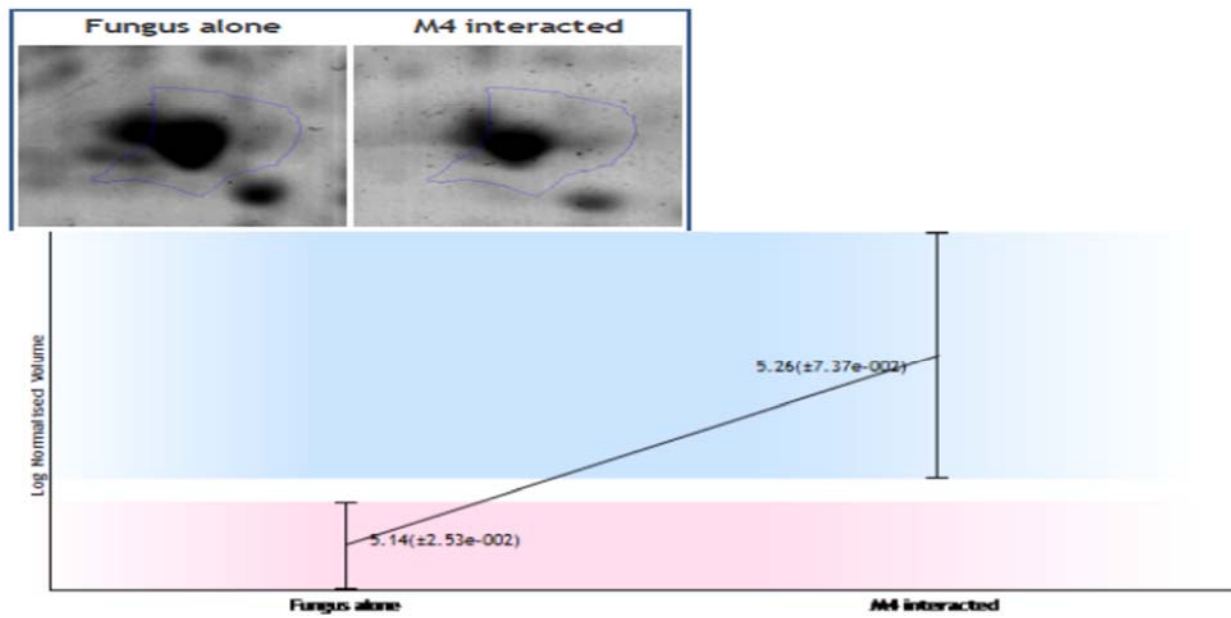
Notes



Identifier 301

Position (-435, 602)

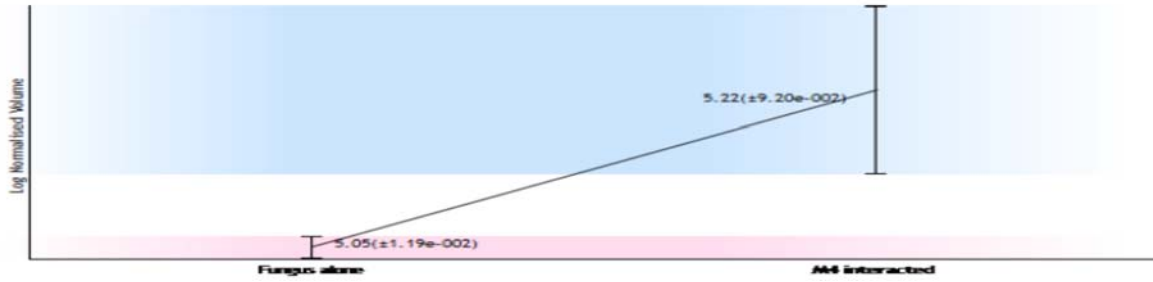
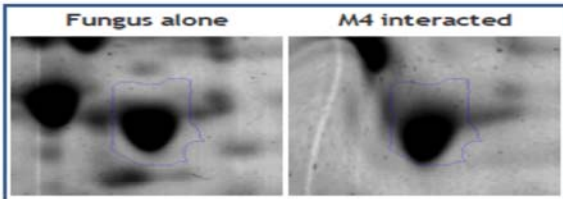
Notes



Identifier 210

Position (418, 420)

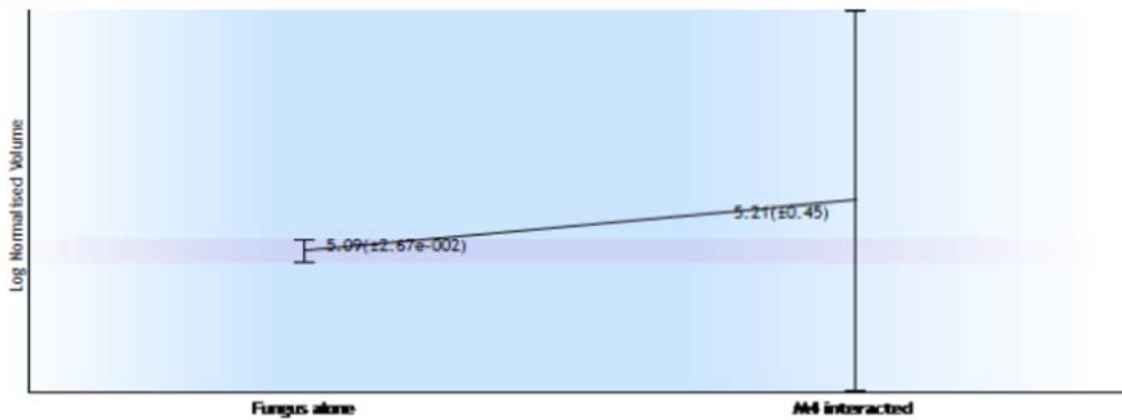
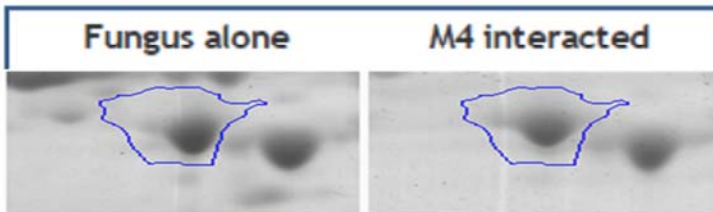
Notes



Identifier 198

Position (371, 402)

Notes



**Figure S5.** The matched peptide list of total sixteen protein spots identified through MALDI-TOF/MS of all three groups.

Spot number 3Wu

hypothetical protein PIIN\_09126 [*Piriformospora indica* DSM 11827]

10	20	30	40	50	60	70	80
MAAYLNRVVG	SDFGGCSMNQ	PYAMANRVNF	DRGFVCGRRK	DVEETKSYRQ	LDPHPHLLIR	YIRDTAGTLR	INNPQTRRTI
90	100	110					
ATLARSTSKG	ARSTHPPAFH	PH					

Spot number 4Wu/4M

hypothetical protein PIIN\_04261 [*Piriformospora indica* DSM 11827]

10	20	30	40	50	60	70	80
MARCVNSCYQ	SSLHITGFI	SLVLIQGAPI	DRAFRRVKV	DLHPLLQFKG	GKAGIAIHTY	RHTQSGFPPI	NALLNLARFY
90	100	110	120	130	140	150	160
AQTVAVLLAS	SAAAVPMIDI	HGLDYSVGT	ATFFLLTGGH	TLPADQGTTE	RDFDVSSSSA	ILLRQDAPYW	CPERFLSTAS
170	180	190	200	210			
FQWEQCTWFI	WLHSLGDHRL	KRLSAQGAPA	STTVEHVLVR	WKKL			

Spot number 6Wu

related to YPT-1 GTP-binding protein ypt1 [*Piriformospora indica* DSM 11827]

10	20	30	40	50	60	70	80
MAGDARPKVE	ETFEPLHLLA	TLTMHASEYD	YLFKLLIGD	SGVGKSCLLL	RFADDTYTES	YISTIGVDFK	IRTIELEGKT
90	100	110	120	130	140	150	160
VKLQIWDTAG	QERFRTITSS	YYRGAHGIIV	VYDVTDTDTF	TNVKQWLQEI	DRYASEGVNK	LLVGNKSDLT	SKKVVEYTVA
170	180	190	200	210	220	230	
KEFADQLGIP	FLETSAKNAT	NVEQAFLTMA	KQIKDKMGAS	GTGGPTSKTN	TITPGTGITT	NTSSGCC	

Spot number 8Wu

hypothetical protein PIIN\_10216 [*Piriformospora indica* DSM 11827]

10	20	30	40	50	60	70	80
MDIIVTTFSS	LSLGTILLLC	AIPWVPVIKI	AITLSFIVFP	VMLFLRHLRN	HPLSEGSTAY	LWSGLWILSY	TRPTTRIHKY
90	100	110	120	130	140	150	160
LQSNQVVRYS	LSRLPTEIWS	KILTFALDMP	EIMDSICTSE	IIWEEPPDA	HQTTNRASIP	IHRRT <b>ESSAR</b>	<b>DTHATKARVE</b>
170	180	190	200	210	220	230	
PSLLGVEQHS	AALSDRVVLR	PSGRLPHGQA	ARTDIGR <b>HSY</b>	<b>ATKLRV</b> LNE	LDEGSRPSSL	AYPCHL	

Spot number 9Wu

predicted protein [*Laccaria bicolor* S238N-H82]

10	20	30	40	50	60	70	80
MLPHQLLDQ	LPLVCEQDPC	ISVEYAWINQ	PSNNPLCQLS	TLKQVTFDLP	FKEWLIITPG	HAKLLQGIMS	DVGQATAEDG
90	100	110	120	130	140	150	160
HQWER <b>LMEGE</b>	<b>KEVDIARQOS</b>	LISLAKPVSM	ILLVNNQLTK	ITHLMMAFIF	<b>NFSVSG</b> TLW	<b>KETNQSKSCI</b>	VKVKVAF

Spot number 11Wu

hypothetical protein PIIN\_02973 [*Piriformospora indica* DSM 11827]

10	20	30	40	50	60	70	80
MVESAKRRWS	YRTFVDTAQV	LFGKAQVPQD	CMLAIQQTVE	LGRWKQNELD	KECLSYRTLA	RCALHLERLL	DQLQLALLH
90	100	110	120	130	140	150	160
SSVLPAEN <b>NPT</b>	TKVEKSDFLQ	LYTHFNEDDM	LYQGTLEILM	QSPALTLALG	GHSWSGGESY	ISLDDVYPPL	APSSLLISSK
170	180	190	200	210	220	230	240
SQSQELESKT	LPSGESPVAL	PYL TALLFLH	AVVSGFSPNV	PEIMETTQRI	LVLILRAP <b>Q</b> N	<b>ITLLQRLPAT</b>	<b>ALVARLSEDK</b>
250	260	270	280				
<b>HAKELFDDLL</b>	LRLEDPALVQ	TARLLSGLGE	PAESSHL				

Spot number 17Wu/17Fc

hypothetical protein PIIN\_05768 [*Piriformospora indica* DSM 11827]

10	20	30	40	50	60	70	80
MSKSTLVPAR	<b>NAIHGT</b> GRAK	LVFGTTASF	AELSYTYPLK	LLSPRQTTAT	NIERLAILY <b>N</b>	<b>LSYGG</b> LIGG	DQLALTLELG
90	100	110	120	130	140	150	160
SDVKLLFLTQ	GSTKIFPSRA	RPRLATGRAE	VGDTRQRLSA	TIGSGACLVM	LPDPVTPFSH	SSYSQVQIFR	LAAPT KD TAG
170	180	190	200	210	220	230	240
GSIVLLDWFT	SGRMSR <b>GEEW</b>	<b>QFDRY</b> RSANE	IWIGNERVAS	DVLLLEQPPS	SSSVDETAKK	INRLRDSLAP	YACYATLLLF
250	260	270	280	290	300	310	320
GPATHALSKE	<b>FAQRYD</b> GLSQ	MQRKVPEDLI	USYSPLYEKT	SINNGKRNSG	QKETGVGAIV	RVAAK <b>D</b> TESV	<b>RQWLRE</b> SLRA
330	340						
GLEAQIGRNA	YSKAFV						



Spot number 18Wu/18Fc

u3 small nucleolar RNA-associated protein 11 [*Coprinopsis cinerea* okayama7#130]

10	20	30	40	50	60	70	80
MTSSLRNSLH	RRNHKERSQL	AHRTKLGFL	KHKDYVKRAR	DYHSKQDRLN	RLKQKAAERN	<b>KDEFYFSMKR</b>	EKTRAGVHIK
90	100	110	120	130	140	150	160
DRGNAAIPTD	IVKVLKTQDE	NYVRTMRLSN	LKKIDRLKRQ	LTEMADLFKS	SLGGEDLEED	EYEVLQEAGI	LPPSGKKRGR
170	180	190	200	210	220	230	240
SKSKHLVFAE	SLEEAQTLGQ	KAKTAAEPDH	SSPPQEPEPT	PEDLGWKTRD	NKKRRRTRQ	TIEELEDVDG	EWEDEDLTT
250	260	270	280	290	300	310	320
HDSGSQSSTE	KRTRLLKEIS	ARLVRDRQLR	YTQ <b>REFEMQR</b>	LLMGKGAACK	IAGVEKFGED	DSEDEDAL	DARGGRPLKK
330	340	350					
SKVVDEATYK	PRVYKWKLER	KR					

Spot number 19Wu/19Fc

related to RTM1 protein [*Piriformospora indica* DSM 11827]

10	20	30	40	50	60	70	80
<b>MERSYFPYKA</b>	SKPAAVLFAV	LYSVSVAAHV	FQMIKLRAFY	MSVLIVGLLV	EVLGYVTRKL	AIDDDPTLWS	FSTSQCILV
90	100	110	120	130	140	150	160
APAFLAASAY	MIVGR <b>MMAYV</b>	<b>GPGASVISHR</b>	<b>LITKVFVI</b> VD	ILCLITQAAG	IAMFVTNVDK	ADRTVVLGR	NILMTGLALQ
170	180	190	200	210	220	230	240
IISYLIFVVI	TIIFDIRAQR	MKGTQLKKLR	PLFWASYSVA	FLIIGRSIYR	AIEFGTVDFK	RRTQGYLYTH	EWPFYVLDAV
250	260	270	280	290	300		
PILAAAVILN	VIHPSSYLP	KKGLRMDGTI	EVPARHWSK	SKSTKEHELE	<b>NATP</b>		

Spot number 21Wu/21Fc

probable ENO1-enolase I (2-phosphoglycerate dehydratase) [*Piriformospora indica* DSM 11827]

10	20	30	40	50	60	70	80
MSITKVHAR <b>Q</b>	<b>IFDSRGNPTV</b>	<b>EVDLYTAKGR</b>	<b>FRAAVPSGAS</b>	<b>TGVHEAVELR</b>	DGDKKSYVGK	<b>GVLNAVKNVN</b>	<b>ETIAPALIDS</b>
90	100	110	120	130	140	150	160
GLSVTQQKDI	DALLIKLDGT	PNKGKLGANA	ILGVSIAVAE	AGAAESGLPL	YAYLAKLAGH	PEGGKMTMPC	PAFNVIINGGS
170	180	190	200	210	220	230	240
HAGNGLAFQE	FMLLPTGATS	FTEAMKIGTE	TYHTLKKVIQ	ARYGLDATNV	GDEGGFAPNV	AGAEESLELL	SEAIKKAGYE
250	260	270	280	290	300	310	320
GKIKIGLDVA	SSEFYKDGKY	DLDFKNANS	PTKWITGKEL	GDFYNKMIK	YPIVSIEDPF	DQDDWEAWSS	<b>FTNGTKVQVV</b>
330	340	350	360	370	380	390	400
<b>GDDLTVTNP</b> E	<b>RIQTAIGKKA</b>	CNGLLLKINQ	<b>IGTISESIQA</b>	<b>AQLAQSDG</b> WG	<b>VNVSHRS</b> GET	ENTVIADLVV	ALGGCQIKTG
410	420						
AP&RSERVAK							

Spot number 5Wd/5M

G protein alpha-subunit [*Laccaria bicolor* S238N-H82]

10	20	30	40	50	60	70
MLEYDQMLYE	DESVDQMEE	LSLFDLVCNS	RWFIKTSIIL	FFNKIDLLTK	KTPPLTTGGL	LPRLCRW

Spot number 12Wd/12M

predicted protein [*Laccaria bicolor* S238N-H82]

10	20	30	40	50	60	70	80
MLSFIVLCGC	IAYAVAQSTT	ARILIYSATA	GFRHDSIPTA	IEALKQGGNP	INVQFDATED	HSQFTTAILS	QYDALLFLST
TGEVLDDPGK	AAFRTYLNMG	GNFIGVHAAS	DCLRNTSSYR	SELGTLFDYH	PPLQNAIVNV	VGPSHPSTRK	<u>LPAANKVQDE</u>
<u>MYNFISDPRA</u>	IGATVILSAD	ESSYVDNGTR	KFDQGTPHPT	AMFQERGAGA	EAGGTRGRSF	YTSLGHLNET	WKDDLFSHI
IGGVSWALQG	<u>NTTRAFN</u> ASA	LVGNSQQSTT	SRVGAASTAA	GPRESAHTSR	SVVSRPAWLL	LGMGVLQNLF	LCNDI

Spot number 13Wd/13Mu

predicted protein [*Laccaria bicolor* S238N-H82]

10	20	30	40	50	60	70	80
NTSSLRNSIH	RRNHKERSQL	AHRAKFCVLE	KHADYVKRAR	DYHSKQDRLT	RFKQKAAEPN	<u>KDEFYFSMKR</u>	EKTGGGVHVK
DRGNVALPSD	IVKVLKTODE	NYVRTMRSAG	LKKIDKIKSQ	LTEMADLLKP	TGAASDDEVE	EELDDEEYQT	LLDAGMLSQR
PGGRKRPPGH	IIFAESSEEA	KKLGSKRKRT	IEEPSHPKEV	QQDLGWASTA	SKKKS IKEVV	ESSPQDDEDA	RETQALARES
KKRLLTELSA	RLGRDQSLRY	AQREFEHQRL	MMCGGCRKKI	RGVEKVEGEN	DEDEEEDQDE	IDARKGRRRK	SSQKVDETTY
KPRVYKWKLE	RKR						

Spot number 20Wd/20Mu

hypothetical protein PIIN\_01661 [*Piriformospora indica* DSM 11827]

10	20	30	40	50	60	70	80
MNTPQRRKRV	GSPAEGDMSG	LSAGIGVELS	MEDKERLIEN	LDIEVTNHRH	RFEAFLEQLL	EGFSLRHGME	ISRIPKAIRN
90	100	110	120	130	140	150	160
MKMKDFDAFG	GNVQRCVQAM	ARQRVAEADG	DANAKRKRKQ	AAIQEEIEER	ASKTPRVAPP	SPVKTSKPSS	QVPNSSRAKG
170	180	190	200	210	220	230	240
LFPKTPTRNM	NNVNPYTKTAL	HGSARKVMPS	PSKRAVSPTK	PQNMPTSSTS	SFKPASTTFN	PVLPPKTPTY	PRRVARADEA
250	260	270	280	290	300	310	320
VMSLNGTPLK	FPSAFMFPRG	VAPIVDEGEE	SEHDSHAKST	GVGPAFLVRR	DPSTVSMGSS	SASTAVSSTG	TLITISTSKG
330	340	350	360	370			
QTVQFDPLMA	SPGSLDRIPD	LTESAKKQVR	EDTARIVQAL	HKWRL			

Spot number 22Wd/22Mu

hypothetical protein PIIN\_01521 [*Piriformospora indica* DSM 11827]

10	20	30	40	50	60	70	80
MASVIPSVTP	NARSTLQREY	FTSELFVNPA	RSDIEDLLAS	FEEAVEQPLK	PFDIFKTVWS	QEGWKTCLY	IWEDTARDQY
90	100	110	120	130	140	150	160
LQTMLRFLFLE	RVKDSSEFAR	QLGAVFGLYT	FFQQQATIKS	LYSVSSIEIT	IDKLEYLCSL	CKESPVAHQF	YVVFILRYFL
170	180	190	200	210	220	230	240
ERDIFHILPH	SSLQPYNPTN	LPASFVVSRE	SSSGADAQSH	GGNSKKTTRG	GRTKAERDRY	GREQWAQLGS	LVRLQRQRQK
250	260	270	280	290	300	310	320
GEVDDVEIAV	GAQPHSDANK	NTSGSTPFPD	KDSSAVVYRE	AKSRULEVLP	KEVEREAEQR	ALQRLKTLAS	SVESDVHSGL
330	340	350	360	370	380	390	400
KKQRLMETDD	SMMEMESVTA	AOKDNORORE	EGDDEGGMVS	QAHKVSHASD	GVARLENMIK	NGHGVLRNQW	ANE

Spot number 23Wd/23M

hypothetical protein PIIN\_03309 [*Piriformospora indica* DSM 11827]

10	20	30	40	50	60	70	80
MFYCHPEHQF	NAANLLWELI	EQDERALQEV	KEEEERLENE	REGILAHLCV	LANDTQVLCQ	LAEVALPNIK	NIIDALKPEI
90	100	110	120	130	140	150	160
SALETKREDG	HFSNYGGWLE	KYKNYIKVTV	GFMEEQHMK	TOOLVREYVE	PESMARLKLD	HIDGLLKETA	DRIQATSIRL
170	180	190	200	210	220	230	240
QTKRLKLSKT	PFSRLTDENW	RLIFGYASIS	FHPHHAGEQV	CDRSISTSIH	ALTRVCHRMY	KVIYQSSKLW	RRVYLNVEGL
250	260	270	280	290	300	310	320
KNDSSRKLLN	LILSKAAEYV	GHILDALPTP	YELAIRSLLM	TNTRLLYHPR	SLDTLEVVEA	TNVELVLETG	RNLPNLRLLK
330	340	350	360	370	380	390	400
LQANTSIITPC	TEFYDYTSKT	STIDLAGGSF	HLPRRVPRLQ	PMDAHSIRGT	LNSILSVFSP	RVVFTQLSEI	TLRFPPPEPAN
410	420	430	440	450	460	470	480
MPDLATWCSF	LSSSKASTVT	SLTLYPMENA	KILSHYVTAL	HNLARLRVHG	SSVDFLLKEL	TWQVEDERSK	VLTFLSVLEI
490	500	510	520	530			
HDDYDGRGSPV	VEFYOSKLAS	SYRTLRTVRF	ANCPNIPOEI	ROIFIDN			

