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CORRECTION **Open Access**

Correction: Genetic variability of mutans streptococci revealed by wide whole-genome sequencing

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Correction

After the publication of this work [1], we became aware of the fact that from No. 10 onwards the numbering of the references in the reference list lost congruence with citations in the body of the text. Please see below the corrected list of references. The citations in the original manuscript refer to the corrected list below.

Furthermore we like to correct two additional errors: In Figure two (Figure 1 here) the strain number KK26 has to be corrected to KK21 and on page 13 of the manuscript, chapter "Antibiotic resistance-related proteins" the unit of the minimum inhibitory concentration of *Streptococcus mutans* against bacitracin has to be changed from μg/l to μg/ml, reading now:

The *S. mutans* species is known to be intrinsically resistant to bacitracin produced by *Bacillus subtilis.* We confirmed this by testing all the 10 strains with a bacitracin-E-test (data not shown). All strains including *S. ratti* DSM 20564 and *S. sobrinus* DSM 20742 had a minimum inhibitory concentration between 128 and >256 μg/ml.

We regret any inconvenience that these inaccuracies might have caused. We wish to thank Prof. Dr. Rudolf Lütticken for bringing this matter to our attention.

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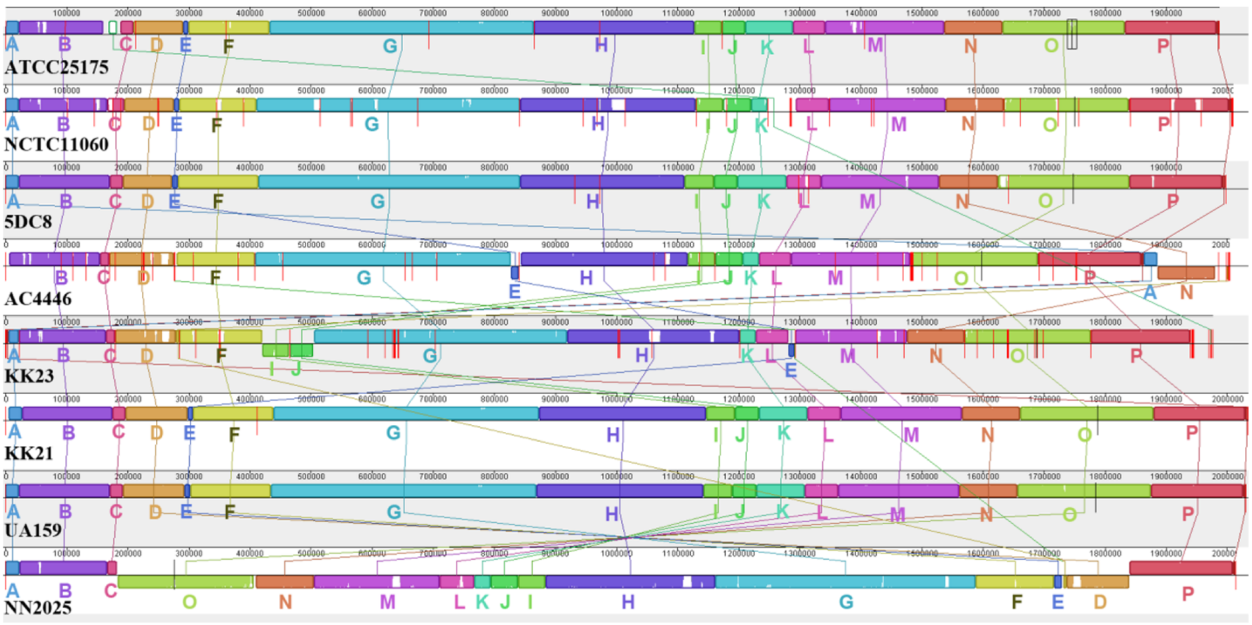

Figure 1 Comparison of local collinear blocks (LCBs) of chromosomal sequences of the eight *S. mutans* strains. In total 16 local LCBs, marked as A to P, were generated and compared by applying the MAUVE software [13,14] with default settings and using strain UA159 as reference. The red vertical bars indicate contig ends. The white areas inside each LCB show regions with low similarities.

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