Table S1 Sequencing data statistics

Sample	Insert length (bp)	Raw data pair reads	Raw data total bases (bp)	Q20 (%)	Clean data pair reads	Cleam data single reads	Clean data total bases (bp)	Average coverage
ZZ21	460	3937952*2	1976851904	92.36	3899252*2	35987	1837619283	428X

Table S2 Indicator statistics of assembly results

Sample	ZZ21
No. of all scaffolds	72
No. of bases in all scaffolds (bp)	4,615,764
No. of large scaffolds (>1000 bp)	39
No of bases in large scaffolds (bp, >1000 bp)	4,600,908
Largest scaffold length (bp)	635,947
Scaffold N50 (bp)	212,981
Scaffold N90 (bp)	89,228
G+C content (%)	65.72
N rate (%)	0.00024
Total no. of contigs	83
No. of bases in all contigs (bp)	4,615,753
No. of large contigs (>1000 bp)	44
No of bases in large contigs (bp, >1000 bp)	4,597,586
Largest contig length (bp)	635,947
Contig N50 (bp)	200,987
Contig N90 (bp)	82,521

Table S3 Gene information statistics

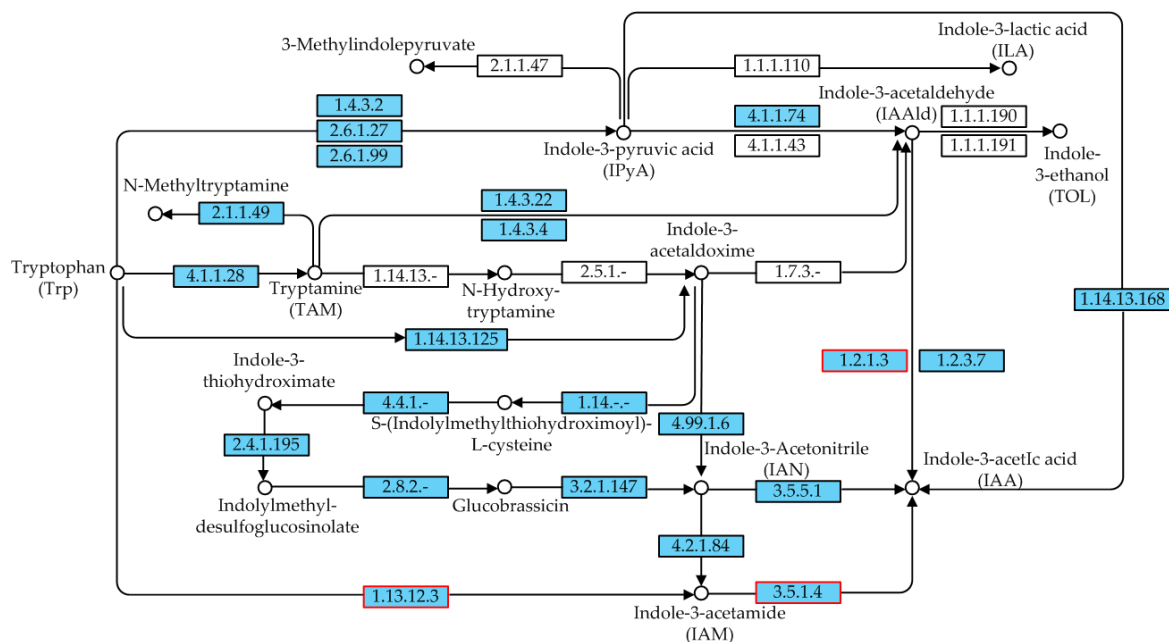| Sample	ZZ21
Number of genes	4321
Total length of genes (bp)	3,992,178
Average length of a gene (bp)	923.9
Gene density (number/kb)	0.94
GC content in gene region (%)	66.37
Gene/Genome (%)	86.49
Intergenic region length (bp)	623,586
GC content in intergenic region (%)	61.56
Intergenic length/Genome (%)	13.51

Figure S1. KEGG pathway involved in tryptophan metabolism (pathway entry number in KEGG: ko00380) and putative pathways involved in IAA biosynthesis in ZZ21. Circular nodes represent metabolic compounds, while rectangular nodes indicate gene products that are either classified as KEGG orthologues (blue) or not (white). A red border of a rectangular internode indicates that this enzyme is encoded by a gene in the *A. pascens* ZZ21 genome. Arrows represent enzymatic reactions or information transfer.
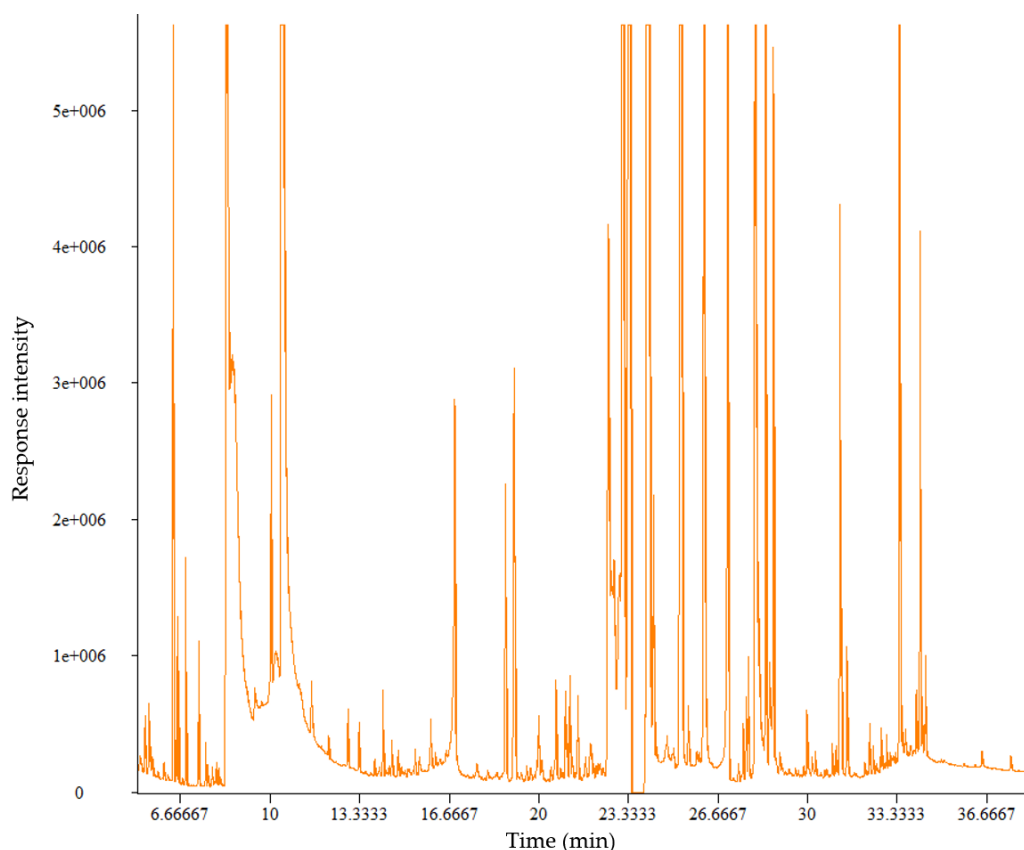

Figure S2. Total ion current (TIC) values of *A. pascens* ZZ21 metabolites. Mass spectrometric analysis was performed from 50 to 450 mass.

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