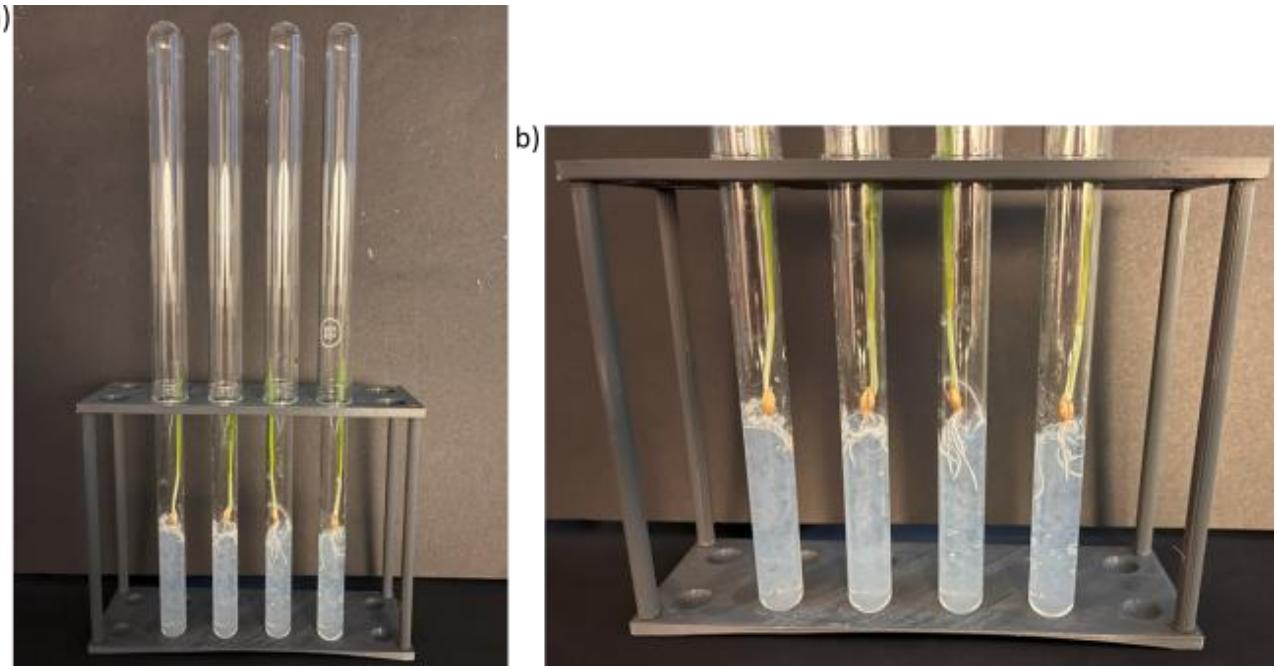
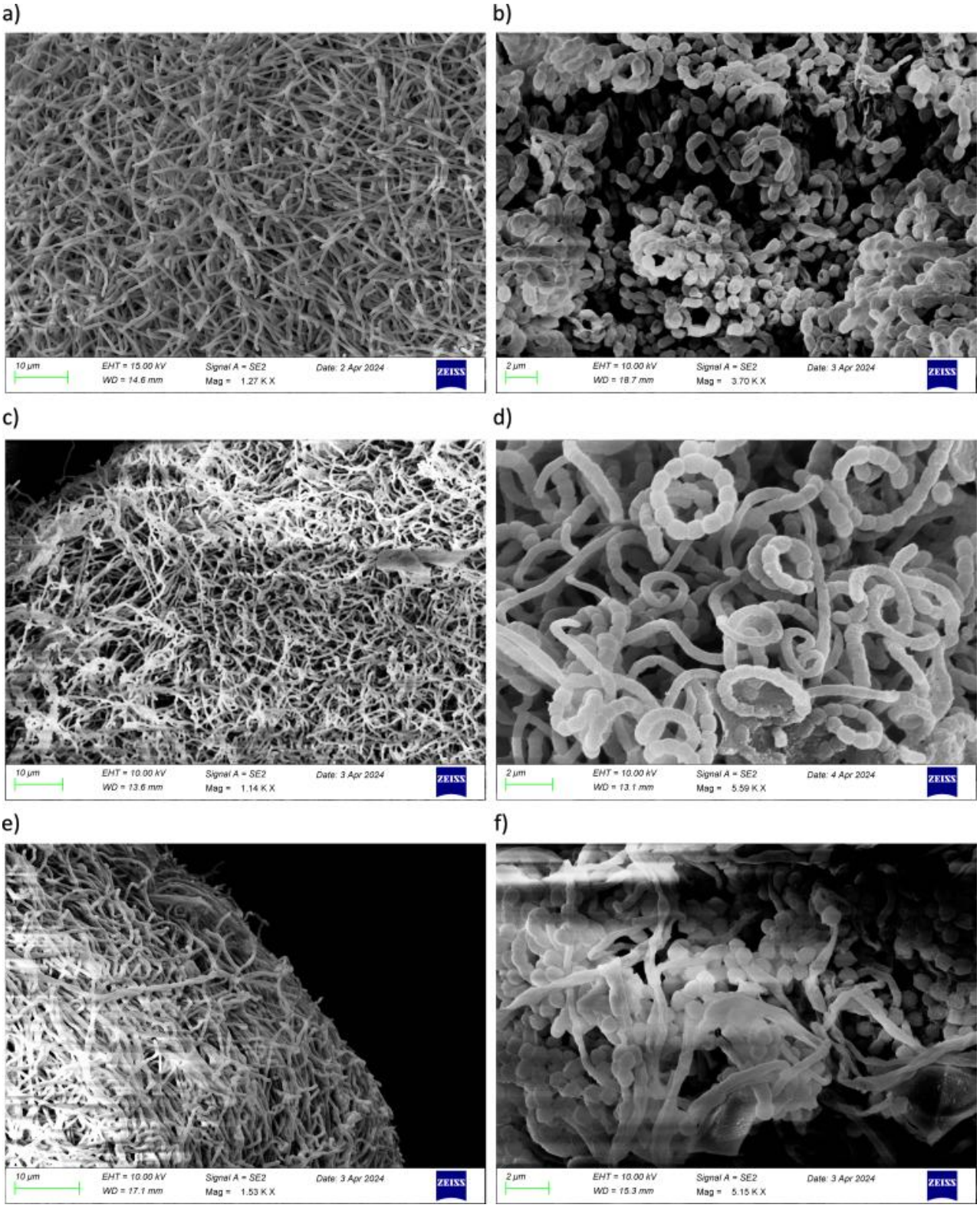


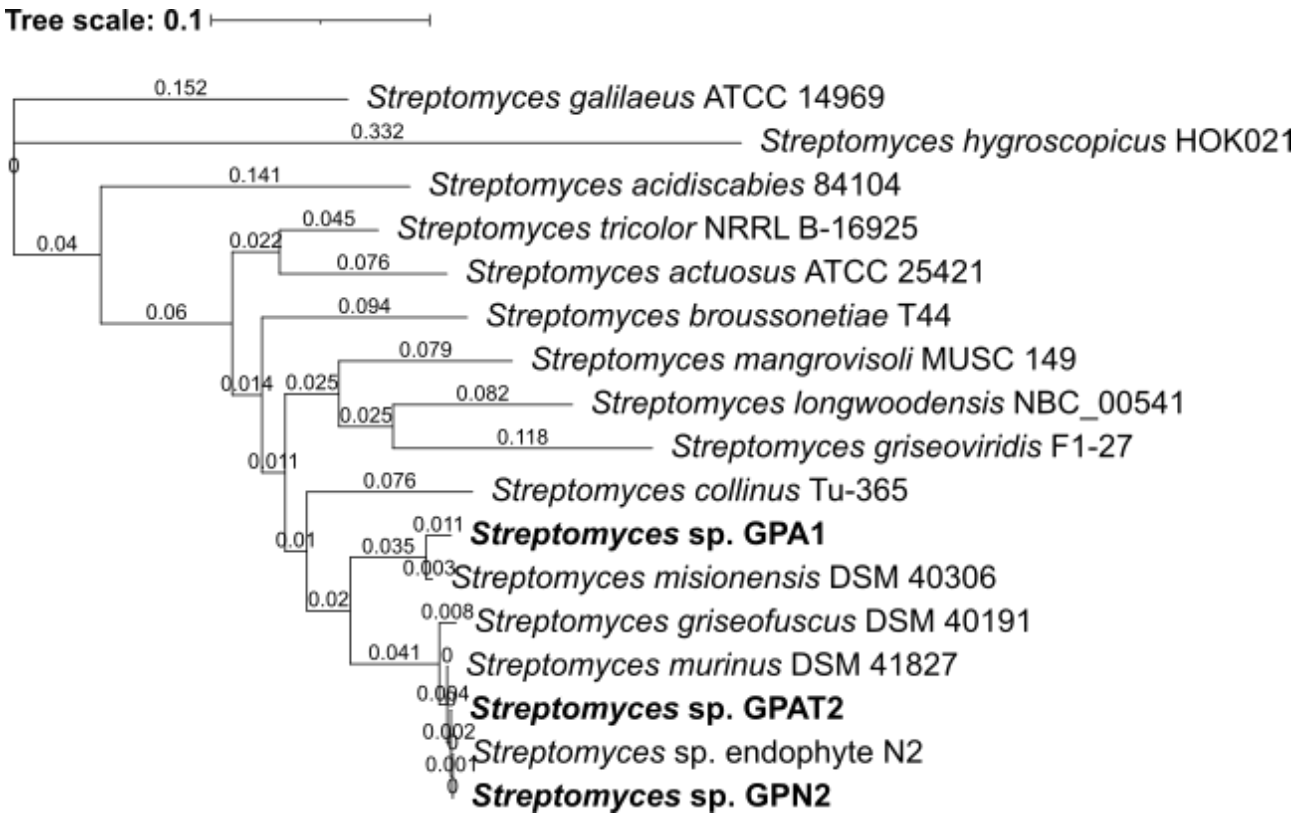
Additional file 1: Barley hydroponic growing system. The system consists of a 16 mm tube containing 9 mL of fragmented sterile semi solid MS medium (agarose 8 g/L). Before seed transfer, an inoculum of 1 mL of bacterial suspension at $1x10^4$ to $5x10^4$ CFU/mL or 1 mL of sterile liquid MS (as a control) was added. The tubes were then vortexed for 5 seconds to distribute the liquid between the agar agglomerates. The germinated seeds were placed in the test tubes using sterile forceps so that the radicle was in contact with the agar medium. Finally, the 16 mm tubes were placed in a raised rack and topped with a 20 mm diameter test tube to cover the smaller diameter tube at a height of 14 cm.

Additional file2: qPCR primers used in this study

Targeted organisms	Targeted genes	Primers	References
Barley	*hsp90*	5'-AGGAGTTTGAGGGCAAGAAGC-3' 5'-CCAGCACCTCCTTGATGACC-3'	Zhang *et al*., 2018
	cyp2	5'-CCTGTCGTGTCGTCGGTCTAAA-3' 5'-ACGCAGATCCAGCAGCCTAAAG-3'	Zhang *et al*., 2018
***Streptomyces* strains**	*rpbA*	5'-CTTCGAGATGCCCTTCTCGG-3' 5'-GGGCTTGGCCTTCTTCTCCT-3'	This study



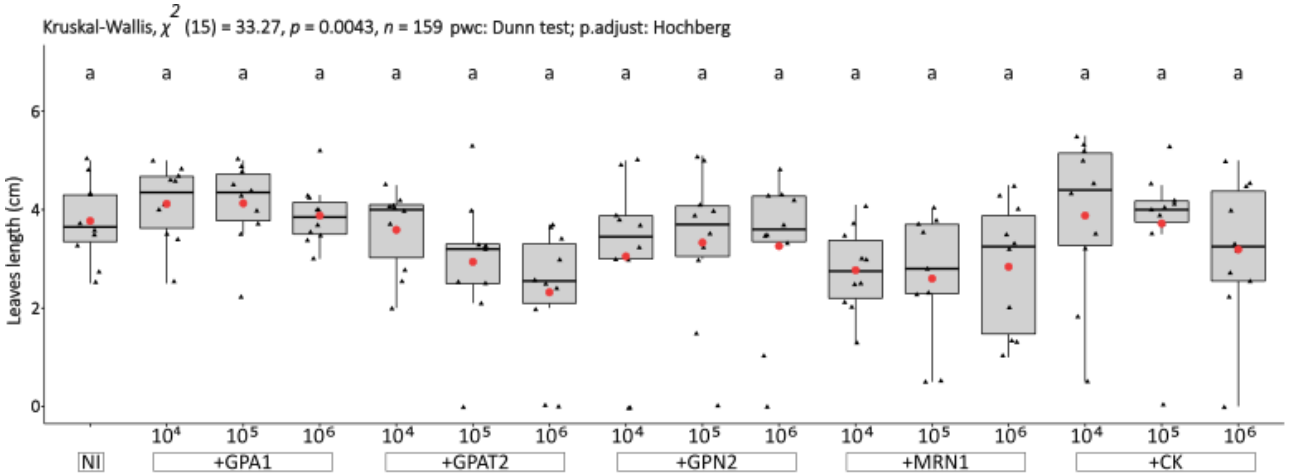
Additional file 3: Scanning electron microscope observation of *Streptomyces* sp. GPA1, GPAT2 and GPN2. a) Filaments and b) spores observation of *Streptomyces* sp. GPA1. c) Filaments and d) spores observation of *Streptomyces* sp. GPAT2. e) Filaments and f) spores observation of *Streptomyces* sp. GPN2. Cultures were prepared on solid GYM medium during 2 days for the filament observations and on Mannitol Mungo solid medium during 7 days for spore observations.



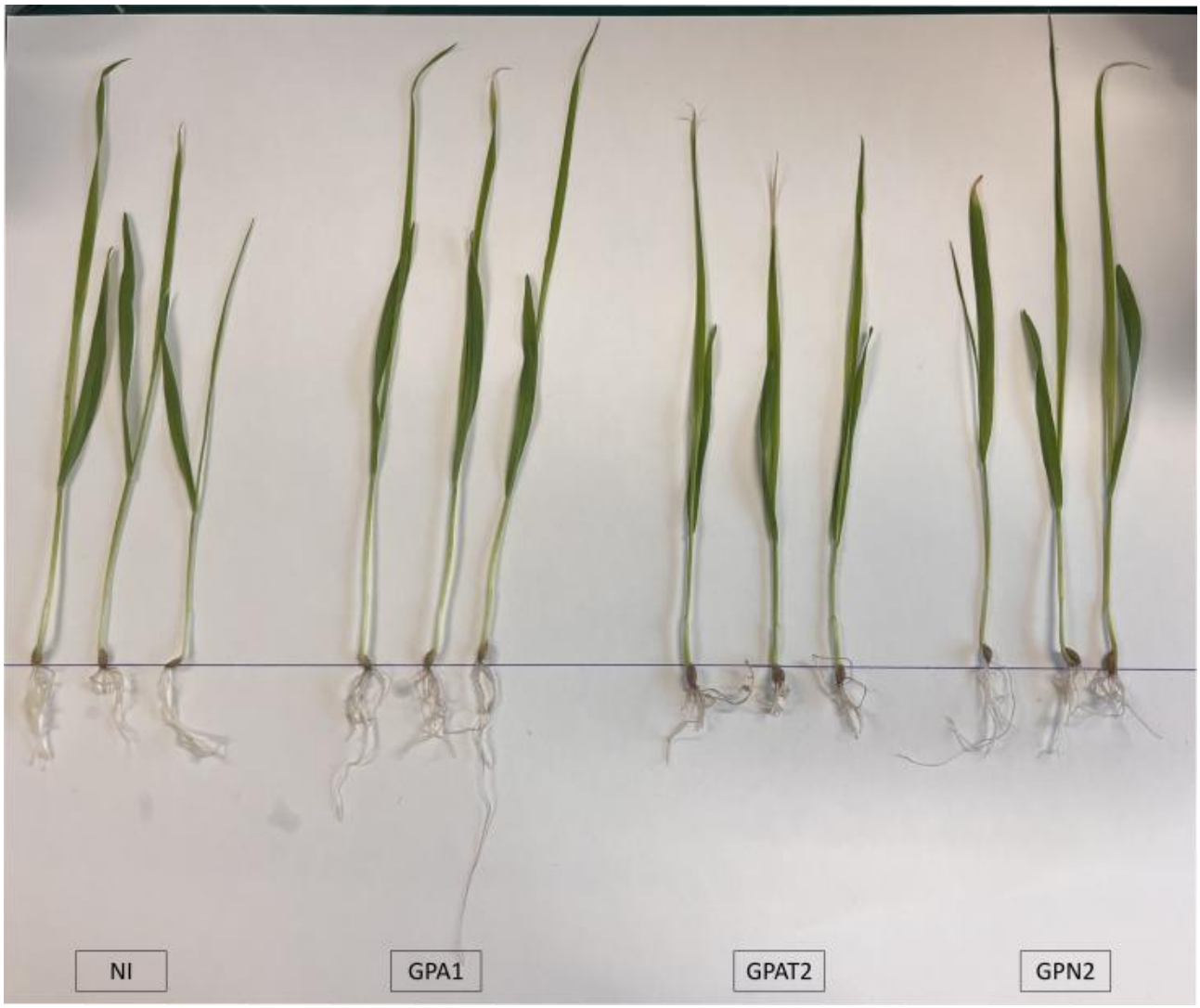
Additional file 4: Phylogenetic trees based on the *rpoB* sequences of *Streptomyces* sp. GPA1, GPAT2 and GPN2. The tree was produced using the BOOSTER plateform (BOOtstrap Support by TransfER) [1] and PhyML-SMS workflow. The tree was implemented in the Interactive Tree Of Life (iTOL) software (v.6.9.1) [2]. The black numbers at the branch level represent branch length values.

Additional file 5: Optical density of *Streptomyces* sp. GPA1/GPAT2/GPN2 and *S. misionensis* in Biolog PM1 and PM2A microarrays. The optical density (590 nm) was measured after one week of growth and the optical density of the control was subtracted from those values. Arbitrarily, we have defined 4 different growth patterns, depending on the optical density measured: no growth for optical densities below 0.05 (-), slight growth for optical densities between 0.05 and 0.2 (+/-), average growth for optical densities between 0.2 and 0.5 (+) and efficient growth for optical densities above 0.5 (++).

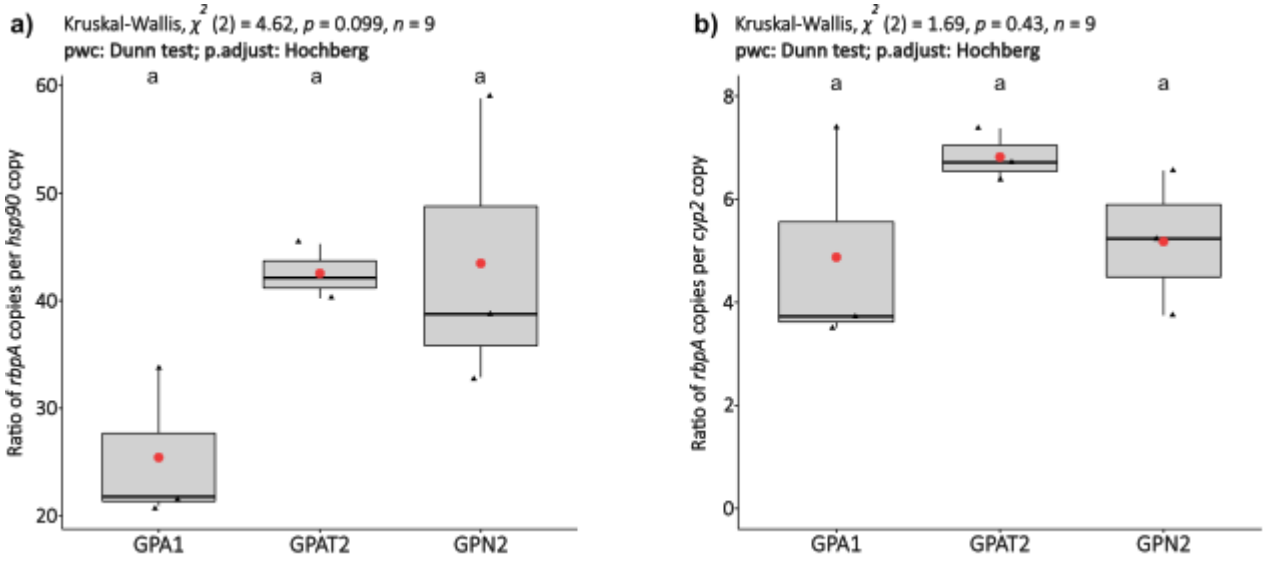
See .xlsx file



Additional file 6: Effects of microorganisms on leaves size during barley germination. Barley Bowman seeds were inoculated by immersion in microbial suspension containing *Streptomyces* sp. GPA1, GPAT2, GPN2, *Pseudomonas* sp. MRN1 or *Fusarium* sp. CK at different concentrations (10^6, 10^5, 10^4 CFU or spores/mL). Inoculated seeds were placed on MS media and incubated in culture chamber in the dark for 5 days. Leaves length was measured 5 days after inoculation and compared to the leave size of non-inoculated seedlings. Differences were statistically tested using a Kruskal-Wallis test followed by a pairwise Dunn test with Hochberg correction. Different letters indicate significant root size differences (p-values < 0.05). 10 replicates per condition were carried out except for *Pseudomonas* sp. MRN1 at concentration 10^5 CFU/mL where 9 seeds were measured.



Additional file 7: Barley seedlings grown in the hydroponic system at 14 dpi. NI: Non-inoculated seedlings, GPA1: seedlings inoculated with GPA1, GPAT2: seedlings inoculated with GPAT2, GPN2: seedlings inoculated with GPN2. Seedlings were selected at random from a pool of 19 for non-inoculated seedlings and 20 for other conditions.

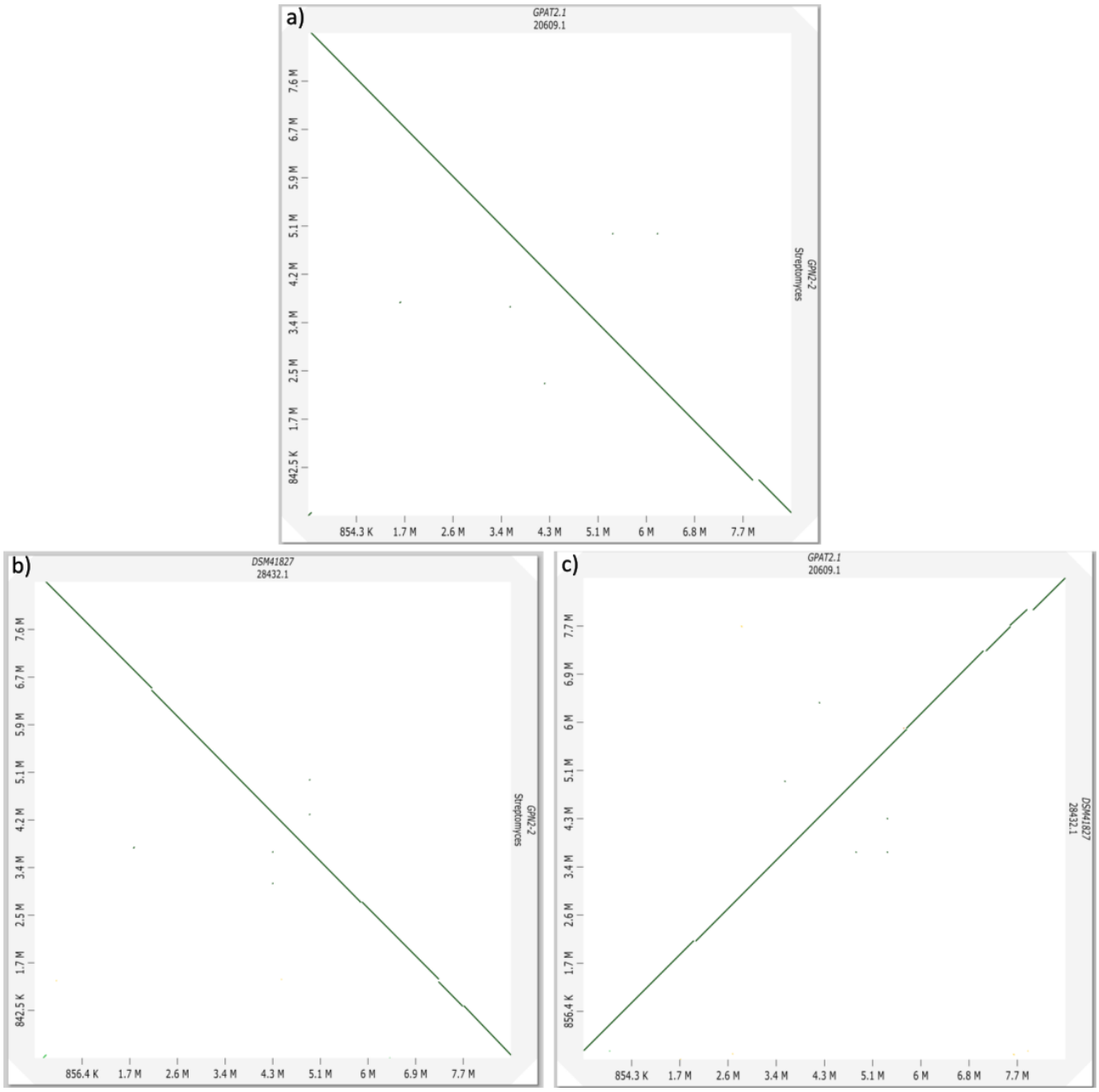


Additional file 8: Quantification of the root colonization of *Streptomyces* sp. GPA1, GPAT2 and GPN2 by qPCR. Quantification of the colonization efficiency of *Streptomyces* strains by qPCR using a) *rbpA/hsp90* primers. b) *rbpA/cyp2* primers. The test used for the qPCR results was a Kruskal-Wallis test followed by a pairwise Dunn test with Hochberg correction. 3 replicates were carried out for each sample. Different letters indicate significant differences (p-values < 0.05).

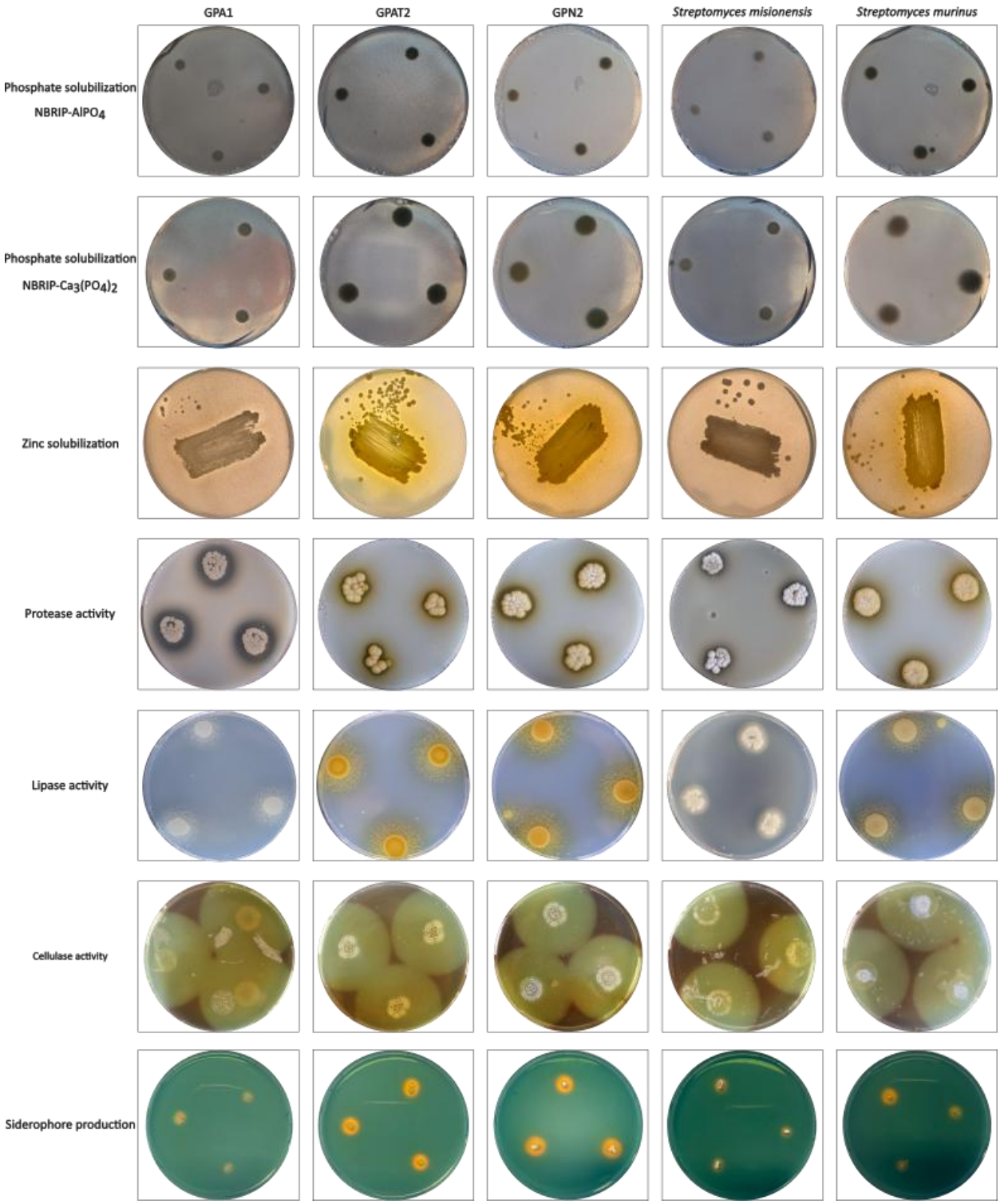
Additional file 9: General characteristics of the *Streptomyces* genomes. [a]Calculation of repetitive regions did not include undetermined ('N') bases. [b]Completeness was estimated using CheckM [3]. In bold: the activity was confirmed using Biologs tests

Genome characteristics	GPA1	*Streptomyces misionensis* DSM 40306	GPAT2	GPN2	*Streptomyces murinus* DSM 41827
Size (bp)	8077379	8474121	8543218	8424890	8564314
GC-content (%)	72.26	72.38	71.79	71,83	71.74
Predicted CDS	9552	7874	7985	7793	7715
Genome coding (%)	90.66	88.57	89.52	89.68	89
Average CDS size (bp)	912.72	967.75	976.52	986.88	1001.67
Number of tRNA	21	21	22	22	22
Number of 16S encoding gene	2	6	7	7	7
Repetitive regions (%)[a]	6.78	8.83	8.28	8.41	8.42
Nb of scaffold	11	5	0 (chromosome)	2	2
Completeness (%)[b]	100	100	99.89	99.89	99.89
Putative genes involved in plant-bacteria interactions					
Polymer degradation	1,4-β-xylan (*xlnA, xlnB*), cellulose (SGPA1_v2_40428-40433), **glycogen**, and chitin (*chi* genes)	1,4-β-xylan (*xlnA, xlnB*), cellulose, **glycogen**, and chitin (*chi* genes)	1,4-β-xylan (*xlnA, xlnB*), cellulose (GPAT2_v1_7842-7846), **glycogen**, and chitin (*chi* genes)	1,4-β-xylan (*xlnA, xlnB*), cellulose (GPN2_v1_20270-20274), **glycogen**, and chitin (*chi* genes)	1,4-β-xylan (*xlnA, xlnB*), cellulose, glycogen, and chitin
Other degradation capacities	**Putrescine** *patD* (SGPA1_v2_11389-11390 and SGPA1_v2_11408), *patA* (SGPA1_v2_10991)	**Putrescine** *patA and D,*	**Putrescine** *patD* (GPAT2_v1_5813 GPAT2_v1_5826), *patA* (GPAT2_v1_6154)	**Putrescine** *patD* (GPN2_v1_22152 - GPN2_v1_22165), *patA* (GPN2_v1_21830)	**Putrescine** *patA and D*
Genes involved in degradation of	**fructose**, **D-mannose**, **L-arabinose**, lactose, **galactose,** maltose, melibiose, **ribose, glycerol** and xylose	**fructose**, **D-mannose**, **L-arabinose**, lactose, **galactose, maltose**, **melibiose**, **ribose, glycerol** and **xylose**	**D-mannose**, lactose, **galactose**, **maltose melibiose**, **ribose, glycerol** and **xylose**	**D-mannose**, lactose, **galactose**, **maltose melibiose**, **ribose, glycerol** and **xylose**	D-mannose, lactose, galactose, maltose, melibiose, ribose, glycerol and xylose

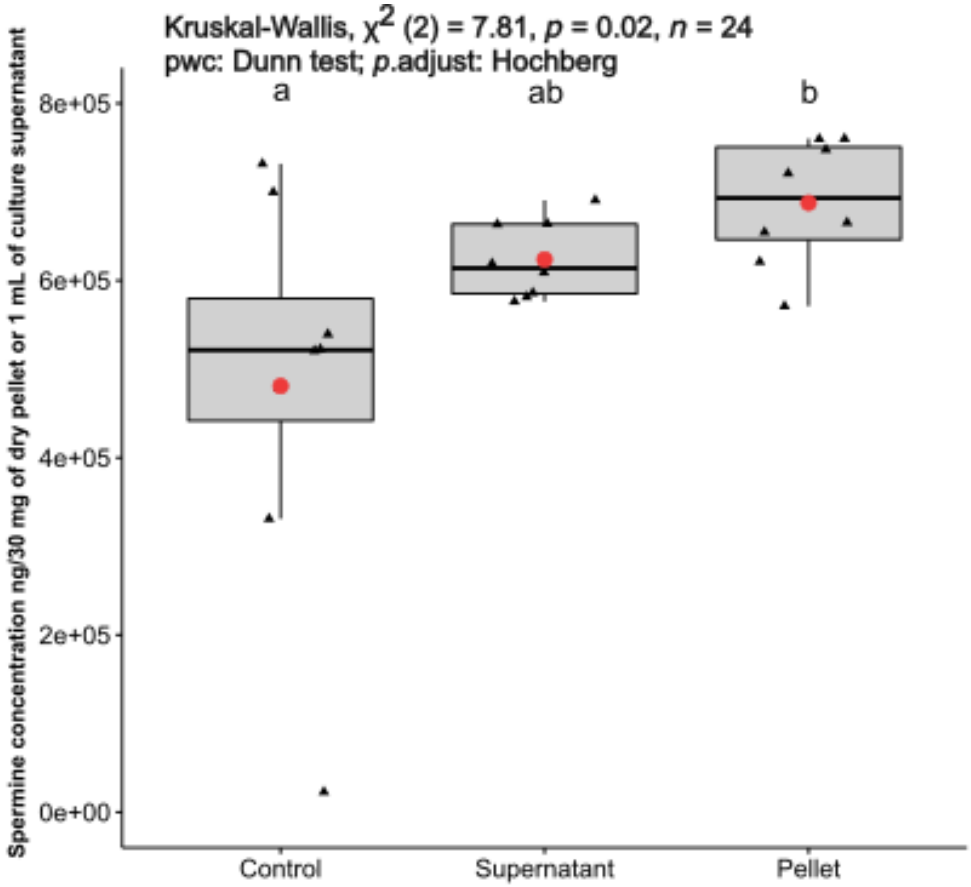
Nitrogen fixation	nd[c]	nd[c]	nd[c]	nd[c]	nd[c]
Siderophore	*rhbEB* (SGPA1_v2_31337-31338), *rhbC* (SGPA1_v2_11231), *feuV-fepDG* (SGPA1_v2_20005-20007)	*rhbEB, rhbC, feuV-fepDG*	*rhbEB* (GPAT2_v1_2287-2288), *feuV-fepDG* (GPAT2_v1_2052-2054), *dhbABCEF* (GPAT2_v1_7361-7368)	*rhbEB* (GPN2_v1_12234-12236), *feuV-fepDG* (GPN2_v1_12476-12478), *dhbABCEF* (GPN2_v1_20605-20612)	*rhbEB, feuV-fepDG, dhbABCEF*
Phosphate solubilization	*gdh* (SGPA1_v2_10359, 31446, 40417), *pqq* (SGPA1_v2_21676,21677,21678,21679,21678,21681)	3 *gdh* genes, 3 *pqq* genes	*gdh* (GPAT2_v1_2205, 6818, 7856)	*gdh* (GPN2_v1_12322, 20259, 21164)	3 *gdh* genes
Quorum sensing					
A-factor synthesis (□-butyrolactone)	*barS*, (SGPA1_v2_21530, 21911)	2 *barS* genes	*barS* (GPAT2_v1_0550)	*barS* (GPN2_v1_13560, 13908)	2 *barS* genes
Phytohormone homeostasis					
IAA synthesis	**Putative *iaaH* (hydrolase, SGPA1_v2_20424) *iaaM* (tryptophan 2-monooxygenase, SGPA1_v2_20425)**	Putative *iaaH* and *iaaM*	Putative *iaaH* (hydrolase, GPAT2_v1_1660) *iaaM* (tryptophan 2-monooxygenase, GPAT2_v1_1659)	Putative *iaaH* (hydrolase, GPN2_v1_12870) *iaaM* (tryptophan 2-monooxygenase, GPN2_v1_12871)	Putative *iaaH* and *iaaM*
Cytokinine synthesis	*log* (SGPA1_v2_11602, SGPA1-v2-12009, SGPA1_v2_40878)	2 *log* genes	*log* (GPAT2_v1_5256, GPAT2_v1_5638)	*log* (GPN2_v1_22341, GPN2_v1_22719)	2 *log* genes
Secondary metabolites					
Number of BGCs (AntiSMASH)	29 (geosmin, albaflavenone, pyrrolizixenamide A, desferrioxamine E, melanin, ectoine)	28 (geosmin, albaflavenone, desferrioxamine E, melanin, ectoine, filipin, curamycin)	36 (geosmin, albaflavenone, desferrioxamine E, melanin, ectoine, pentamycin, albusnodin, curamycin, 2-methylisoborneol)	34 (geosmin, albaflavenone, desferrioxamine E, melanin, ectoine, pentamycin, albusnodin, curamycin, 2-methylisoborneol)	34 (geosmin, albaflavenone, desferrioxamine E, melanin, ectoine, pentamycin, albusnodin, curamycin, 2-methylisoborneol)
Biofilm formation and regulation	*vbfA* , (SGPA1_v2_31568)	*vbfA*	*vbfA* (GPAT2_v1_2102)	*vbfA* (GPN2_v1_12428)	*vbfA*



Additional file 10: Syntenies between *Streptomyces* sp GPAT2, GPN2 and *S. murinus* DSM 41827. Dot plot showing the genomic similarities between a) *Streptomyces* sp. GPAT2 and *Streptomyces* sp. GPN2, b) *S. murinus* DSM 41827 and *Streptomyces* sp. GPN2 and c) *S. murinus* DSM 41827 and *Streptomyces* sp. GPAT2. These figures were produced using the D-genies platform [4].



Additional file 11: PGP activities test in vitro of *Streptomyces* strains. In vitro tests were carried out jointly for all *Streptomyces* strains. For that, 50 mL of GYM liquid medium was inoculated with the *Streptomyces* strains. 10 µL of unwashed bacterial culture were deposited in triplicate on the different media. Controls were performed with 10 µL of non-inoculated GYM medium. Petri dishes were incubated at 28°C for 7 days. The different media used are described in the Methods section.



Additional file 12: Spermine concentration measured in *Streptomyces* sp. GPA1 pellet and culture supernatant. Targeted metabolomics were performed by ultrahigh-performance liquid chromatography on GPA1 cell pellet, culture supernatant and non-inoculated control medium. Analyses were carried out on 8 biological replicates. Spermine (100 ng/mL) standard was injected during the analysis to calibrate and quantify the samples. Differences were statistically tested using a Kruskal-Wallis test followed by a pairwise Dunn test with Hochberg correction. Different letters indicate statistically significant differences (p-values < 0.05).

References

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3. Parks DH, Imelfort M, Skennerton CT, Hugenholtz P, Tyson GW. CheckM: assessing the quality of microbial genomes recovered from isolates, single cells, and metagenomes. Genome Res. 2015;25:1043–55.

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