Correction to: Development of an LC-MS Method for the Identification of β -Casein Genetic Variants in Bovine Milk

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This article was originally published with errors in Figs. 3b, 4a, b and 5, that were introduced during the production process. The correct versions are given below.

The original article has been corrected.

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Fig. 3 **a** Experimental procedure for milk sample processing; **b** extracted chromatograms for A1-like and A2-like peptides, obtained by applying different milk processing conditions; signals are extracted as the sum of the three most intense m/z values of the Gaussian isotopic distribution for the tetra-charged state of each peptide (i.e., for A1-like peptide: 1340.47201+ 1340.72285+ 1340.97369; for A2-like peptide: 1330.47048+ 1330.72131+ 1330.97215). Correspondent m/z spectra

are reported. Blank: digestion buffer; β -CN: processed standard β -casein. Mass error < 5 ppm; **c** percentage recovery, calculated based on peak area values, following filtration and ultracentrifugation of a commercial milk sample, compared with the untreated sample. Black: A1-like peptide; gray: A2-like peptide. Data represent the average values $\pm$ standard deviation of three replicates

Fig. 4 Extracted chromatograms for A1-like and A2-like peptides, detected in seven samples of commercial milk (**a**) and in six samples of A2 milk (**b**). Signals are extracted as the sum of the three most intense m/z values of the Gaussian isotopic distribution for the tetra-charged state of each peptide (for A1-like peptide: 1340.47201+ 1340.72285+ 1340.97369; for A2-like pep-tide:

1330.47048+ 1330.72131+ 1330.97215). β -CN: processed standard β casein (1 mg/ml). Mass error < 5 ppm; **c** peak area values for A1-like peptide signals detected in commercial milk samples (left) and A2 milk samples (right). Data represent the average values $\pm$ standard deviation of three replicates

Fig. 5 **a** Evaluation of response linearity, obtained by plotting commercial milk spike level in A2 milk (% spike, v/v) versus peak areas of the A1-like peptide signal, in the tetra-charged state; **b** extracted chromatograms for A1-like peptide, detected in A2 milk sample no. 6 spiked at 1% (v/v) with commercial milk no. 4. Signals are extracted as the sum of the three most intense m/z values of the Gaussian isotopic

distribution for the tetracharged form of each peptide. A2 milk: unspiked A2 milk; β -CN: processed standard β -casein (1 mg/ml). Mass error < 5 ppm; **c** peak area values for A1-like and A2-like tetra-charged peptide species, measured in each replicate spiked sample. CV, coefficient of variation