

Figure S1. Rarefaction curves generated for 16S rRNA gene sequences obtained from samples. Panels represent the rarefaction curves of aggregates of the 16 samples of bulk soil (BS) and samples of the rhizosphere soil of durum wheat (cv. Iride, IR) and Tritordeum (cv. Bulel, cv. HTC-444) under organic (org) and conventional (conv) management.

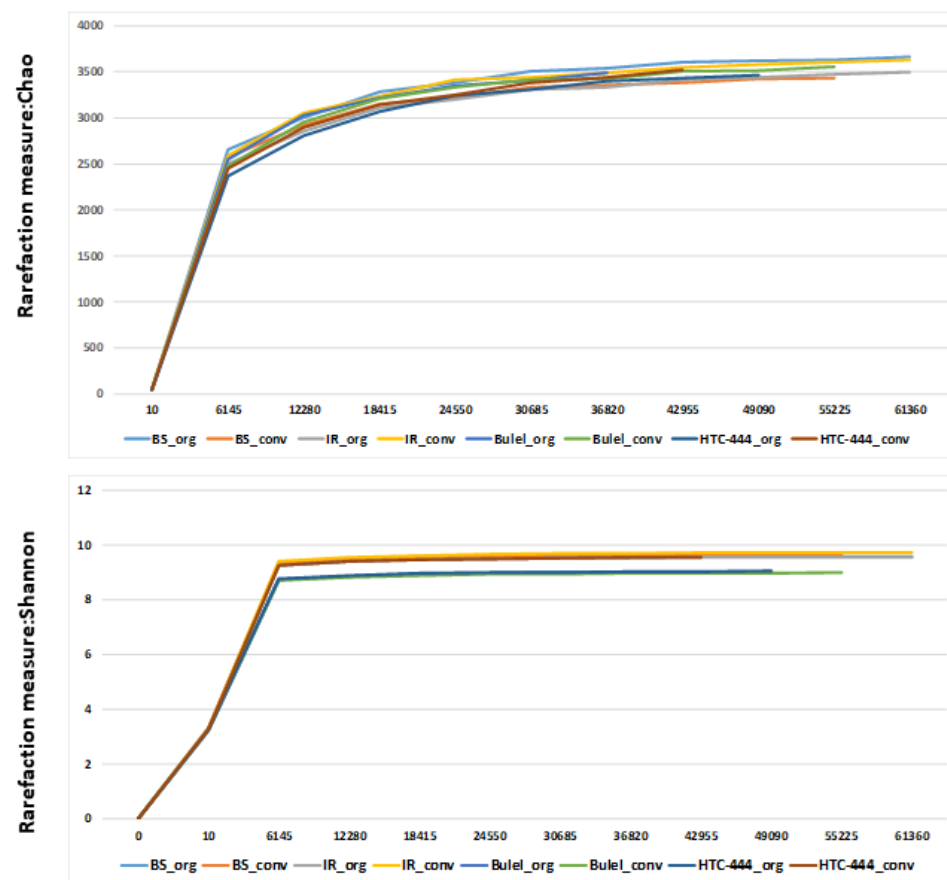


Table S1: Data filtering report of sample runs.

Sample	Number of sequenced pe reads	Number of pe reads with mean quality > 20	Number of merged pe reads	No bacterial sequences	Length outside bounds of 100 and 400	Ambiguous bases	Homopolymers > 7	Mismatch in primers >1	Reverse primer not found	Final Read Number
BS_org	97958	95229	86817	162	0	0	28	3454	95	83078
BS_conv	83767	82606	75158	29	0	0	26	2758	70	72275
IR_org	94210	92781	83085	20	0	0	55	2737	66	80207
IR_conv	94875	93622	84905	171	0	0	30	3375	96	81233
Bulel_org	61146	57636	51827	174	0	0	30	1482	44	50097
Bulel_conv	92449	84147	77235	256	0	0	30	2770	73	74106
HTC_444_org	78528	72267	64918	95	0	0	26	2317	51	62429
HTC_444_conv	74165	66420	60712	82	0	0	38	2100	48	58444

Table S2: Bacterial phyla with relative variations (var) and significance level (*p*-value) in bulk soil and rhizosphere soil of durum wheat (cv. Iride) and tritordeum (cv. HTC-444 and Bulel) cultivated under organic (org) and conventional (conv) agricultural managements. Data reported are presented as percentages of abundance of the mean values of 2 biological replicates.

Taxonomy	Bulk soil				Iride				Bulel				HTC-444			
	org (%)	conv (%)	var (%)	<i>p</i> -value	org (%)	conv (%)	var (%)	<i>p</i> -value	org (%)	conv (%)	var (%)	<i>p</i> -value	org (%)	conv (%)	var (%)	<i>p</i> -value
<i>Acidobacteria</i>	15.75	17.15	-8.20	0.526	11.85	13.07	-9.28	0.307	8.90	12.97	-31.37	0,001*	11.53	8.50	35.63	0.206
<i>Actinobacteria</i>	31.60	26.52	19.14	<0,001**	34.19	25.16	35.89	<0,001**	24.71	27.76	-10.97	0,022*	27.17	21.47	26.58	0.022
<i>Bacteroidetes</i>	2.93	3.31	-11.38	0.983	5.60	6.82	-17.95	0.302	15.47	6.77	128.37	<0,001**	8.42	17.96	-53.14	<0,001**

<i>Chloroflexi</i>	7.96	8.36	-4.75	0.980	7.04	7.22	-2.45	0.881	4.39	6.50	-32.38	0.184	5.21	4.45	17.04	0.748
<i>Cyanobacteria</i>	0.08	0.19	-55.44	1.000	1.08	0.55	95.15	0.656	0.68	0.61	11.25	1.000	0.21	0.43	-50.55	0.926
<i>Firmicutes</i>	3.61	4.87	-25.76	0.618	3.56	5.49	-35.19	0.109	2.37	3.53	-32.84	0.676	3.05	3.33	-8.35	0.906
<i>Gemmatimonadetes</i>	4.32	4.84	-10.70	0.958	3.78	3.86	-1.99	0.948	3.26	4.40	-25.91	0.686	3.95	3.04	29.59	0.703
<i>Latescibacteria</i>	0.52	0.20	152.33	0.990	0.00	0.00	0.00	0	0.30	0.29	4.23	1.000	0.00	0.00	0.00	0
<i>Nitrospirae</i>	1.22	0.82	49.51	0.979	1.13	1.02	11.45	0.921	0.71	0.89	-20.58	0.998	1.28	0.72	76.96	0.814
<i>Planctomycetes</i>	0.88	0.60	47.22	0.993	0.71	0.58	22.85	0.911	0.38	0.73	-47.39	0.987	1.22	1.08	12.49	0.954
<i>Proteobacteria</i>	25.63	28.48	-10.00	0.037*	25.77	31.22	-17.45	<0.001**	34.47	30.48	13.10	0.002*	33.23	34.74	-4.36	0.523
<i>Tectomicrobia</i>	1.03	0.80	29.17	0.996	0.76	0.71	7.59	0.964	0.62	0.84	-25.88	0.999	0.80	0.59	35.44	0.929
<i>Verrucomicrobia</i>	1.52	1.38	9.96	0.999	1.67	1.72	-3.28	0.962	1.54	1.68	-8.21	0.999	1.54	1.76	-12.47	0.926
U. m. of Bact. Kingdom	2.69	2.17	23.95	0.962	2.16	1.99	8.55	0.885	1.59	2.09	-23.88	0.962	1.81	1.36	33.20	0.848
Taxa below 0.5	0.24	0.30	-21.36	1.000	0.69	0.59	16.29	0.144	0.59	0.46	29.02	0.999	0.58	0.55	4.29	0.886

*: significant at $p \leq 0.05$

**: significant at $p \leq 0.01$

***: significant at $p \leq 0.001$

Table S3: Bacterial families with relative variations (var) and significance level (p -value) in bulk soil and rhizosphere soil of durum wheat (cv. Iride) and tritordeum (cv. HTC-444 and Bulel) cultivated under organic (org) and conventional (conv) agricultural managements. Data reported are presented as percentages of abundance of the mean values of 2 biological replicates.

Taxonomy	Bulk soil				Iride				Bulel				HTC-444			
	org (%)	conv (%)	var (%)	p -value	org (%)	conv (%)	var (%)	p -value	org (%)	conv (%)	var (%)	p -value	org (%)	conv (%)	var (%)	p -value
<i>Blastocatellaceae</i>	3.20	5.37	-40.38	<0.001**	2.67	4.02	-33.49	0.008*	2.01	3.13	-35.80	0.025*	2.62	2.47	5.78	0.869
U. m. of Acidobacteria phylum	10.65	8.80	21.06	<0.001**	8.01	7571	5.83	0.382	5.92	7.96	-25.66	<0.001**	7.26	4.84	50.13	0.005*

U. m. of <i>Actinobacteria</i> phylum	4.04	3.03	33.45	0.051	3.74	2.52	48.41	0.016*	2.86	2.88	-0.73	1	3.49	2.20	58.90	0.137
U. m. of <i>Gaiellales</i> order	6.88	5.77	19.17	0.026*	6.90	4.91	40.53	<0.001**	5.60	5.58	0.45	0.838	6.21	3.19	94.67	<0.001**
<i>Flavobacteriaceae</i>	1.07	0.04	2354.53	0.046*	2.48	2.90	-14.48	0.402	6.06	2.47	145.30	<0.001**	3.28	11.50	-71.46	<0.001**
<i>Micrococcaceae</i>	0.92	0.80	15.77	0.989	1.30	1.46	-10.96	0.762	1.44	1.37	5.54	0.998	1.05	3.20	-67.26	0.013*
<i>Sphingobacteriaceae</i>	0.31	0.12	150.91	0.967	0.62	0.85	-27.06	0.648	7.33	1.03	609.80	<0.001**	2.93	3.57	-17.86	0.463
<i>Propionibacteriaceae</i>	2.52	1.24	102.65	0.007*	2.78	1.45	91.72	0.009*	1.52	2.03	-25.19	0.569	2.06	1.44	42.94	0.477
<i>Bacillaceae</i>	2.20	3.11	-29.38	0.096	2.24	3.55	-36.90	0.010*	1.03	2.29	-55.19	0.008*	1.53	2.00	-23.68	0.586
<i>Oxalobacteraceae</i>	0.89	2.52	-64.68	<0.001**	1.48	5.50	-73.09	<0.001**	9.65	5.66	70.64	<0.001**	9.58	6.69	43.23	<0.001**
<i>Enterobacteriaceae</i>	0.01	0.04	-79.03	1	0.08	0.07	14.29	0.977	1.46	0.36	307.21	0.027*	0.13	3.44	-96.13	<0.001**
<i>Pseudomonadaceae</i>	0.11	0.06	86.58	0.999	0.28	0.90	-68.89	0.224	0.90	0.77	16.42	0.989	0.99	3.07	-67.83	0.017*
<i>Sphingomonadaceae</i>	1.66	4.08	-59.31	<0.001**	2.46	4.54	-45.81	<0.001**	3.43	3.19	7.36	0.934	3.04	4.59	-33.88	0.074
Taxa below 0.5	12.10	11.73	3.15	0.787	10.67	10.12	5.43	0.27	9.59	11.04	-13.12	0.001*	8.88	8.29	7.18	0.494

*: significant at $p \leq 0.05$.

**: significant at $p \leq 0.01$.

***: significant at $p \leq 0.001$.