**TABLE S1** Observed diversity and estimated sample coverage in 16S rRNA sequencing analysis of Canestrato Pugliese cheese during manufacture and ripening

| Days of ripening | No. of reads | No. of OTUs | Chao1 richness | Shannon diversity index | ESC (%) |
|---|---|---|---|---|---|
| Milk | 5727 | 14 | 17.33 | 1.43 | 99% |
| Curd[a] | 3555 | 44 | 46.57 | 3.05 | 99% |
| 1[b] | 5001 | 34 | 38.66 | 1.15 | 99% |
| 3 | 2206 | 23 | 26.33 | 0.75 | 99% |
| 7 | 6334 | 36 | 49.75 | 0.92 | 99% |
| 15 | 9357 | 39 | 43.20 | 1.75 | 99% |
| 30 | 8945 | 40 | 42.50 | 1.27 | 99% |
| 45 | 3687 | 41 | 44.00 | 2.06 | 99% |
| 60 | 7843 | 45 | 52.33 | 2.08 | 99% |
| 75 | 7965 | 43 | 51.25 | 1.65 | 99% |
| 90 | 6304 | 43 | 47.00 | 1.99 | 99% |

Abbreviations: OTU, operational taxonomic unit; ESC, estimated sample coverage. Chao1 richness, Shannon diversity, and ESC were calculated with Qiime at the 3% distance level.
[a]Curd after moulding.
[b]Curd after dry salting.

**TABLE S2** Community Level Catabolic Profiles (CLCPs) of Canestrato Pugliese cheese during manufacture and ripening

| Days of ripening | *H'* | *S* | E |
|---|---|---|---|
| Milk | 2.68 ± 0.2 D | 12.33 ± 1.5D | 2.64 ± 0.2BC |
| Curd[a] | 3.00 ± 0.1C | 16.67 ± 2.5 B | 2.46 ± 0.1A |
| 1[b] | 2.71 ± 0.1 E | 12.68 ± 1.5 D | 2.47 ± 0.2A |
| 3 | 3.25 ± 0.1 A | 20.33 ± 0.2 A | 2.49 ± 0.1A |
| 7 | 3.09 ± 0.3 BC | 15.67 ± 1.1 B | 2.59 ± 0.2B |
| 15 | 3.15 ± 0.2 B | 16.00 ± 1.5 B | 2.61 ± 0.3B |
| 30 | 3.03 ± 0.2 C | 16.67 ± 0.6B | 2.48 ± 0.1A |
| 45 | 3.00 ± 0.3 C | 15.23 ± 2.1B | 2.53 ± 0.3AB |
| 60 | 3.03 ± 0.1C | 13.67 ± 1.5C | 2.68 ± 0.2 BC |
| 75 | 3.09 ± 0.2 BC | 13.67 ± 1.1C | 2.72 ± 0.1C |
| 90 | 2.84 ± 0.1D | 13.33 ± 0.6C | 2.53 ± 0.2AB |

Each value was expressed as the mean ± standard deviations for two batches of each type of cheese, analysed in triplicate.

Means within the column with different letters (A-D) are significantly different ($P<0.05$).

*H'*, Shannon's diversity; *S*, substrate richness; *E*, substrate evenness.

[a]Curd after moulding.

[b]Curd after dry salting

**TABLE S3** Correlations[a] between the abundance of operational taxonomic units (OTUs) and total free amino acid (FFA), concentration of Asp, Glu, Leu, Phe, and Val, area of hydrophilic and hydrophobic peaks[b], and carbon substrates[c] (polimers, amines, carboxylic acids, carbohydrates, and amino acids)

| **Descriptors** | **Significance** | **Abundance of OTUs** | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | *L. plantarum* group | *L. casei* group | *Lactobacillus* sp. | *L. sakei* group | *Lactobacillaceae* family | *L. brevis* | *Lc. lactis* | *St. thermophilus* |
| FAA | P | 3.92E-08 | 7.90E-05 | 0.00013 | 0.00028 | 0.0012 | 0.0019 | | |
| | FDR | 8.23E-07 | 0.0008 | 0.0009 | 0.0015 | 0.0049 | 0.0067 | | |
| | r | 0.89 | 0.74 | 0.72 | 0.70 | 0.64 | 0.62 | | |
| Asp | P | 1.49E-07 | 6.12E-05 | 0.0003 | 0.0004 | | | | |
| | FDR | 3.14E-06 | 0.0006 | 0.002 | 0.0025 | | | | |
| | r | 0.87 | 0.75 | 0.69 | 0.69 | | | | |
| Glu | P | 4.05E-07 | 0.0001 | 0.00064 | 0.0004 | | | | |
| | FDR | 8.50E-06 | 0.0012 | 0.0034 | 0.0029 | | | | |
| | r | 0.85 | 0.73 | 0.67 | 0.68 | | | | |
| Leu | P | 5.40E-08 | 2.61E-05 | 0.00013 | 0.0002 | | 0.0027 | | |
| | FDR | 1.13E-06 | 0.0003 | 0.0009 | 0.0009 | | 0.011 | | |
| | r | 0.88 | 0.77 | 0.72 | 0.72 | | 0.61 | | |
| Phe | P | 3.36E-08 | 3.52E-05 | 0.0002 | 0.0002 | | 0.0024 | | |
| | FDR | 7.07E-07 | 0.0004 | 0.0011 | 0.0013 | | 0.01 | | |
| | r | 0.89 | 0.76 | 0.71 | 0.71 | | 0.61 | | |
| Val | P | 9.21E-08 | 5.29E-05 | 0.0002 | 0.0002 | | | | |
| | FDR | 1.93E-06 | 0.0005 | 0.0013 | 0.0011 | | | | |
| | r | 0.88 | 0.75 | 0.71 | 0.71 | | | | |

**TABLE S3** (continued)

| Descriptors | Significance | Abundance of OTUs | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | *L. plantarum* group | *L. casei* group | *Lactobacillus* sp. | *L. sakei* group | *Lactobacillaceae* family | *L. brevis* | *Lc. lactis* | *St. thermophilus* |
| Area hydrophilic peaks | P | 3.56E-07 | 0.0001 | 0.0002 | 8.80E-05 | 0.0009 | 0.0015 | | |
| | FDR | 7.47E-06 | 0.0009 | 0.0010 | 0.0009 | 0.003 | 0.005 | | |
| | r | 0.86 | 0.72 | 0.71 | 0.74 | 0.65 | 0.63 | | |
| Area hydrophobic peaks | P | | | | | | | | 0.002 |
| | FDR | | | | | | | | 0.04 |
| | r | | | | | | | | 0.62 |
| Polymers | P | | | | | | | 5.69E-09 | |
| | FDR | | | | | | | 1.19E-07 | |
| | r | | | | | | | 0.91 | |
| Amines | P | | | | | | | 0.0061 | |
| | FDR | | | | | | | 0.043 | |
| | r | | | | | | | 0.60 | |
| Carbohydrates | P | | | | | | | 0.0003 | |
| | FDR | | | | | | | 0.007 | |
| | r | | | | | | | 0.69 | |
| Amino acids | P | | | | | | | 3.77E-07 | |
| | FDR | | | | | | | 7.92E-06 | |
| | r | | | | | | | 0.85 | |

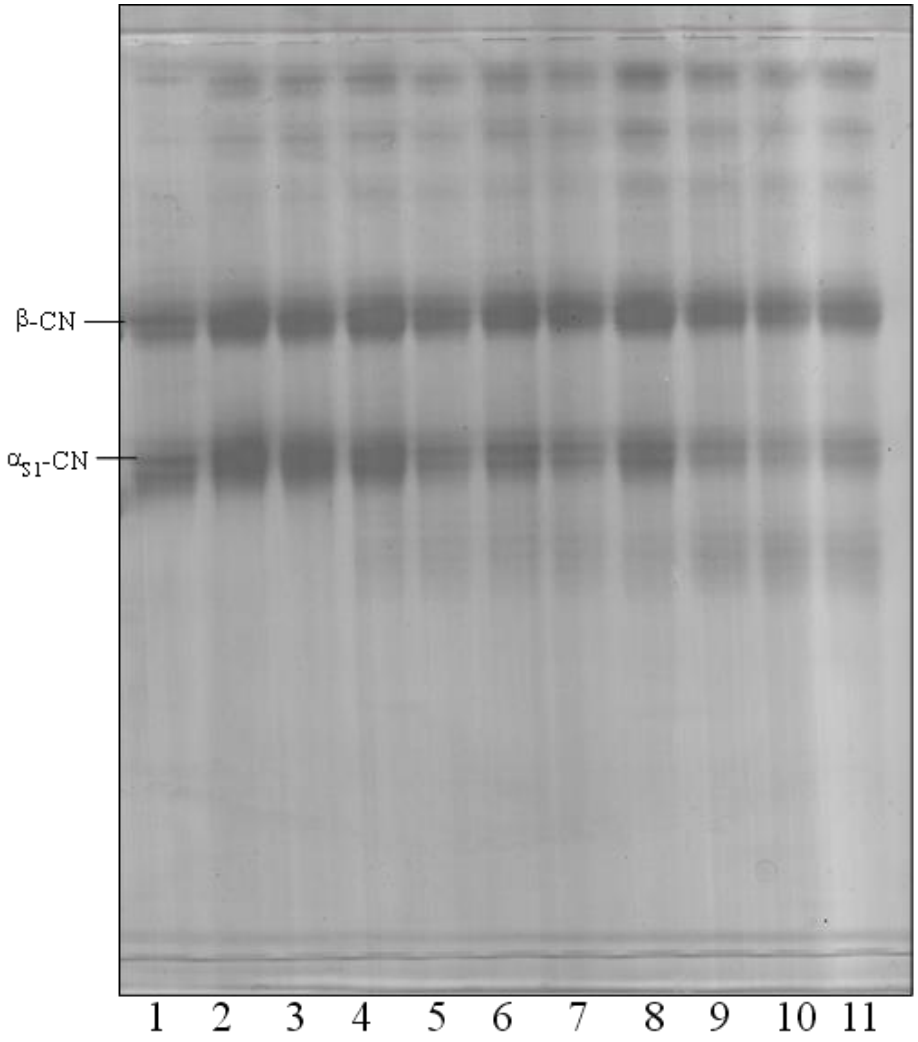
[a]Only the positive correlations with a $P<0.05$, $FDR<0.05$ and $r>0.06$ are reported.

[b]Area of hydrophilic and hydrophobic peaks of the pH 4.6-soluble nitrogen fractions analyzed by reverse phase high pressure liquid chromatography (RP-HPLC) were recognized and matched visually with the Unicorn program (Amersham Biosciences).

[c]Utilization of carbon substrates was carried out by using Biolog Eco-Microplates containing 31 carbon substrates grouped for chemical class (polimers, amines, carbohydrates, and amino acids).

**FIGURE S1** Urea-polyacrylamide gel electrophoresis (PAGE) of the pH 4.6-insoluble (A) and -soluble (B) nitrogen fractions during manufacture and ripening of Canestrato Pugliese cheese. Lanes: 1, ovine casein (CN) standard; 2, curd after moulding; 3 - 11, cheese (post dry salting) after 1, 3, 7, 15, 30, 45, 60, 75 and 90 days of ripening, respectively.

(A)



(B)