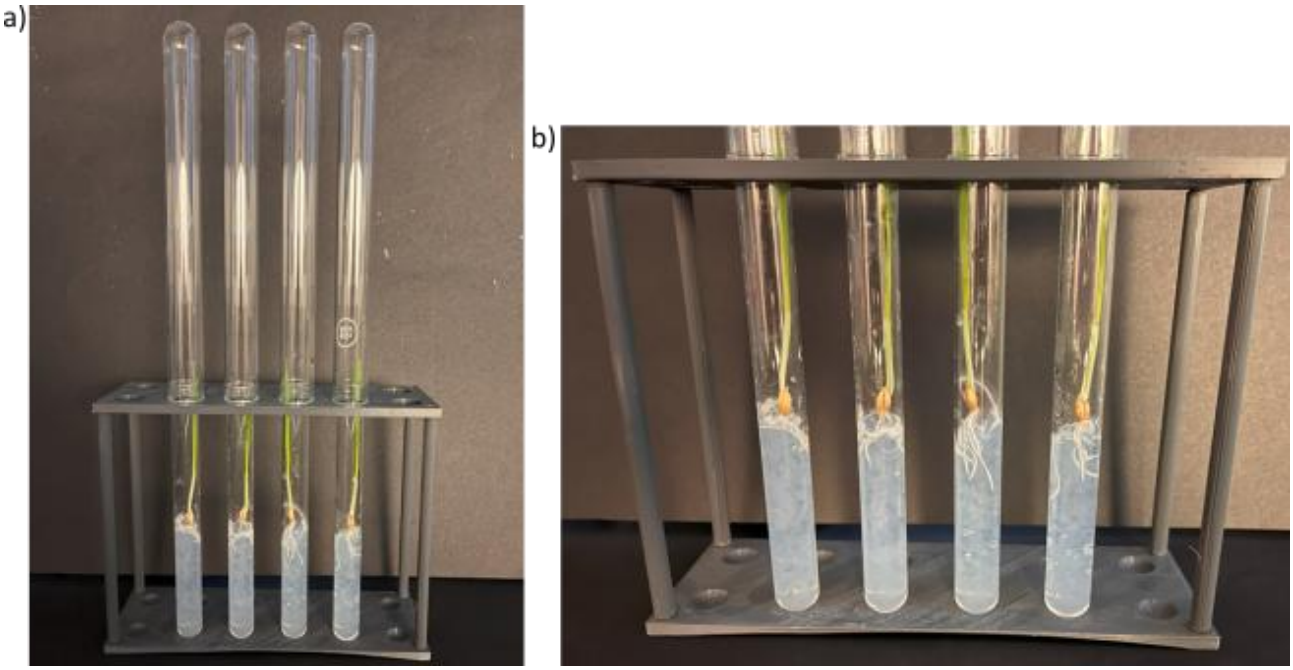


Additional file 1: Barley hydroponic growing system. The system consists of a 16 mm tube containing 9 mL of fragmented sterile semi solid MS medium (agarose 8 g/L). Before seed transfer, an inoculum of 1 mL of bacterial suspension at $1x10^4$ to $5x10^4$ CFU/mL or 1 mL of sterile liquid MS (as a control) 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.

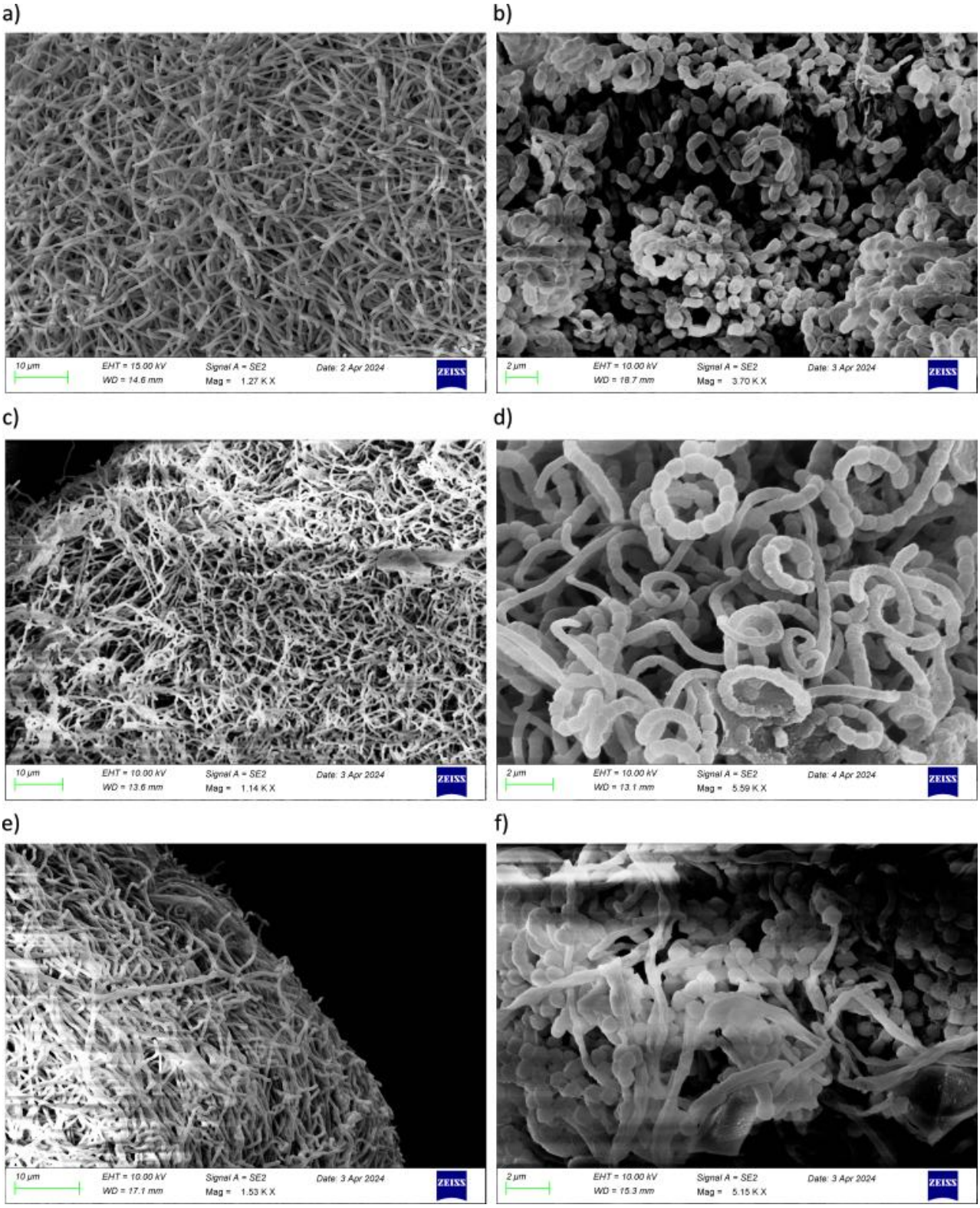
Additional file2: qPCR primers used in this study.

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: Summary of morphological aspects of isolated strains.

microrganism	Culture medium	Macroscopic observation after short time (<7 days)	Macroscopic observation after long time (1 month)	Microscopic observation
GPA1	GYM	Round, regular, yellowish and granular colonies	Irregular colonies. Grey aerial mycelia	Hyphal networks composed of intertwined filaments with few branches. Spores arranged in chains
GPN2	GYM	Round, regular, yellowish and granular colonies	Irregular colonies. Black aerial mycelia on the edge and grey aerial mycelia on the center. Production of an orange-colored pigment	Hyphal networks composed of intertwined filaments with few branches. Spores arranged in chains
GPAT2	GYM	Round, regular, yellowish and granular colonies	Irregular colonies. Black aerial mycelia on the edge and grey aerial mycelia on the center. Production of an orange-colored pigment	Hyphal networks composed of intertwined filaments with few branches. Spores arranged in chains
MRN1	LB	Yellowish, smooth, and regular colonies	No change	ND
Fusarium sp. CK	GYM	White filaments, with occasional development of dark purple pigmentation	Black pigmentation	ND

ND: Not determined



Additional file 4: Scanning electron microscope observation of *Streptomyces* sp. GPA1, GPAT2 and GPN2. a) Filaments and b) spores observation of GPA1. c) Filaments and d) spores observation of GPAT2. e) Filaments and f) spores observation of 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 5: Quality parameters of bacterial genomes.

Strain (assembly software)	Date	Marker lineage	Number of genomes	Number of markers	Number of marker sets	0	1	2	3	4	5+	Completeness	Contamination	Strain heterogeneity	N50 (Kbp)
GPAT2 (Unicycler)	2021-07-06	Streptomycetaceae (UID2048)	60	460	233	1	456	3	0	0	0	99.89	0.68	0.00	8 543.22
GPN2 (Unicycler)	2020-11-02	Streptomycetaceae (UID2048)	60	460	233	1	456	3	0	0	0	99.89	0.68	0.00	4,708.30
GPA1 (sPADEs)	2021-05-20	Streptomycetaceae (UID2048)	60	460	233	0	457	3	0	0	0	100	1.07	0.00	1,145.98
MRN1 (Nextdenovo v2.5.2)	2023-09-08	Pseudomonadaceae (UID4490)	183	845	321	3	837	5	0	0	0	99.84	0.83	60.00	6,140.29

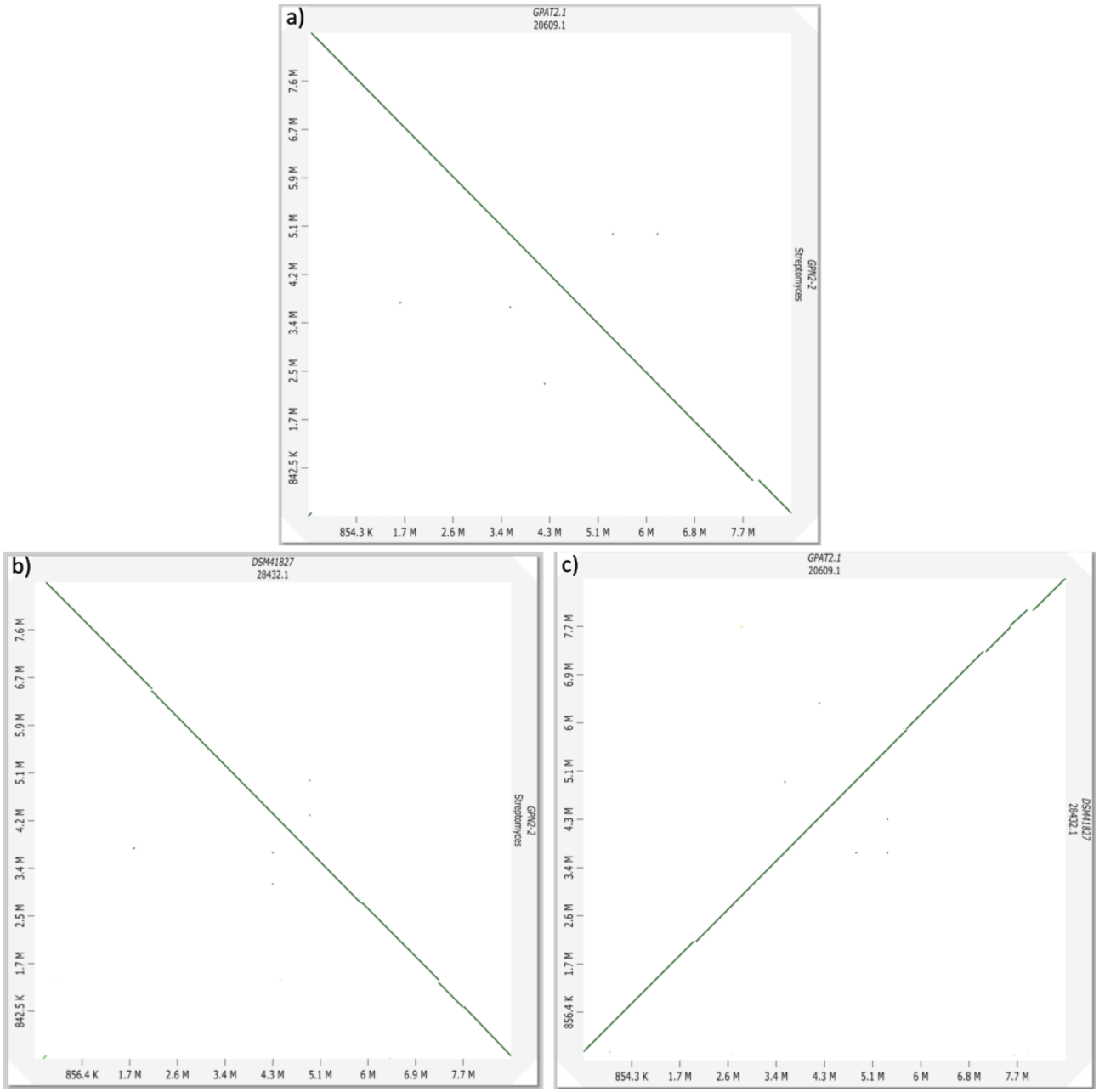
These parameters were estimated using CheckM [1]

Additional file 6: General characteristics of the *Streptomyces* genomes.

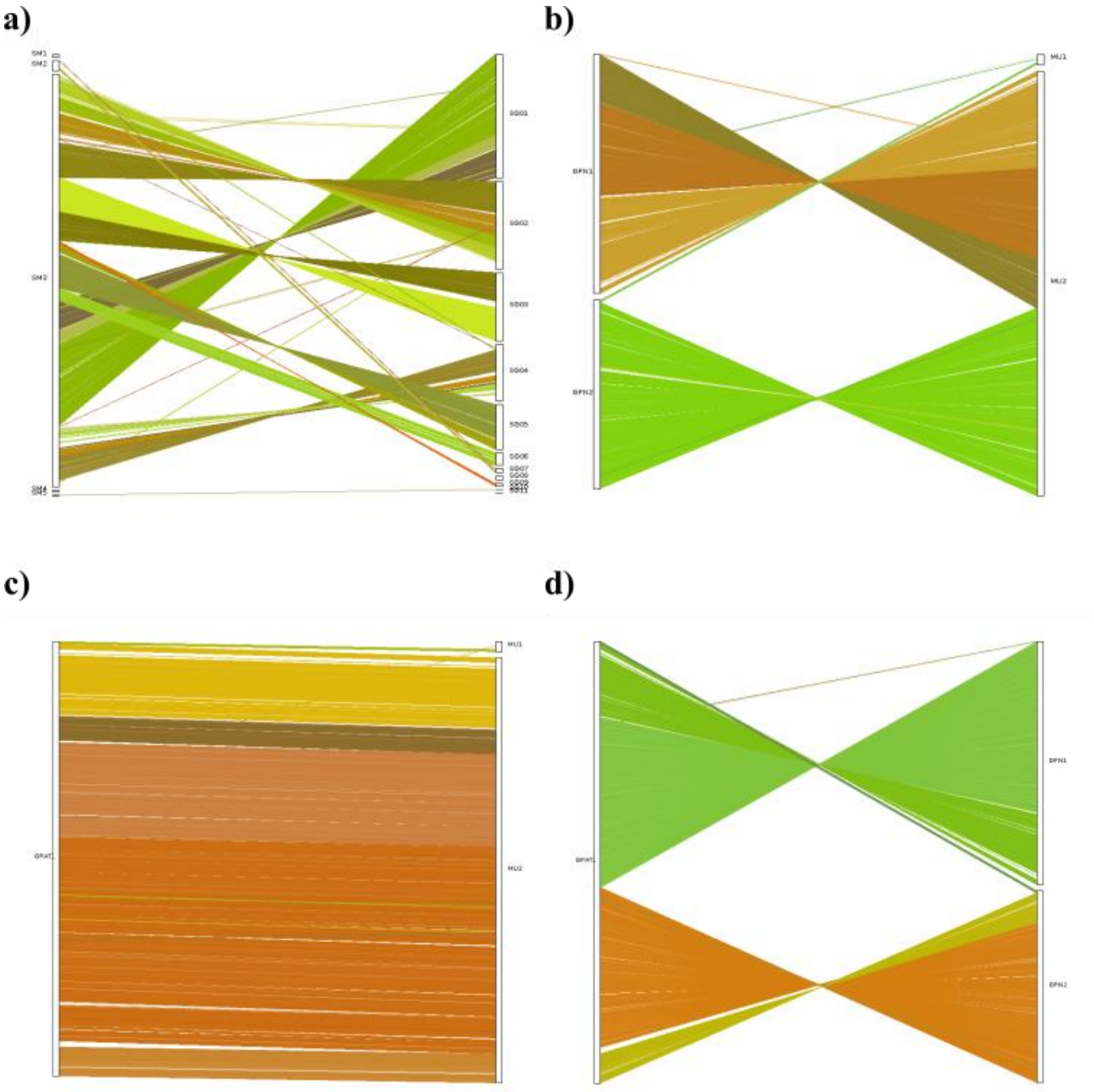
Genome characteristics	GPA1	*Streptomyces misionensis* DSM 40306	GPAT2	GPN2	*Streptomyces murinus* DSM 41827
Size (bp)	8077379	8474121	8543218	8424890	8564314
GC-content (%)	72.26	72.38	71.79	71,83	71.74
Predicted CDS	9552	7874	7985	7793	7715
Genome coding (%)	90.66	88.57	89.52	89.68	89
Average CDS size (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	1 chromosome	2	2
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, 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 (γ- 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)

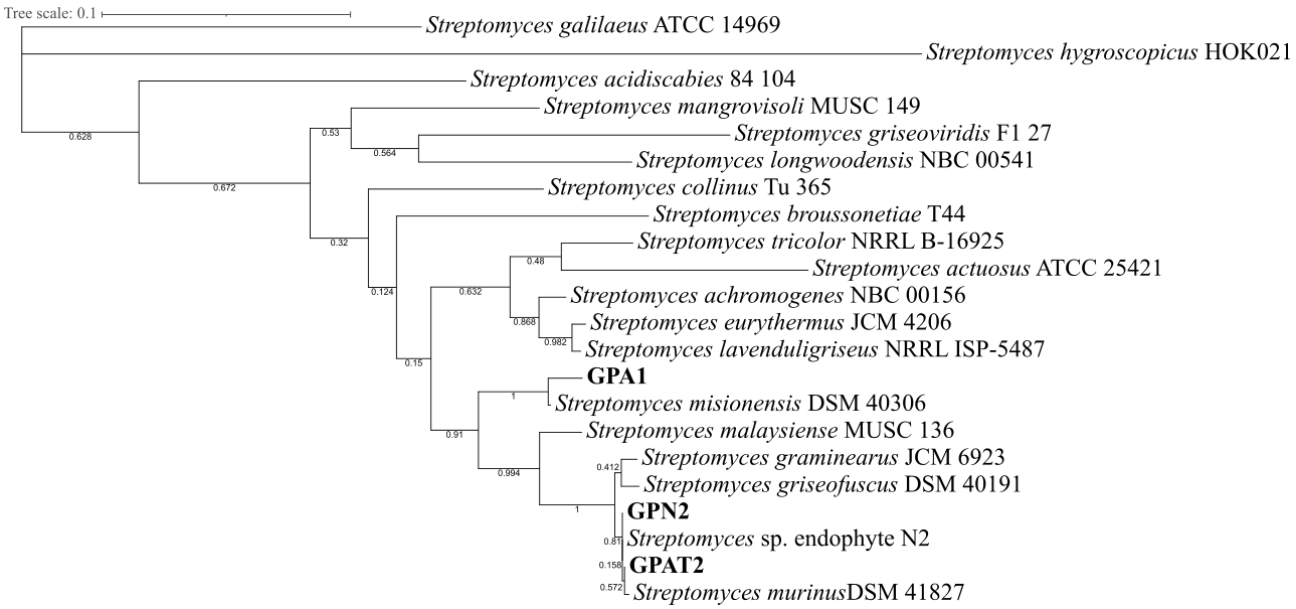
[a]Calculation of repetitive regions did not include undetermined ('N') bases. In bold: the activity was confirmed using Biologs tests



Additional file 7: Syntenies between *Streptomyces* genomes. Dot plot showing the genomic similarities between a) GPAT2 and GPN2, b) *S. murinus* DSM 41827 and GPN2 and c) *S. murinus* DSM 41827 and GPAT2. These figures were produced using the D-genies platform [2].



Additional file 8: Syntenies between *Streptomyces* genomes. This figure was generated using McScanX [3]. a) *S. misionensis* DSM 40306 and GPA1, b) GPN2 and *S. murinus* DSM 41827, c) GPAT2 and *S. murinus* DSM 41827 and d) GPAT2 and GPN2. Each curved line links a pair of syntenic genes between or within the given set of chromosomes. Different colors of lines, generated randomly, represent different syntenic blocks.

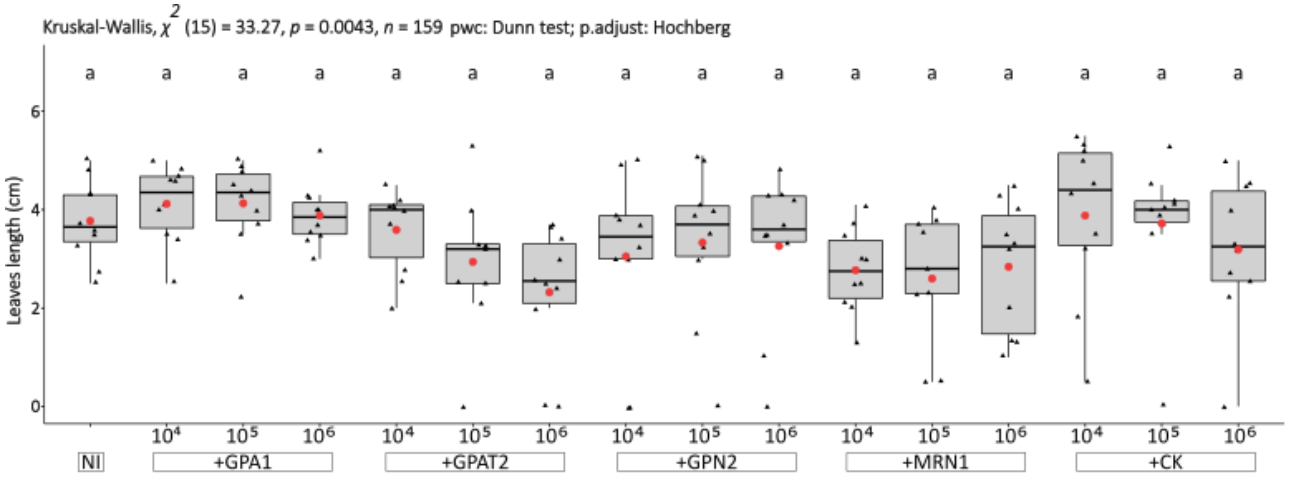


Additional file 9: Phylogenetic trees based on the *rpoB* sequences of GPA1, GPAT2 and GPN2.

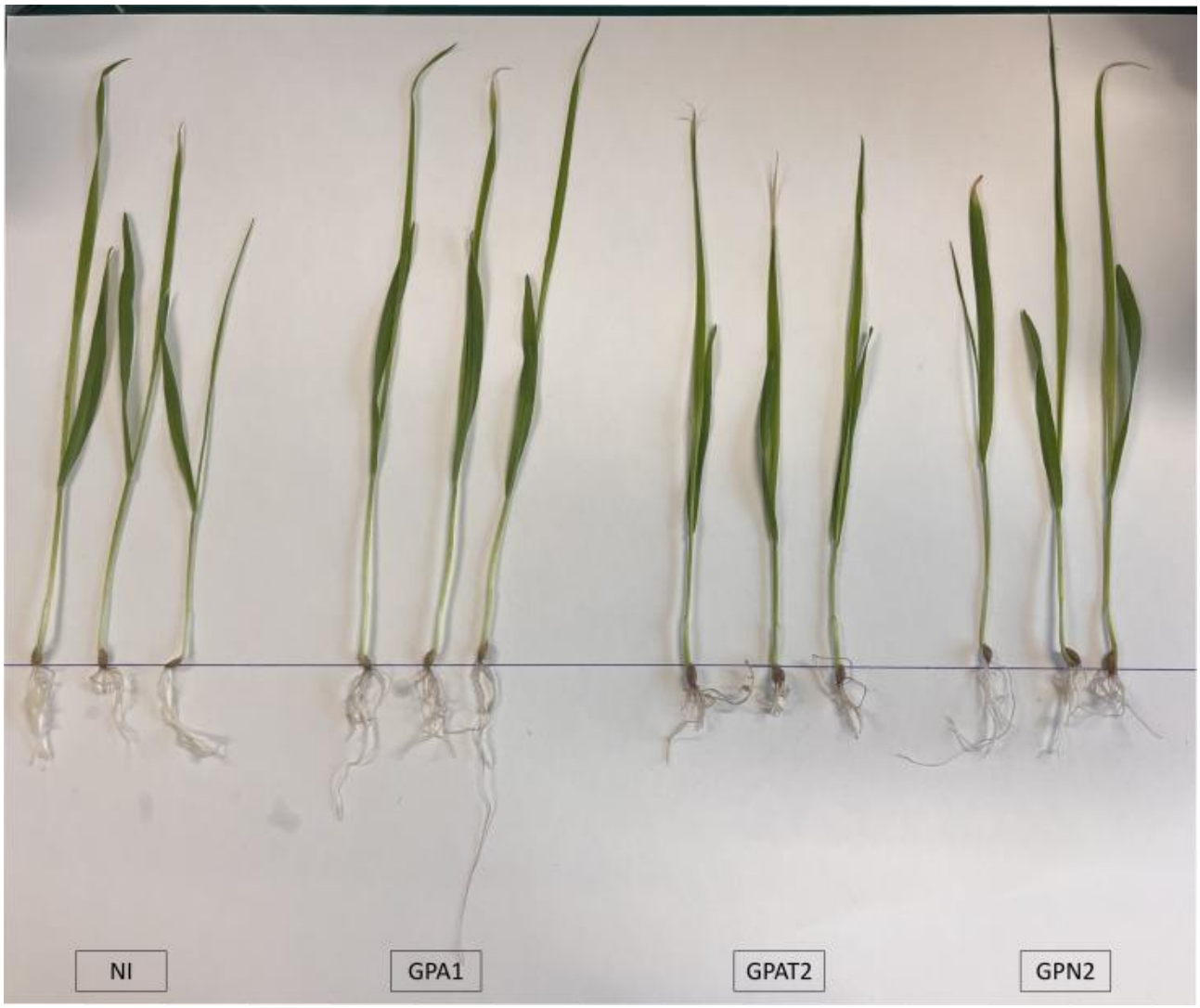
The tree was produced using the BOOSTER plateform (BOOtstrap Support by TransfER) [4] and PhyML-SMS workflow. The tree was implemented in the Interactive Tree Of Life (iTOL) software (v.7) [5]. The black numbers at the branch level represent the bootstrap values.

Additional file 10: Optical density of 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 (++).

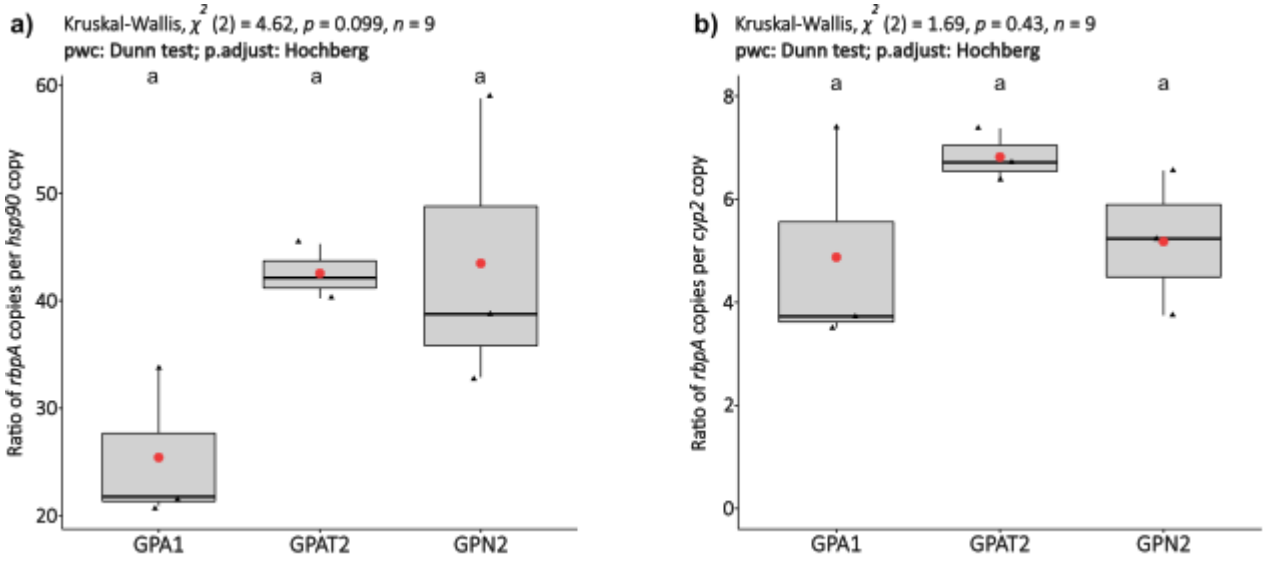
See .xlsx file, Supplementary Material 2



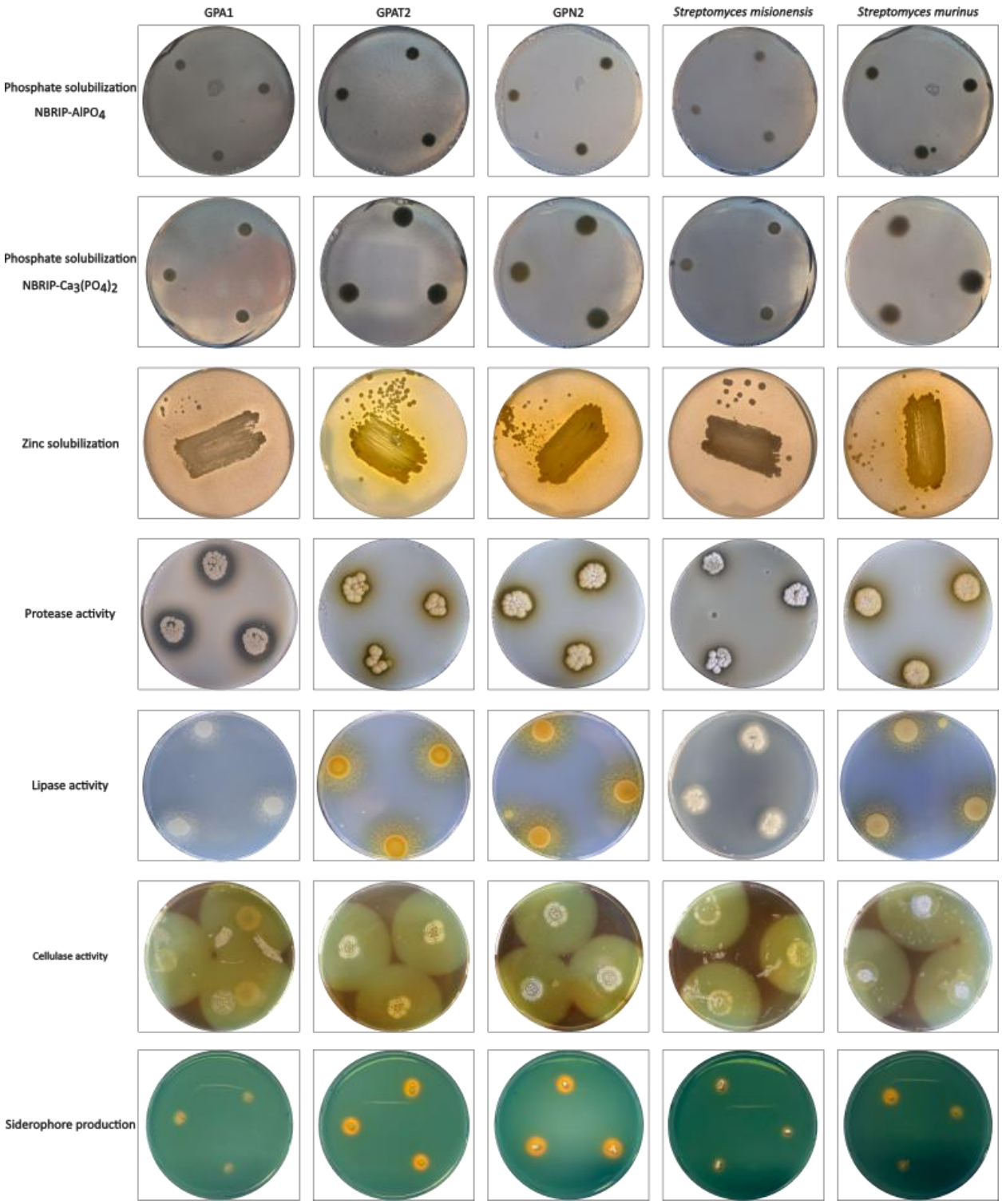
Additional file 11: Effects of microorganisms on leaves size during barley germination. Barley Bowman seeds were inoculated by immersion in microbial suspension containing GPA1, GPAT2, GPN2, MRN1 or *Fusarium* sp. CK at different concentrations (10^6, 10^5, 10^4 CFU or spores/mL). Inoculated seeds were 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 MRN1 at concentration 10^5 CFU/mL where 9 seeds were measured.



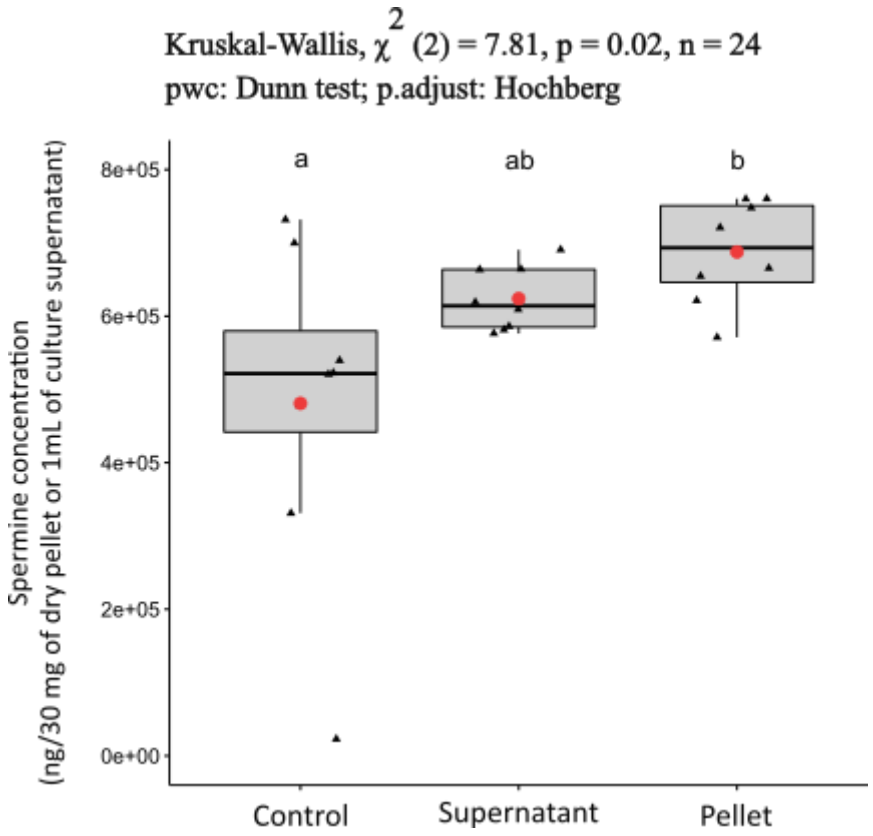
Additional file 12: Barley seedlings grown in the hydroponic system at 14 dpi. NI: Non-inoculated seedlings, GPA1: seedlings inoculated with GPA1, GPAT2: seedlings inoculated with GPAT2, GPN2: seedlings inoculated with GPN2. Seedlings were selected at random from a pool of 19 for non-inoculated seedlings and 20 for other conditions.



Additional file 13: 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 14: 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 15: Spermine concentration measured in 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

1. 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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