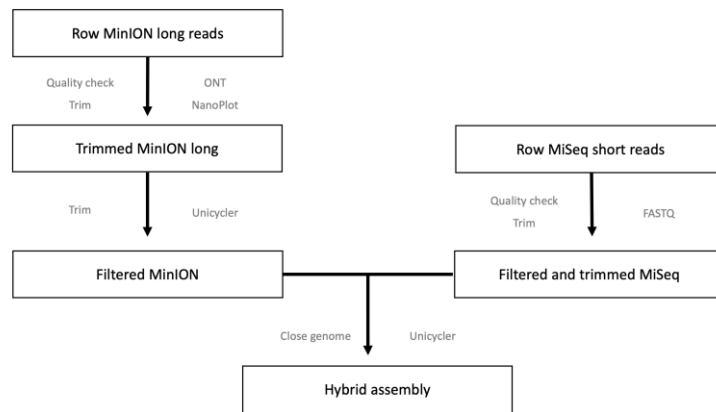
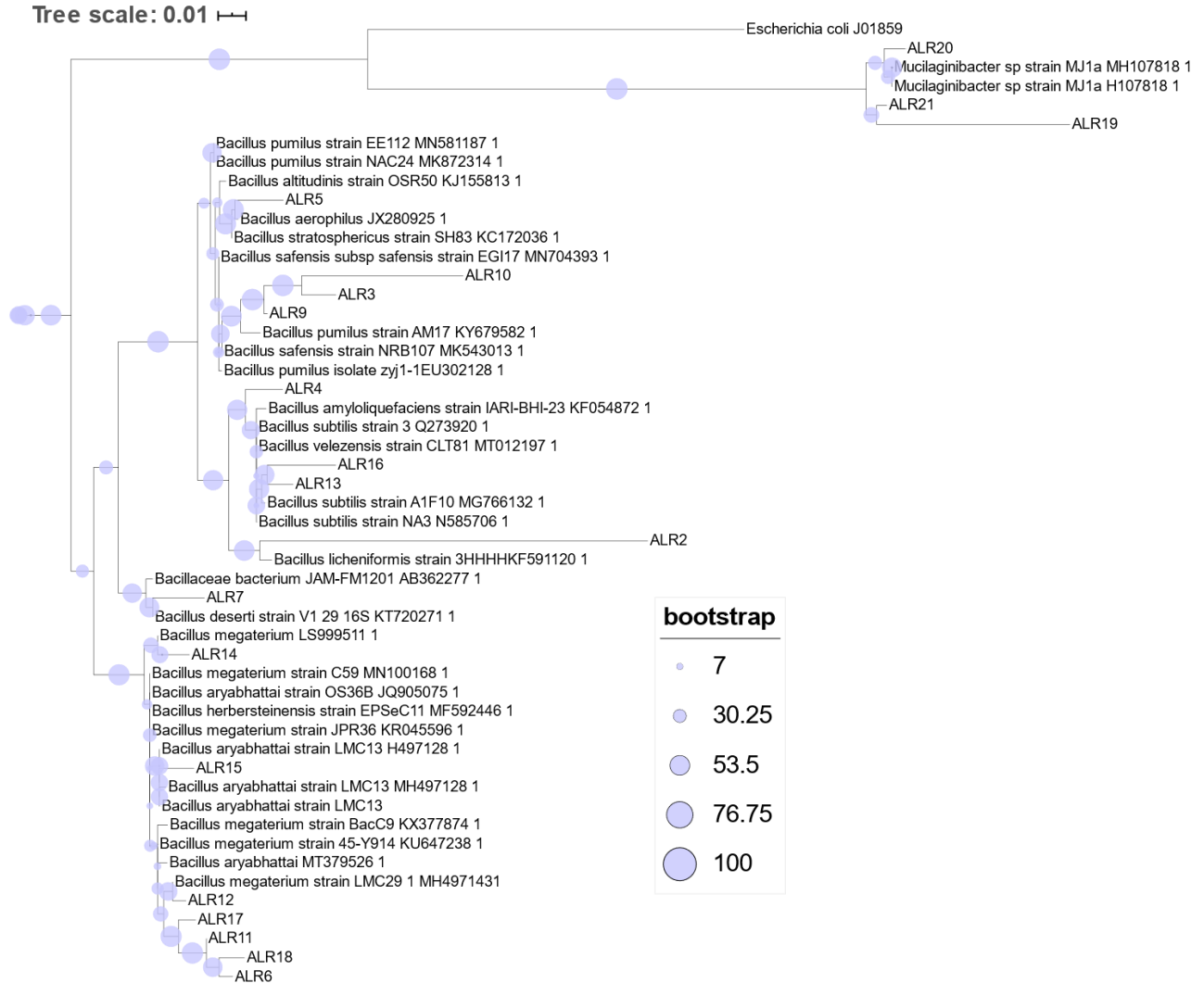


## Supplementary data



**Figure S1.** Bioinformatic workflow of the hybrid, MinION and MiSeq assembly.



**Figure S2.** Neighbor-joining phylogenetic tree constructed based on the 16S ribosomal RNA (rRNA) gene sequences from bacteria isolated showing the phylogenetic relationships between all isolated strains including *Mucilaginibacter* sp. 21p. Values indicate percentages of identical branching in 100 bootstrapping. The sequence of *Escherichia coli* J01859 was used as an out-group.

**Table S1: Direct submission of sequence data to GenBank**

Submission Number and Taxonomic		
SUB8325601 ALR1	MW187503	<i>Bacillus</i> sp.
SUB8325601 ALR2	MW187504	<i>Bacillus licheniformis</i>
SUB8325601 ALR3	MW187505	<i>Bacillus pumilus</i>
SUB8325601 ALR4	MW187506	<i>Bacillus</i> sp.
SUB8325601 ALR5	MW187507	<i>Bacillus aerophilus</i>
SUB8325601 ALR6	MW187508	<i>Bacillus</i> sp.
SUB8325601 ALR7	MW187509	<i>Bacillus</i> sp.
SUB8325601 ALR9	MW187510	<i>Bacillus pumilus</i>
SUB8325601 ALR10	MW187511	<i>Bacillus pumilus</i>
SUB8325601 ALR11	MW187512	<i>Bacillus</i> sp.
SUB8325601 ALR12	MW187513	<i>Bacillus megaterium</i>
SUB8325601 ALR13	MW187514	<i>Bacillus subtilis</i>
SUB8325601 ALR14	MW187515	<i>Bacillus megaterium</i>
SUB8325601 ALR15	MW187516	<i>Bacillus aryabhatai</i>
SUB8325601 ALR16	MW187517	<i>Bacillus subtilis</i>
SUB8325601 ALR17	MW187518	<i>Bacillus</i> sp.
SUB8325601 ALR18	MW187519	<i>Bacillus</i> sp.
SUB8325601 ALR19	MW187520	<i>Mucilaginibacter</i> sp.
SUB8325601 ALR20	MW187521	<i>Mucilaginibacter</i> sp.
SUB8325601 ALR21	MW187522	<i>Mucilaginibacter</i> sp.
<b>SUB8286515 PRJNA667924</b>		<b>SAMN16392370 <i>Mucilaginibacter</i> sp. 21p</b>

**Table S2.** Chemical Analysis of the soil where the strains were selected.

Sample	Total metal in mg kg <sup>-1</sup>												
	Al	Cd	Co	Cr	Cu	Fe	Mn	Ni	P	Pb	Zn	pH	Eh
Contaminated soil	7370	3.1	8.8	30.3	10.7	30396	459.8	10.1	387.4	13.6	48.4	6.5	370
Pristine Soil	1082	--	1.2	4,1	3.6	10489	50.0	2.3	--	4.8	2.4	--	--

\* Data based on Gomes et al. 2017, study that collect samples 2 days before the disaster in the same that this study; Cd, pH and Eh was not informed.

**Table S3.** Average Nucleotide Identification (Blast algorithm).

	Nome	ANiB [%]	Aligned [%]	Aligned [bp]	Total [bp]	RefSeq
1	<i>Mucilaginibacter paludis</i>	69.38	36.33	1722017	4739655	NZ_CM001403.1
2	<i>Mucilaginibacter psychrotolerans</i>	71.83	46.90	2222846	4739655	NZ_SOZE000000000.1

3	<i>Mucilaginibacter phyllosphaerae</i>	73.76	51.95	2462155	4739655	NZ_SNQG000000000.1;
4	<i>Mucilaginibacter kameinonensis</i>	70.41	45.97	2178982	4739655	NZ_RCWZ000000000.1;
5	<i>Mucilaginibacter gotjawali</i>	69.80	38.06	1804141	4739655	NZ_AP017313.1
6	<i>Mucilaginibacter lappiensis</i>	70.50	44.25	2097240	4739655	NZ_FTMG000000000.1;
7	<i>Mucilaginibacter polytrichastri</i>	69.90	39.83	1887980	4739655	NZ_FPAM000000000.1
8	<i>Mucilaginibacter gossypii</i>	70.72	44.74	2120667	4739655	NZ_CP043449.1
9	<i>Mucilaginibacter hurinus</i>	70.08	32.92	1560174	4739655	NZ_QGDC000000000.1
10	<i>Mucilaginibacter corticis</i>	70.39	37.13	1759804	4739655	NZ_VLPK000000000.1
11	<i>Mucilaginibacter terrigena</i>	73.88	49.65	2353321	4739655	NZ_SEWG000000000.1;
12	<i>Mucilaginibacter limnophilus</i>	70.30	37.44	1774487	4739655	NZ_SACK000000000.1
13	<i>Mucilaginibacter endophyticus</i>	70.47	46.14	2186976	4739655	NZ_QPCG000000000.1
14	<i>Mucilaginibacter xinganensis</i>	70.21	39.86	1889277	4739655	NZ_CP022743.1
15	<i>Mucilaginibacter ginsenosidivorax</i>	70.59	43.98	2084666	4739655	NZ_CP042437.1
16	<i>Mucilaginibacter ginsenosidivorans</i>	69.54	36.84	1746029	4739655	NZ_CP042436.1
17	<i>Mucilaginibacter frigoritolerans</i>	70.02	39.00	1848280	4739655	NZ_VLLI000000000.1
18	<i>Mucilaginibacter gracilis</i>	69.62	33.99	1611240	4739655	NZ_RBKU000000000.1
19	<i>Mucilaginibacter rubeus</i>	70.39	46.65	2211131	4739655	NZ_CP043450.1
20	<i>Mucilaginibacter oryzae</i>	70.70	43.84	2077853	4739655	NZ_QGHA000000000.1
21	<i>Mucilaginibacter yixingensis</i>	70.14	33.37	1581560	4739655	NZ_QAOQ000000000.1
22	<i>Mucilaginibacter auburnensis</i>	70.12	33.74	1599015	4739655	NZ_PGFJ000000000.1
23	<i>Mucilaginibacter pedocola</i>	71.96	49.97	2368607	4739655	NZ_MBTf000000000.1
24	<i>Mucilaginibacter gossypicola</i>	70.47	46.54	2205933	4739655	NZ_FOCL000000000.1;
25	<i>Mucilaginibacter mallensis</i>	70.20	38.57	1827886	4739655	NZ_LT629740.1
26	<i>Mucilaginibacter pineti</i>	70.66	44.07	2088850	4739655	NZ_FNAI000000000.1
27	<i>Mucilaginibacter boryungensis</i>	70.36	33.57	1639307	4882537	NZ_JADFFM010000001.1
28	<i>Mucilaginibacter glaciei</i>	69.84	35.18	1709210	4857968	NZ_JACWMX000000000.1
29	<i>Mucilaginibacter galii</i>	72.21	50.55	2322903	4595613	NZ_BMDO01000018.1
30	<i>Mucilaginibacter myungsuensis</i>	69.63	33.89	1723720	5086043	NZ_JADFFL000000000.1
31	<i>Mucilaginibacter pankratovii</i>	72.08	37.34	2378066	6368633	NZ_JACWMY000000000.1
32	<i>Mucilaginibacter rigui</i>	74.11	53.22	2506078	4708985	NZ_JACWMW000000000.1

1

**Table S4.** List of alleles that is not present in assembly *M. 21p* e according to Pirate.

Gene	Description	Frequency*
<i>chonabc</i>	Chondroitin sulfate ABC exolyase	1
<i>abnA</i>	Extracellular endo- $\alpha$ -(1 $\rightarrow$ 5)-L-arabinanase 1	1
<i>nagAa</i>	Naphthalene C2-salicylate 5-hydroxylase systems ferredoxin--NAD(P)(+)%2C reductase	1
<i>narX</i>	Nitrate/nitrite sensor protein NarX	1
<i>nap</i>	putative carboxylesterase nap	1
<i>narS</i>	putative sensor histidine kinase NarS	2
<i>tnaA1</i>	Tryptophanase 1	2
<i>nasC</i>	Assimilatory nitrate reductase catalytic subunit	2
<i>phnA</i>	Phosphonoacetate hydrolase	2
<i>xynA</i>	Endo-1%2C4-beta-xylanase A	2
<i>nagJ</i>	hypothetical protein	4

<i>arnA</i>	Bifunctional polymyxin resistance protein ArnA	6
<i>nanR</i>	HTH-type transcriptional repressor NanR	6
<i>nanM</i>	N-acetylneuraminate epimerase	7
<i>napA</i>	Periplasmic nitrate reductase	15
<i>nasD</i>	Nitrite reductase [NAD(P)H]	16
<i>nasF</i>	Uroporphyrinogen-III C-methyltransferase	18

---

\*Comparative analyze of frequency of each specie contain respective gene.