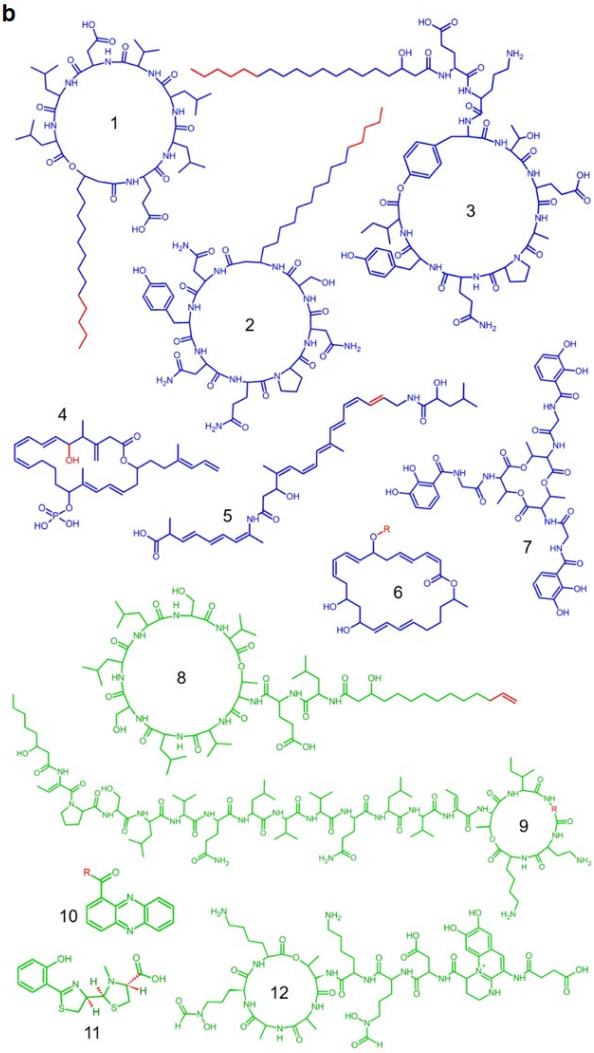
a

***Bacillus velezensis* GA1 *and Pseudomonas* sp. CMR12a detectable Bioactive Secondary Metabolite (BSMs) differential production**

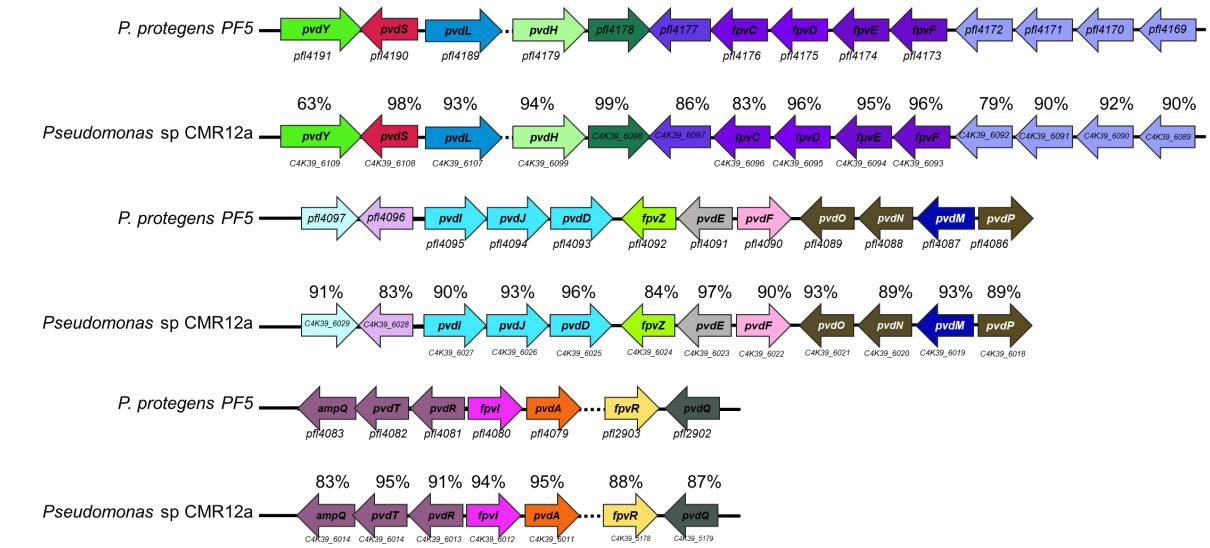
BSM	Main described activities	Raw formula of variants	Detected m/z (mass error (ppm))	EM	CAA
1 Surfactins	ISR Motility	**C12** : $C_{90}H_{157}N_7O_{13}$ **C13** : $C_{91}H_{159}N_7O_{13}$ **C14** : $C_{92}H_{161}N_7O_{13}$ **C15** : $C_{93}H_{163}N_7O_{13}$ **C16** : $C_{94}H_{165}N_7O_{13}$	994.6420 (1,5) 1008.6582 (0,9) 1022,6743 (0,5) 1036.6904 (4,8) 1050.7061 (1,7)		
2 Iturins	Antifungal	**C14** : $C_{86}H_{134}N_{12}O_{14}$ **C15** : $C_{87}H_{136}N_{12}O_{14}$ **C16** : $C_{88}H_{138}N_{12}O_{14}$ **C17** : $C_{89}H_{140}N_{12}O_{14}$	1043.5510 (1,0) 1057.5653 (2,2) 1071.5809 (2,3) 1085.5967 (2,1)		
3 Fengycins	Antifungal	**C15** : $C_{71}H_{109}N_7O_{20}$ **C16** : $C_{72}H_{111}N_7O_{20}$ **C17** : $C_{73}H_{113}N_7O_{20}$ **C18** : $C_{74}H_{114}N_7O_{20}$ **C19** : $C_{75}H_{116}N_7O_{20}$	1449.7806 (4,8) 1463.8004 (1,9) 1477.8171 (2,5) 1491.8305 (2,7) 1505.8440 (4,1)		
4 Difficidins	Antibacterial	**Difficidin** : $C_{71}H_{45}O_{19}P$ **Oxydifficidin** : $C_{71}H_{45}O_{21}P$	567.2828 (3,2) 583.2795 (7,8)		
5 Bacillaenes	Antibacterial	**Bacillaene** : $C_{35}H_{48}N_2O_8$ **Dihydro-** : $C_{34}H_{50}N_2O_8$	581.3585 (2,3) 583.3726 (2,7)		
6 Macrolactins	Antibacterial	**A**:$C_{31}H_{54}O_8$(R=H) ***7-O-malonyl*-A**:$C_{37}H_{58}O_{11}$ (R=CO-CH_2-COOH) ***7-O-succinyl*-A**:$C_{38}H_{60}O_{11}$ (R=CO-CH_2-CH_2-COOH) **D**:$C_{34}H_{48}O_{13}$ (R=6-*O*-syccinyl-β-gluc.)	425.2298 (6,7) 511,2292 (2,0) 525.2459 (0,0) 687.2991 (0,6)		
7 Bacillibactin	Siderophore	$C_{20}H_{21}N_3O_{18}$	883.2620 (0,1)		
8 Orfamides	Antifungal ISR	**B** : $C_{83}H_{112}N_{10}O_{17}$ **D** : $C_{81}H_{108}N_{10}O_{17}$ **E** : $C_{83}H_{110}N_{10}O_{17}$	1281.8387 (8,4) 1253.8054 (7,0) 1279.8157 (2,6)		
9 Sessilins	Antifungal ISR	**A**:$C_{56}H_{100}N_{22}O_{25}$(R=Hse) **B**:$C_{56}H_{100}N_{22}O_{24}$(acyclic A) **C** :$C_{54}H_{102}N_{22}O_{24}$(R=Gly)	1014.6457 (18,4) 1023.6473 (14,7) 992.6264 (12,6)		
10 Phenazines	Antibiotic ISR	**PCA** : $C_{13}H_8N_2O_2$ (R=OH) **PCN** : $C_{13}H_9NO_3$ (R=NH_2)	225.0681 (10,0) 224.0814 (2,0)		
11 Pyochelins	Siderophore	**Enantio-** : $C_{14}H_{18}N_2O_3S_2$ (4'*S*,2"*S*,4"*S*)	325.0665 (3,1)		
12 Pyoverdine	Siderophore	$C_{53}H_{82}N_{15}O_{21}$	1289.5928 (3,5)		

b



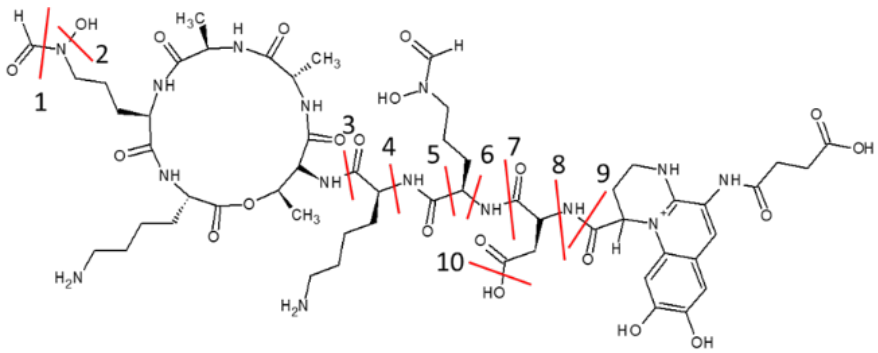
Supplementary Figure 1. Diversity of predicted and detectable BSMs produced by *B. velezensis* GA1 and *Pseudomonas* sp. CMR12a. a, *B. velezensis* GA1 and *Pseudomonas* sp. CMR12a BSMs and their corresponding main described activities, the raw formula of detected variants with molecular mass and mass chromatograms. BSMs were detected in exudate mimicking media (EM) and casamino acid media (CAA) The numbers next to the molecule name indicate the corresponding BSMs structure depicted in **b. b,** BSMs structural formulas are represented and changes observed in variants are indicated in red.

a

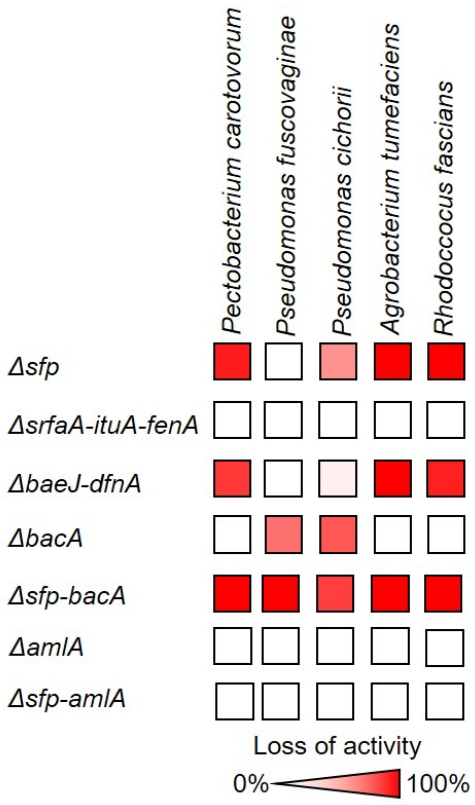


b

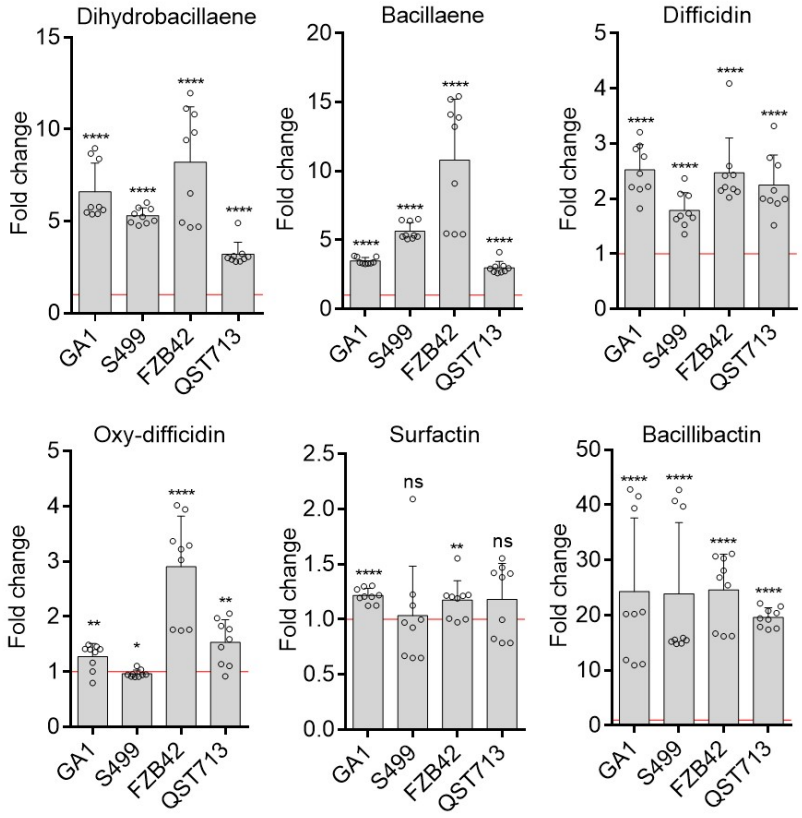
FRAGMENTS	m/z	FRAGMENT INTENSITY
1	1260.5857	2980.48
2/10	1270.5686	2025.38
3	759.2935	1620.38
4	648.2229	944.03
5	603.2024	829.93
6	490.1537	716.68
7	473.1280	21347.25
8	375.1266	2453.58
9	358.1015	1312.32
10	1270.5686	2025.38



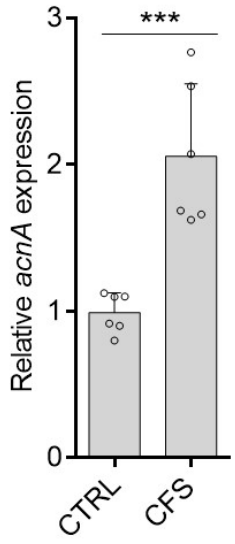
Supplementary Figure 2: ***Pseudomonas* sp. CMR12a produces a pyoverdine similar to the one of *Pseudomonas protegens* Pf-5. a,** Genes of pyoverdine clusters identified in *Pseudomonas* sp. CMR12a and *P. protegens* Pf-5. *P. protegens* Pf-5 pyoverdine genes described by Hartney et al., 2013 were compared to *Pseudomonas* sp. CMR12a genes. The corresponding locus tag and the nucleotide identity calculated by blast in MAGE platform (https://mage.genoscope.cns.fr/microscope/home/index.php) are indicated for each gene. **b,** The assigned fragments of *Pseudomonas* sp. CMR12a pyoverdine confirm the structural similarity with the pyoverdine described for *P. protegens* Pf-5 [1].



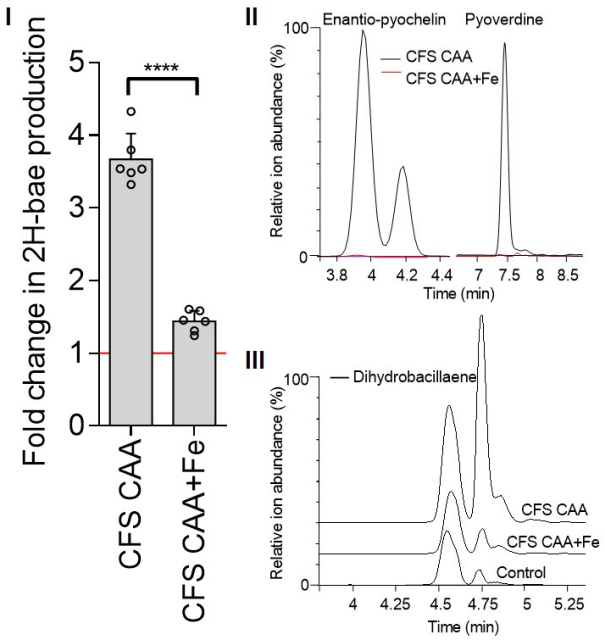
Supplementary Figure 3. Anti-bacterial activity of *B. velezensis* GA1 relies on its production of a wide range of diverse BSMs. The heatmap shows the loss of anti-bacterial activity of *B. velezensis* GA1 mutants against *Pectobacterium carotovorum, Pseudomonas fuscovaginae, Pseudomonas cichorii, Agrobacterium tumefaciens* and *Rhodoccocus fascians*. The mutants are impaired in the production of NRPs and PKs (Δ*sfp*), surfactins, iturins and fengycins (Δ*srfA-ituA-fenA*), difficidins and bacillaenes (Δ*dfnA-baeJ*), bacilysin (Δ*bacA*), NRPs, PKs and bacilysin (Δ*sfp-bacA*), amylolysin (Δ*amlA*) and NRPs, PKs and amylolysin (Δ*sfp-amlA*). The intensity of mutant's activity loss is represented as the intensity of red color where the darkest red indicates loss of 100 % and white color indicated no loss compared to the wild-type.



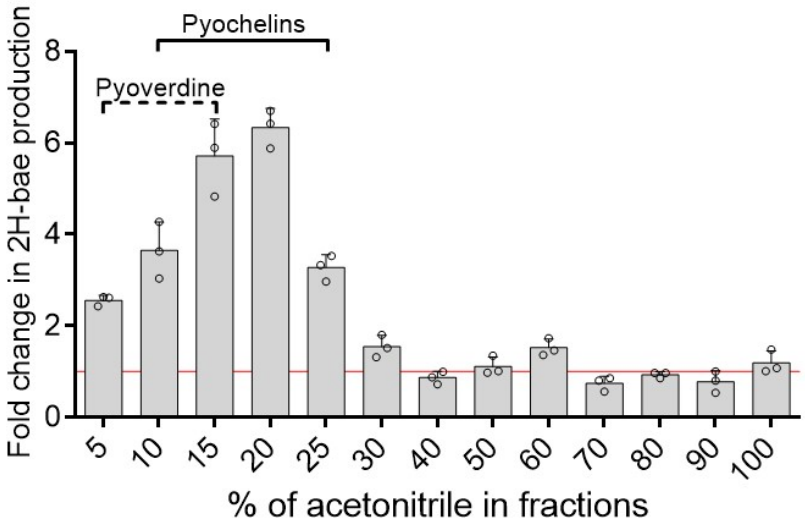
Supplementary Figure 4: Effect of *Pseudomonas* sp. CMR12a metabolites on the BSMs production by *B. velezensis* strains GA1, S499, FZB42 and QST713. BSMs production by *B. velezensis* GA1, S499, FZB42 and QST713 after 24 h of interaction with 4 % (v/v) of *Pseudomonas* sp. CMR12a Δ*sesA-ofaBC* CFS. Fold change equals to 1 is represented as a red line and corresponds to the production of metabolites in *B. velezensis* strains monocultures. Error bars indicate standard error (n=9 within three biological repetitions and three technical replicates). Statistical significance of each condition was calculated as a comparison of BSMs production by *B. velezensis* strains in treated cultures with the production in related monocultures, by using Mann–Whitney test where ''ns'' represents no significant difference (P>0.05); ''**'', significant difference (0.001>P<0.05) and ''****'' significant difference (P<0.0001).



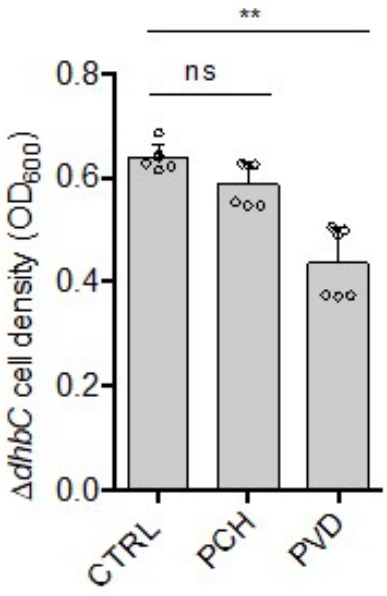
Supplementary Figure 5. Enhanced expression of the *acnA* gene by *B. velezensis* S499 in presence of Pseudomonas CFS. Expression of *acnA*, encoding the amylocyclicin precursor, after 8h of *B. velezensis* S499 interaction with 2% of *Pseudomonas* cell-free supernatant (CFS) compared to the *B. velezensis* S499 monoculture (CTRL). Error bars indicate standard error (n=6 within two biological repetitions). The statistical difference, in *acnA* gene expression, between the two conditions was calculated by using T-test where ''***'' represents a statistically significant difference between the two conditions (0.0001>P<0.001).



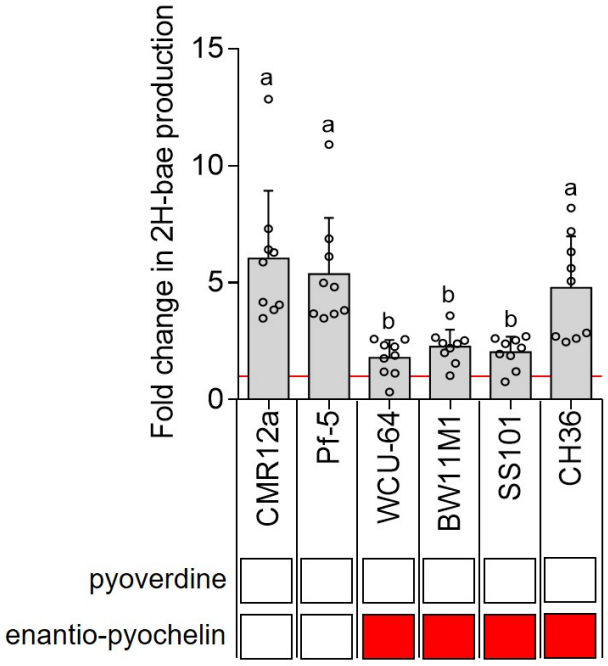
Supplementary Figure 6: Effect of iron supplementation to *Pseudomonas* sp. CMR12a culture on dihydrobacillaene production by *B. velezensis*. I, Iron supplementation to *Pseudomonas* sp. CMR12a culture significantly reduced enhancement of dihydrobacillaene (2H-bae) production by *B. velezensis* GA1. *B. velezensis* GA1 culture was supplemented with 4 % of CFS obtained in CAA medium (CAA) or with iron supplemented CFS (CFS CAA+Fe). The production of 2H-bae was evaluated after 24 h of co-culture. Fold change equals to 1 is represented as a red line and corresponds to the production of 2H-bae in *B. velezensis* GA1 monoculture. Error bars indicate standard error (n=6 within two biological repetitions and three technical replicates). Statistical difference between two conditions was calculated by using Mann–Whitney test where **** represents a significant difference ($P<0.0001$). **II**, LC-MS analysis of pyochelin and pyoverdine production by *Pseudomonas* sp. CMR12a in CAA (black line) or CFS CAA+Fe (red line) medium after 48h. **III**, Chromatogram of dihydrobacillaene production by *B. velezensis* GA1 monoculture (Control), *B. velezensis* GA1 growing with CFS CAA or *B. velezensis* GA1 growing with CFS CAA+Fe.



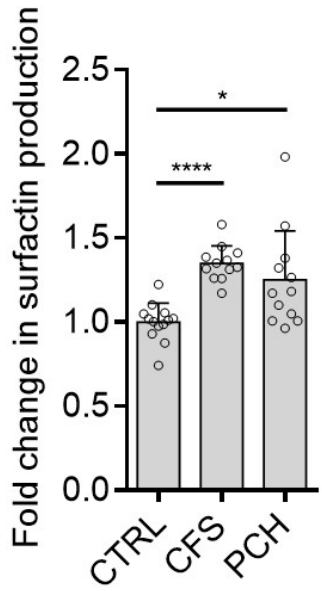
Supplementary Figure 7: Fractions containing enantio-pyochelin are the main inducers of dihydrobacillaene production by *B. velezensis* GA1. The impact of *Pseudomonas* sp. CMR12a Δ*sesA-ofaBC* CFS fractions, eluted from C18 cartridge with increasing stepwise acetonitrile-water ratio expressed in %(v/v) , on 2H-bae production by *B. velezensis* GA1 is linked to the presence of *Pseudomonas* sp. CMR12a siderophore in the fractions. The fractions with pyoverdine and/or enantio-pyochelin are labeled as dashed and solid lines, respectively. *B. velezensis* GA1 cultures were co-cultured with 4 % (v/v) of the fractions of *Pseudomonas* sp. CMR12a during 24 h. The *Pseudomonas* sp. CMR12a siderophores content is expressed in % of the crude sample. Fold change equals to 1 is represented as a red line and corresponds to the production of 2H-bae in *B. velezensis* GA1 monoculture. Data show a representative result of one of two biological repetitions. Error bars indicate standard error (n=3).



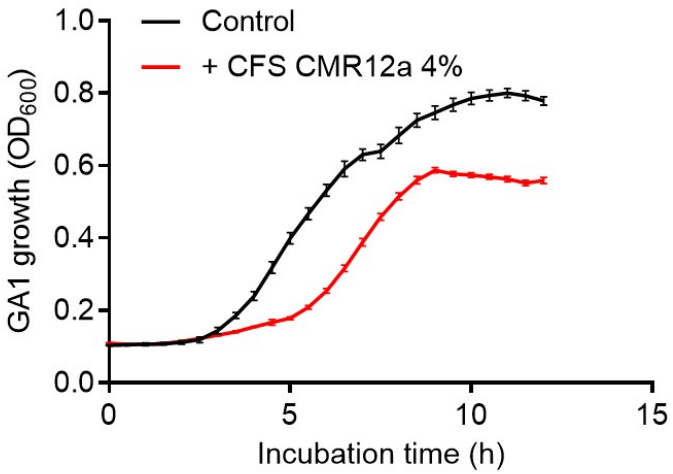
Supplementary Figure 8: Effect of pure pyoverdine and pyochelin on the growth of the bacillibactin-suppressed mutant of *B. velezensis* GA1. Pure compounds were added at a concentration corresponding to the one resulting from the addition of culture supernatant (CFS CAA) at 4 % v/v in the *Bacillus* culture. Growth expressed as cell density or OD_{600nm} was measured at the mid-exponential phase. Error bars indicate standard error (n=6 with two biological repetitions and three technical replicates). Statistical difference between different conditions was calculated by using T- test where ''ns'' represents no significant difference (P>0.05); and ''**'', significant difference (0.001>P<0.05).



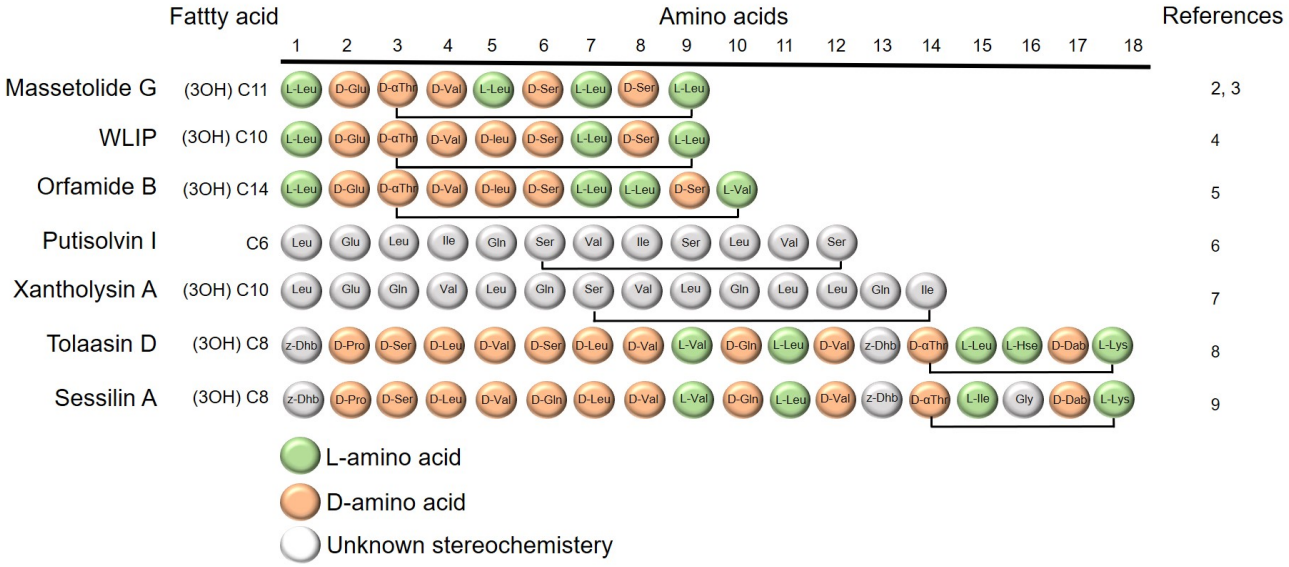
Supplementary Figure 9: Induction of 2H-bae by *Pseudomonas* strains. The 2H-bae production by *B. velezensis* GA1 is differently impacted by *P. protegens* Pf-5, WCU-84, *P. putida* BW11M1, *P. lactis* SS101 and *P. tolaasii* CH36, and is dependent on the production of pyoverdine and enantio-pyochelin by the *Pseudomonas* strains. *B. velezensis* GA1 culture was supplemented with 4 %(v/v) of *Pseudomonas* CFSs and the production of 2H-bae was evaluated after 24h of culture. Fold change equals to 1 is represented as a red line and corresponds to the production of 2H-bae in *B. velezensis* GA1 monoculture. Error bars indicate standard error (n=9 within three biological repetitions and three technical replicates). Different letters indicate groups of statistically different conditions (one-way ANOVA and Tukey test; $P<0.05$). Production of metabolites in *B. velezensis* GA1 monoculture is not statistically different from the conditions within group b. Siderophores production (white boxes) or lack thereof (red boxes) by aforementioned *Pseudomonas* strains, used in this study are represented below the corresponding strain.



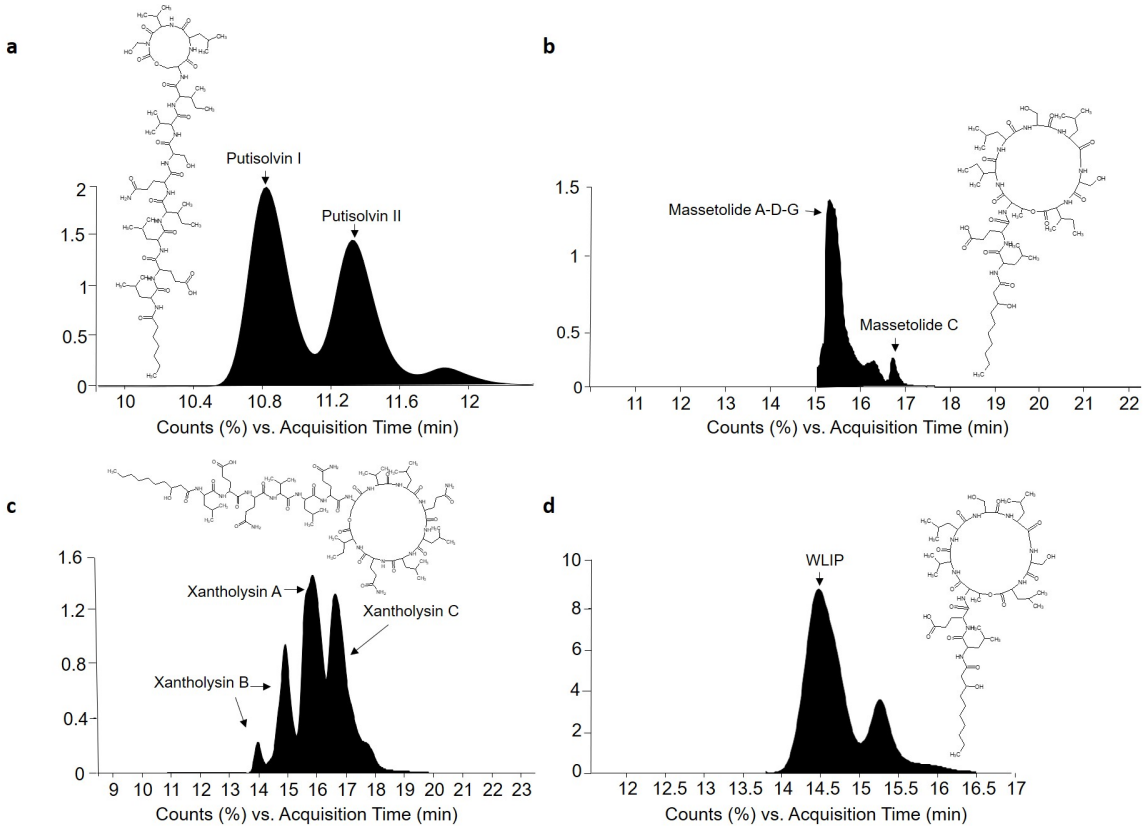
Supplementary Figure 10. Enantio-pyochelin partially triggers surfactin production by *B. velezensis* GA1. Surfactin production by *B. velezensis* monoculture (CTRL) in comparison with the production upon addition of *Pseudomonas* sp. CMR12a cell-free supernatant (CFS, added at 4 % (v/v)) and 1.4 µM of pure PCH. Analysis of surfactin in the culture broth was performed after 20 h of incubation. Error bars correspond to standard error (n=12 to 9 within four biological repetitions and three technical replicates). Statistical difference between the controlled and other conditions was calculated by using Mann–Whitney test where ‘’****’’ represents significant difference (P<0.0001) and ‘’*’’, significant difference (0.01>P<0.05).



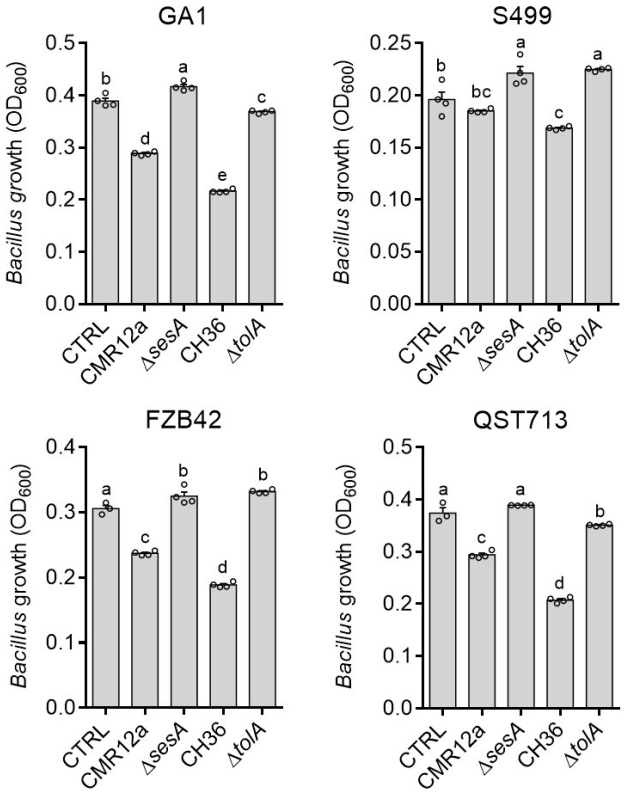
Supplementary Figure 11: Effect of *Pseudomonas* CFS on *Bacillus* growth: The dose-effect (4 % (v/v)) of *Pseudomonas* sp. CMR12a CFS was tested on *B. velezensis* GA1 growth. Growth inhibition is expressed as a change in the cell density of *B. velezensis* GA1. Error bars indicate standard error (n=6 within two biological repetitions and three technical replicates).



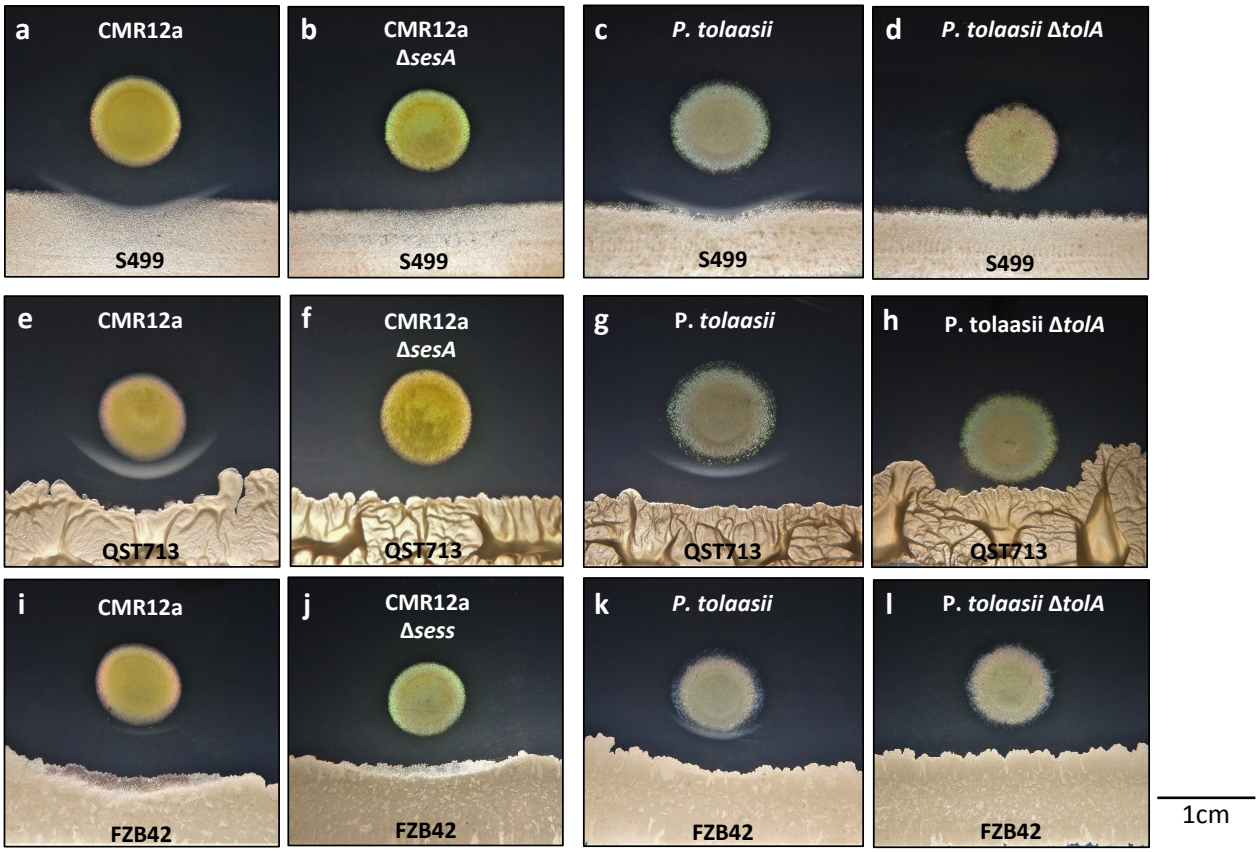
Supplementary Fig. 12: **Structures and amino acids composition of the different *Pseudomonas* CLPs used**. The structures including the fatty chain length and the amino acid composition of the CLPs produced by the different *Pseudomonas* strains used in this study are depicted. Circle colors represented the stereochemistry of the CLPs. Only the main detected forms are indicated (for more details about minor variants see the corresponding associated references[2–7]).



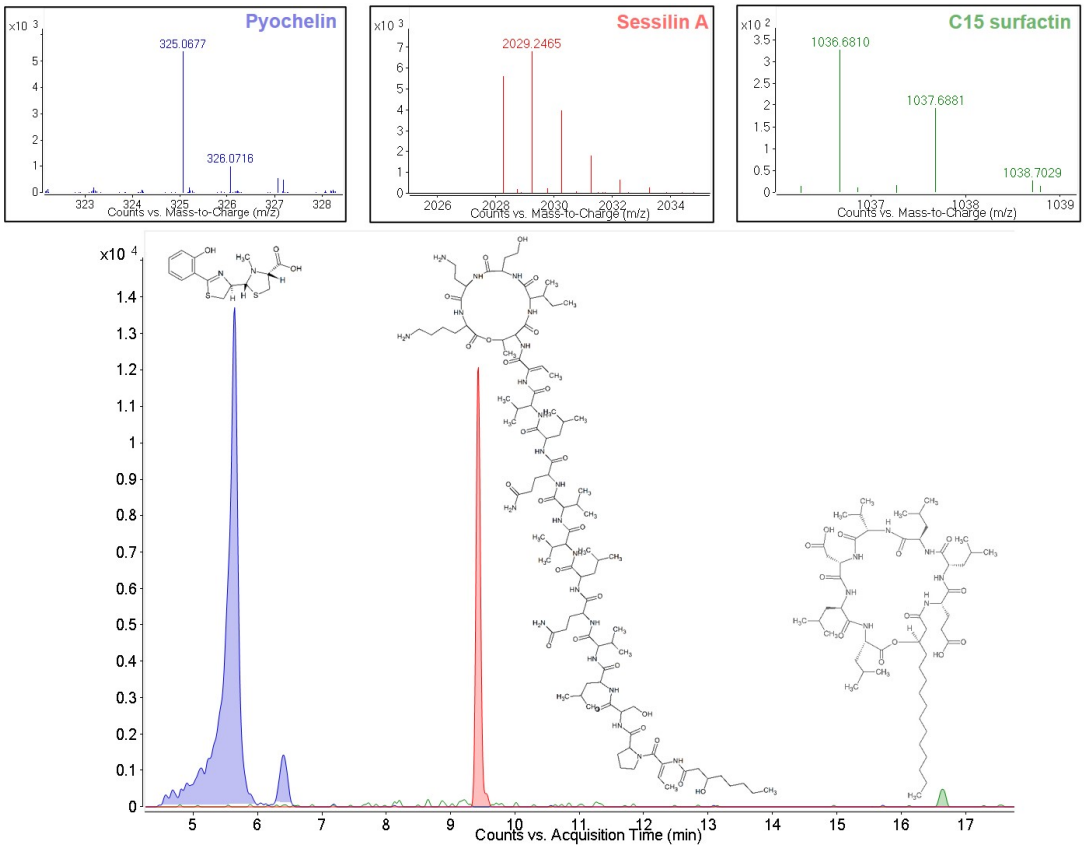
Supplementary Figure 13: Mains CLPs produce by *P. putida* WCU-84, *P. lactis* SS101, *P. putida* BW11M1 and *P. putida* RW10S2. a, Relative ion abundance of putisolvin I and II produced by *P. putida* WCU-84. The structural formula of putisolvin I is presented. **b,** Relative ion abundance massetolide A-D-G, C and WILP produced by *P. lactis* SS101. The structural formula of WLIP is indicated. **c,** Relative ion abundance of xantholysin A, B and C produced by *P. putida* BW11M1. Structural formula of xantholysin A is presented. **d,** Relative ion abundance of massetolide A-D-G, E, H by *P. putida* RW10S2. The structural formula of massetolide A for *P. putida* RW10S2 is represented.



Supplementary Figure 14: Sessilin and tolaasin inhibit the growth of different *B. velezensis* strains. The effects of CFS of *Pseudomonas* sp. CMR12a wild type or Δ*sesA* mutant impaired in sessilin production, and *P. tolaasii* or Δ*tolA* mutant CFS impaired in tolaasin on *B. velezensis* strains (FZB42, S499, QST713 and GA1) growth. Growth inhibition, expressed as change in the cell density of *B. velezensis* GA1, was measured after 7 h culture while 4 %(v/v) of the CFS of *Pseudomonas* sp. wild types or mutants CFS were added to the *B. velezensis* GA1 cultures. Error bars indicate standard error (n=4 within two biological repetitions and two technical replicates). Different letters indicate groups of statistically different conditions (one-way ANOVA and Tukey test; $P<0.05$).



Supplementary Figure 15: White line formation between surfactin and sessilin/tolaasin is conserved in the *B. velezensis* species. The white line formation is dependent on the co-presence of surfactin and sessilin/tolaasin producers while during interaction between *B. velezensis* wild-type strains and *Pseudomonas* sp. mutant impaired in the production of sessilin/tolaasin no white-line are observed. Sessilin/tolaasin production induces slight growth inhibition of all *B. velezensis* (**a, c, e, g, e and k**) whereas no inhibition is observed in confrontation assays with *Pseudomonas* mutants unable to produce these metabolites (**b, d, f, h, j and l**).



Supplementary Figure 16: Quantification of sessilin, surfactin and pyochelin produced *in planta*. LC-MS analysis of extracts from co-inoculated plants (n=16 of 3 independent experiments including at least 4 plants per condition) with *B. velezensis* GA1 and *Pseudomonas* sp. CMR12a after 3 days of co-inoculation on tomato plant roots.

References:

1. Hartney, S. L. *et al.* Ferric-pyoverdine recognition by Fpv outer membrane proteins of pseudomonas protegens pf-5. *J. Bacteriol.* **195**, 765–776 (2013).
2. Sinnaeve, D. *et al.* Structure and X-ray conformation of pseudodesmins A and B, two new cyclic lipodepsipeptides from Pseudomonas bacteria. *Tetrahedron* **65**, 4173–4181 (2009).
3. Li, W. *et al.* The Antimicrobial Compound Xantholysin Defines a New Group of Pseudomonas Cyclic Lipopeptides. *PLoS One* **8**, e62946 (2013).
4. Ma, Z., Hoang Hua, G. K. H., Ongena, M. & Höfte, M. Role of phenazines and cyclic lipopeptides produced by pseudomonas sp. CMR12a in induced systemic resistance on rice and bean. *Environ. Microbiol. Rep.* **8**, 896–904 (2016).
5. Kuiper, I. *et al.* Characterization of two Pseudomonas putida lipopeptide biosurfactants, putisolvin I and II, which inhibit biofilm formation and break down existing biofilms. *Mol. Microbiol.* **51**, 97–113 (2003).
6. Bassarello, C. *et al.* Tolaasins A−E, Five New Lipodepsipeptides Produced by *Pseudomonas tolaasii*. *J. Nat. Prod.* **67**, 811–816 (2004).
7. D'aes, J. *et al.* To settle or to move? The interplay between two classes of cyclic lipopeptides in the biocontrol strain Pseudomonas CMR12a. *Environ. Microbiol.* **16**, 2282–2300 (2014).