

Supplemental material

(a)

```
.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130
1  MIVTVSSR--RPSPPVQNL LLHPLSKSSL QTFHFP--FS LMRLIV--C PASVVRGLLF LBDTPGHLSL LSGKPNPDTF PFTSFTEFAR SPINSKEDAI LTTECKELAQ GLQYGFAGE KQLLSWIEGL
2  NSQIFDPTS-----ISHDAP VRRLKRYNT DFLSDIAKRF KPSAIRSLHF LHPHGLISL LAGKPNPSTF PFTSISEFAR SEVHBEETIT INLSGADLAQ GLQYGDYAGI KQLLDWIYGL
3  MIOISDTN-----SHDAP VRRLKRYNT NFLSNIAKRF KPSAIRSLHF LHPHGLISL LAGKPNPSTF PFTSISEFAR SEGHSDBEIT INLSGADLAQ GLQYGDYAGI KQLLDWIYGL
4  MKKSTDSGE INGS-----OPLTSSDG VKVLEDAFYT SFLSDIAKRF KPSAIRSLHF LBSRPLISF LAGKPNATTF PFTSISEFAR DPLNPDRTDA ITTDCPALAQ GLQYGDYAGI HGLLDWIYGL
5  MPKEANG-----NGISD VKVLEDAFYT PFLSEANRF KPSAIRSLHF LBNTPGLISL LAGKPNASCF PFKSISEKTR SEITDESADVI LEVDKADLRD GLQYGMACD SSIIVNWIEGL
```

```
.....140.....150.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260
1  QEPFHGRKRN EGWRVSIIGCG SQDLIKAVTI AVVNPQDSVL LEPHYVAFV FVVPHTPLLN MGCVWVGLI YIFAA-----I YRKLASROAK ACGFVYSECK DVDIRQRYCC NPTGTMATLE RRKEVILLAR
2  QBINHGRKRN EGWRVSIIGCG SQDLIKAVTI AVVNPQDSVL VESFYVAGVI PMFSLHCOO I--EVETDSO GIRSSLRMTI LEQWBEKPKR PKVLYTVF-----YCC NPTGTMATLE RRKEVILLAR
3  QBINHGRKRN EGWRVSIIGCG SQDLIKAVTI AVVNPQDSVL VESFYVAGVI PMFSLHCOO I--EVETDSR GIRSSLRMTI LEQWBEKPKR PKVLYTVF-----YCC NPTGTMATLE RRKEVILLAR
4  QEAQHGRKRG EGWRVSVGAG SQDLIKAVA AVVNPQDSVL VESFYVAGVI PMFOSLNCOO I--EVETDAH GICASSLRSTI LENWESGKPK PKVLYSVF-----YCC NPTGTMATLE RRKEVILLAR
5  QEPFHGRKRG EGWRVSVGCG SQDLIKAVTI AVVNPQDSVL VESFYVAGVI HILLE--HCL V--EVSADSO GVNPAISRSI YENWEAKPKR PKVLYTVF-----FCS NPTGTMATLE RRKEVILLAR
```

```
.....270.....280.....290.....300.....310.....320.....330.....340.....350.....360.....370.....380.....390
1  EHNFIILEGM DPYFYLKYG TAPRPSYFA LELEPEVGR VLRFDLSLKV LSAGIRIGVF SGPEPILVAI DQHTSFLNLO TFSLTQIHHI KLLNSWGYDC BATHVNVAA FYREKRDIFF RAMRHLISGL
2  EHNFIILEGM DPYFYLKYG TAPRPSYFA LELEPEVGR VLRFDLSLKV LSAGIRIGVF SGPEPILVAI DQHTSFLNLO TFSLTQIHHI KLLNSWGYDC BATHVNVAA FYREKRDIFF RAMRHLISGL
3  EHNFIILEGM DPYFYLKYG TAPRPSYFA LELEPEVGR VLRFDLSLKV LSAGIRIGVF SGPEPILVAI DQHTSFLNLO TFSLTQIHHI KLLNSWGYDC BATHVNVAA FYREKRDIFF RAMRHLISGL
4  EHNFIILEGM DPYFYLKYG TAPRPSYFA LELEPEVGR VLRFDLSLKV LSAGIRIGVF SGPEPILVAI DQHTSFLNLO TFSLTQIHHI KLLNSWGYDC BATHVNVAA FYREKRDIFF RAMRHLISGL
5  EHNFIILEGM DPYFYLKYG TAPRPSYFA LELEPEVGR VLRFDLSLKV LSAGIRIGVF SGPEPILVAI DQHTSFLNLO TFSLTQIHHI KLLNSWGYDC BATHVNVAA FYREKRDIFF RAMRHLISGL
```

```
.....400.....410.....420.....430.....440.....450.....460.....470.....480.....
1  VEWSPEVAGM EFWFKLLING EPGEE--D SYVILSRGI ERGVIALPGA GEPNRSKRTA YVRSFSAAP EPEVDEAIRR LRDAILDARA TNKK---
2  AEWSPEVAGM EFWFKLLIND NKAADDDSGD SEVWIKTKAF ERGVIALPGT VFLPNRPTPE YVRASFSLTG EDVDRAIOR IRDAILDARA TAVAIPIA
3  AEWSPEVAGM EFWFKLLIND NKAADDDSGD SEVWIKTKAF ERGVIALPGT VFLPNRPTPE YVRASFSLTG EDVDRAIOR IRDAILDARA SVNGISA
4  AEWSPEVAGM EFWFKLLIND QDGA---GD SBSIIRTKAL ERGVIALPGT VFLPNRPTPE YVRASFSLTG EPEVDEAIRR LRDAILDARA AKLS-TV
5  AEWSPEVAGM EFWFKLLIND TGSPE--D SEVWIKTKAF ERGVIALPGT VEPNRSKRTA YVRASFSLTD EQOIDEAIRR LRDAILDARA ASTAGKA
```

(b)

```
.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130
1  M--SSS--EAT LQAEVDRLRN EVDVLRPEQL GRSYKLSIGN YLLRRLAQLG IIVRQSMFGV PGDFNLGFLV RVFFVYQDLV BEHEFDWVG NWCYCLGSLY LLYAADRTDR CNELNAYAA DGYARVKE--S
2  MATTS--AES LQAEVNRIRI ELDQKVED-- GSEYDYGD YLLRRLAQLG VT---SMFGV PGDFNLGFLV -----DLV EDHFDWVG N----- CNELNAYAA DGYARVKE--S
3  MASOT--VAA LQAEVNRIRI ELDQKVED-- GSEYDYGD YLLRRLAQLG AN---SMFGV PGDFNLGFLV -----DLV EDHFDWVG N----- CNELNAYAA DGYARVKE--S
4  M--SNE--EAT LQAEVDRLRN EVDVLRPEQL GRSYKLSIGN YLLRRLAQLG IIVRQSMFGV PGDFNLGFLV -----DLV EDHFDWVG N----- CNELNAYAA DGYARVKE--S
5  M--SSHPPASV LQAEVDRLRI QLFHQAPE-- GVNYSIGN YLLRRLAQLG VT---SMFGV PGDFNLGFLV -----DLV EDHFDWVG N----- CNELNAYAA DGYARVKE--S
```

```
.....140.....150.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260
1  IGVVLTTFGV GELSAINGIA GAFSEMVFVL HIVGVPESTAC QKAKFLHHT LGDGRVYVIR HVT--EHRHD SLDLDTHTMR LQNNRIR-- COARFVVL VFNVLVAKI SSAPRTPIN RNPANRDE
2  IGVVLTTFGV GELSAINGIA GAFSEMVFVL HIVGVPESTAC QKAKFLHHT LGDGRVYVIR HVT--EHRHD SLDLDTHTMR LQNNRIR-- COARFVVL VFNVLVAKI SSAPRTPIN RNPANRDE
3  IGVVLTTFGV GELSAINGIA GAFSEMVFVL HIVGVPESTAC QKAKFLHHT LGDGRVYVIR HVT--EHRHD SLDLDTHTMR LQNNRIR-- COARFVVL VFNVLVAKI SSAPRTPIN RNPANRDE
4  IGVVLTTFGV GELSAINGIA GAFSEMVFVL HIVGVPESTAC QKAKFLHHT LGDGRVYVIR HVT--EHRHD SLDLDTHTMR LQNNRIR-- COARFVVL VFNVLVAKI SSAPRTPIN RNPANRDE
5  IGVVLTTFGV GELSAINGIA GAFSEMVFVL HIVGVPESTAC QKAKFLHHT LGDGRVYVIR HVT--EHRHD SLDLDTHTMR LQNNRIR-- COARFVVL VFNVLVAKI SSAPRTPIN RNPANRDE
```

```
.....270.....280.....290.....300.....310.....320.....330.....340.....350.....360.....370.....380.....390
1  BAVVLDLHNR QVREAGDGVV VIVDACVIRH CVREAVDQL RKTGFVYAA PMGRTAVDEE YERYGGIYVC SITHPEIRK VESAKLIHSI GSKLSDFNTC NFSYKPTLR TIE----- YAVVAGV
2  BAVVLDLHNR QVREAGDGVV VIVDACVIRH CVREAVDQL RKTGFVYAA PMGRTAVDEE YERYGGIYVC SITHPEIRK VESAKLIHSI GSKLSDFNTC NFSYKPTLR TIE----- YAVVAGV
3  BAVVLDLHNR QVREAGDGVV VIVDACVIRH CVREAVDQL RKTGFVYAA PMGRTAVDEE YERYGGIYVC SITHPEIRK VESAKLIHSI GSKLSDFNTC NFSYKPTLR TIE----- YAVVAGV
4  BAVVLDLHNR QVREAGDGVV VIVDACVIRH CVREAVDQL RKTGFVYAA PMGRTAVDEE YERYGGIYVC SITHPEIRK VESAKLIHSI GSKLSDFNTC NFSYKPTLR TIE----- YAVVAGV
5  BAVVLDLHNR QVREAGDGVV VIVDACVIRH CVREAVDQL RKTGFVYAA PMGRTAVDEE YERYGGIYVC SITHPEIRK VESAKLIHSI GSKLSDFNTC NFSYKPTLR TIE----- YAVVAGV
```

```
.....400.....410.....420.....430.....440.....450.....460.....470.....480.....490.....500.....510.....520
1  MKQLLEKITE RLHFFNAEAR HIEVREAVNT VNEGDQKHT HSEWFRVGD FFKPKDVIIT ERGTSFGIL EVPLPESVL VQQLWGSIG WVGSTLGA LAARDVGLGR TILFVGDGSL QLTVOELSM
2  MKQLLEKITE RLHFFNAEAR HIEVREAVNT VNEGDQKHT HSEWFRVGD FFKPKDVIIT ERGTSFGIL EVPLPESVL VQQLWGSIG WVGSTLGA LAARDVGLGR TILFVGDGSL QLTVOELSM
3  MKQLLEKITE RLHFFNAEAR HIEVREAVNT VNEGDQKHT HSEWFRVGD FFKPKDVIIT ERGTSFGIL EVPLPESVL VQQLWGSIG WVGSTLGA LAARDVGLGR TILFVGDGSL QLTVOELSM
4  MKQLLEKITE RLHFFNAEAR HIEVREAVNT VNEGDQKHT HSEWFRVGD FFKPKDVIIT ERGTSFGIL EVPLPESVL VQQLWGSIG WVGSTLGA LAARDVGLGR TILFVGDGSL QLTVOELSM
5  MKQLLEKITE RLHFFNAEAR HIEVREAVNT VNEGDQKHT HSEWFRVGD FFKPKDVIIT ERGTSFGIL EVPLPESVL VQQLWGSIG WVGSTLGA LAARDVGLGR TILFVGDGSL QLTVOELSM
```

```
.....530.....540.....550.....560.....570.....580.....590.....600.....610.....620.....630
1  IRKGLKPIIE VLNNSGYTIE RLHIGRRRY NDLSNWVIA LRSVGDGDE RUSAFVNT KGLSKLLD AIFARAKICQ LVEVMMDKFD APRALQVQAE LSA-----
2  IRKGLKPIIE VLNNSGYTIE RLHIGRRRY NDLSNWVIA LRSVGDGDE RUSAFVNT KGLSKLLD AIFARAKICQ LVEVMMDKFD APRALQVQAE LSA-----
3  IRKGLKPIIE VLNNSGYTIE RLHIGRRRY NDLSNWVIA LRSVGDGDE RUSAFVNT KGLSKLLD AIFARAKICQ LVEVMMDKFD APRALQVQAE LSA-----
4  IRKGLKPIIE VLNNSGYTIE RLHIGRRRY NDLSNWVIA LRSVGDGDE RUSAFVNT KGLSKLLD AIFARAKICQ LVEVMMDKFD APRALQVQAE LSA-----
5  IRKGLKPIIE VLNNSGYTIE RLHIGRRRY NDLSNWVIA LRSVGDGDE RUSAFVNT KGLSKLLD AIFARAKICQ LVEVMMDKFD APRALQVQAE LSA-----
```

(c)

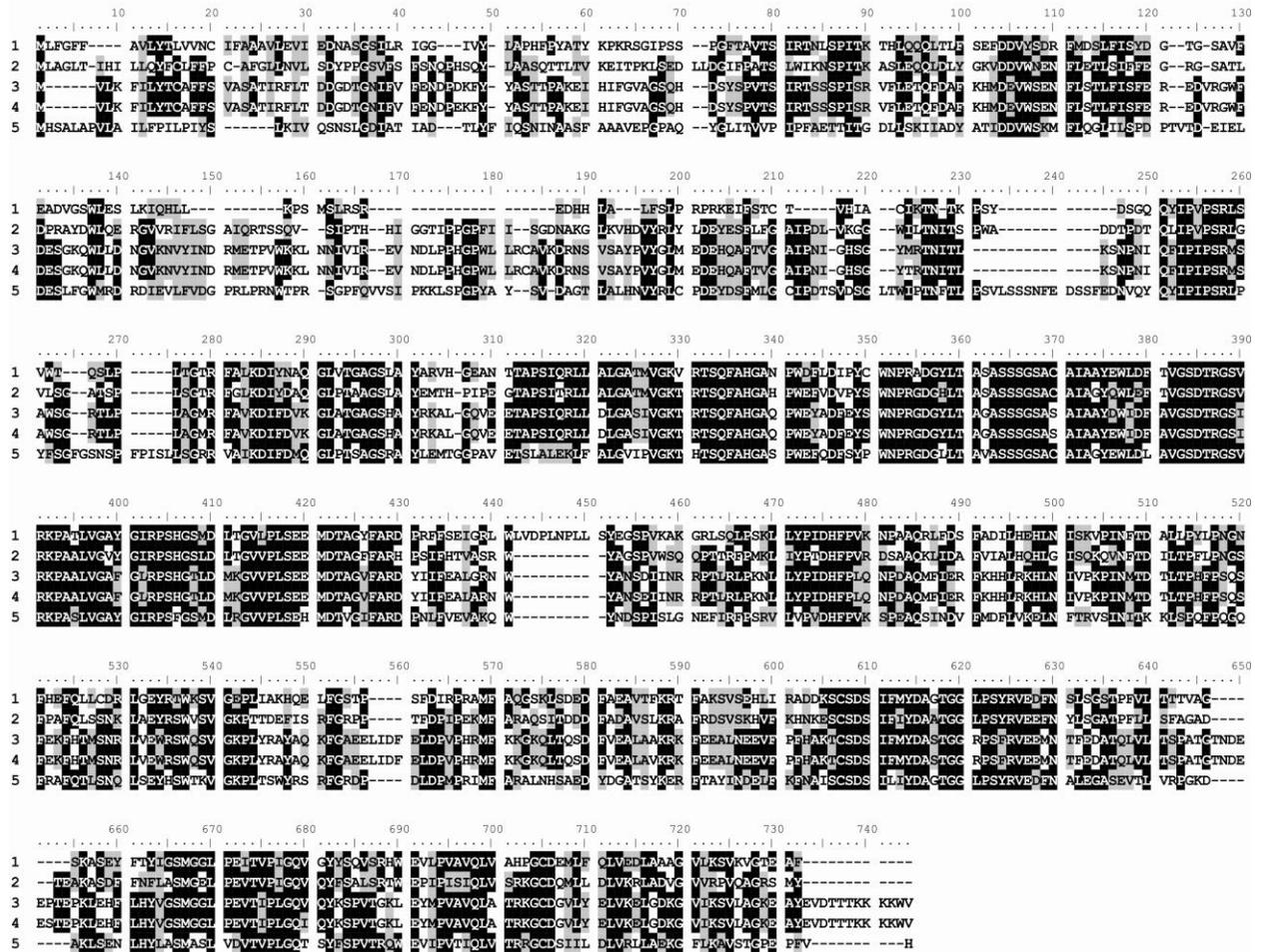


Fig. S1: Alignments for identification of IAA biosynthesis genes from *T. vaccinum*. Conceptually translated sequences for *tam1*, *ipd1* and *iah1* were aligned with four most similar sequences in BLASTp using MAFFT and BioEdit alignments. *Tam1* (1: KP096350) was aligned to sequences 2 (KDR75974 of *Galerina marginata*), 3 (KDQ24236 of *Pleurotus ostreatus*), 4 (KDR77824 of *Galerina marginata*) and 5 (XP_007868862 of *Gloeophyllum trabeum*) (a), *Ipd1* (1: KP096351) was aligned to 2 (XP_007845706 of *Moniliophthora roreri*), 3 (KDQ25837 of *Pleurotus ostreatus*), 4 (KDR82740 of *Galerina marginata*) and 5 (XP_001875889 of *Laccaria bicolor*) (b); *Iah1* (1: KP096352) was similar to 2 (KDR84180 of *Galerina marginata*), 3 (XP_007329104 of *Agaricus bisporus*), 4 (XP_006456935 of *Agaricus bisporus*) and 5 (XP_007846638 of *Moniliophthora roreri*) (c).

Tab. S1: Orthologs in mycorrhizal, plant-pathogenic/parasitic as well as saprobic fungi for the enzymes Tam1, Ipd1, Ald1 and Iah1 suggested to be involved in IAA production in *T. vaccinum* (protein-IDs, JGI <http://genome.jgi-psf.org>, in brackets).

Protein	Mycorrhizal	Plant-pathogenic/parasitic	Saprobic
Tam1	<i>Laccaria bicolor</i> (191053); <i>Paxillus involutus</i> ATCC 200175 (103787); <i>Tricholoma matsutake</i> 945 (1422813); <i>Suillus luteus</i> UH-Slu-Lm8-n1 (801906)	<i>Armillaria mellea</i> (7757)	<i>Heterobasidion annosum</i> (458781); <i>Schizophyllum commune</i> H4-8 (2616666);
Ipd1	<i>Laccaria bicolor</i> (188370); <i>Paxillus involutus</i> ATCC 200175 (175618); <i>Tricholoma matsutake</i> 945 (1425307); <i>Suillus luteus</i> UH-Slu-Lm8-n1 (94806)	<i>Armillaria mellea</i> (6628)	<i>Heterobasidion annosum</i> (440059); <i>Schizophyllum commune</i> H4-8 (2626643); <i>Schizophyllum commune</i> H4-8 (2637783)
Ald1	<i>Laccaria bicolor</i> (256254); <i>Laccaria bicolor</i> (191009); <i>Paxillus involutus</i> ATCC 200175 (182543); <i>Paxillus involutus</i> ATCC 200175 (76843); <i>Tricholoma matsutake</i> 945 (1284147); <i>Tricholoma matsutake</i> 945 (1444458); <i>Tricholoma matsutake</i> 945 (1295949); <i>Tricholoma matsutake</i> 945 (1308658); <i>Suillus luteus</i> UH-Slu-Lm8-n1 (803802); <i>Suillus luteus</i> UH-Slu-Lm8-n1 (807535); <i>Suillus luteus</i> UH-Slu-Lm8-n1 (807087)	<i>Armillaria mellea</i> (9343); <i>Armillaria mellea</i> (5490); <i>Armillaria mellea</i> (3731); <i>Armillaria mellea</i> (13567)	<i>Heterobasidion annosum</i> (454399); <i>Schizophyllum commune</i> H4-8 (1156481); <i>Schizophyllum commune</i> H4-8 (2606953)
Iah1	<i>Tricholoma matsutake</i> 945 (290237)		

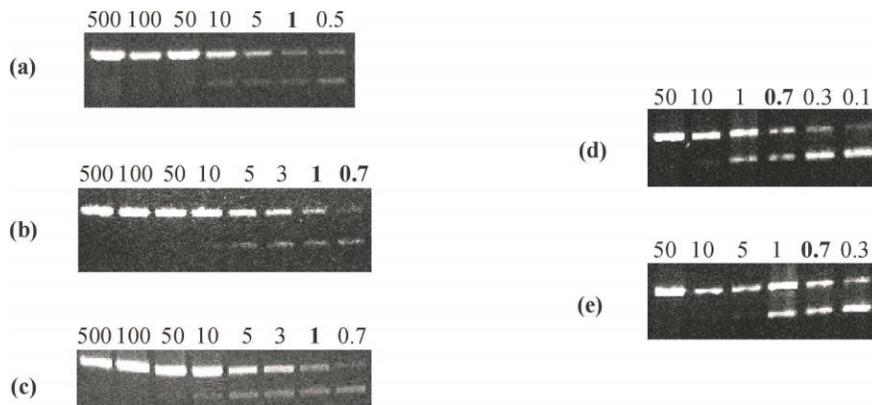


Fig. S2: Expression of *ald1* in *T. vaccinum* mycorrhiza. Competitive PCR was used to estimate the relative amount of the transcript using 1 ng cDNA for the control with mycelium from pure culture (a), and 0.02 ng fungal cDNA from mycorrhizal tissues Hartig' net (b) and hyphal mantle (c) from 3 weeks and (d) 3 months co-cultures with the compatible host, spruce and (e) the low compatible host, pine; the bold numbers indicate bands of the same intensity with the competitor. 1 pg *ald1* transcript was found in the pure culture, making it 10^{-3} of cDNA. In Hartig' net 0.7 to 1 pg was found making it 1:20 of all cDNA and thus approximately 40-fold more compared to pure culture. For mantle, 50-fold and in compatible interaction (45-fold) or for low compatibility (30-fold) can be calculated.

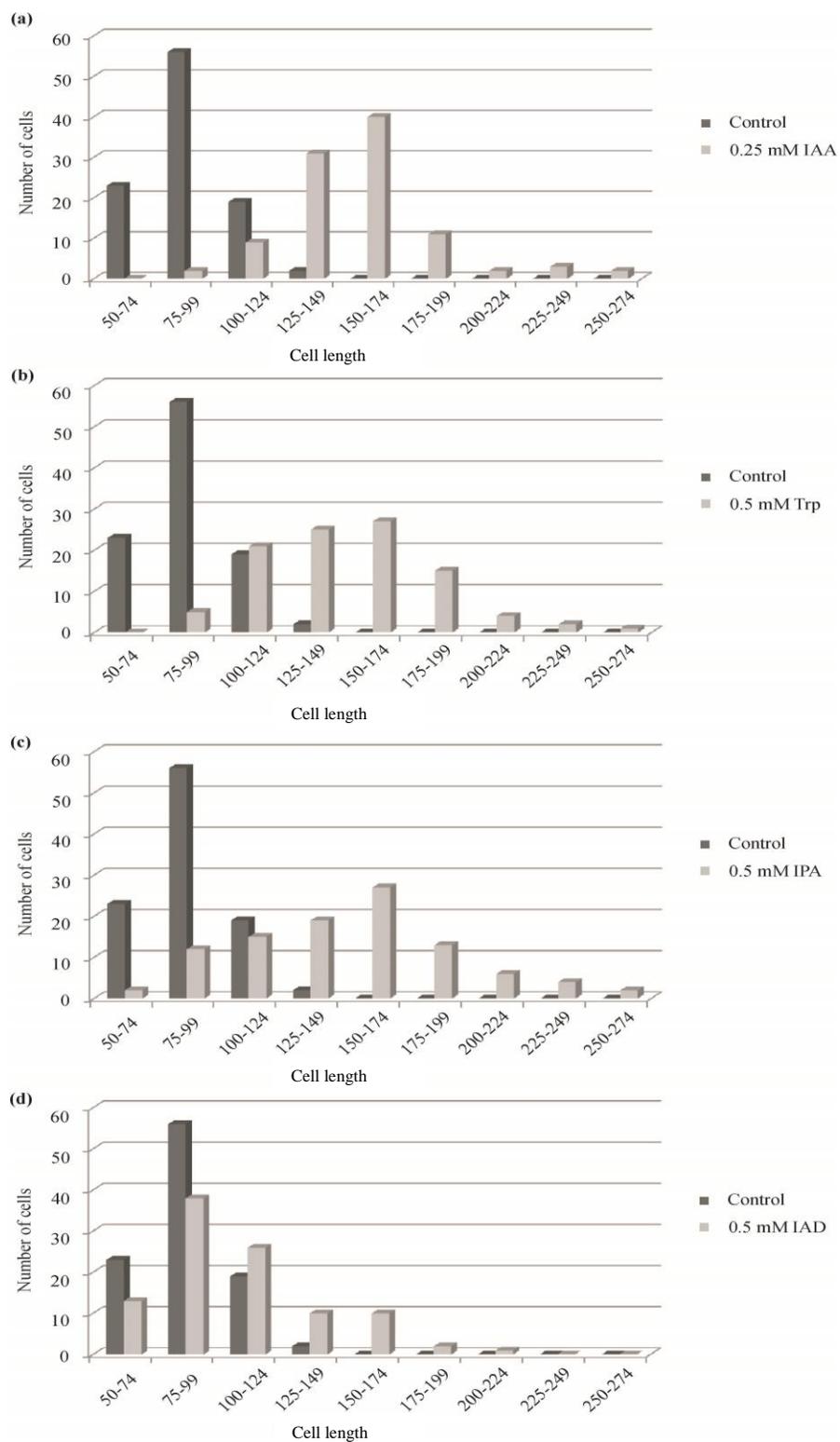


Fig. S3: Influence of IAA and precursors on cell length distribution. MMNb control was compared to 0.25 mM IAA (a), 0.5 mM Trp (b), 0.5 mM IPA (c) and 0.5 mM IAD (d) treatments.

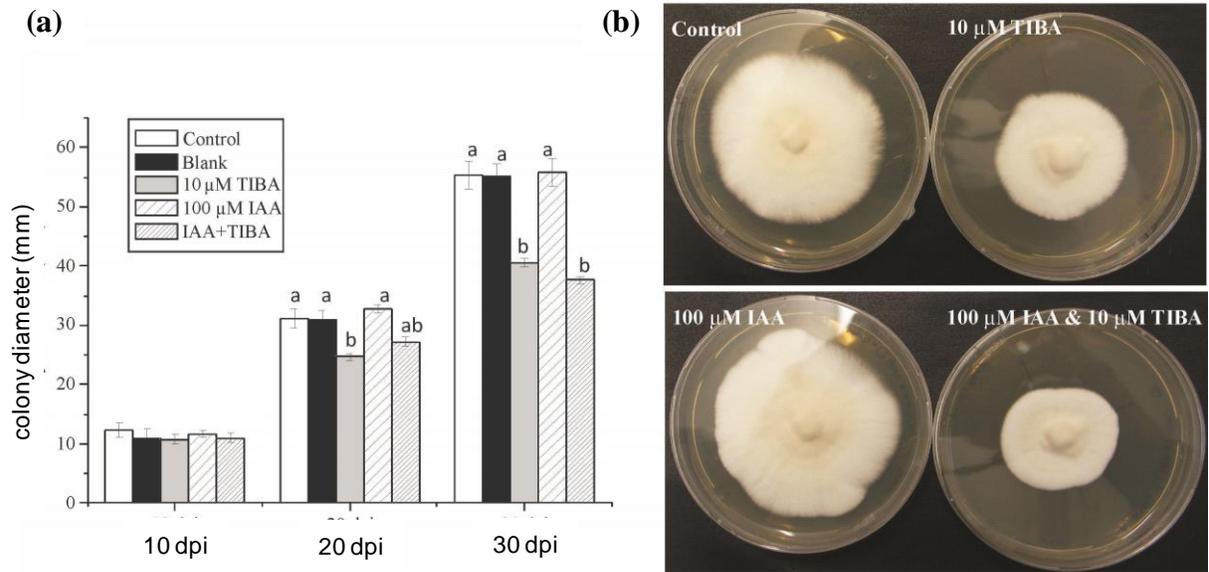


Fig. S4: Growth of *T. vaccinum* after 4-week application of IAA with or without addition of TIBA blocking IAA uptake. Fungal growth was measured as colony diameter, bars denote standard error, letters indicate significant differences (a); representative plate cultures (b).

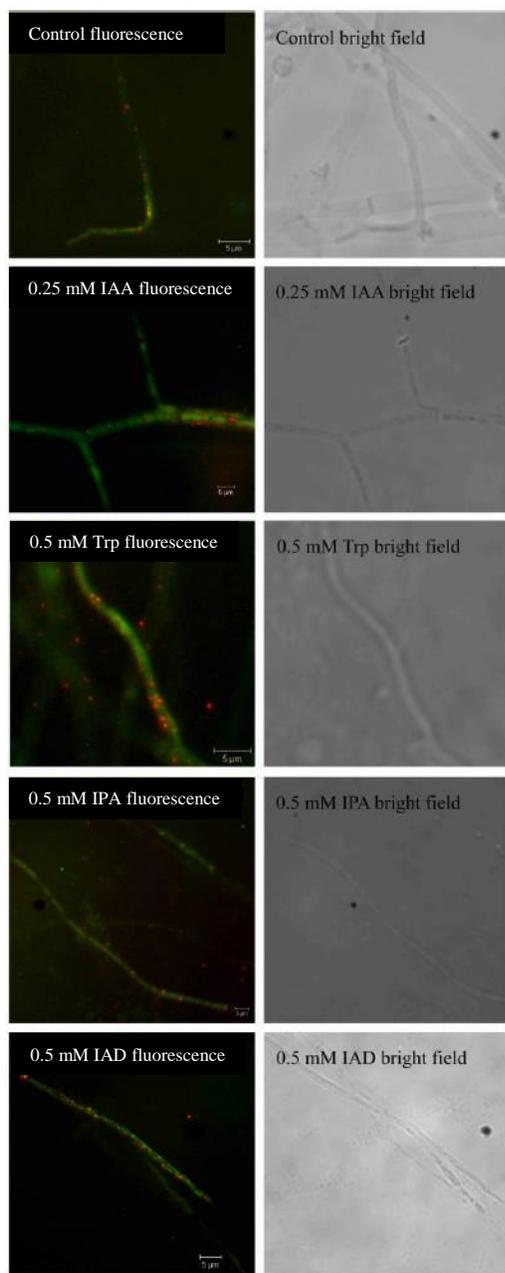


Fig. S5: Cytoskeleton of hyphae of *T. vaccinum* stained with immunofluorescence for actin (red) and tubulin (green) after treatment with 0.25 mM IAA and 0.5 mM of different IAA precursors in the tryptophan dependent pathway. Corresponding bright field picture is given on the right side.