Additional file 5



x-axes = Terminal restriction fragments (bp)

Figure AF5.1 – Comparison of mirror plots obtained on raw (left) and on denoised (right) pyrosequencing datasets

Examples are given for the sample GRW01 pyrosequenced with the HighRA method (A) and for the samples GRW07 (B) and AGS01 (C) pyrosequenced with the LowRA method. Relative abundances are given next to the cut predominant peaks.



x-axes = Terminal restriction fragments (bp)

Figure AF5.2 – Comparison of mirror plots obtained on raw (left) and on denoised (right) pyrosequencing datasets (zoom of Figure AF5.1 to detect low abundant peaks).

Examples are given for the sample GRW01 pyrosequenced with the HighRA method (A) and for the samples GRW07 (B) and AGS01 (C) pyrosequenced with the LowRA method. Relative abundances are given next to the cut predominant peaks.