

Table S1: Summary of bacterial (16S rRNA) sequence library sizes, filtered sequences, operational taxonomic units (OTUs), diversity, richness and coverage estimates. OTUs were defined as sequences sharing >97% similarity and served as the basis for the Shannon, Simpson, Chao I and Coverage calculations. ¹ = the number corresponds to which planting (1-3) the samples are from. wap =weeks after planting.

Farm	Sample name	Time of sampling	Seq library size	Filtered sequences	OTUs identified	Simpson	Shannon	Chao I richness	Coverage	
Farm Leafy green	6	3 wap 1 ¹	91727	21172	1290	12.05	3.97	2645.28	0.97	
	7	3 wap 1	110250	15673	717	2.67	2.24	1496.22	0.97	
	8	3 wap 1	157490	18586	1249	6.66	3.59	2528.10	0.96	
	9	harvest 1	196746	11673	263	11.74	3.02	683.75	0.99	
	10	harvest 1	277806	58353	362	11.09	2.70	862.11	1.00	
	11	harvest 1	217801	43980	269	3.18	1.59	764.34	1.00	
	12	harvest 1	1130173	165898	653	2.75	1.58	1607.76	1.00	
	17	3 wap 2	692820	44150	1384	9.96	3.44	2741.02	0.98	
	18	3 wap 2	510421	72234	1718	9.22	3.25	3098.13	0.99	
	19	3 wap 2	436110	30188	572	6.20	2.48	1198.54	0.99	
	20	3 wap 2	294271	56678	2011	21.73	4.25	3610.73	0.98	
	Farm Vestfold, <i>Lactuca sativa</i>	21	harvest 2	807594	102974	1460	6.01	2.90	2712.85	0.99
		22	harvest 2	457194	25190	701	9.57	3.09	1419.18	0.98
		23	harvest 2	501525	30295	740	8.90	3.01	1550.27	0.99
		24	harvest 2	898390	108861	3531	18.36	4.46	6267.76	0.98
		29	3 wap 3	674589	35191	1635	18.15	4.16	3054.85	0.98
		30	3 wap 3	455331	59711	949	7.42	2.81	1747.41	0.99
		31	3 wap 3	1035950	52441	2568	37.59	4.89	4514.55	0.98
		32	3 wap 3	418170	13076	1169	33.46	4.82	2096.84	0.96
		33	harvest 3	781248	80143	363	2.66	1.67	781.75	1.00
34		harvest 3	760765	121620	822	11.49	3.10	1616.59	1.00	
35		harvest 3	1185772	88886	524	7.57	2.70	949.04	1.00	
36		harvest 3	441797	51756	337	7.34	2.56	687.07	1.00	
41		3 wap 1	479982	143644	3161	11.92	3.93	5273.26	0.99	

	42	3 wap 1	698430	171939	1641	4.76	2.56	3071.56	1.00
	43	3 wap 1	570076	380083	2696	8.00	2.79	4447.42	1.00
	45	harvest 1	398169	33698	166	4.31	2.07	312.71	1.00
	46	harvest 1	695062	25076	247	4.81	2.12	546.09	0.99
	47	harvest 1	601617	10260	272	7.69	2.70	664.70	0.98
	48	harvest 1	265463	32386	170	3.99	1.75	383.90	1.00
	53	3 wap 2	526668	9549	650	13.13	3.66	1304.64	0.96
	54	3 wap 2	778255	335039	795	1.03	0.14	1977.51	1.00
	55	3 wap 2	154569	2998	465	13.34	4.10	952.80	0.91
	56	3 wap 2	153097	1720	418	26.77	4.54	866.93	0.85
Farm Buskerud, <i>Lactuca sativa</i>	57	harvest 2	309820	26389	727	13.13	3.41	1315.49	0.99
	58	harvest 2	405115	59683	610	5.05	2.32	1229.68	0.99
	59	harvest 2	321777	82509	637	5.23	2.46	1259.13	1.00
	60	harvest 2	507530	14305	397	7.78	2.85	815.69	0.98
	65	3 wap 3	230143	12987	160	3.63	1.82	418.67	0.99
	66	3 wap 3	448708	19353	225	5.34	2.23	427.97	0.99
	67	3 wap 3	933063	29076	631	4.97	2.39	1477.46	0.99
	69	harvest 3	392534	33861	238	7.82	2.62	442.00	1.00
	70	harvest 3	300931	85677	211	2.54	1.62	493.55	1.00
	71	harvest 3	295638	11271	199	7.10	2.71	401.22	0.99
	72	harvest 3	621195	27858	177	4.07	2.16	400.25	1.00
	73	harvest 1	674194	442820	500	4.37	2.18	1155.12	1.00
	74	harvest 1	210420	141315	319	8.86	2.70	578.22	1.00
	75	harvest 1	705941	474117	809	8.95	2.73	1966.88	1.00
Farm Buskerud, <i>Diplotaxis tenuifolia</i>	76	harvest 2	109001	62636	332	11.31	3.04	696.79	1.00
	77	harvest 2	294116	202935	526	16.12	3.26	1020.02	1.00
	78	harvest 2	281344	181957	521	19.62	3.46	975.28	1.00

Table S2. Differentially abundant phyla and genera in selected groups using Metastats analysis ($P < 0.05$) (1). Only taxa with most differences between groups are shown (abundance $\geq 0.002 \pm \text{SE}$). The groups with most abundant phylum and genus are underlined. wap = weeks after planting.

<i>Lactuca sativa</i> , Buskerud and Vestfold			
Phyla	3wap, total	harvest, total	P-value
Acidobacteria	<u>0.008 ± 0.002</u>	0.001 ± 0.0004	0.002
Actinobacteria	<u>0.046 ± 0.01</u>	0.007 ± 0.002	0.002
Planctomycetacia	<u>0.002 ± 0.0005</u>	0.0002 ± 0.00009	0.002
Proteobacteria	0.09 ± 0.02	<u>0.22 ± 0.04</u>	0.002
Verrucomicrobia	<u>0.002 ± 0.0005</u>	0.0001 ± 0.00007	0.002
Genera	3wap, total	harvest, total	
Duganella	0.07 ± 0.015	<u>0.19 ± 0.03</u>	0.001
Pedobacter	0.002 ± 0.0004	<u>0.007 ± 0.0017</u>	0.001
Rhizobium	0.003 ± 0.001	<u>0.028 ± 0.007</u>	0.001
<i>Lactuca sativa</i> , Buskerud			
Phyla	harvest planting 1, 3	harvest planting 2	P-value
Acidobacteria	0.00005 ± 0.00003	<u>0.001 ± 0.0004</u>	0.02
Actinobacteria	<u>0.03 ± 0.009</u>	0.003 ± 0.001	0.02
Bacteroidetes	<u>0.03 ± 0.01</u>	0.003 ± 0.001	0.02
Firmicutes	0.0006 ± 0.0003	<u>0.003 ± 0.001</u>	0.03
Proteobacteria	<u>0.35 ± 0.1</u>	0.31 ± 0.07	0.03
Genera	harvest planting 1, 3	harvest planting 2	
Arthrobacter	0.002 ± 0.0007	<u>0.006 ± 0.002</u>	0.02
Hymenobacter	0.0002 ± 0.0001	<u>0.033 ± 0.009</u>	0.001
Nocardioides	0.0002 ± 0.00008	<u>0.004 ± 0.002</u>	0.01
Paracoccus	0.00009 ± 0.00006	<u>0.003 ± 0.002</u>	0.04
Pseudomonas	<u>0.36 ± 0.09</u>	0.28 ± 0.05	0.009
Rhizobium	<u>0.02 ± 0.007</u>	0.008 ± 0.002	0.04
Sphingomonas	0.08 ± 0.03	<u>0.3 ± 0.07</u>	0.004
<i>Lactuca sativa</i> , Vestfold			
Phyla	harvest, planting 1, 3	harvest, planting 2	P-value
Acidobacteria	0.0003 ± 0.0002	<u>0.004 ± 0.001</u>	0.03
Actinobacteria	0.008 ± 0.005	<u>0.09 ± 0.02</u>	0.02
Bacteroidetes	<u>0.02 ± 0.01</u>	0.003 ± 0.001	0.03
Firmicutes	0.0009 ± 0.0004	<u>0.013 ± 0.005</u>	0.02
Proteobacteria	<u>0.37 ± 0.1</u>	0.15 ± 0.04	0.03

Genera	harvest, planting 1, 3	harvest, planting 2	
Arthrobacter	0.007 ± 0.004	<u>0.08 ± 0.01</u>	0.0003
Brevundimonas	0.006 ± 0.003	<u>0.03 ± 0.009</u>	0.009
Chryseobacterium	<u>0.02 ± 0.009</u>	0.00003 ± 0.00003	0.03
Massilia	0.03 ± 0.006	<u>0.06 ± 0.01</u>	0.02
Nocardioides	0.0003 ± 0.0001	<u>0.002 ± 0.0004</u>	0.002
Pantoea	<u>0.22 ± 0.06</u>	0.004 ± 0.002	0.002
Paracoccus	0.001 ± 0.0001	<u>0.003 ± 0.0007</u>	0.002
Rhizobium	<u>0.05 ± 0.02</u>	0.01 ± 0.005	0.03
Sphingomonas	<u>0.05 ± 0.02</u>	0.03 ± 0.008	0.02

References:

1. **White JR, Nagarajan N, Pop M.** 2009. Statistical methods for detecting differentially abundant features in clinical metagenomic samples. *PLoS Comput Biol* **5**:10.