

## Supplementary data

M5a1	MQPTYTIGDYLLDRLVDCGIDRLFGVPGDYNLQFLDSVIAHRNLGWVGCANLNAAYAAD	60
SGM81	MQPTYTIGDYLLDRLVDCGIDRLFGVPGDYNLQFLDRVIAHNALGWVGCANELNAAYAAD	60
SSN1	MQPTYTIGDYLLDRLVDCGIDRLFGVPGDYNLQFLDRVIAHNALGWVGCANELNAAYAAD	60
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M5a1	GYARIKAGALLTTYGVGELSALNGIAGSYAEHVPVLHIVGAPCTGAQQRGELLHHTLGD	120
SGM81	GYARIKAGALLTTYGVGELSALNGVAGSYAEHIPVLHIVGAPSTGAQQRGELLHHTLGD	120
SSN1	GYARIKAGALLTTYGVGELSALNGVAGSYAEHIPVLHIVGAPSTGAQQRGELLHHTLGD	120
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M5a1	GDFSHFSRMSEQITCSQAVLAAGNACHEIDRVLSEMLTHHRPGYLMLPADVAKAKTTPPA	180
SGM81	GDFRHFARMSEQITCSQALLTAGNACHEIDRVLRDMLTHHRPGYLMLPADVARAAAIAPA	180
SSN1	GDFRHFARMSEQITCSQALLTAGNACHEIDRVLRDMLTHHRPGYLMLPADVARAAAIAPA	180
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M5a1	HRLLIQGLPADENQLAGFREHAGRMLRSSRRVSLADFLAQRYGLQNALREWVAKVPVAY	240
SGM81	QRLLEAAPADENQFAGFCEHASRLLRGSRISLLADFLAQRYGLQNTLREWVAKTPVAH	240
SSN1	QRLLEAAPADENQLAGFCEHASRLLRGSRISLLADFLAQRYGLQNTLREWVAKTPVAH	240
	:***:..*****:*** **.*:*** **.*:*****:*****:***:	
M5a1	ATMLMGKGLFDEQQSGFVGTYSGLASAEETRAIENADTIICIGTRFTDTITAGFTQHLP	300
SGM81	ATMLMGKGLFDEQQRGFVGTYSGLASAPQTREAIENADTIICIGTRFTDTITAGFTQHLP	300
SSN1	ATMLMGKGLFDEQQRGFVGTYSGLASAPQTREAIENADTIICIGTRFTDTITAGFTQHLP	300
	***** *****:***:*****	
M5a1	LEKTIEIQPFAPVRVADRWFSPRIPEKALAILIELSASLAAEWVSPNIQAPGVSGAPEGSL	360
SGM81	RDKTIEIQPFAPVRVGDHWFSGVPMQALALMTLSAPLAAEWAAPQVVAPEVEEGADGEL	360
SSN1	RDKTIEIQPFAPVRVGDHWFSGVPMQALALMTLSAPLAAEWAAPQVVAPEVEEGADGEL	360
	:*****.*:*** **:*** *: *** **.*:***: ** *. .:*.*	
M5a1	TQKNFWNTVQKQLRPGDIIADQGAFAFGAAALKLPVDATLIVQPLWGSIGFTLPAAYGA	420
SGM81	TQKNFWATVQGALRPGDIIADQGTAAFGIAALKLPSEASLIVQPLWGSIGFTLPAAYGA	420
SSN1	TQKNFWATVQGALRPGDIIADQGTAAFGIAALKLPSEASLIVQPLWGSIGFTLPAAYGA	420
	***** ** ***** *****:***:*****	
M5a1	QIAAAERRVVLIVGDGAQLTIQELGSMRLDKQRPLILLNNEGYTVRAIHGPEQRYND	480
SGM81	QTAAAEERRVVLIVGDGAQLTIQEMGSMRLDKQKPLILLNNEGYTVRAIHGPEQRYND	480
SSN1	QTAAAEERRVVLIVGDGAQLTIQEMGSMRLDKQKPLILLNNEGYTVRAIHGPEQRYND	480
	* *****:*****:*****	
M5a1	IALWDWNRLPDAFAPDVPSRCWRVTRTQELQEAMNSSVASDRLTLVEVMLPKMDIPDFLR	540
SGM81	IALWDWRRLPEAFAPDVASRCWRVTHTDELREAMAESITSDMLTLVEVMLPKMDIPDFLR	540
SSN1	IALWDWRRLPEAFAPDVASRCWRVTHTDELREAMAESITSDMLTLVEVMLPKMDIPDFLR	540
	*****.*:***** *****:***:*** *:*** *****	
M5a1	TVTQALEERNRSRV	553
SGM81	AVTQALEERNRSRV	553
SSN1	AVTQALEERNRSRV	553
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**Figure S1.** Multiple Sequence alignment of ipdC derived amino acid sequence of indole pyruvate decarboxylase of *Klebsiella* SGM 81, *Klebsiella* SSN1 and *Klebsiella* M5a1, using Clustal O. Highlighted motifs (yellow) and residues involved in Mg<sup>2+</sup> binding (red), thiamine pyrophosphate binding (blue highlighted) are identical to those of the functional IpdC of *Enterobacter cloacae*, for which the structure and function has been detailed [1][3]

>SGM81 *ipdC* promoter seq (400nt before the translational start codon ATG)

CCGCCGAGCCCCGGCGGGCCCCATAGTTGTTGGCCAGGTCGAAATGGGTAATGCCGAGGTCA  
AACGCGTGCTGGAGCATCTGCCGGCTGGTTTCCACCCGCGTTTCATCGCCAAAGTTATGCCAC  
AGACCGAGAGAAATTGCCGGCAGCTGAAGGCCGCTGCGGCCGAGCGACGATAGGCCATCG  
TTTGATATCGCGTGGTACTTGCCTGGTAAACATTCTTCCTCCGCAGATAAAACAGGGTGTGTA  
TACGTTTACACTAATCAATGTTCTGCGTGGAGTACATCGCTTTTTTGGCGTAATTATTGCTTTA  
CACCGCCTTTATCACCCCTTTCTGGACAGGCGGATCGCTTATTCAATACTCAAATTACACCT  
GCGCCAAAATGAGGAAAATGGAT

>M5a1 *ipdC* promoter seq (400nt before the translational start codon ATG)

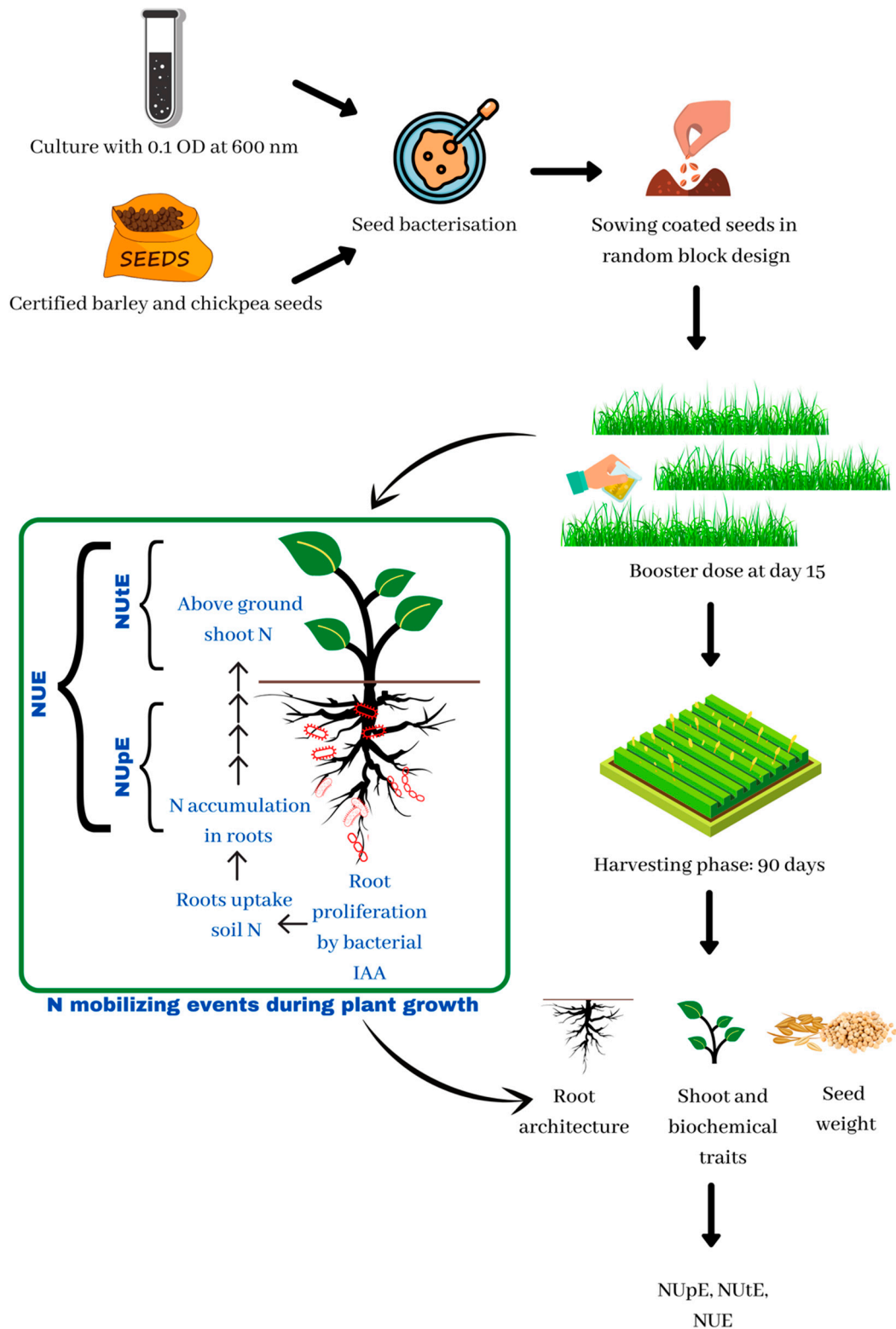
CTCTCCGCCGATCCCGCGGTGGCCCGTAGTTATTGGCTAAATCGAAATGGGTTATGCCGAGA  
TCGAATGCGTGACGCAGAAGCTGACGGCTGGTTTCCACCCGCGTTTCATCGCCAAAATTATGC  
CAAAGCCCCAGAGAACTGCCGGTAGCTTTAGTCCGCTATGACCGCAGCGGCGGTATTCCAT  
CGTTTGATATCGCGTGGCGTTTGCCTGGTAAACCATACTTCCTCCGCAGATAAAACAGGGTTG  
TGTATACGTTTACACTAAAGAATCTTTGGCGCCGAGTATACTCCCTGAACGCGTAAATTTTAC  
TTGCCACCGCATTTGTTGGGTGCAATGTGGACAGCGCAACTGCTTATTCAATACTCAACTTAT  
CTGCATGAGAGGAGAGTGGGGAT

**Figure S2.** Inspection of potential  $s^{54}$  promoters of *ipdC* in SGM81 and M5a1, 400 nucleotides before the translational start codon ATG. SGM81 has two near perfect  $s^{54}$  promoters with regards to the near invariable putative -24 GG and the -12 GC motifs (red) and their conserved next neighbour nucleotides according to Barrios et al. [2](T at -25, CA at -22-21, TT at -14-13). Importantly the exact spacing of 10 nucleotides between the -24 GG and -12 CC is stringent for  $s^{54}$  recognition and has been validated experimentally to be required for various  $s^{54}$  dependent promoters [3]. The spacing between the two putative GG – GC motifs of M5a1 (red) are 9 and 11 nucleotides, suggesting these are pseudo  $s^{54}$  binding motifs.



**Figure S3.** Plant morphology of barley (**A**) and chickpea (**B**) From left to right, no bacteria control, SSN1, SGM81, M5a1,  $\Delta nifH$  treatments

Supplementary Fig S4. Image Schema



Supplementary Fig S4. Schematic representation of plant experimental set up.

Referen Flow chart shows the steps conducted for plant study

1. Schütz, A.; Sandalova, T.; Ricagno, S.; Hübner, G.; König, S.; Schneider, G. Crystal Structure of Thiamindiphosphate-dependent Indolepyruvate Decarboxylase from *Enterobacter Cloacae*, an Enzyme Involved in the Biosynthesis of the Plant Hormone Indole-3-acetic Acid. *Eur. J. Biochem.* **2003**, *270*, 2312–2321.
2. Barrios, H.; Valderrama, B.; Morett, E. Compilation and Analysis of  $\Sigma 54$ -Dependent Promoter Sequences. *Nucleic Acids Res.* **1999**, *27*, 4305–4313.
3. Buck, M. Deletion Analysis of the *Klebsiella Pneumoniae* Nitrogenase Promoter: Importance of Spacing between Conserved Sequences around Positions-12 and-24 for Activation by the NifA and NtrC (GlnG) Products. *J. Bacteriol.* **1986**, *166*, 545–551.