

1 Supplementary Figure Legends:

2 Supplementary Table 1: Summary of reads generated for each individual sample, at
3 Phylum, Family and Genus level, post quality filtering.

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5 Supplementary Table 2: Summary of read percentages and relative abundances, at
6 Phylum, Family and Genus level, for early and late day production continental-type
7 cheese (Early Day [ED], Late Day [LD]). Results depicted are mean values of reads
8 generated from individual core/rind samples from each respective cheese block and
9 were standardised to equi-molar concentrations prior to library preparation.

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11 Supplementary Table 3: Summary of read percentages and relative abundances, at
12 genus level, for core and rind samples of continental-type cheese (Early Day [ED],
13 Late Day [LD]). Results depicted are mean values of reads generated from individual
14 core/rind samples from each respective cheese block and were standardised to equi-
15 molar concentrations prior to library preparation.

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17 Supplementary Figures:

18 Supplementary Figure 1: Rarefaction curves of microbial populations using the
19 Shannon, Simpson and Chao1 indices

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21 Supplementary Figure 2: Relative abundance of individual samples at genus level for
22 a Continental-type cheese produced early and late (ED and LD) in the production day

23 Supplementary Table 1

	TP1, LD, B1, Rind	TP1, LD, B2, Rind	TP1, LD, B1, Core	TP1, LD, B2, Core	TP1, ED, B1, Rind	TP1, ED, B2, Rind	TP1, ED, B1, Core	TP1, ED, B2, Core	Total
Phylum	13736	9403	6724	7422	14682	10614	9204	15371	87156
Family	13649	9327	6669	7352	14618	10562	9174	15322	86673
Genus	13548	9202	6575	7127	14297	10157	8713	14884	84503
	TP2, LD, B1, Rind	TP2, LD, B2, Rind	TP2, LD, B1, Core	TP2, LD, B2, Core	TP2, ED, B1, Rind	TP2, ED, B2, Rind	TP2, ED, B1, Core	TP2, ED, B2, Core	
Phylum	16797	11854	11097	18525	16528	5690	7248	9306	97045
Family	16746	11794	11080	18484	16485	5663	7231	9247	96730
Genus	16521	11518	10912	18168	16374	5549	7162	9161	95365
	TP3, LD, B1, Rind	TP3, LD, B2, Rind	TP3, LD, B1, Core	TP3, LD, B2, Core	TP3, ED, B1, Rind	TP3, ED, B2, Rind	TP3, ED, B1, Core	TP3, ED, B2, Core	
Phylum	8694	6553	11510	5735	5604	6015	9528	8609	62248
Family	8672	6547	11500	5727	5579	5988	9508	8554	62075
Genus	8192	6327	11403	5655	5435	5679	9465	8442	60598
	TP4, LD, B1, Rind	TP4, LD, B2, Rind	TP4, LD, B1, Core	TP4, LD, B2, Core	TP4, ED, B1, Rind	TP4, ED, B2, Rind	TP4, ED, B1, Core	TP1, ED, B2, Core	
Phylum	6885	7484	4651	Sequencing Failed	5295	7942	6671	9476	48404
Family	6869	7469	4627		5279	7907	6638	9450	48239
Genus	6817	7419	4474		5205	7830	6515	9346	47606

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25 Supplementary Table 1: Summary of reads generated for each individual sample, at Phylum, Family and Genus level, post quality filtering

Supplementary Table 2:

Phylum (%)	TP1 ED	TP1 LD	TP2 ED	TP2 LD	TP3 ED	TP3 LD	TP4 ED	TP4 LD
<i>Proteobacteria</i>	2.14	3.02	0.61	0.33	1.50	0.46	0.25	0.28
<i>Bacteroidetes</i>	0.08	0.25	0	0.06	0	0	0	0.04
<i>Actinobacteria</i>	0.07	0.17	0.02	0.01	0.04	0.03	0	0
<i>Firmicutes</i>	97.53	85.56	99.33	83.96	93.46	76.62	99.75	75.26
<i>Deinococcus-Thermus</i>	0.18	10.99	0.04	15.64	5.01	22.89	0	24.42
Relative Abundance (%)	100	100	100	100	100	100	100	100
Family (%)	TP1 ED	TP1 LD	TP2 ED	TP2 LD	TP3 ED	TP3 LD	TP4 ED	TP4 LD
<i>Pseudoalteromonadaceae:</i>	0.07	0.22	0.03	0.01	0.09	0.02	0	0
<i>Moraxellaceae:</i>	0.80	1.45	0.26	0.11	0.73	0.21	0.05	0.10
<i>Vibrionaceae:</i>	0.53	1.25	0.11	0.10	0.41	0.14	0.03	0.09
<i>Brevibacteriaceae:</i>	0	0.01	0	0	0	0	0	0
<i>Micrococcaceae:</i>	0.07	0.13	0.02	0.01	0.03	0	0	0
<i>Corynebacteriaceae:</i>	0	0.01	0	0	0	0	0	0
<i>Streptococcaceae:</i>	32.59	18.57	24.03	12.35	18.50	9.34	27.06	13.70
<i>Lactobacillaceae:</i>	64.42	63.51	74.61	68.76	72.62	65.44	69.10	59.77
<i>Staphylococcaceae:</i>	0	0	0.35	0.66	0	0	0	0
<i>Lachnospiraceae:</i>	0.06	0.01	0.01	0	0.14	0.15	0.14	0.62
<i>Ruminococcaceae:</i>	0.03	0	0.01	0	0.04	0.07	0.05	0.19
<i>Thermaceae</i>	0.18	10.99	0.04	15.64	5.01	22.89	0	24.42
<i>Pseudomonadaceae</i>	0.26		0.03	0	0	0	0	0
<i>Leuconostocaceae</i>	0.08	0.01	0	0	0.26	0.02	0	0

<i>Enterobacteriaceae</i>	0.06		0	0	0	0.03	0	0
<i>Flavobacteriaceae</i>	0.08	0.25	0	0.05	0	0	0	0
<i>Bacillaceae</i>	0	3.20	0	1.49	0.11	0.65	0	0.42
<i>Clostridiaceae</i>	0	0	0.12	0.53	1.64	0.87	3.20	0.38
<i>Bifidobacteriaceae</i>	0	0	0	0	0	0.03	0	0
<i>Acetobacteraceae</i>	0	0	0	0	0	0	0	0.03
Unassigned	0.77	0.39	0.38	1.06	0.43	0.14	0.37	0.29
Relative Abundance (%)	99.23	99.23	99.62	99.71	99.57	99.86	99.63	99.71
Genus (%)	TP1 ED	TP1 LD	TP2 ED	TP2 LD	TP3 ED	TP3 LD	TP4 ED	TP4 LD
<i>Pseudoalteromonas:</i>	0.0697	0.2166	0.0335	0.0137	0.0907	0.02	0	0
<i>Psychrobacter:</i>	0.4881	1.4457	0.2295	0.1047	0.7091	0.21	0.0374	0.0894
<i>Vibrio:</i>	0.5257	1.2352	0.1057	0.0995	0.4134	0.14	0.0272	0.0894
<i>Brevibacterium:</i>	0	0.0120	0	0	0	0	0	0
<i>Arthrobacter:</i>	0.0697	0.1283	0.0232	0.0103	0.0302	0	0	0
<i>Corynebacterium:</i>	0	0.0120	0	0	0	0	0	0
<i>Streptococcus:</i>	31.1788	18.3072	23.0914	12.2715	17.3746	9.26	26.0686	13.6225
<i>Lactococcus:</i>	0.1180	0.2346	0.0800	0.0618	0.2924	0.04	0.1225	0.0421
<i>Lactobacillus:</i>	64.4227	63.5119	74.5100	68.5789	71.7267	63.71	68.9729	59.5899
<i>Staphylococcus:</i>	0	0	0.3508	0.6590	0	0	0	0
<i>Thermus:</i>	0.1797	10.9883	0.0413	15.6436	5.0074	22.89	0	24.4217
<i>Acinetobacter</i>	0.3031	0	0.0206	0	0	0	0	0
<i>Pseudomonas</i>	0.2575	0	0.0310	0	0	0	0	0
<i>Leuconostoc</i>	0.0751	0.0100	0	0	0	0	0	0

<i>Flavobacterium</i>	0.0778	0.2486	0	0.0480	0	0	0	0
<i>Clostridium</i>	0	0	0.1135	0.5285	1.6333	0.87	3.0901	0.3733
<i>Ruminococcaeae Incertae Sedis</i>	0	0	0.0129	0	0	0	0.0204	0.1104
<i>Bifidobacterium</i>	0	0	0	0	0	0.03	0	0
<i>Weisella</i>	0	0	0	0	0.2521	0.02	0	0
<i>EU622674</i>	0	0	0	0	0	0	0	0.0315
Unassigned	2.2341	3.6494	1.3566	1.9803	2.4701	2.82	1.6608	1.6299
Relative Abundance (%)	97.7659	96.3506	98.6434	98.0197	97.5299	97.18	98.3392	98.3701

26 Supplementary Table 2: Summary of read percentages and relative abundances, at Phylum, Family and Genus level, for early and late day
27 production continental-type cheese (Early Day [ED], Late Day [LD]). Results depicted are mean values of reads generated from individual
28 core/rind samples from each respective cheese block and were standardised to equi-molar concentrations prior to library preparation.

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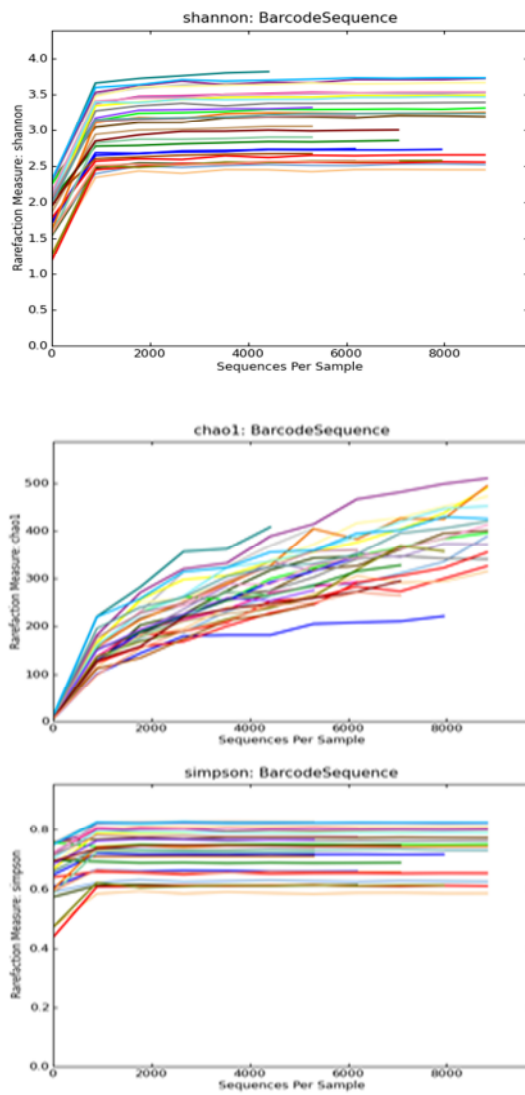
Genus (%)	TP1 ED	TP1 ED	TP1 LD	TP1 LD	TP2 ED	TP2 ED	TP2 LD	TP2 LD	TP3 ED	TP3 ED	TP3 LD	TP3 LD	TP4 ED	TP4 ED	TP4 LD	TP4 LD
	Core	Rind	Core	Rind	Core	Rind	Core	Rind	Core	Rind	Core	Rind	Core	Rind	Core	Rind
<i>Pseudoalteromonas</i>	0	0.112	0.028	0.399	0	0.059	0.027	0	0.149	0	0	0.033	0	0	0	0
<i>Psychrobacter</i>	0	0.787	0.256	2.601	0.205	0.248	0.206	0	1.130	0.052	0.128	0.302	0.068	0	0.129	0.077
<i>Vibrio</i>	0	0.847	0.187	2.253	0.060	0.140	0.196	0	0.678	0	0.081	0.203	0.050	0	0.194	0.056
<i>Brevibacterium:</i>	0	0	0	0.024	0	0	0	0	0	0	0	0	0	0	0	0
<i>Arthrobacter</i>	0	0.112	0.020	0.233	0	0.041	0.020	0	0.050	0	0	0	0	0	0	0
<i>Corynebacterium</i>	0	0	0	0.024	0	0	0	0	0	0	0	0	0	0	0	0
<i>Streptococcus</i>	23.215	36.047	13.400	23.075	19.011	26.132	5.898	18.861	9.268	30.028	6.153	12.783	11.086	44.345	5.289	16.320
<i>Lactococcus</i>	0.163	0.091	0.057	0.407	0.060	0.095	0.064	0.059	0.342	0.215	0.052	0.033	0.111	0.136	0	0.056
<i>Lactobacillus</i>	72.303	59.605	74.604	52.736	78.791	71.321	79.515	57.272	76.220	64.713	70.977	55.486	81.253	53.993	69.490	56.385
<i>Staphylococcus</i>	0	0	0	0	0	0.612	0	1.340	0	0	0	0	0	0	0	0
<i>Thermus</i>	0.276	0.121	7.438	14.437	0.060	0.027	11.164	20.275	8.215	0	19.884	26.281	0	0	19.093	26.147
<i>Acinetobacter</i>	0.467	0.203	0	0	0.048	0	0	0	0	0	0	0	0	0	0	0
<i>Pseudomonas</i>	0.339	0.207	0	0	0.072	0	0	0	0	0	0	0	0	0	0	0
<i>Leuconostoc</i>	0.099	0.061	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Flavobacterium</i>	0.000	0.125	0.028	0.463	0	0	0.041	0.056	0	0	0	0	0	0	0	0
<i>Clostridium</i>	0	0	0	0	0.266	0	1.040	0	2.680	0	1.641	0	5.623	0	1.419	0
<i>Ruminococcaeae</i>																
<i>Incertae Sedis</i>	0	0	0	0	0.030	0	0	0	0	0	0	0	0.037	0	0.452	0
<i>Bifidobacterium</i>	0	0	0	0	0	0	0	0	0	0	0	0.066	0	0	0	0
<i>Weisella</i>	0	0	0	0	0	0	0	0	0	0.645	0	0.039	0	0	0	0

<i>EU622674</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.129	0
Unassigned	3.139	1.681	3.980	3.329	1.395	1.328	1.830	2.136	1.268	4.346	1.084	4.775	1.771	1.526	3.806	0.926
Relative																
Abundance (%)	96.861	98.319	96.020	96.671	98.605	98.672	98.170	97.864	98.732	95.654	98.916	95.225	98.229	98.474	96.194	99.074

40 Supplementary Table 3: Summary of read percentages and relative abundances, at genus level, for core and rind samples of continental-type
41 cheese (Early Day [ED], Late Day [LD]). Results depicted are mean values of reads generated from individual core/rind samples from each
42 respective cheese block and were standardised to equi-molar concentrations prior to library preparation.

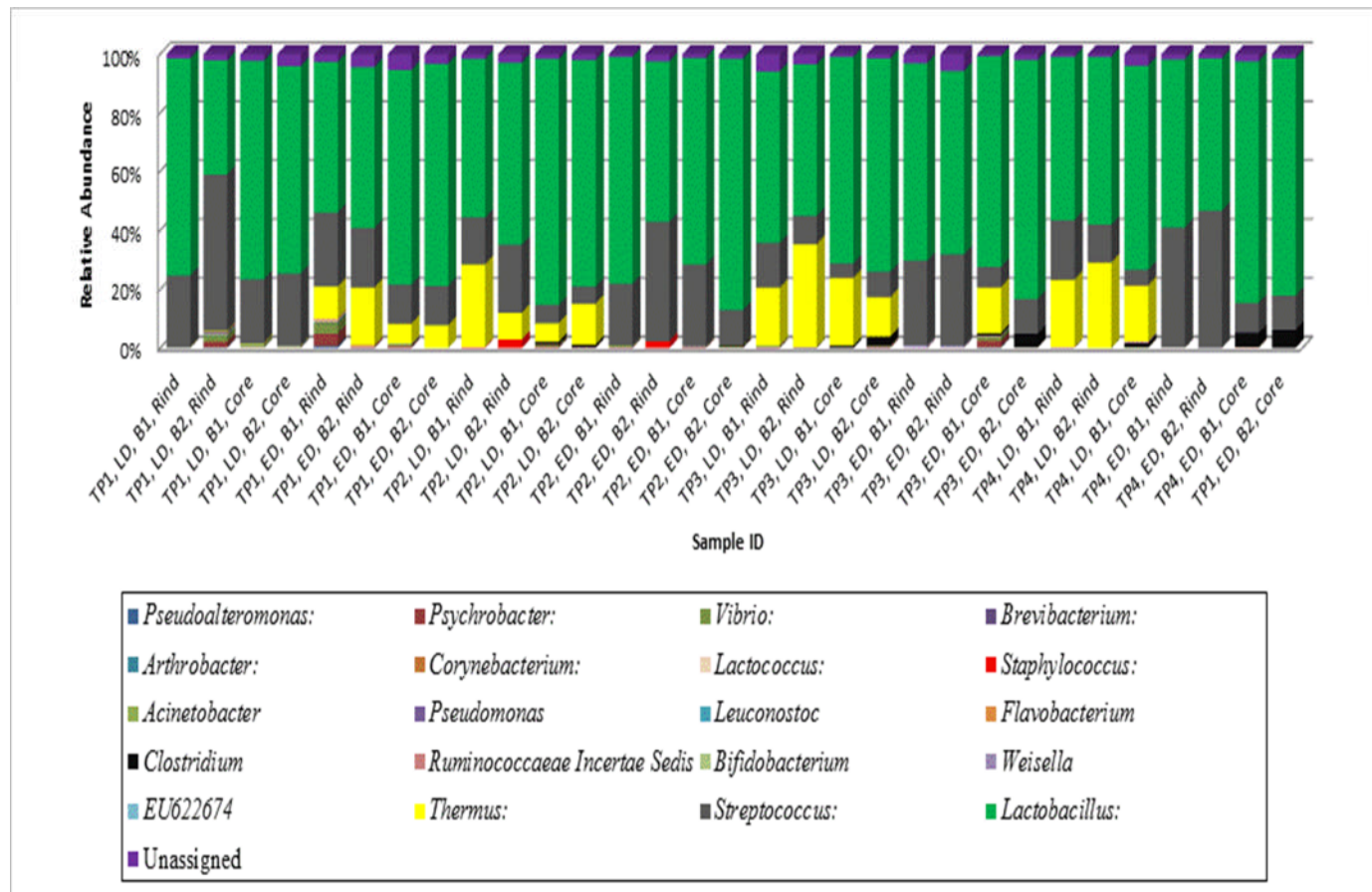
Supplementary Figures:

Supplementary Figure 1:



Supplementary Figure 1: Rarefaction curves of microbial populations using the Shannon, Simpson and Chao1 indices

Supplementary Figure 2:



Supplementary Figure 2: Relative abundance of individual samples at genus level for a Continental-type cheese produced early and late (ED and LD) in the production day.