

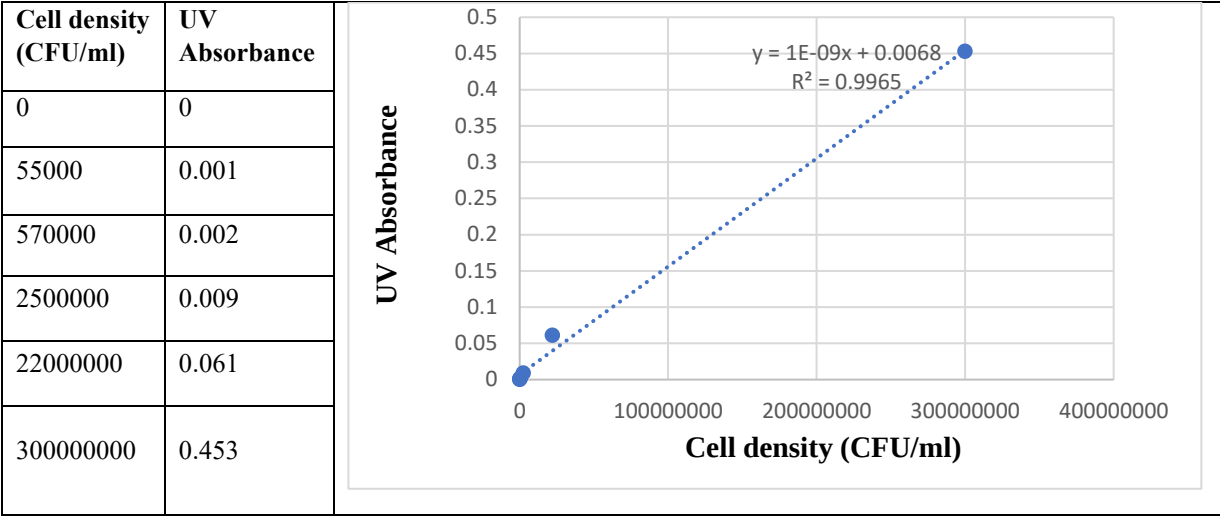


Fig S1. OD reference curve for NL1 strain

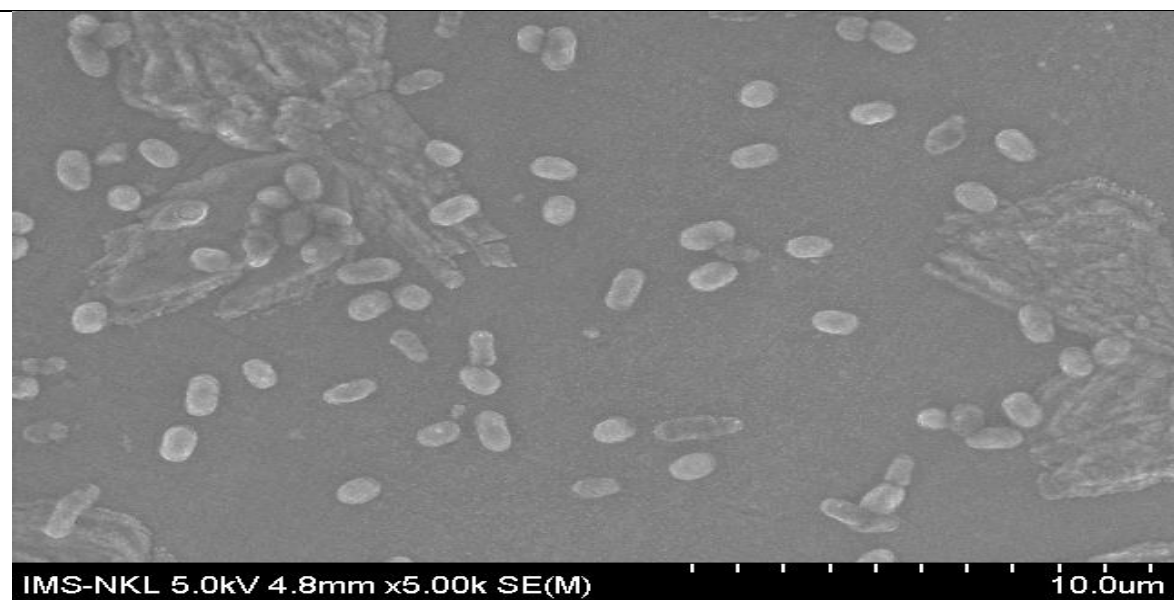


Fig S2. Cell morphology

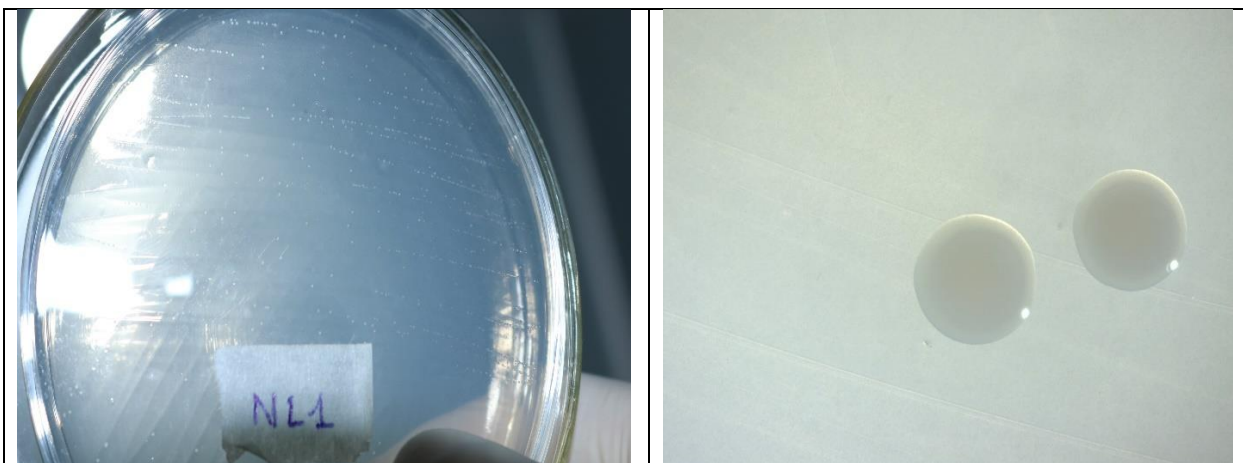


Fig S3. Colony morphology

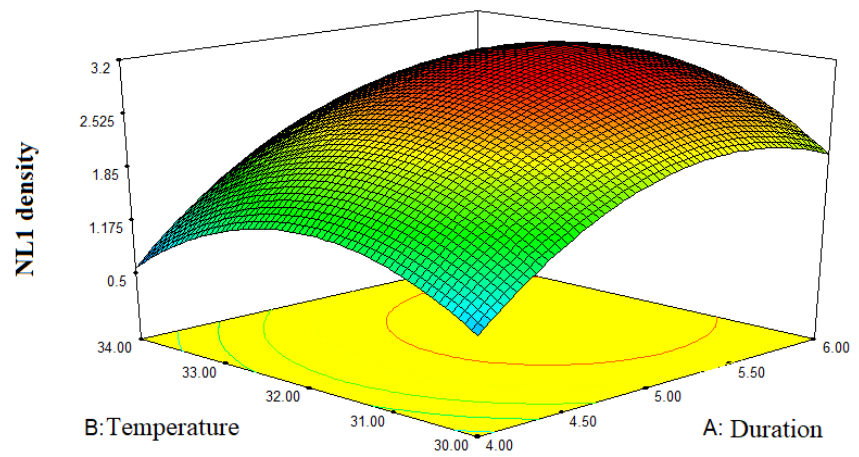
Design-Expert® Software

NL1 density



X1 = A: Duration
X2 = B: Temperature

Actual Factor
C: pH = 6.61



(a)

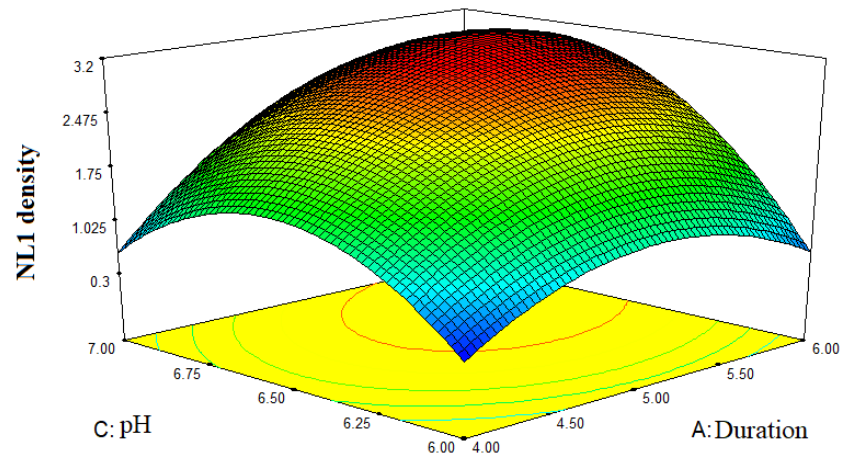
Design-Expert® Software

NL1 density



X1 = A: Duration
X2 = C: pH

Actual Factor
B: Temperature = 31.73



(b)

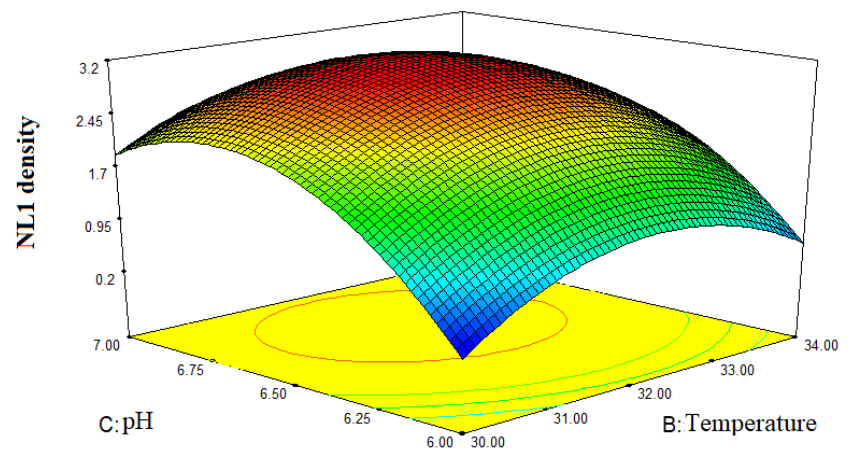
Design-Expert® Software

NL1 density



X1 = B: Temperature
X2 = C: pH

Actual Factor
A: Duration = 5.22



(c)

Fig S4. Surface meets NL1 cell density

Notes: (a): Interaction model between culture time and culture temperature

(b): Interaction model between culture time and pH

(c): Temperature and pH interaction model

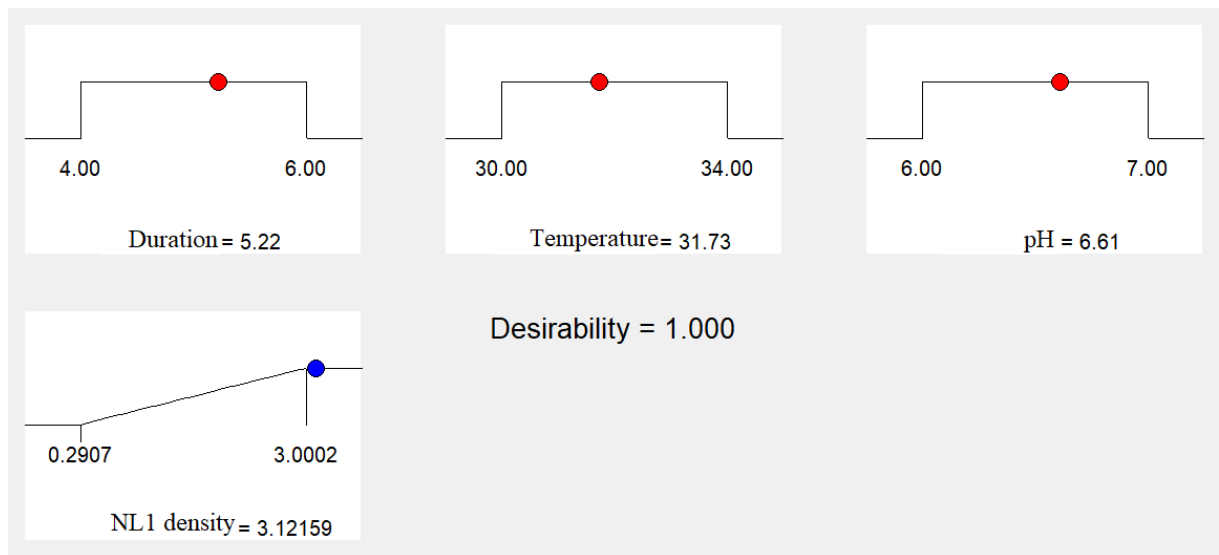


Fig S5. NL1 cell density expectation and optimal conditions

NITROGEN METABOLISM

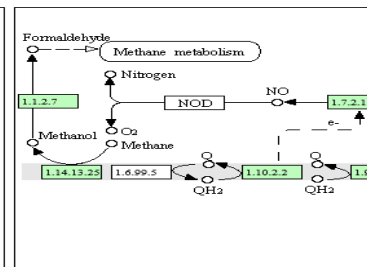
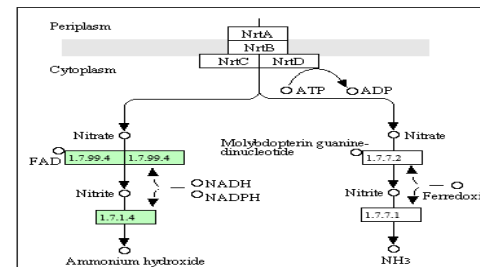
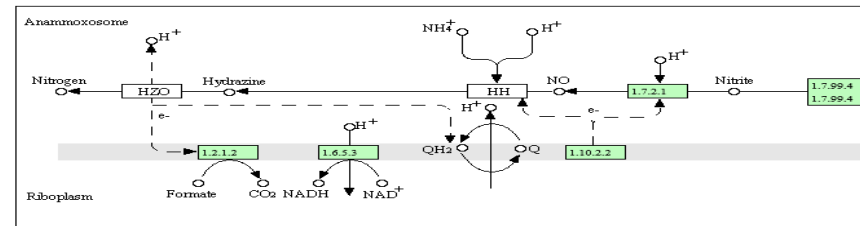
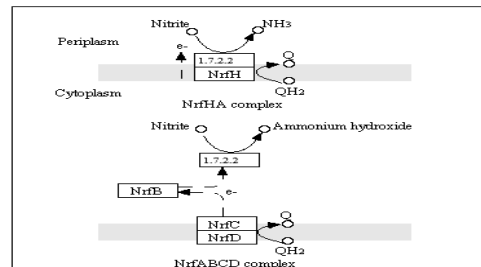
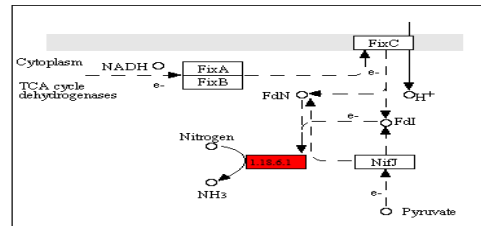
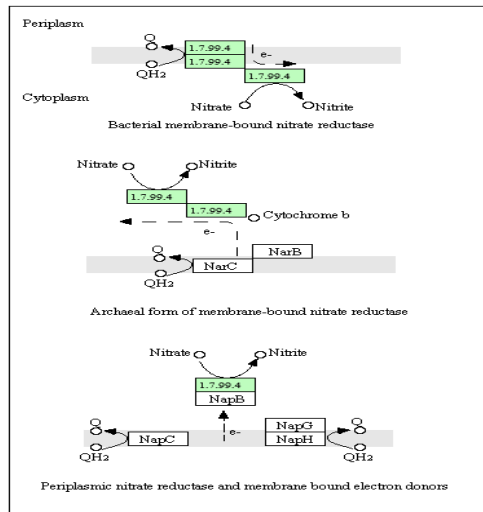
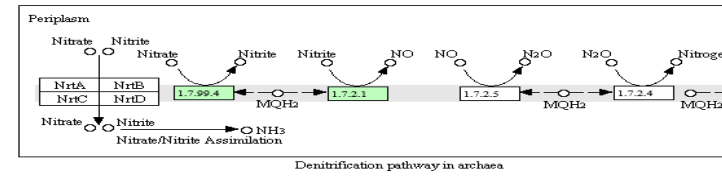
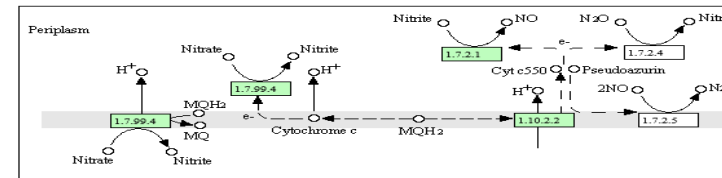
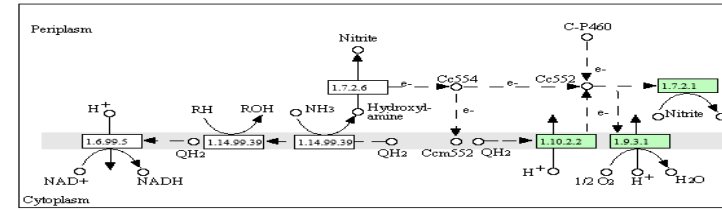
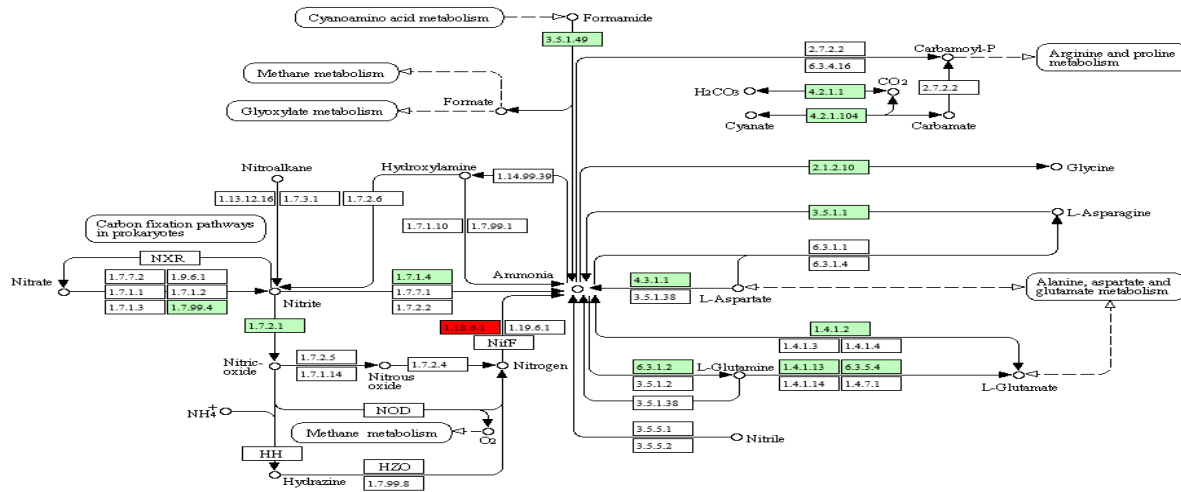


Fig S6. Nitrogen fixation pathway by *Azospirillum* sp. NL1 strain

TRYPTOPHAN METABOLISM

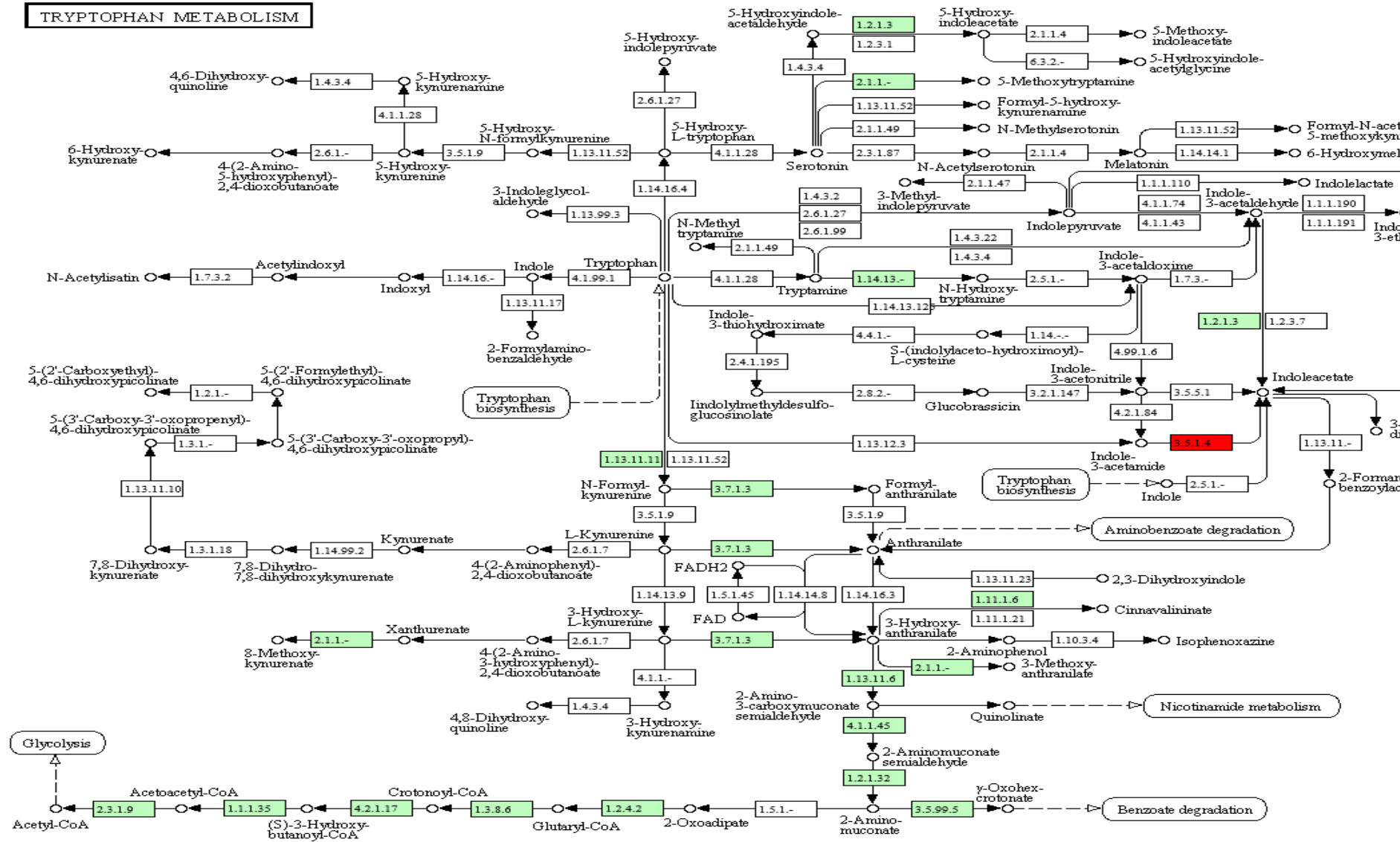


Fig S7. Mechanism of IAA production of *Azospirillum* sp. NL1 strain

Table S1. Description of cell morphology, colony morphology, and Gram-staining properties of screened strains.

TT	Strain symbol	Colony morphology	Cell morphology	Gram Dyeing Properties	Portability
1	NL1	Round, ivory white, convex, entire margin, smooth, with pili that firmly adhere to the environment	Short rod	-	+
2	NL35	Round, opaque white, convex, smooth, shiny, slimy	Oval - round	-	+
3	NL38	Round, opaque white, wrinkled, concave, rough surface	Short rod	-	+
4	NL321	Milky white, round with core, smooth and shiny, convex, without pili	Oval	-	+
5	NL335	Round, ivory white, wet shiny surface, without pili, slimy, convex	Short rod	-	+
6	NL338	Round, ivory white, wet shiny surface, without pili, slimy, convex	Comma	-	+
7	NL324	Round, ivory white, shiny surface, neat and slimy	Short rod	-	+
8	NL341	Opaque white, round, without pili, rough surface	Oval	-	+

Table S2. Enzymatic production capacity of NL1 strains

TT	Ability to produce enzymes	NL1
1	Control	-
2	Alkaline phosphatase	+
3	Esterase (C4)	+
4	Lipase esterase (C8)	+
5	Lipase (C14)	+
6	Leucine arylamidase	+
7	Valine arylamidase	+
8	Cystine arylamidase	-
9	Trypsin	-
10	D-chymotrypsin	-
11	Acid phosphatase	+
12	Naphthol-AS-BI-phosphohydrolase	+
13	D-galactosidase	-
14	β -galactosidase	-
15	β -glucuronidase	+
16	D-glucosidase	-
17	β -glucosidase	+
18	N-acetyl- β -glucosaminidase	+
19	D-mannosidase	-
20	D-fructosidase	-

Table S3. Some biochemical characteristics of the NL1 strain

TT	Biochemistry minor threads	Activity
1	Nitrate to nitrite conversion	+
2	Indole generation	+
3	D-glucose fermentation	-
4	L-arginine assimilation	-
5	Urea assimilation	+
6	Esculin ferric citrate assimilation	+
7	Gelatin assimilation	-
8	4-nitrophenyl- β D-galactopyranoside assimilation	+
9	D-glucose assimilation	+
10	L-arabinose assimilation	+
11	D-mannose assimilation	+
12	D-mannitol assimilation	+
13	N-acetyl-glucosamine assimilation	+
14	D-maltose assimilation	-
15	Potassium gluconate assimilation	+
16	Capric acid assimilation	-
17	Adipic acid assimilation	+
18	Malic acid assimilation	+
19	Trisodium citrate assimilation	+
20	Phenylacetic acid assimilation	-
21	L-rhamnose assimilation	-
22	D-ribose assimilation	+
23	Inositol assimilation	+
24	D-saccharose assimilation	-
25	Itaconic acid assimilation	-
26	Suberic acid assimilation	+
27	Sodium malonate assimilation	+
28	Sodium acetate assimilation	+

TT	Biochemistry minor threads	Activity
29	Lactic acid assimilation	+
30	L-alanine assimilation	+
31	Potassium 5-ketogluconate	-
32	Glycogen assimilation	+
33	3-hydroxybenzoic acid assimilation	-
34	L-serine assimilation	+
35	Salicin assimilation	-
36	D-melibiose assimilation	-
37	L-fucose assimilation	+
38	D-sorbitol assimilation	+
39	Propionic acid assimilation	+
40	Valeric acid assimilation	+
41	L-histidine assimilation	+
42	Potassium 2-ketogluconate assimilation	+
43	3-hydroxybutyric acid assimilation	+
44	4-hydroxybenzoic acid assimilation	-
45	L-proline assimilation	+
46	D-xylose assimilation	-
47	D-fructose assimilation	+
48	Lactose assimilation	-
49	Catalase activity	+
50	Oxidase activity	+
51	Methyl red reaction	+
52	Voges-Proskauer reaction	+
53	H ₂ S production	+

Table S4. Sequencing quality of NL1 strains by Illumina method

Sample	Total read	Total bases(bp)	Length(bp)	%GC	% Q30
Before purification					
Downstream Sequencing R1	3,900,453	588,968,403	35-151	66.9	95.5
Reverse Sequencing R2	3,900,453	588,968,403	35-151	66.9	94.7
After purification					
Downstream Sequencing R1	3,734,385	563,311,743	35-151	66.9	96.6
Reverse Sequencing R2	3,734,385	563,311,743	35-151	66.9	96.1

Table S5. De novo assembly results of the NL1 strain

Characteristic	Amount
Number of contigs	7
Number of circles contig	7
%GC (contigs > 500 bp)	67.23
Total length of contig (bp)	8,071,173
Maximum contig length (bp)	2,813,755
N50 value (contigs > 500 bp)	1,395,693
L50 value (contigs > 500 bp)	2
Coding sequence (CDS)	7313
tRNA	79
rRNA	26
The number of genes that regulate protein function:	
Hypothesis protein	2362
Functional protein	4951
Protein with EC indicator	1483
Protein with GO arrangement	1298
Signaling proteins	1156
Systematic protein	1854
Protein for PLfam especially for PATRIC genus	6444
Protein with family-genus mission of PATRIC (PGfam)	6630
Protein with FIGfam mission	0

Table S6. Genes in the nitrogen fixation pathway and IAA biosynthesis are present in the genome of the NL1 strain

Number of functional genes	Function
Genes in the nitrogen fixation pathway:	
1	Nitrogenase (molybdenum-iron)-specific transcriptional regulator <i>NifA</i>
2	4Fe-4S ferredoxin
3	LRV (FeS) ₄ cluster domain protein clustered with nitrogenase cofactor synthesis
4	Nitrogenase FeMo-cofactor synthesis FeS core scaffold and assembly protein <i>NifB</i>
5	NifZ protein
6	NifZ protein
7	NifT protein
8	Cysteine desulfurase (EC 2.8.1.7), NifS
9	4Fe-4S ferredoxin, nitrogenase associated
10	Uncharacterized protein RPC_4456
11	NifX-associated protein
12	Nitrogenase FeMo-cofactor scaffold and assembly protein NifE
13	Nitrogenase FeMo-cofactor carrier protein NifX
14	Nitrogenase FeMo-cofactor scaffold and assembly protein, NifN
15	Nitrogenase (molybdenum-iron) alpha chain (EC 1.18.6.1)
16	Nitrogenase (molybdenum-iron) reductase and maturation protein NifH
17	Nitrogenase-associated protein NifO
18	Nitrogenase (molybdenum-iron) beta chain (EC 1.18.6.1)
19	Homocitrate synthase (EC2.3.3.14)
20	Nitrogenase stabilizing/protective protein NifW
21	Cysteine desulfurase (EC 2.8.1.7), NifS
22	Iron-sulfur cluster assembly scaffold protein NifU
23	probable iron binding protein from the HesB_IscA_SufA family in Nif operon
24	Nitrogenase FeMo-cofactor synthesis molybdenum delivery protein NifQ
25	Nitrogenase-associated protein NifO
26	Electron transfer flavoprotein, beta subunit FixA

27	Electron transfer flavoprotein, alpha subunit FixB
28	Electron transfer flavoprotein quinone oxidoreductase FixC
29	Ferredoxin-like protein FixX
Genes in IAA biosynthesis:	
1	Aliphatic amidase AmiE (EC 3.5.1.4)
2	Aliphatic amidase AmiE (EC 3.5.1.4)
3	Amidase (EC 3.5.1.4)
4	Nitrilase (EC 3.5.5.7)