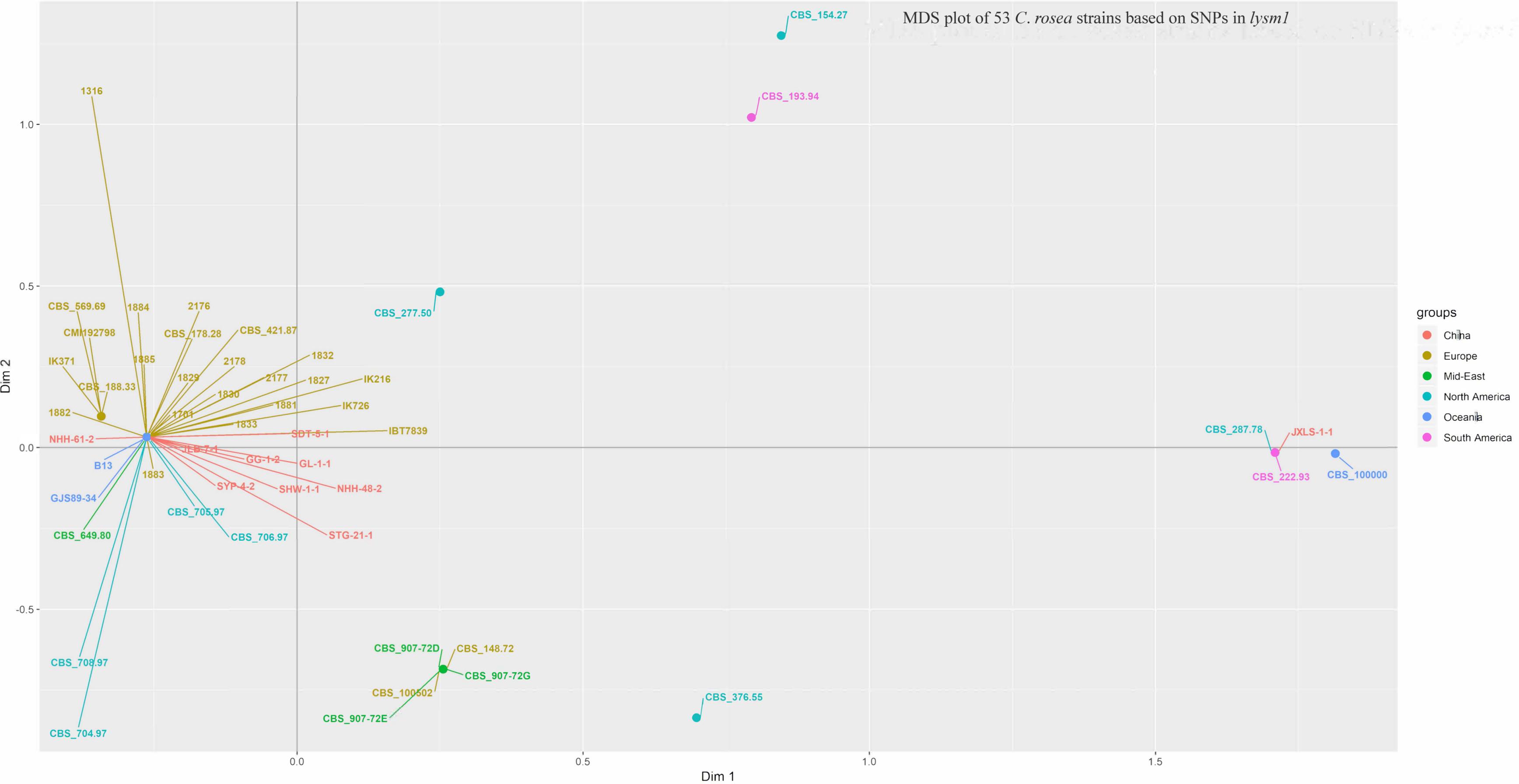


MDS plot of 53 *C. rosea* strains based on SNPs in *lysm1*



MDS plot of 53 *C. rosea* strains based on SNPs in *lysm2*



Figure S2: Multidimensional scaling (MDS) plots of SNP genotypes from a world-wide collection of 53 *Clonostachys rosea* strains in *lysm1*, *lysm2* and *chiC2*.

A multi-dimensional scaling (MDS) analysis of the distribution of *lysm1* SNPs, did not indicate any correlation between sequence variation in *lysm1* and the geographical origin of the strains (Fig S2). The 3'-end of the *lysm1* alleles from three strains (CBS 10000, CBS 222.93 and CBS 287.78) were different from the other 50 strains in that the last 177 bp (from pos. 355) were replaced by a different 117 bp DNA fragment. This effectively removed the LysM module from these alleles, while preserving the trans-membrane domain. After removing the 117 bp DNA fragment from the sequence alignment, a test for the presence of recombination using GARD indicated ($P < 0.001$) one potential recombination event at position 192. Furthermore, analysis with the codon-based maximum likelihood method REL provided no evidence for positive selection in *lysm1*.

MDS analysis of sequence polymorphism in *lysm2* showed that strains originating from China, except GG-1-2 and JXLS-1-1, grouped together, while European strains were found in two groups where one group clustered together with strains originating from North America while second group clustered with strains from the Middle East (Fig S2). REL analysis indicated one site evolving under positive selection (Bayes factor = 46), at codons 205 (Fig. 1).

Based on a MDS analysis of sequence polymorphism in *chiC2*, strains from China grouped together, with the exception for JXLS-1-1, SDT-5-1 and GG-1-2. Strains originating from Europe formed two groups where one group only contained European strains, while the other group included strains with a wide geographical distribution (Fig S2). GARD analysis indicated ($P < 0.001$) one potential recombination event at position 531. REL analysis indicated one site to evolve under positive selection (Bayes factor = 699), at codon 826 in the GH18 module (Fig. 1).