

The mycobiome of root canal infections is correlated to the bacteriome. *Clinical Oral Investigations*
Ilona F. Persoon¹, Mark J. Buijs¹, Ahmet R. Özok², Wim Crielaard¹, Bastiaan P. Krom¹, Egija Zaura¹,
Bernd W. Brandt¹

Affiliations:¹Department of Preventive Dentistry; ²Department of Endodontology, Academic Centre for
Dentistry Amsterdam (ACTA), University of Amsterdam and Vrije Universiteit Amsterdam, The
Netherlands

Correspondence: Ilona F. Persoon, i.persoon@acta.nl

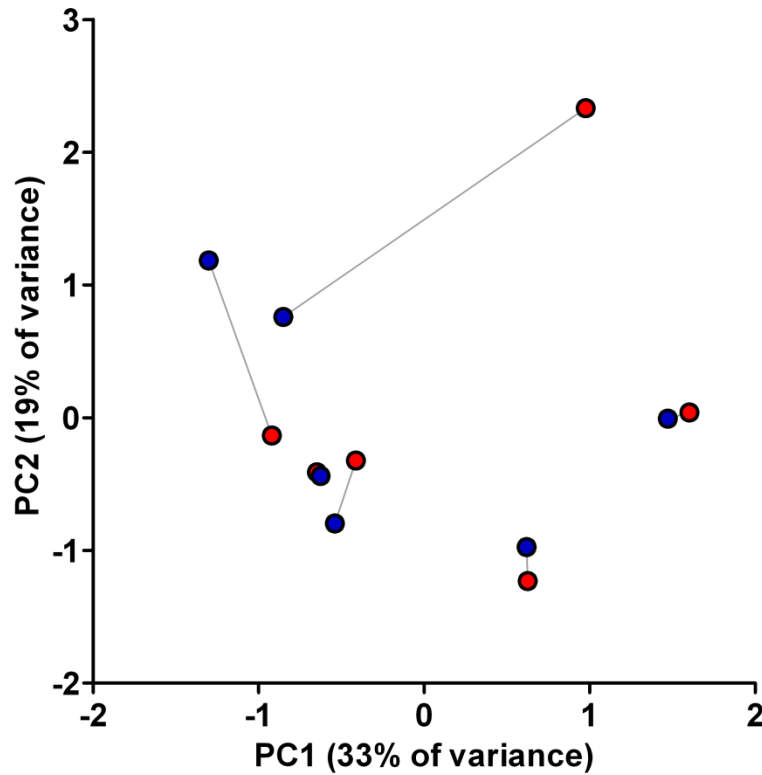


Fig. A two-dimensional ordination by principal component analysis (PCA) of the mycobiomes, as determined through ITS1 sequencing, of apical (N = 6; red) and coronal root segments (N = 6; blue) were not statistically significantly different ($F = 0.327$, $p = 0.966$, PERMANOVA). Principal components PC1, PC2 and PC3 (not shown) explained 33%, 19% and 13% of the overall variance among samples, respectively. Corresponding apical and coronal root segments are connected with a line