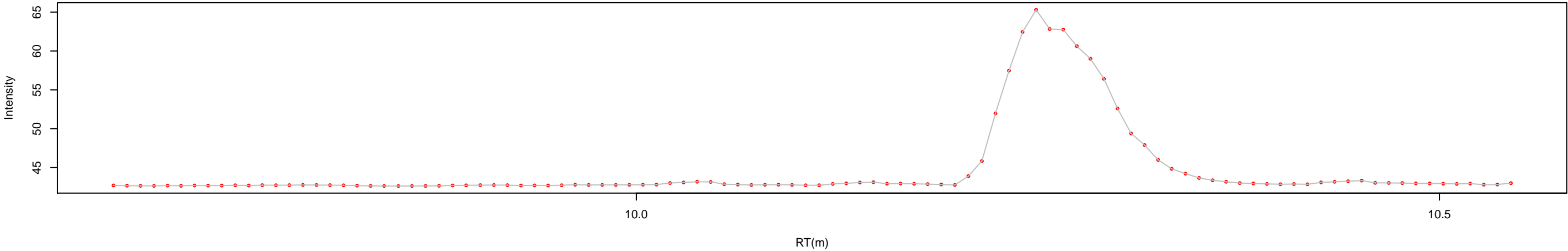
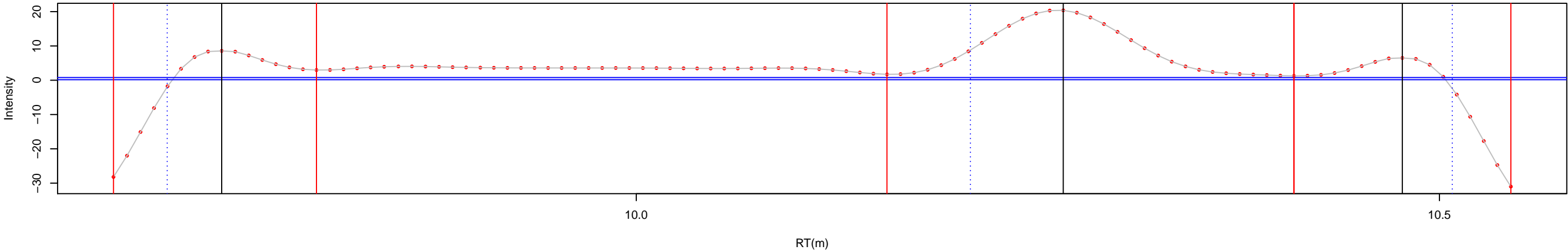


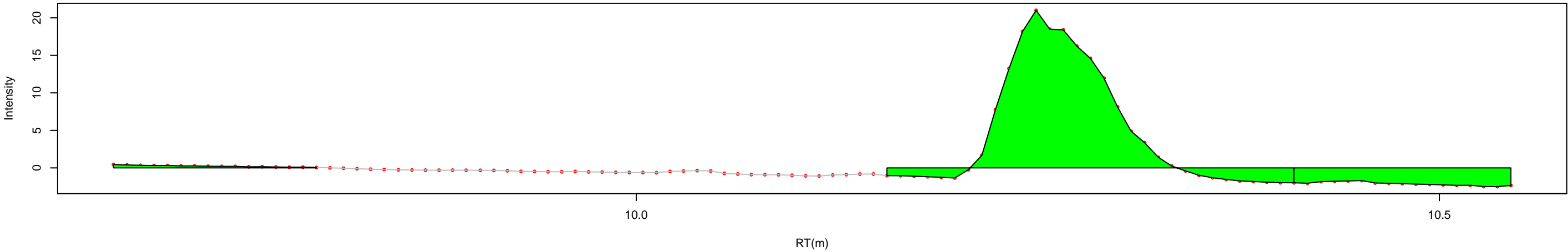
raw chromatogram | batch: 1   sample: female-y-1   conc: 50   function: 278   mass: 548 > 142.8



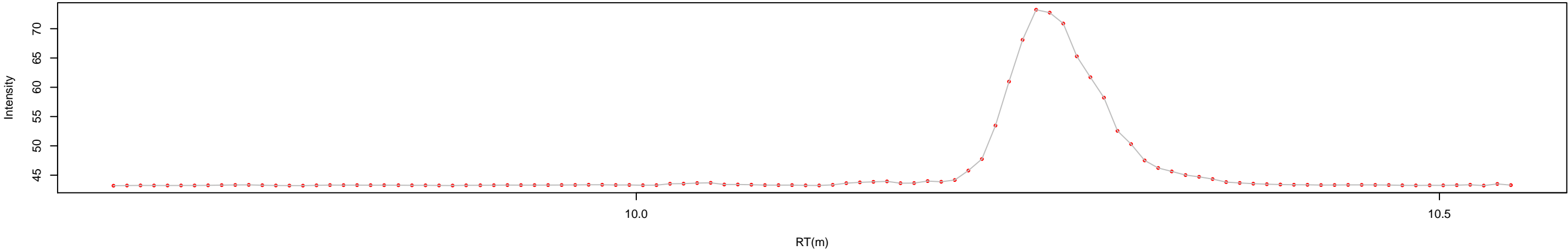
peak picking | window size: 19   iteration: 11   lp: 2   rp: 2   snr: 5   peak location: all   noise: 0.157   BLine: yes



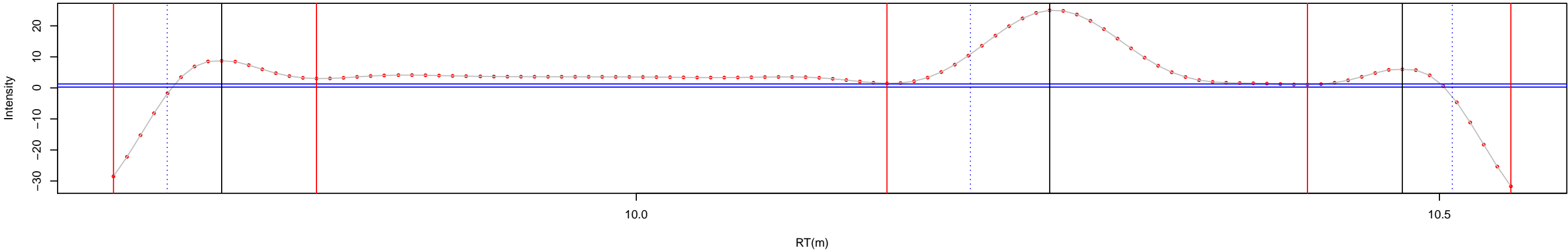
peak area | window size:3   BLine: yes



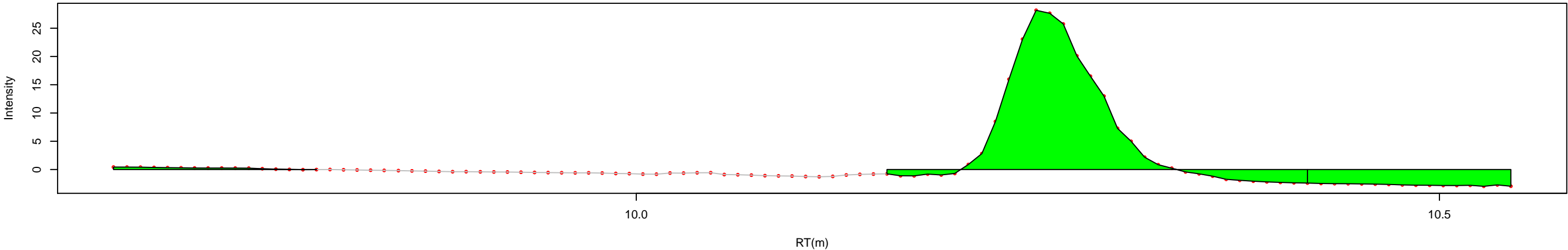
raw chromatogram | batch: 1   sample: female-y-m-7   conc: 50   function: 278   mass: 548 > 142.8



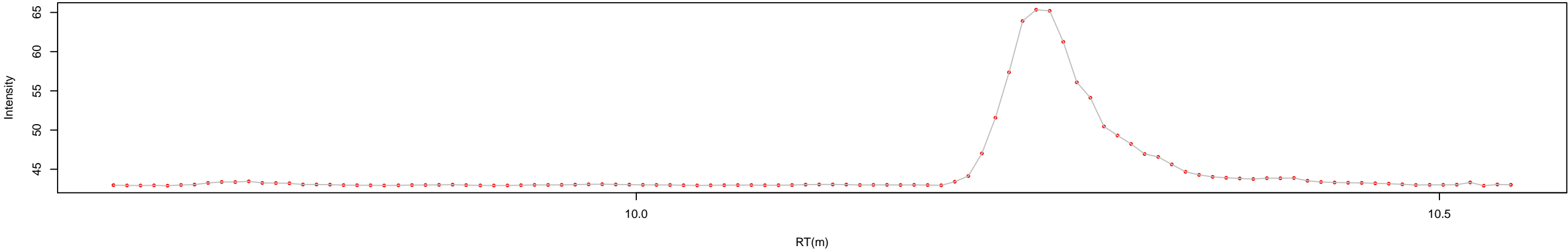
peak picking | window size: 19   iteration: 11   lp: 2   rp: 2   snr: 5   peak location: all   noise: 0.253   BLine: yes



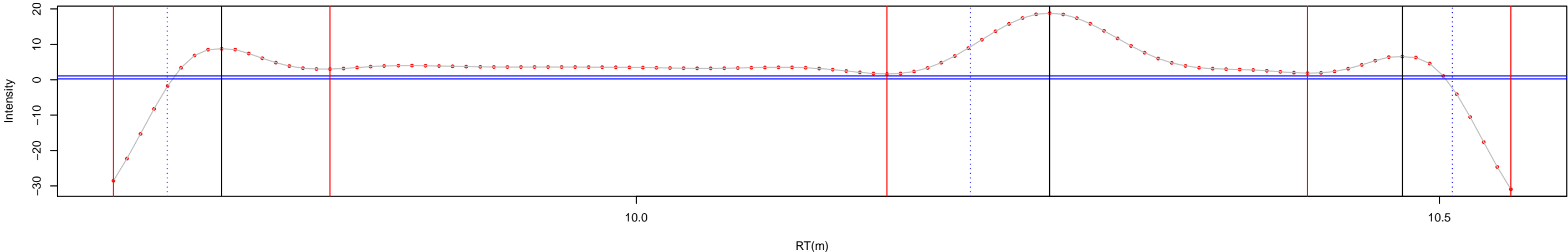
peak area | window size:3   BLine: yes



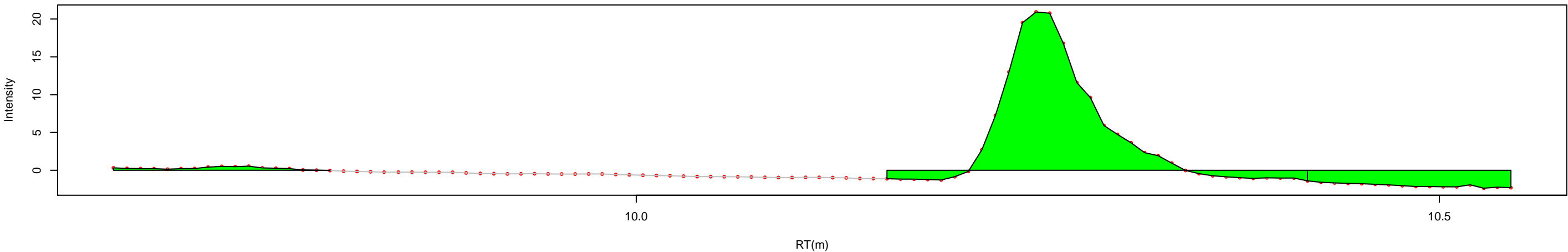
raw chromatogram | batch: 1   sample: female-o-13   conc: 50   function: 278   mass: 548 > 142.8



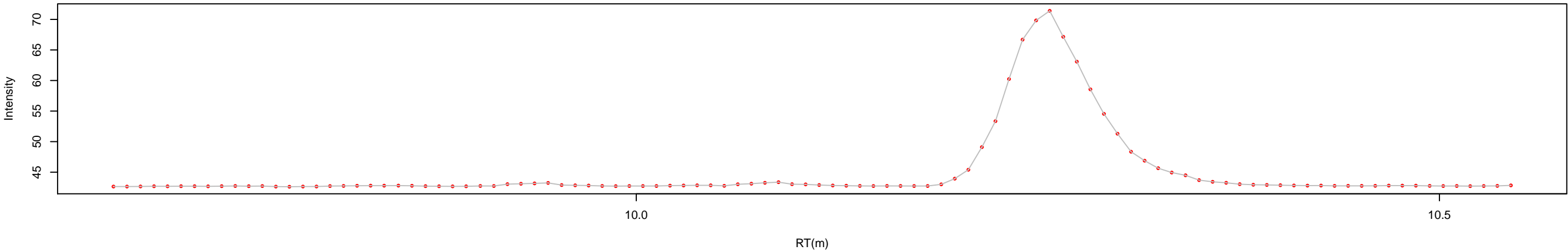
peak picking | window size: 19   iteration: 11   lp: 2   rp: 2   snr: 5   peak location: all   noise: 0.218   BLine: yes



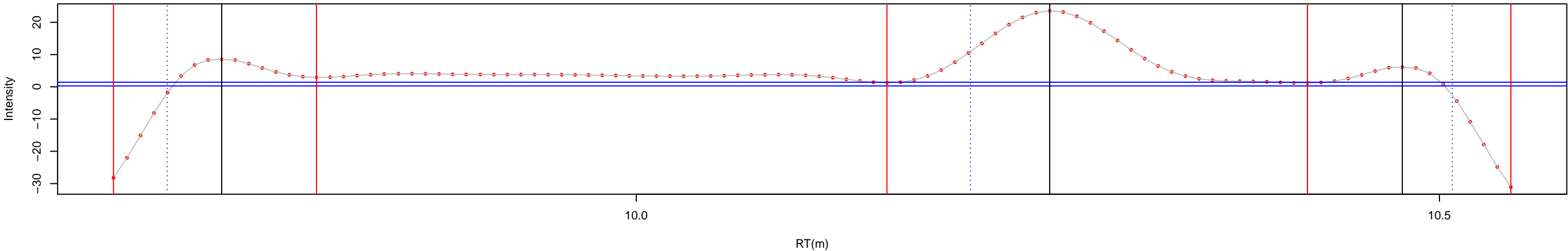
peak area | window size:3   BLine: yes



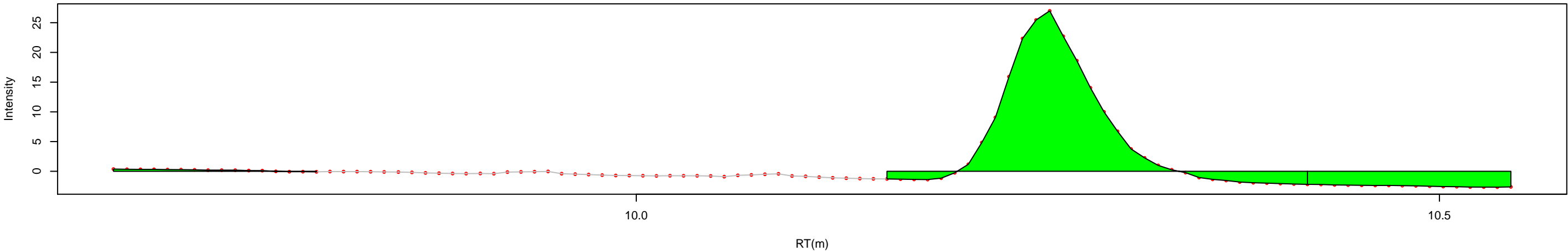
raw chromatogram | batch: 1 sample: female-o-m-20 conc: 50 function: 278 mass: 548 > 142.8



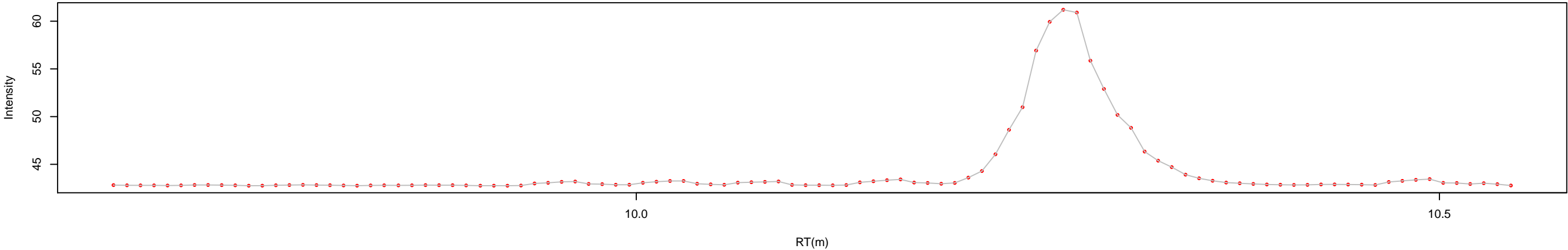
peak picking | window size: 19 iteration: 11 lp: 2 rp: 2 snr: 5 peak location: all noise: 0.285 BLine: yes



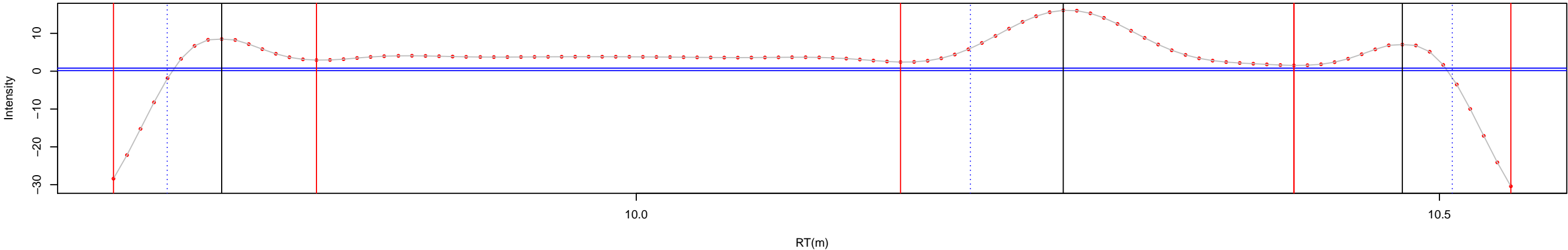
peak area | window size:3 BLine: yes



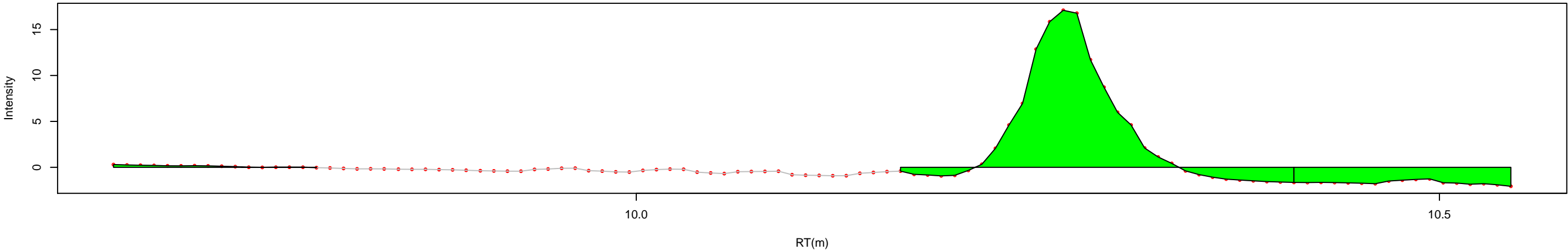
raw chromatogram | batch: 1   sample: female-y-2   conc: 50   function: 278   mass: 548 > 142.8

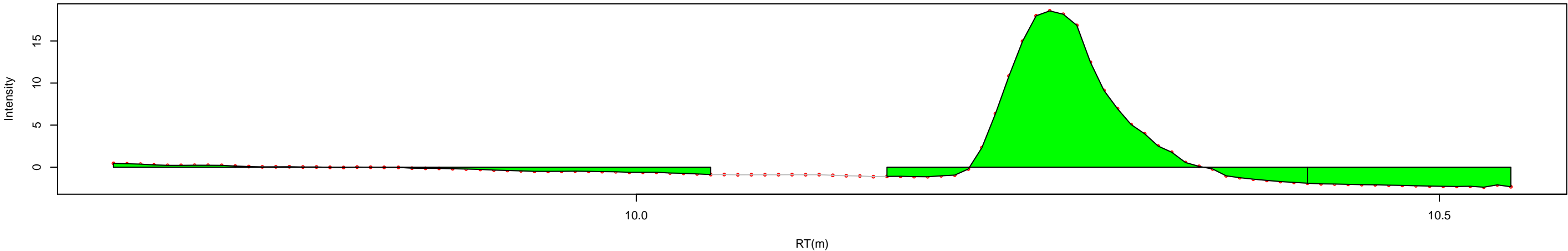
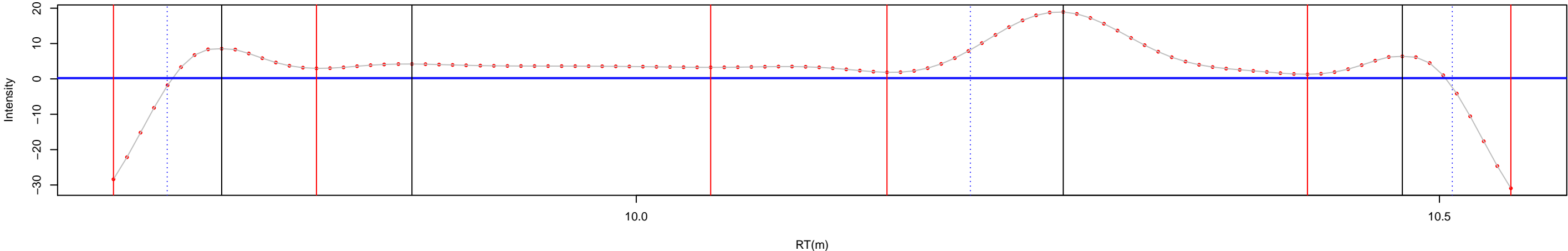
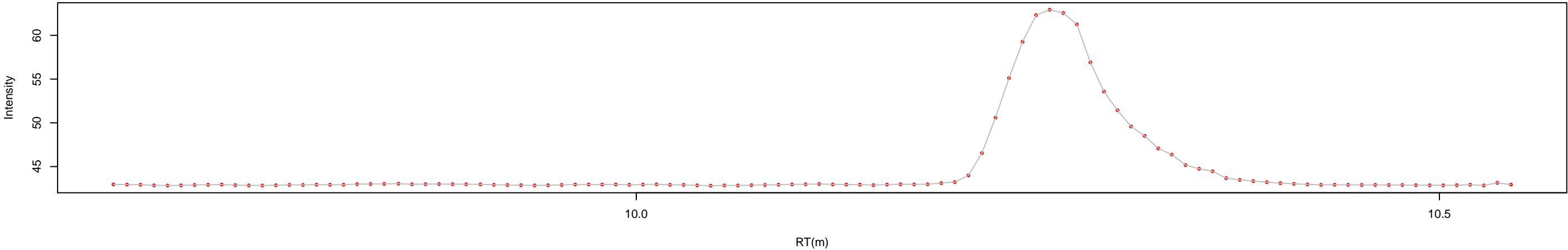


peak picking | window size: 19   iteration: 11   lp: 2   rp: 2   snr: 5   peak location: all   noise: 0.164   BLine: yes

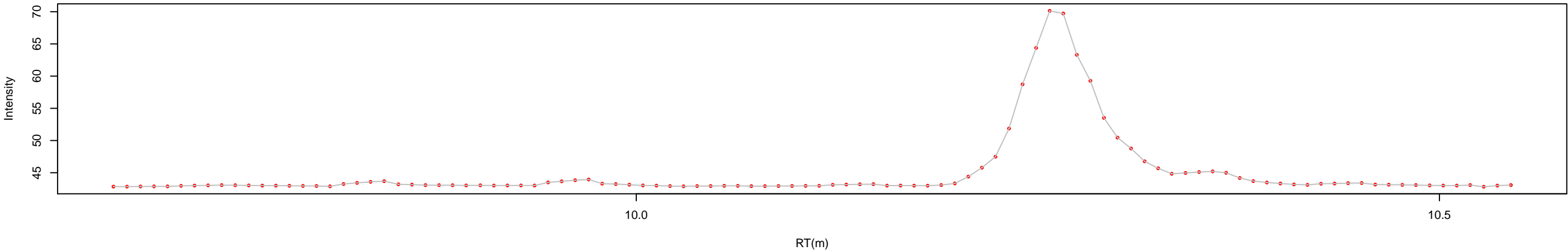


peak area | window size:3   BLine: yes

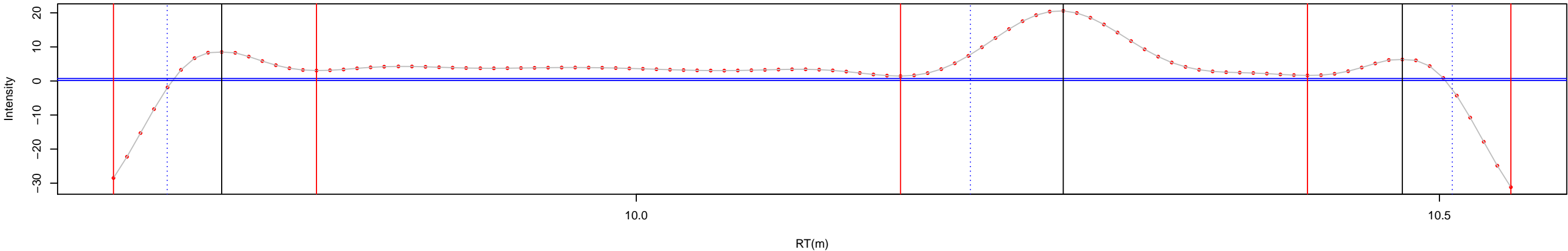




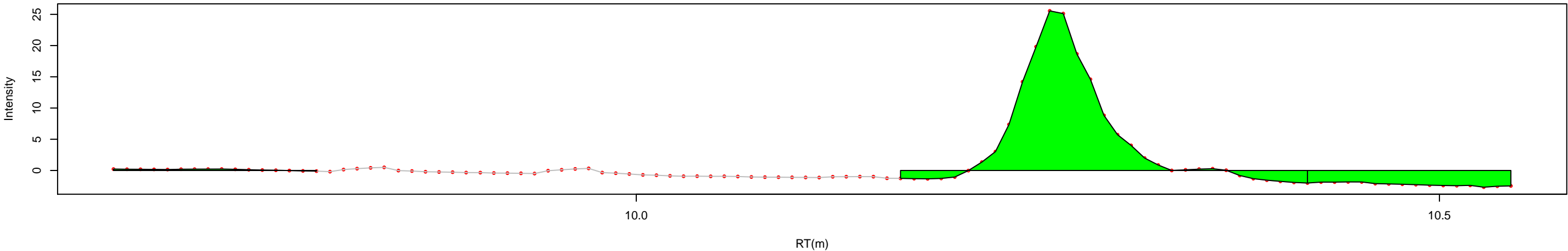
raw chromatogram | batch: 1   sample: female-o-14   conc: 50   function: 278   mass: 548 > 142.8



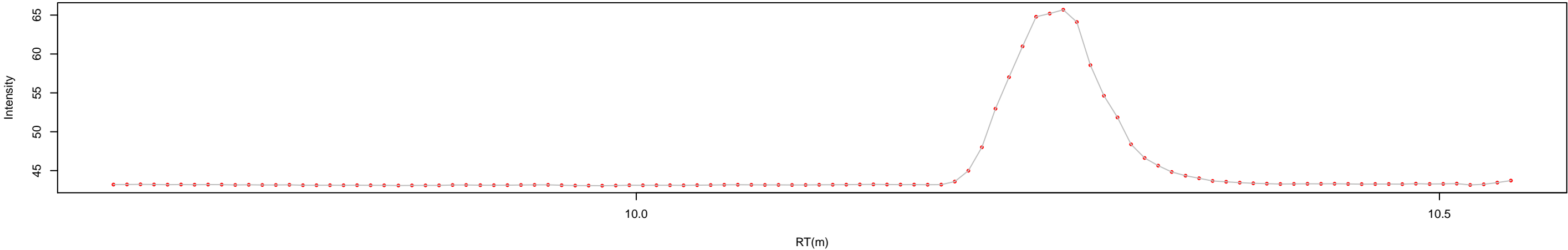
peak picking | window size: 19   iteration: 11   lp: 2   rp: 2   snr: 5   peak location: all   noise: 0.145   BLine: yes



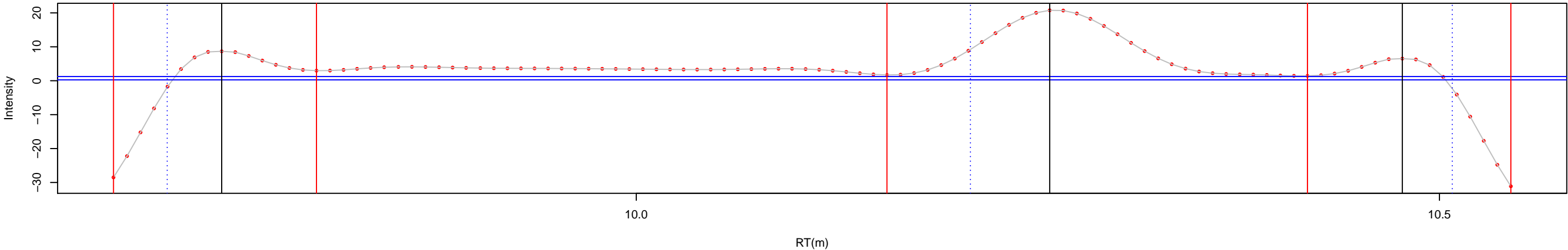
peak area | window size:3   BLine: yes



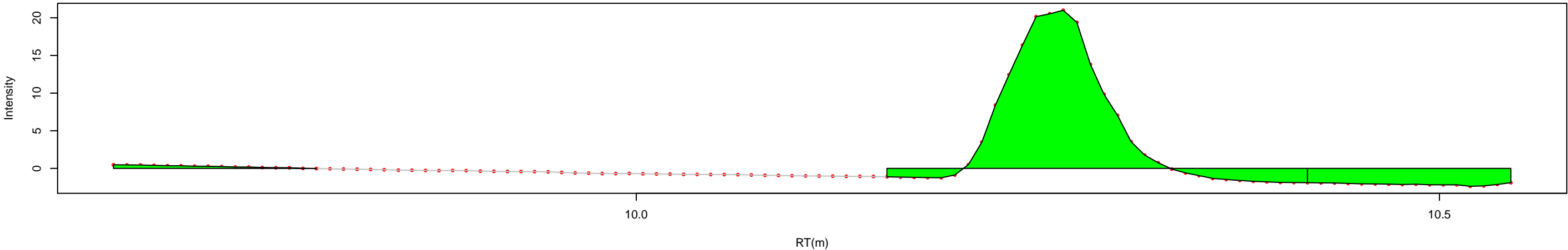
raw chromatogram | batch: 1   sample: female-o-m-21   conc: 50   function: 278   mass: 548 > 142.8



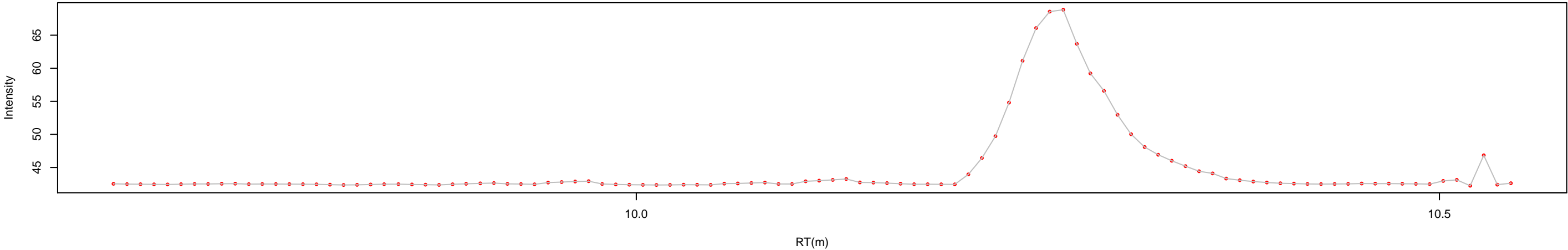
peak picking | window size: 19   iteration: 11   lp: 2   rp: 2   snr: 5   peak location: all   noise: 0.248   BLine: yes



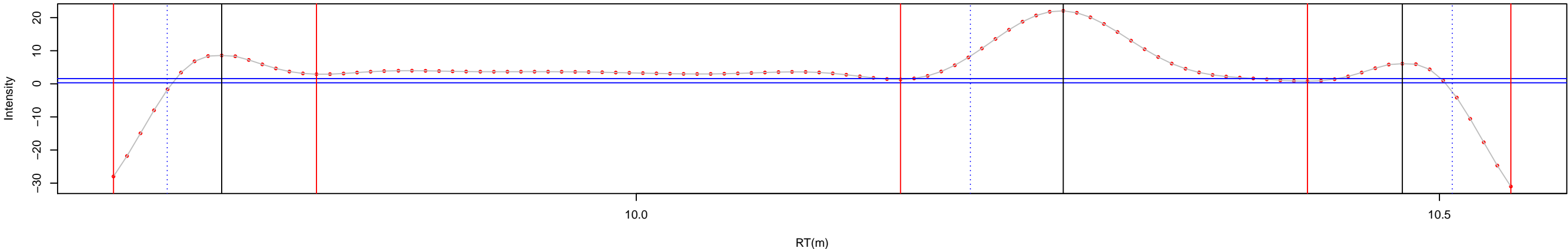
peak area | window size:3   BLine: yes



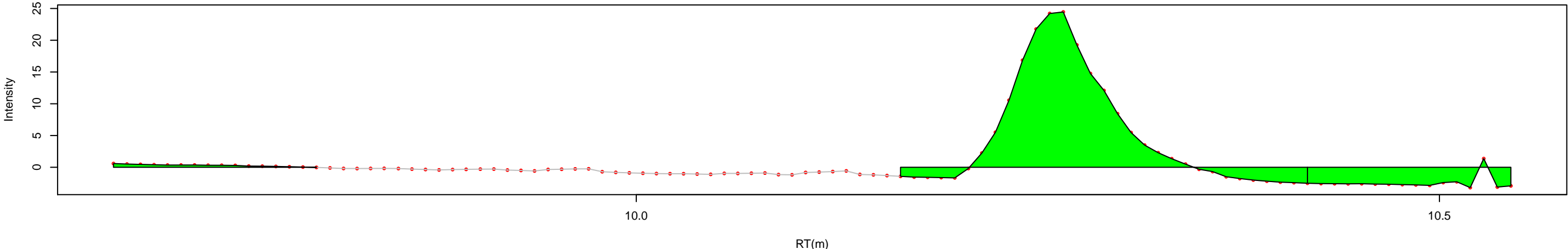
raw chromatogram | batch: 1 sample: female-y-3 conc: 50 function: 278 mass: 548 > 142.8



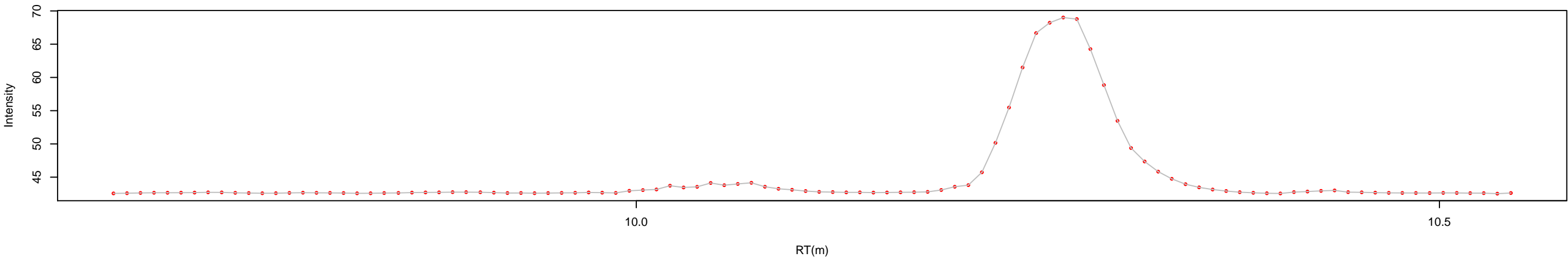
peak picking | window size: 19 iteration: 11 lp: 2 rp: 2 snr: 5 peak location: all noise: 0.315 BLine: yes



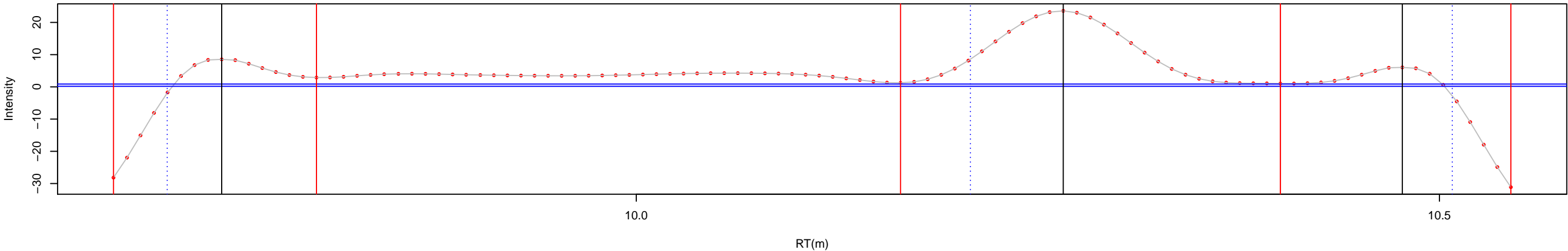
peak area | window size:3 BLine: yes



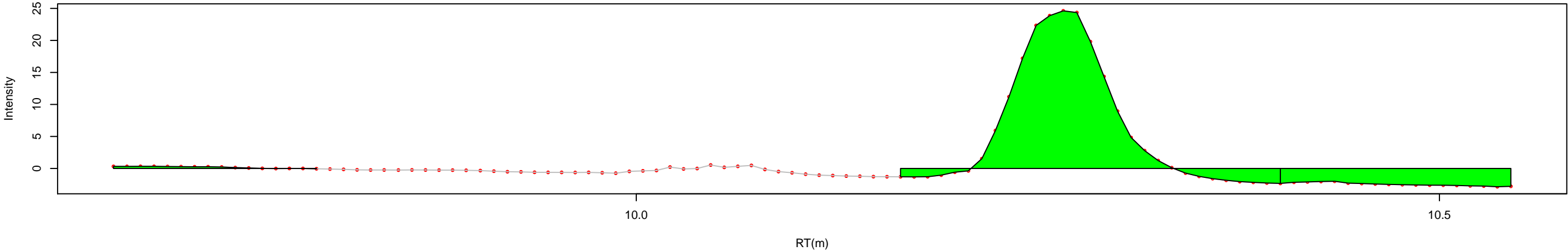
raw chromatogram | batch: 1   sample: female-y-m-9   conc: 50   function: 278   mass: 548 > 142.8



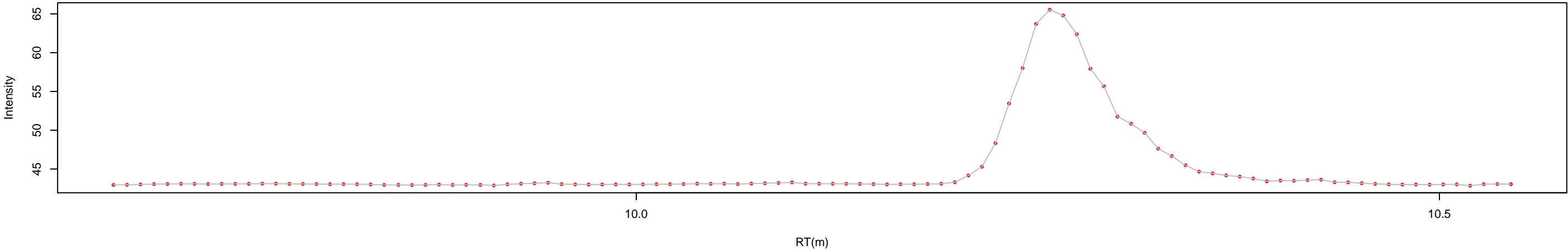
peak picking | window size: 19   iteration: 11   lp: 2   rp: 2   snr: 5   peak location: all   noise: 0.175   BLine: yes



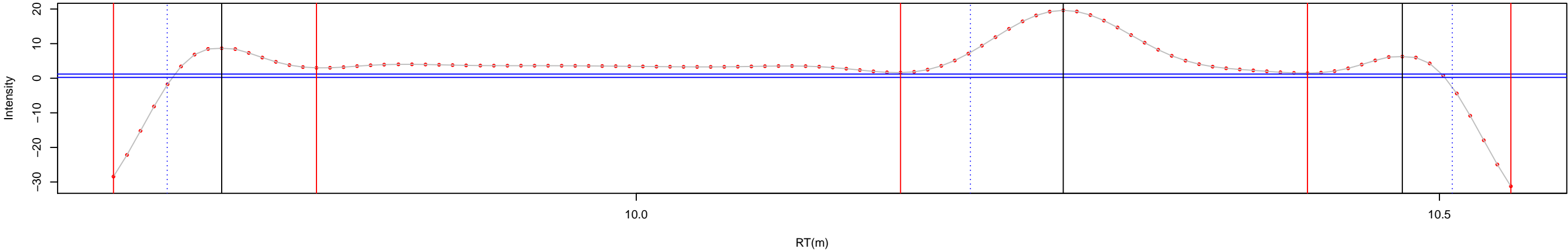
peak area | window size:3   BLine: yes



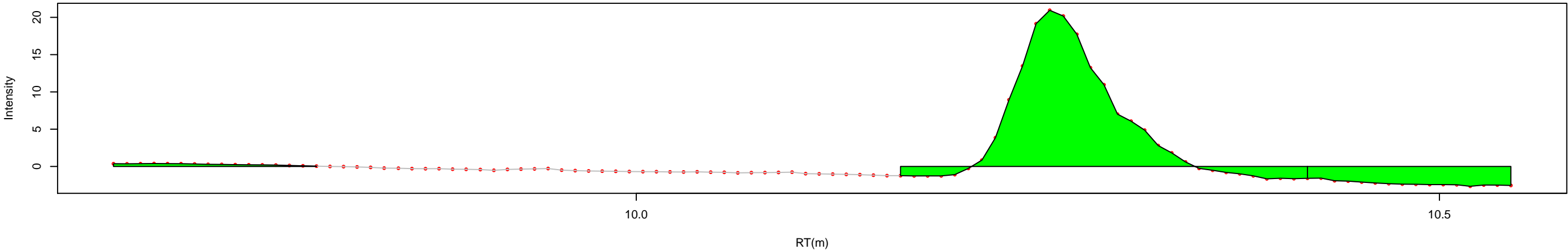
raw chromatogram | batch: 1   sample: female-o-15   conc: 50   function: 278   mass: 548 > 142.8



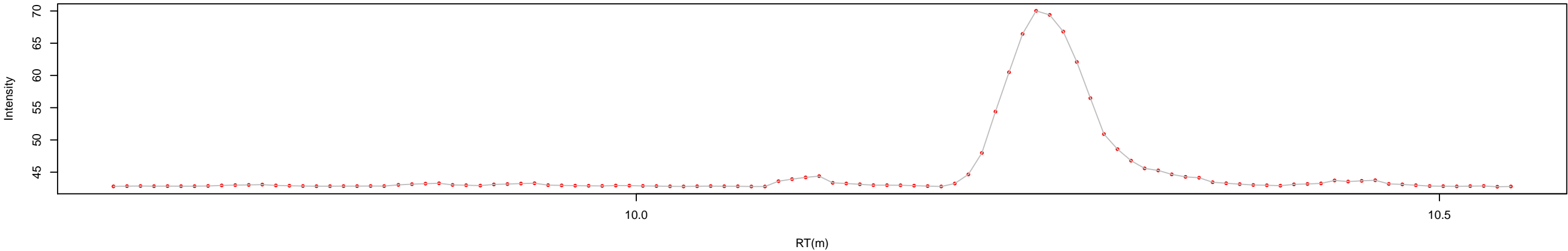
peak picking | window size: 19   iteration: 11   lp: 2   rp: 2   snr: 5   peak location: all   noise: 0.241   BLine: yes



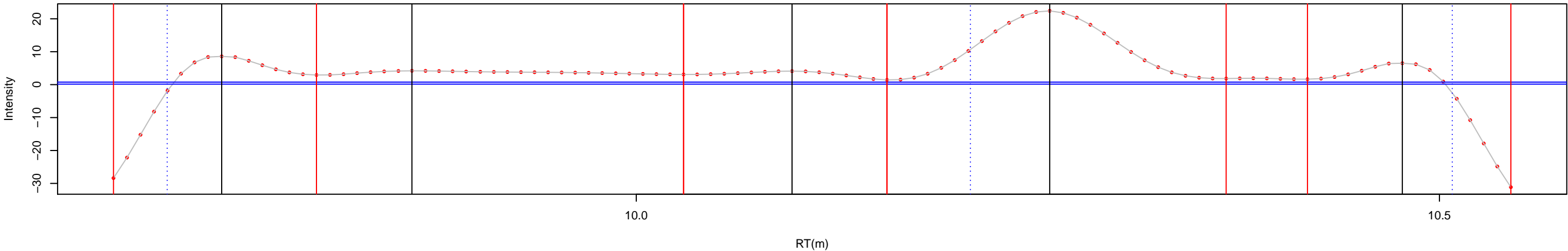
peak area | window size:3   BLine: yes



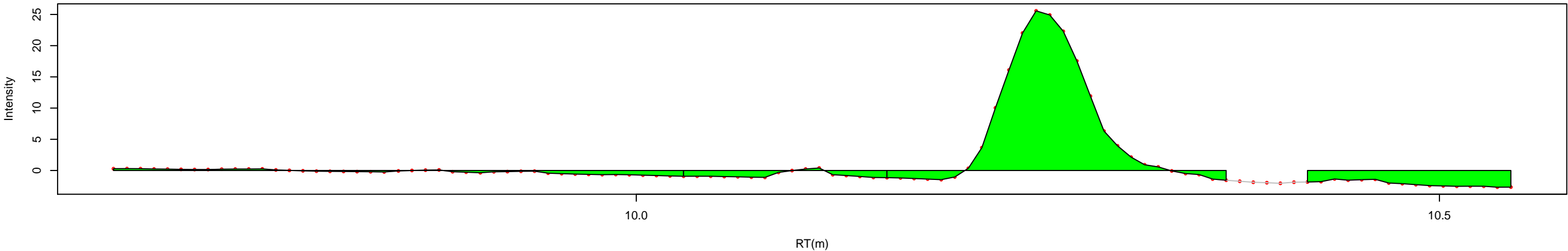
raw chromatogram | batch: 1 sample: female-o-m-22 conc: 50 function: 278 mass: 548 > 142.8



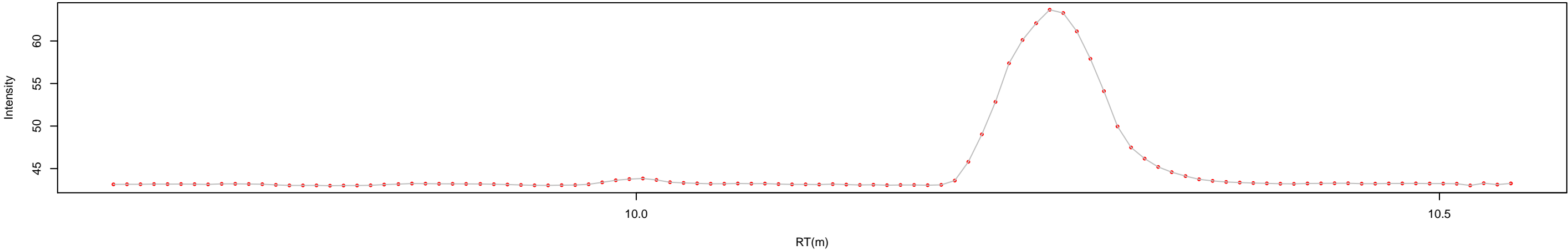
peak picking | window size: 19 iteration: 11 lp: 2 rp: 2 snr: 5 peak location: all noise: 0.154 BLine: yes



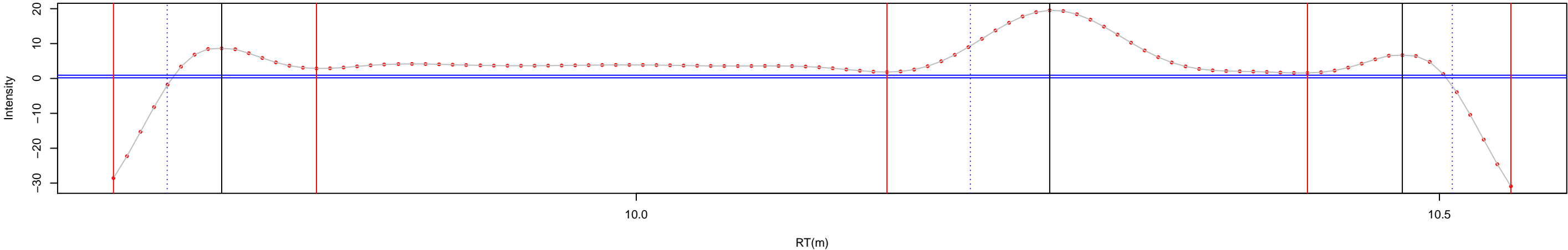
peak area | window size:3 BLine: yes



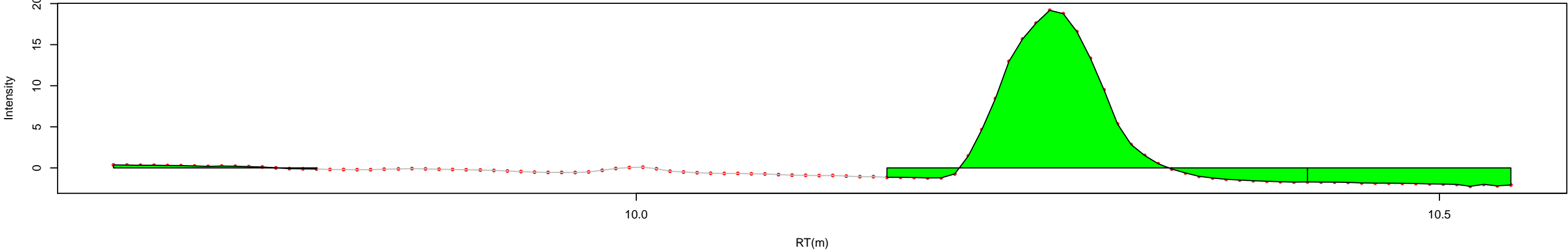
raw chromatogram | batch: 1   sample: female-y-4   conc: 50   function: 278   mass: 548 > 142.8



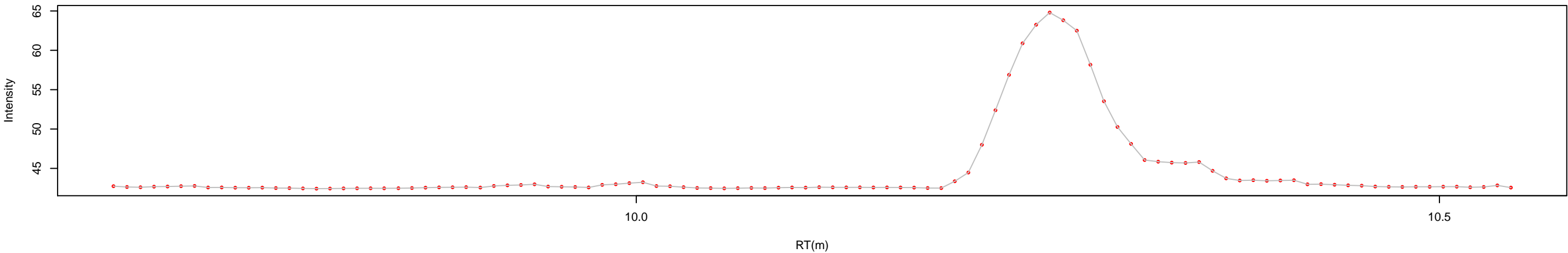
peak picking | window size: 19   iteration: 11   lp: 2   rp: 2   snr: 5   peak location: all   noise: 0.185   BLine: yes



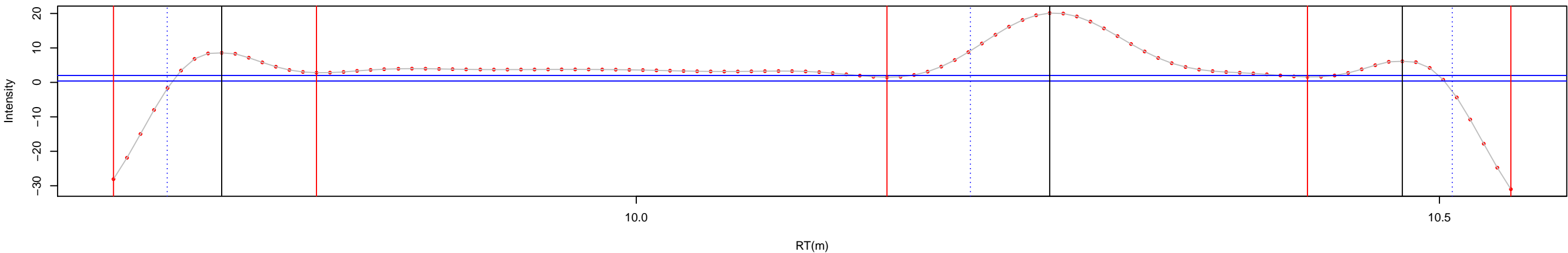
peak area | window size:3   BLine: yes



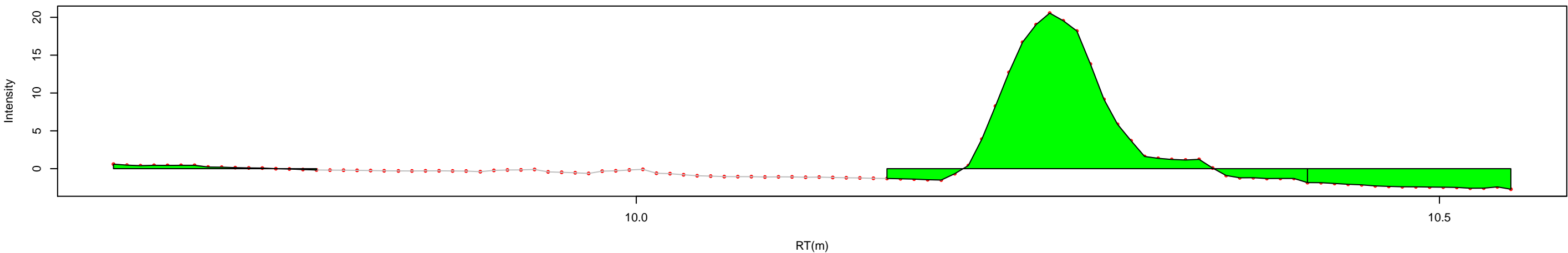
raw chromatogram | batch: 1 sample: female-y-m-10 conc: 50 function: 278 mass: 548 > 142.8



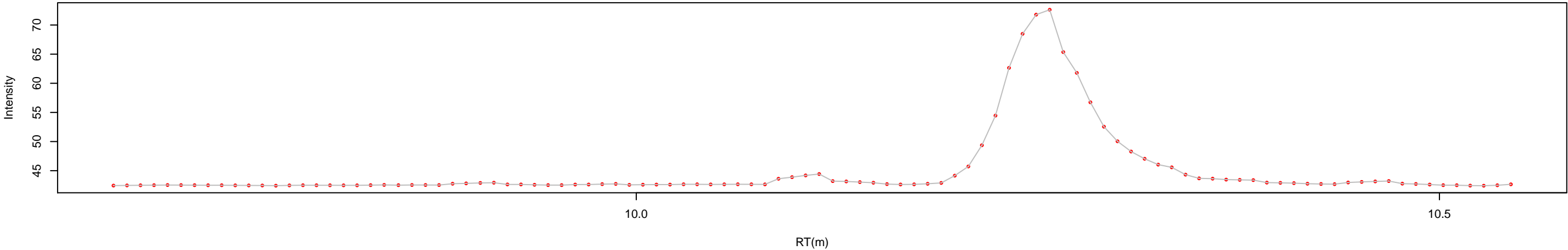
peak picking | window size: 19 iteration: 11 lp: 2 rp: 2 snr: 5 peak location: all noise: 0.401 BLine: yes



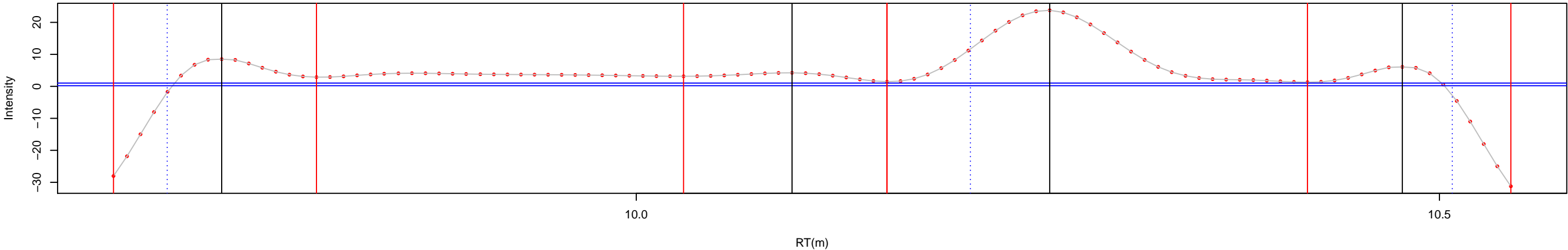
peak area | window size:3 BLine: yes



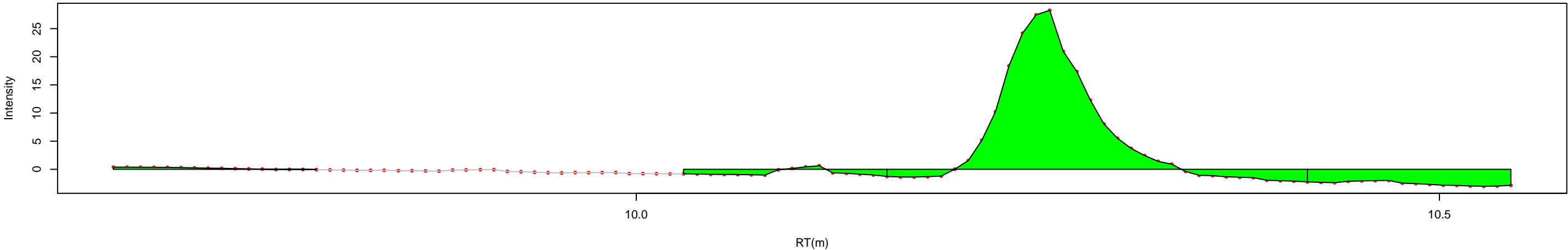
raw chromatogram | batch: 1 sample: female-o-16 conc: 50 function: 278 mass: 548 > 142.8



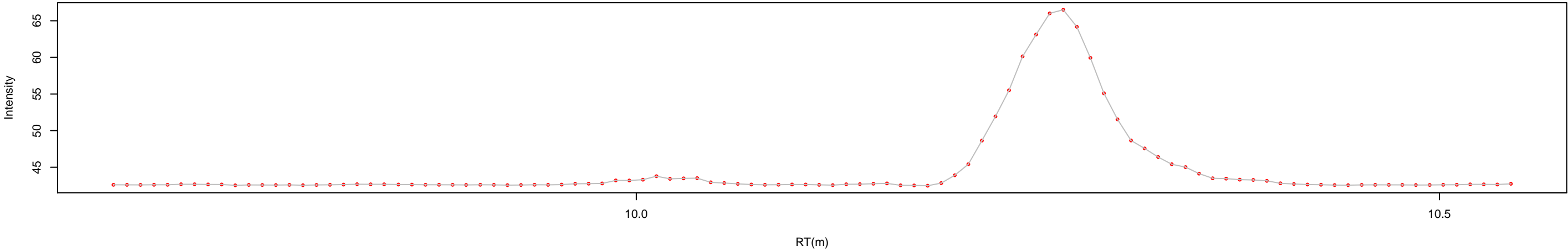
peak picking | window size: 19 iteration: 11 lp: 2 rp: 2 snr: 5 peak location: all noise: 0.206 BLine: yes



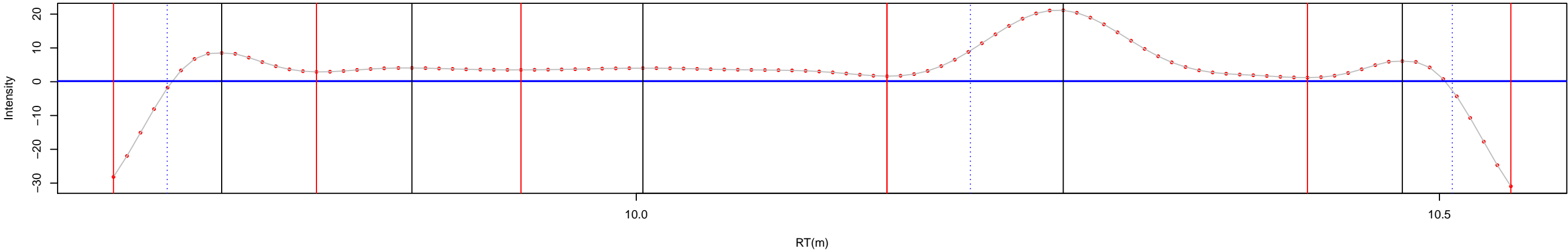
peak area | window size:3 BLine: yes



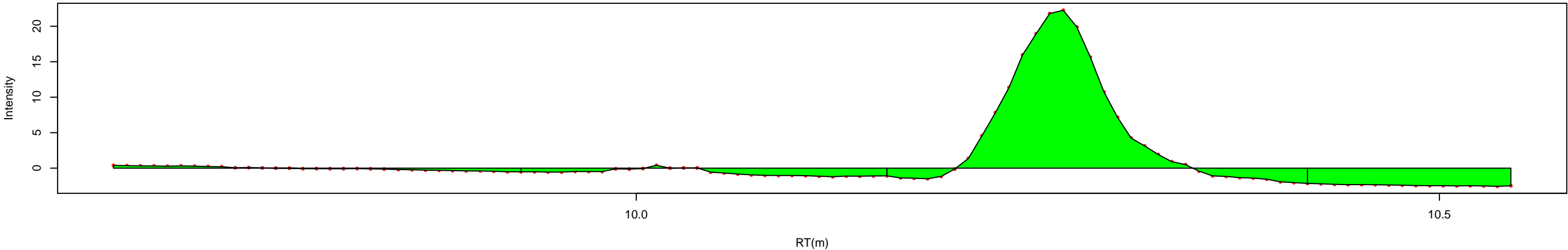
raw chromatogram | batch: 1 sample: female-o-m-23 conc: 50 function: 278 mass: 548 > 142.8



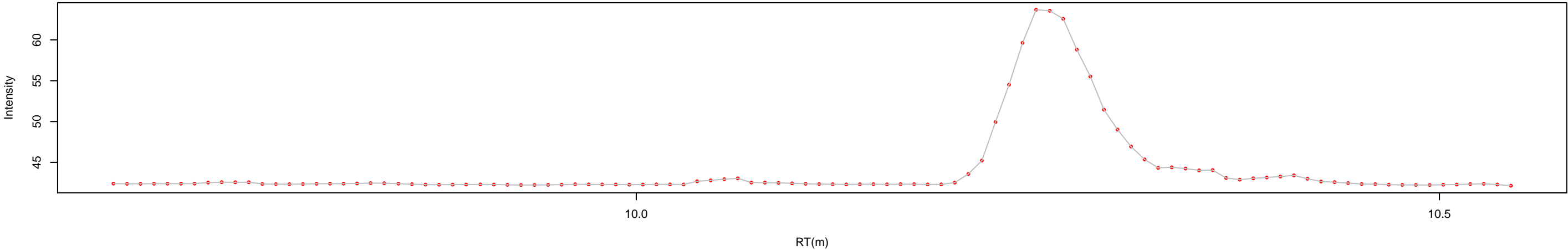
peak picking | window size: 19 iteration: 11 lp: 2 rp: 2 snr: 5 peak location: all noise: 0.0594 BLine: yes



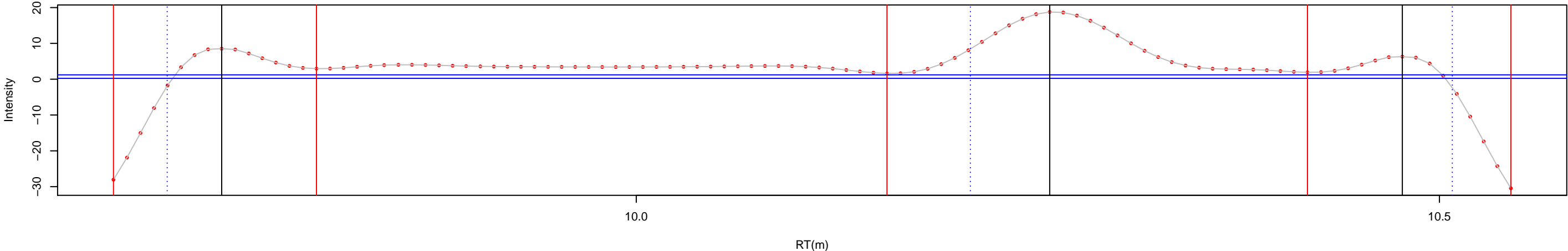
peak area | window size:3 BLine: yes



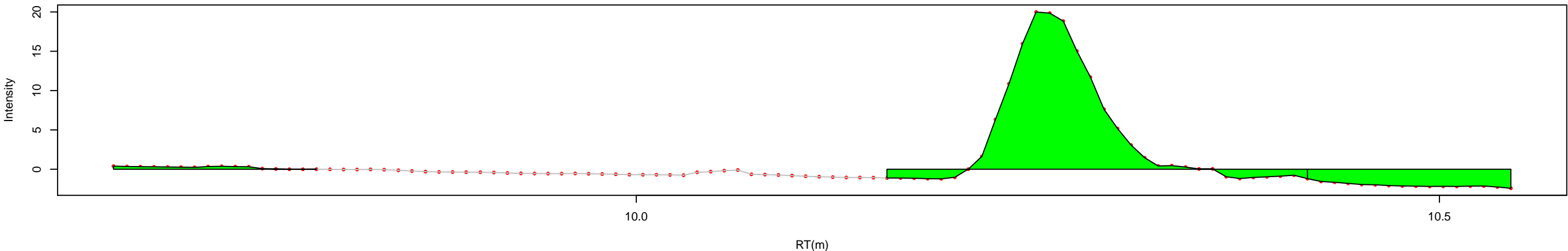
raw chromatogram | batch: 1 sample: female-y-5 conc: 50 function: 278 mass: 548 > 142.8



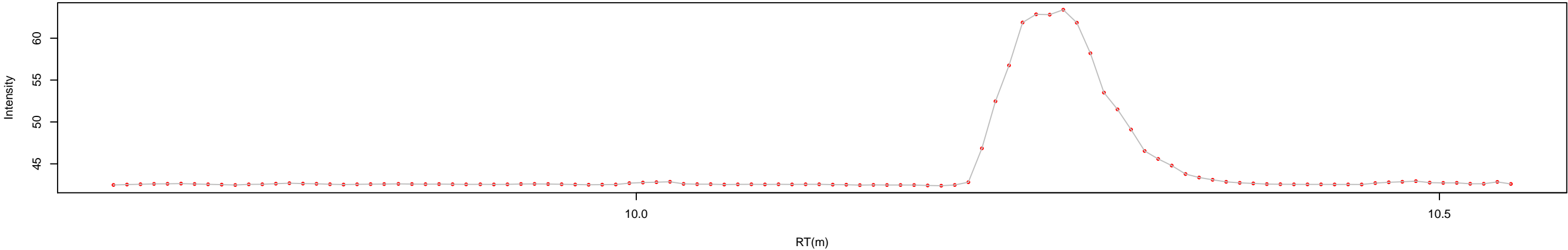
peak picking | window size: 19 iteration: 11 lp: 2 rp: 2 snr: 5 peak location: all noise: 0.243 BLine: yes



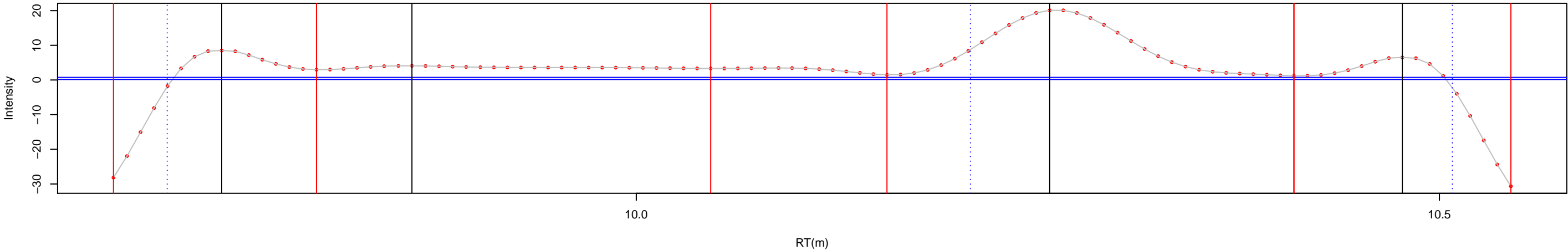
peak area | window size:3 BLine: yes



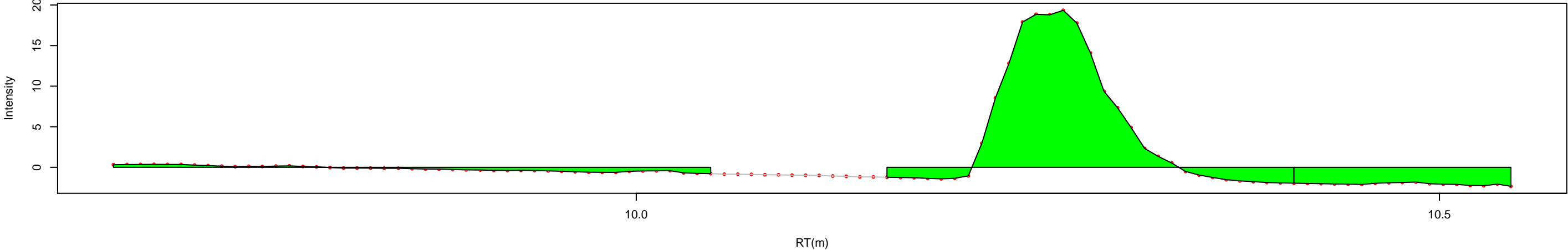
raw chromatogram | batch: 1   sample: female-y-m-11   conc: 50   function: 278   mass: 548 > 142.8



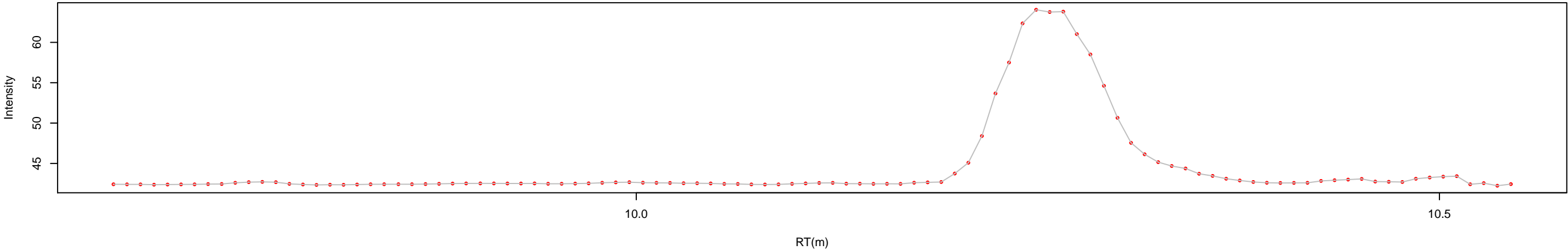
peak picking | window size: 19   iteration: 11   lp: 2   rp: 2   snr: 5   peak location: all   noise: 0.149   BLine: yes



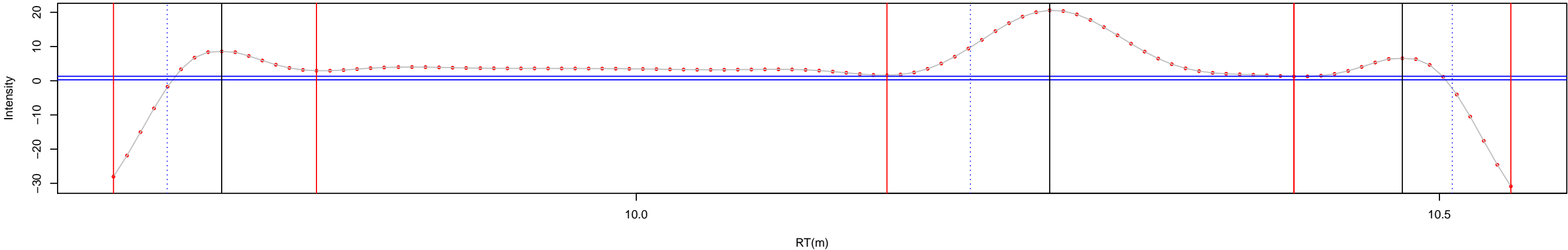
peak area | window size:3   BLine: yes



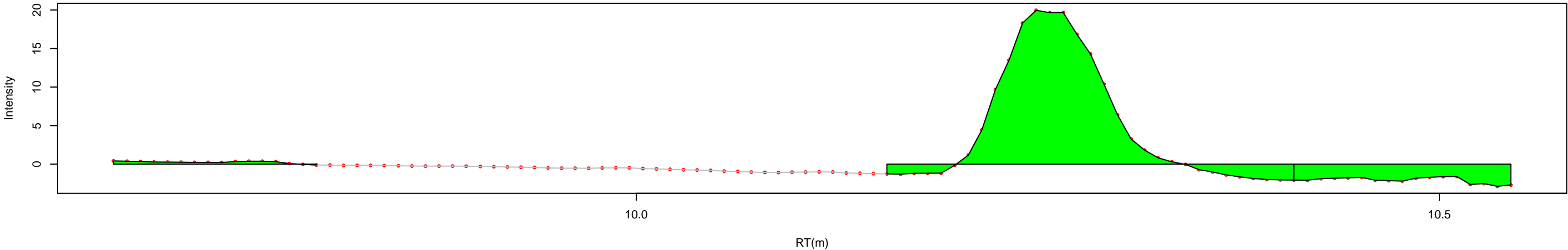
raw chromatogram | batch: 1   sample: female-o-17   conc: 50   function: 278   mass: 548 > 142.8



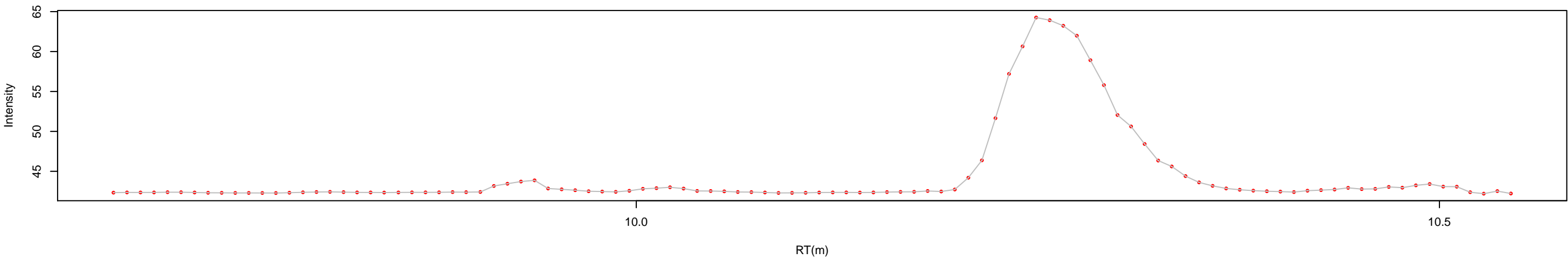
peak picking | window size: 19   iteration: 11   lp: 2   rp: 2   snr: 5   peak location: all   noise: 0.261   BLine: yes



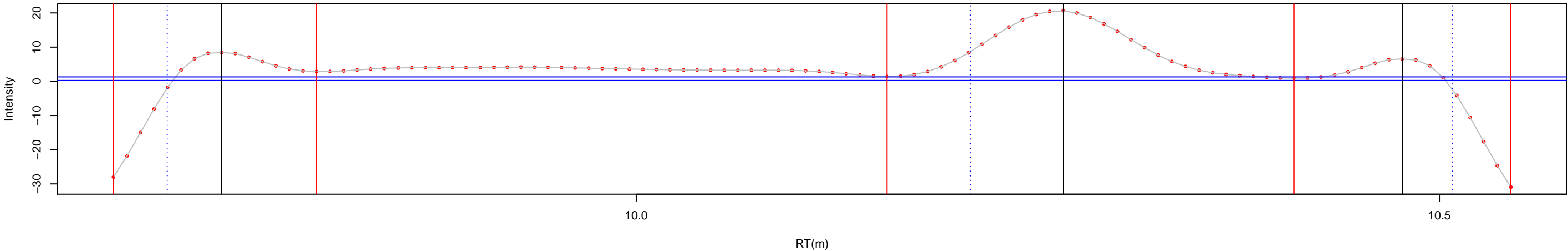
peak area | window size:3   BLine: yes



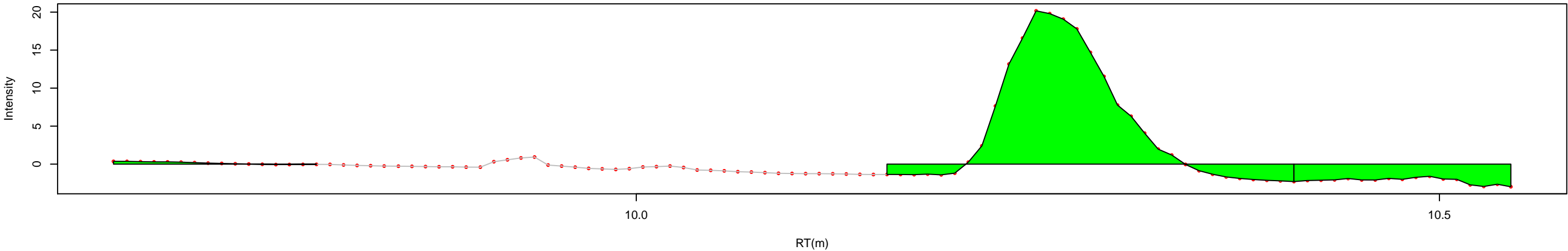
raw chromatogram | batch: 1 sample: female-o-m-24 conc: 50 function: 278 mass: 548 > 142.8



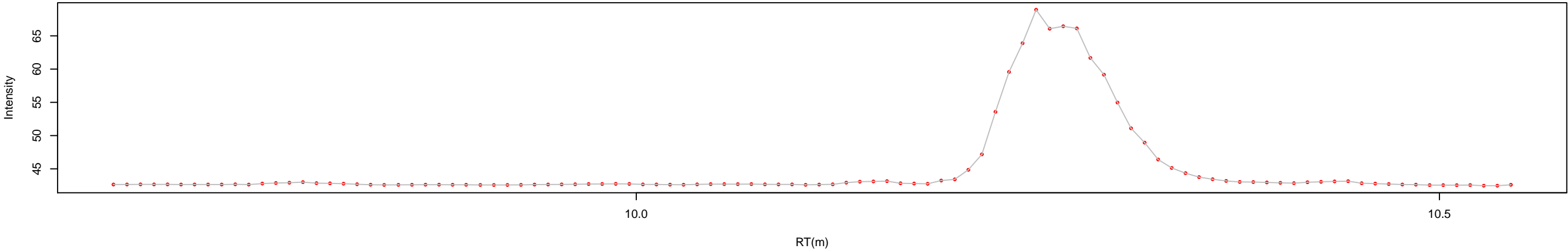
peak picking | window size: 19 iteration: 11 lp: 2 rp: 2 snr: 5 peak location: all noise: 0.259 BLine: yes



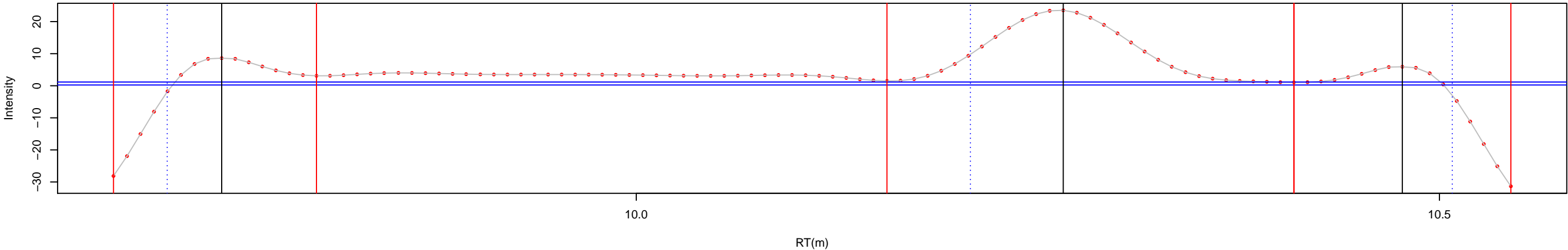
peak area | window size:3 BLine: yes



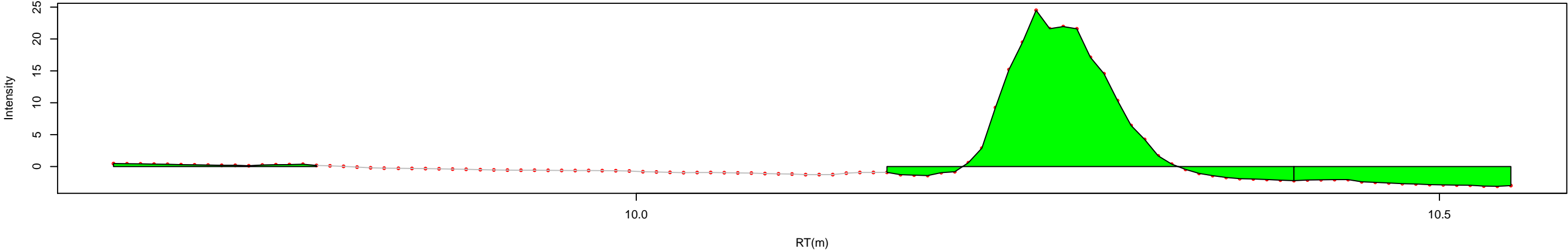
raw chromatogram | batch: 1 sample: female-o-18 conc: 50 function: 278 mass: 548 > 142.8



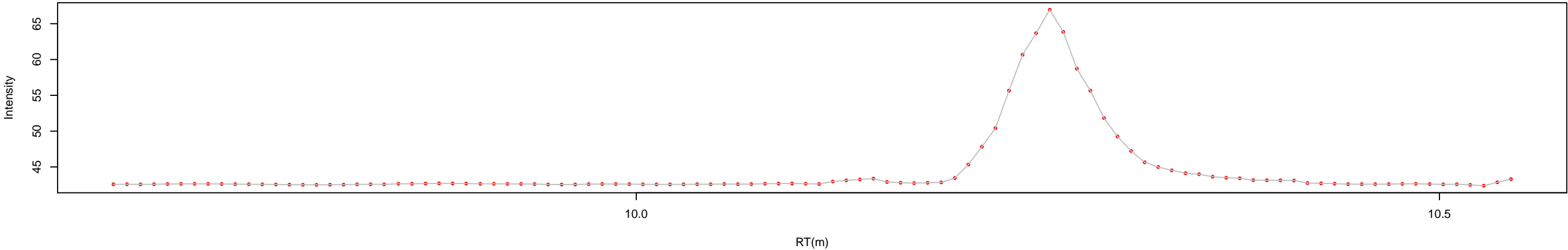
peak picking | window size: 19 iteration: 11 lp: 2 rp: 2 snr: 5 peak location: all noise: 0.233 BLine: yes



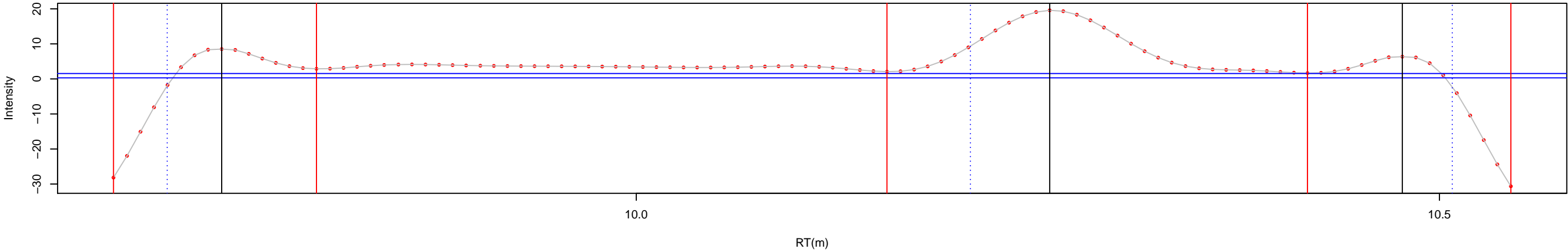
peak area | window size:3 BLine: yes



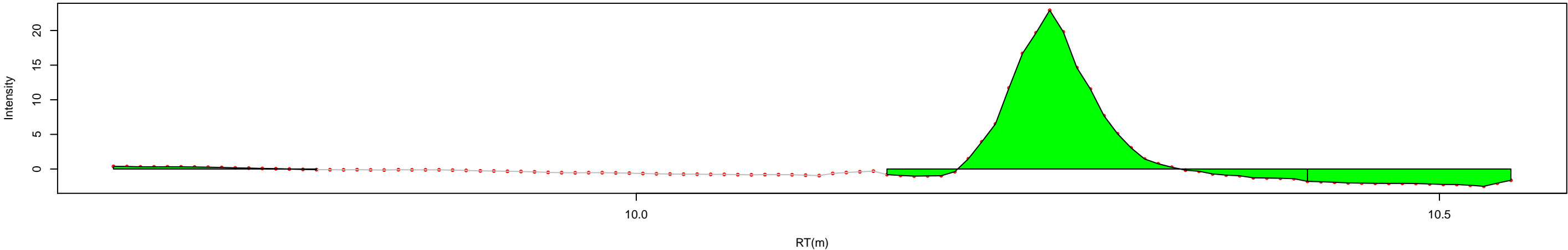
raw chromatogram | batch: 1 sample: female-o-m-25 conc: 50 function: 278 mass: 548 > 142.8



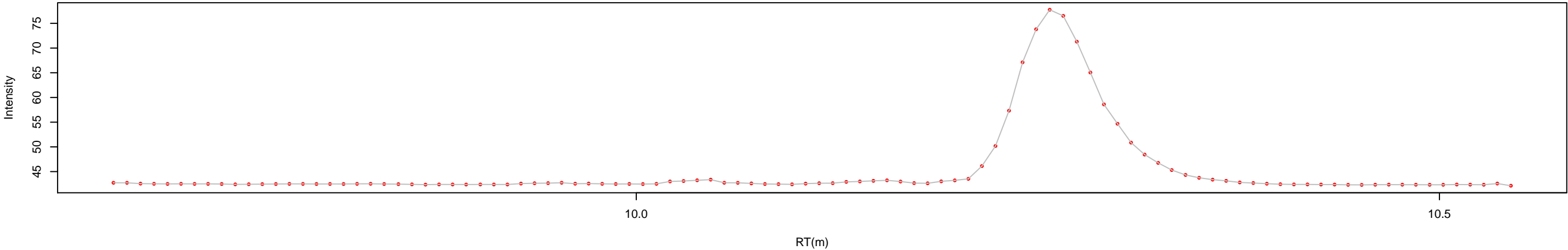
peak picking | window size: 19 iteration: 11 lp: 2 rp: 2 snr: 5 peak location: all noise: 0.308 BLine: yes



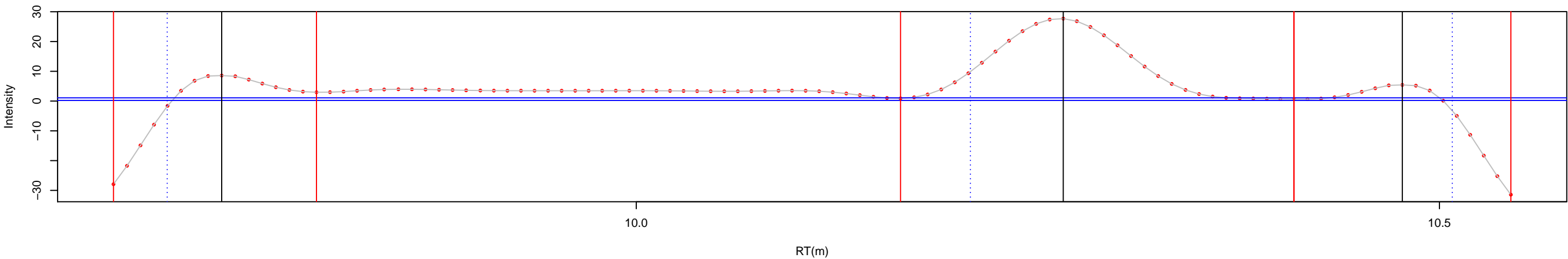
peak area | window size:3 BLine: yes



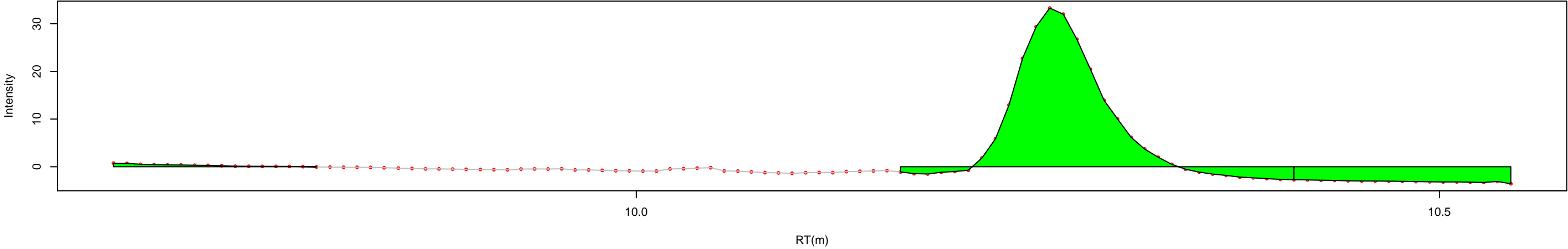
raw chromatogram | batch: 1 sample: female-o-19 conc: 50 function: 278 mass: 548 > 142.8



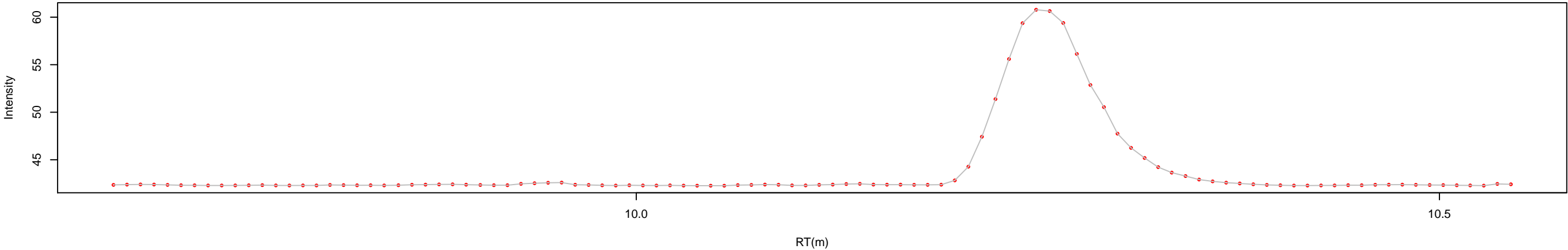
peak picking | window size: 19 iteration: 11 lp: 2 rp: 2 snr: 5 peak location: all noise: 0.219 BLine: yes



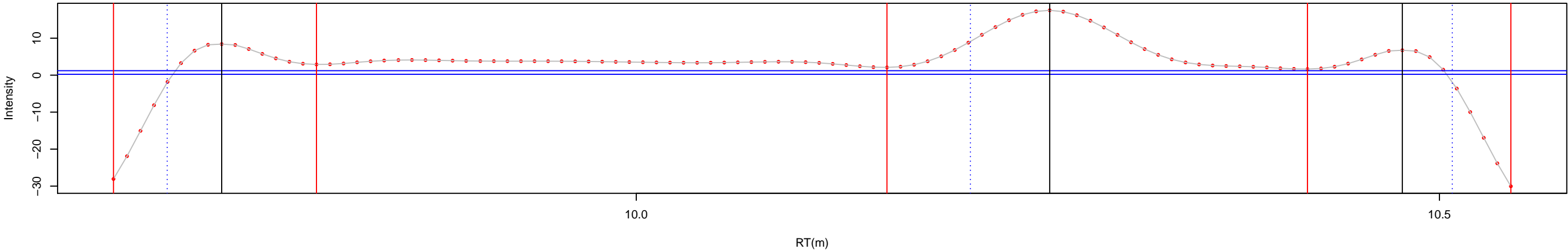
peak area | window size:3 BLine: yes



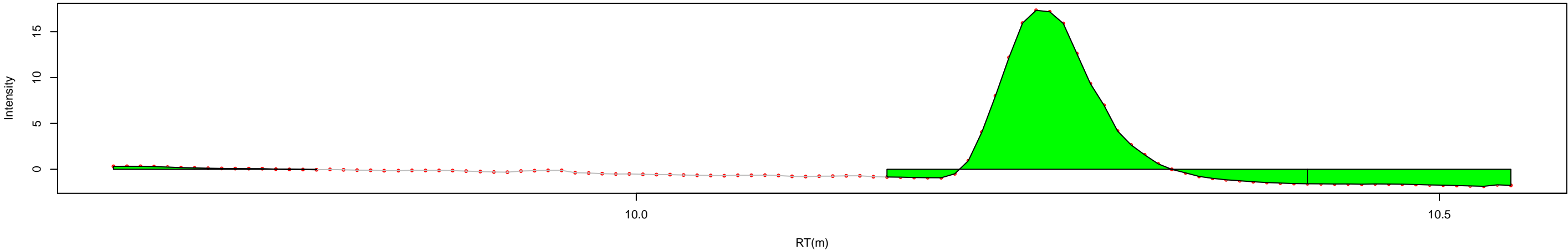
raw chromatogram | batch: 1 sample: female-o-m-26 conc: 50 function: 278 mass: 548 > 142.8



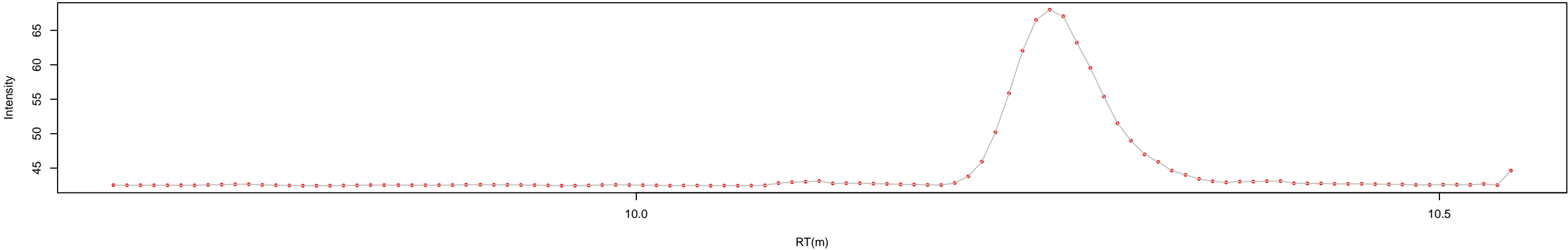
peak picking | window size: 19 iteration: 11 lp: 2 rp: 2 snr: 5 peak location: all noise: 0.242 BLine: yes



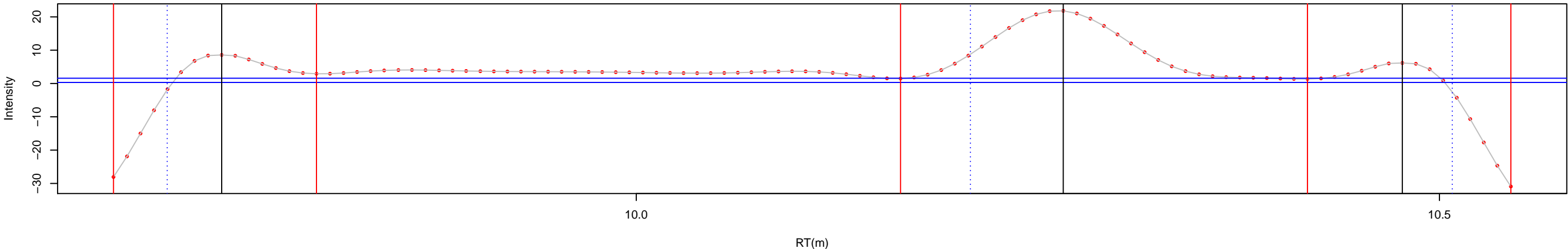
peak area | window size:3 BLine: yes



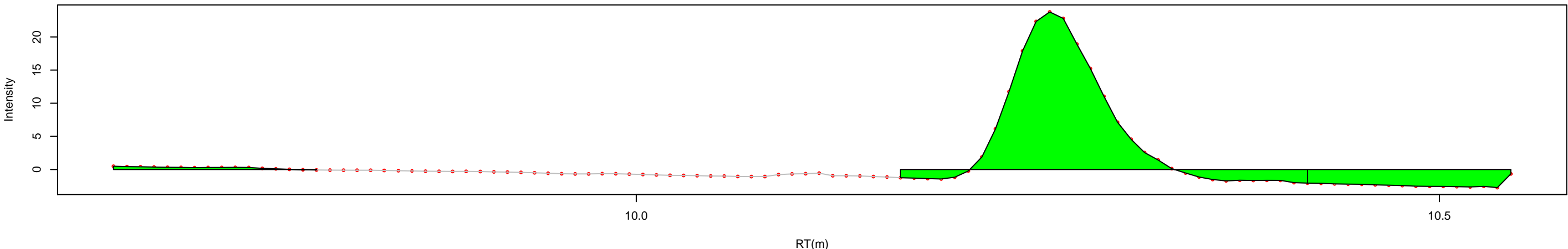
raw chromatogram | batch: 1   sample: std-1   conc: 50   function: 278   mass: 548 > 142.8



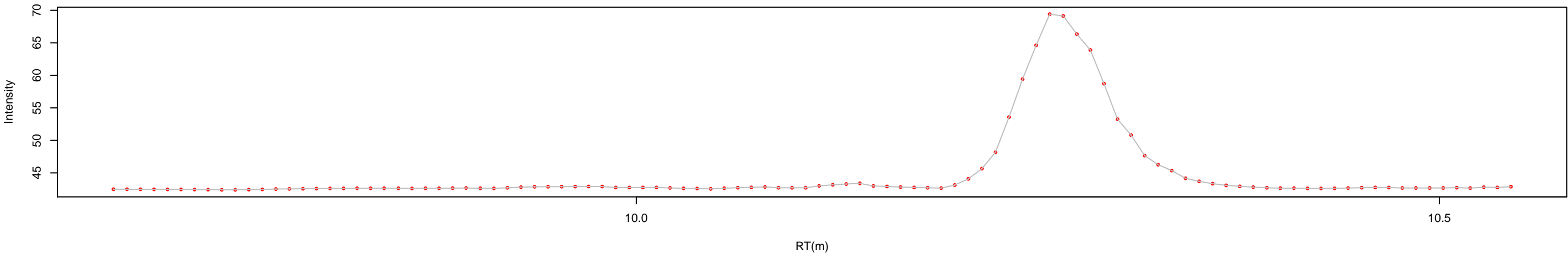
peak picking | window size: 19   iteration: 11   lp: 2   rp: 2   snr: 5   peak location: all   noise: 0.315   BLine: yes



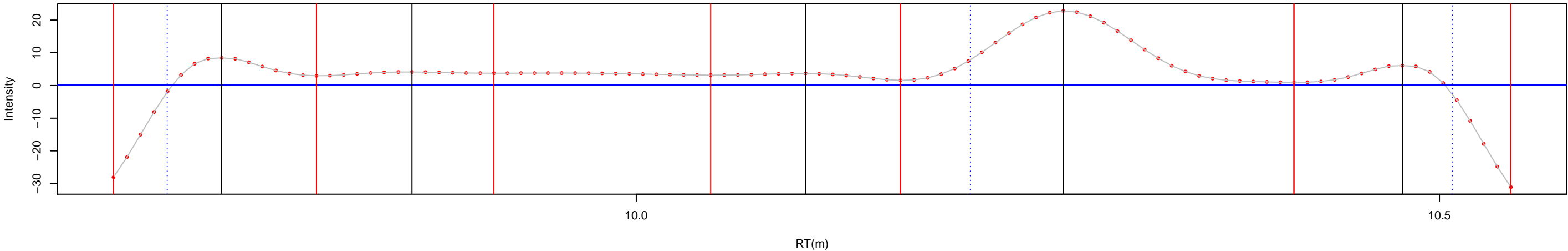
peak area | window size:3   BLine: yes



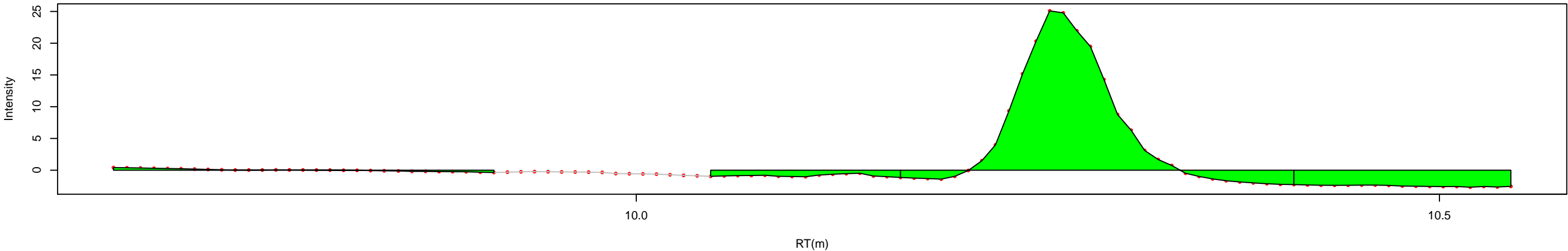
raw chromatogram | batch: 1 sample: std-2 conc: 50 function: 278 mass: 548 > 142.8



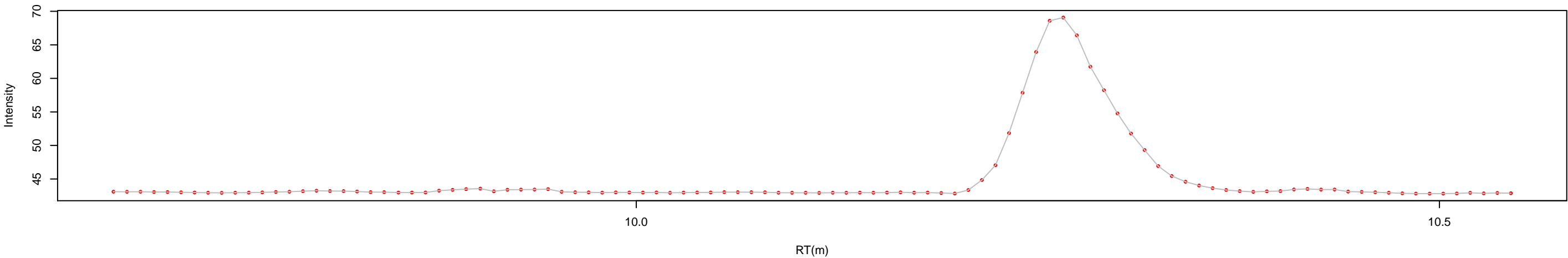
peak picking | window size: 19 iteration: 11 lp: 2 rp: 2 snr: 5 peak location: all noise: 0.048 BLine: yes



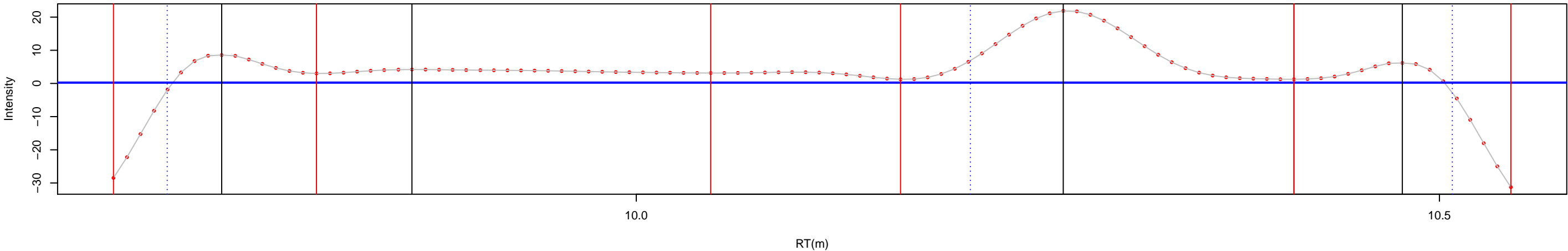
peak area | window size:3 BLine: yes



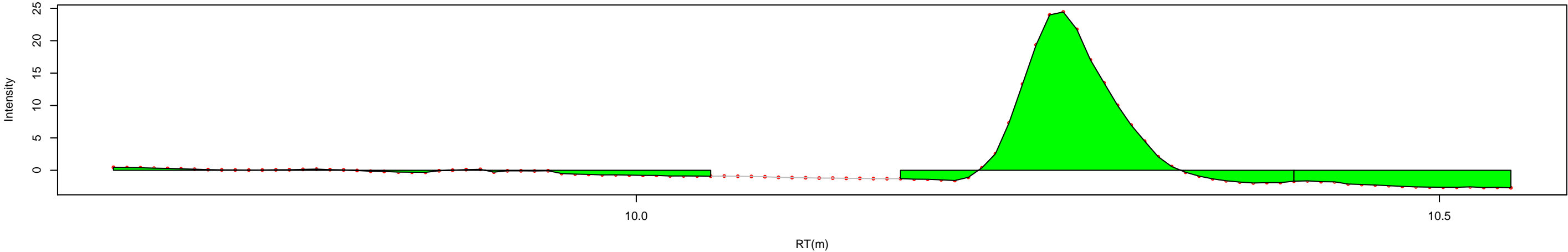
raw chromatogram | batch: 1   sample: std-3   conc: 50   function: 278   mass: 548 > 142.8



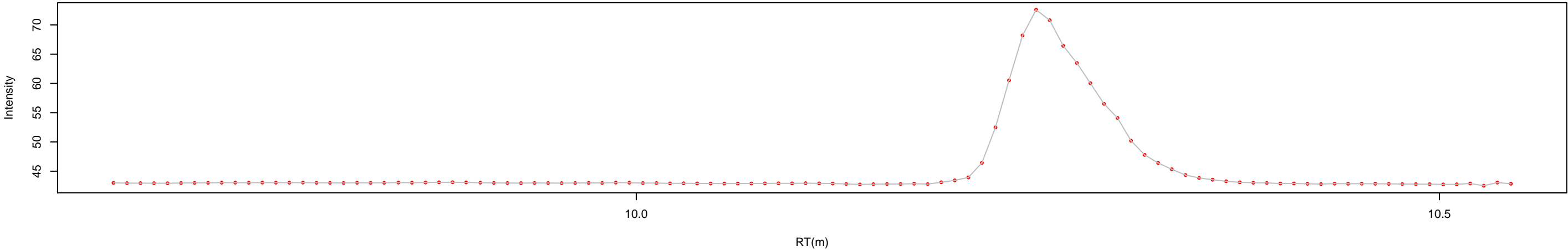
peak picking | window size: 19   iteration: 11   lp: 2   rp: 2   snr: 5   peak location: all   noise: 0.083   BLine: yes



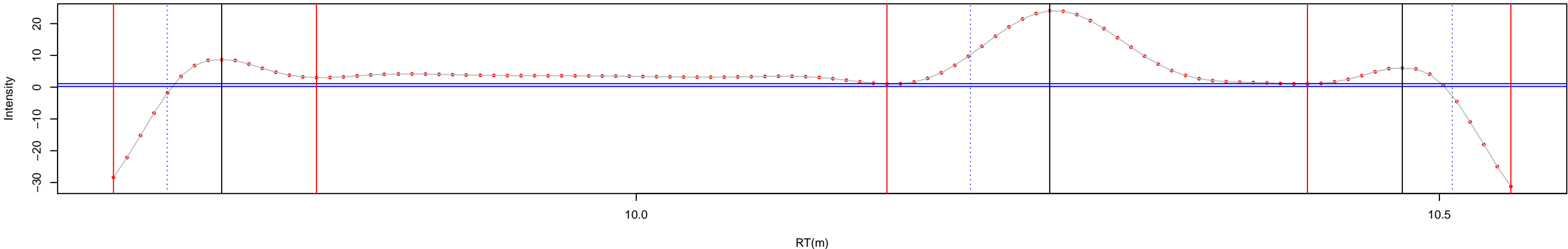
peak area | window size:3   BLine: yes



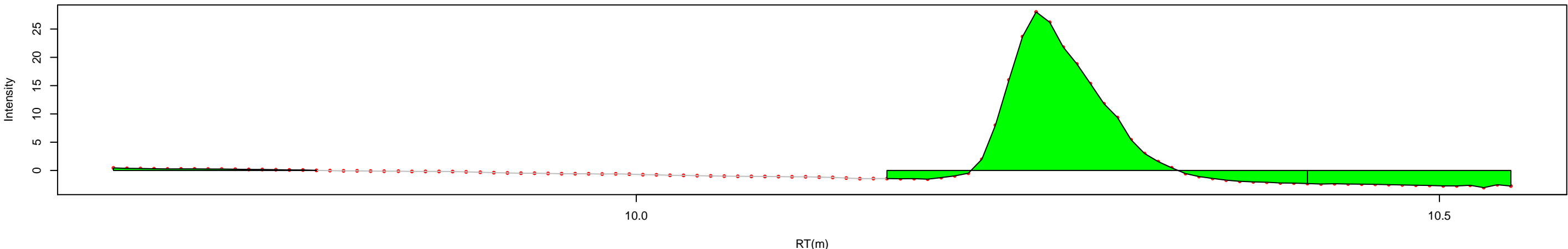
raw chromatogram | batch: 1   sample: std-4   conc: 50   function: 278   mass: 548 > 142.8



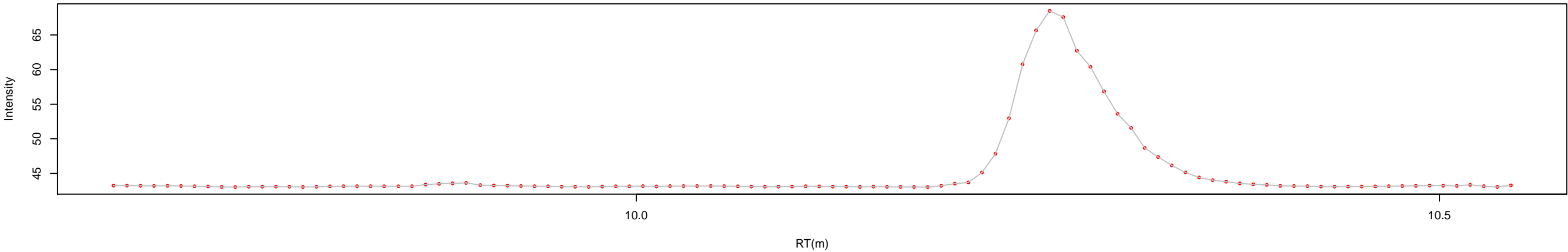
peak picking | window size: 19   iteration: 11   lp: 2   rp: 2   snr: 5   peak location: all   noise: 0.221   BLine: yes



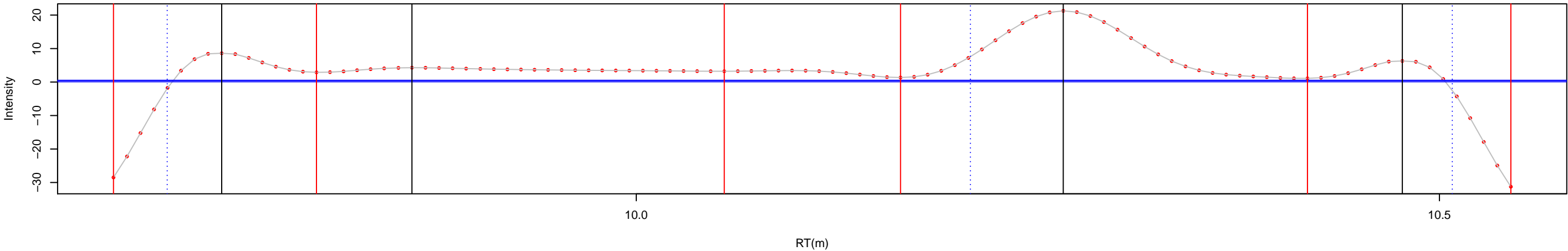
peak area | window size:3   BLine: yes



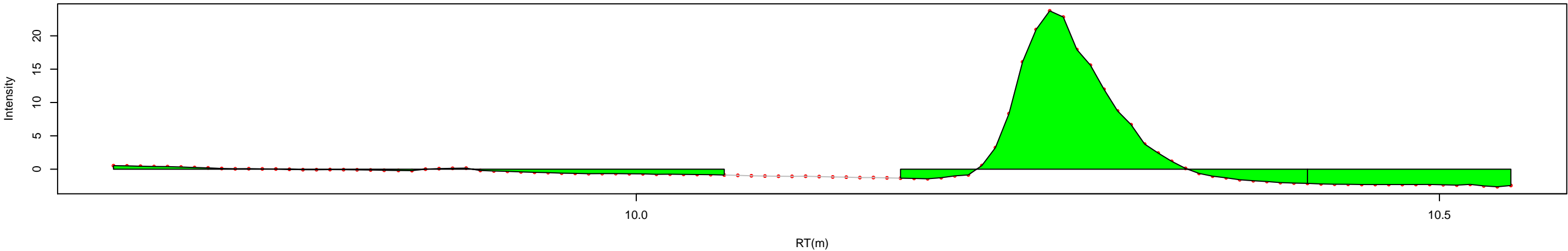
raw chromatogram | batch: 1 sample: std-5 conc: 50 function: 278 mass: 548 > 142.8



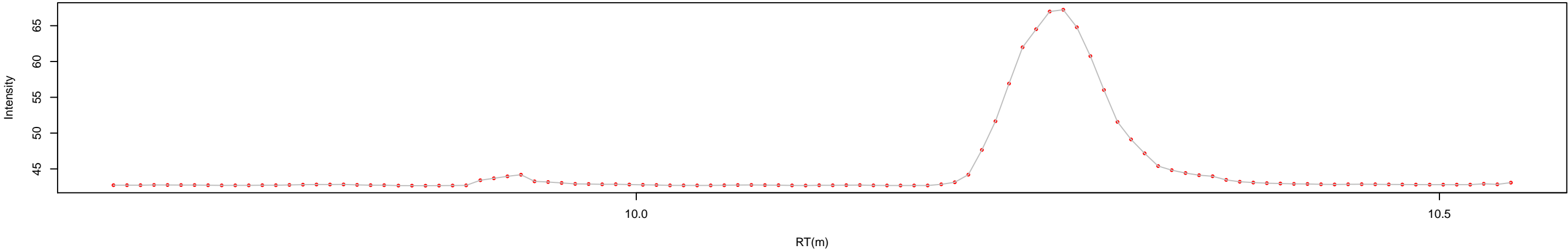
peak picking | window size: 19 iteration: 11 lp: 2 rp: 2 snr: 5 peak location: all noise: 0.104 BLine: yes



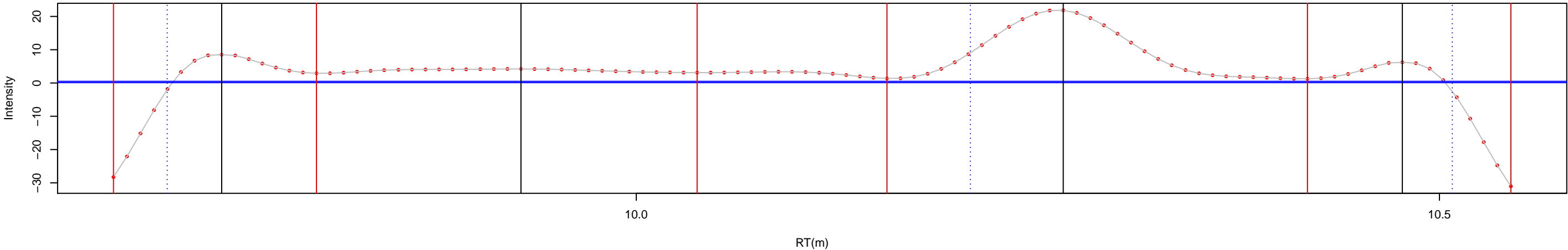
peak area | window size:3 BLine: yes



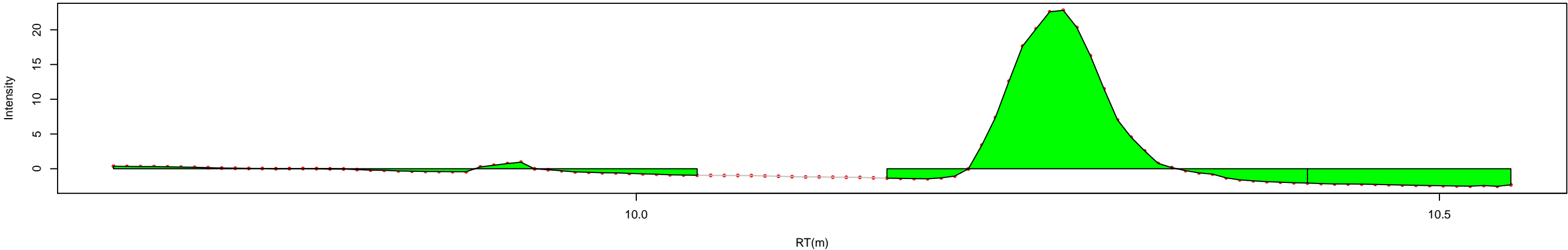
raw chromatogram | batch: 1 sample: std-6 conc: 50 function: 278 mass: 548 > 142.8



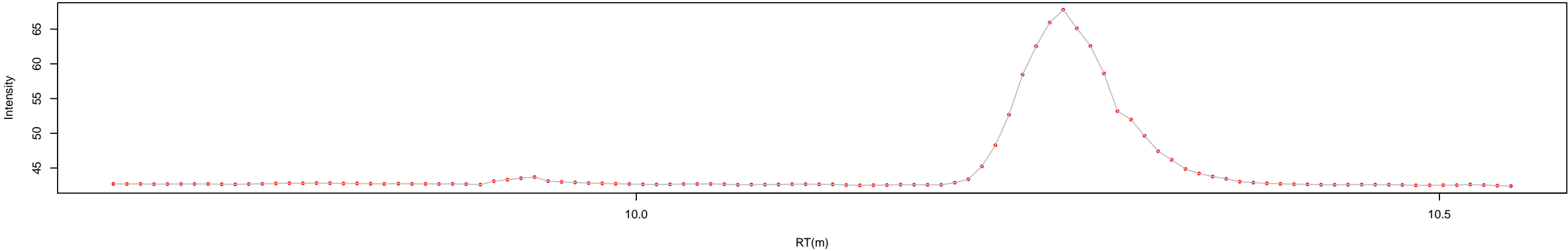
peak picking | window size: 19 iteration: 11 lp: 2 rp: 2 snr: 5 peak location: all noise: 0.0992 BLine: yes



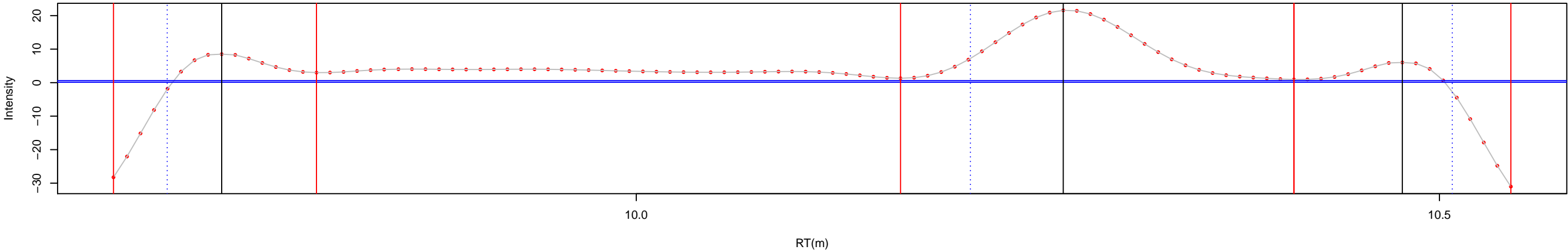
peak area | window size:3 BLine: yes



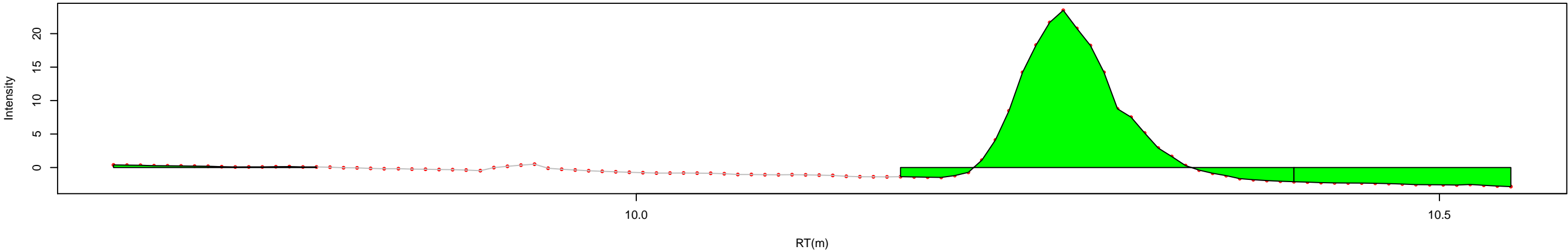
raw chromatogram | batch: 1 sample: std-7 conc: 50 function: 278 mass: 548 > 142.8



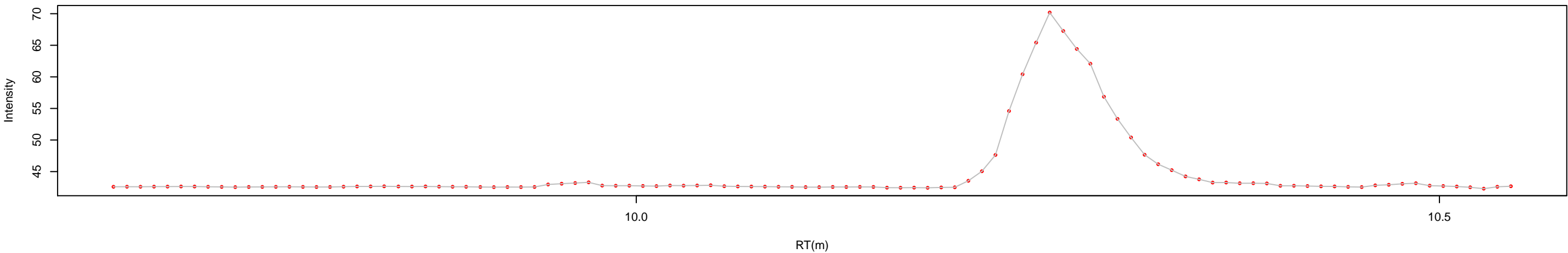
peak picking | window size: 19 iteration: 11 lp: 2 rp: 2 snr: 5 peak location: all noise: 0.121 BLine: yes



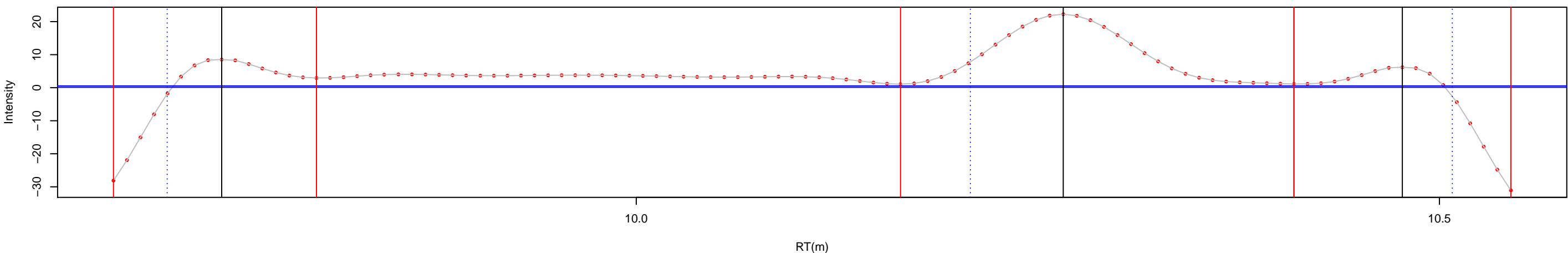
peak area | window size:3 BLine: yes



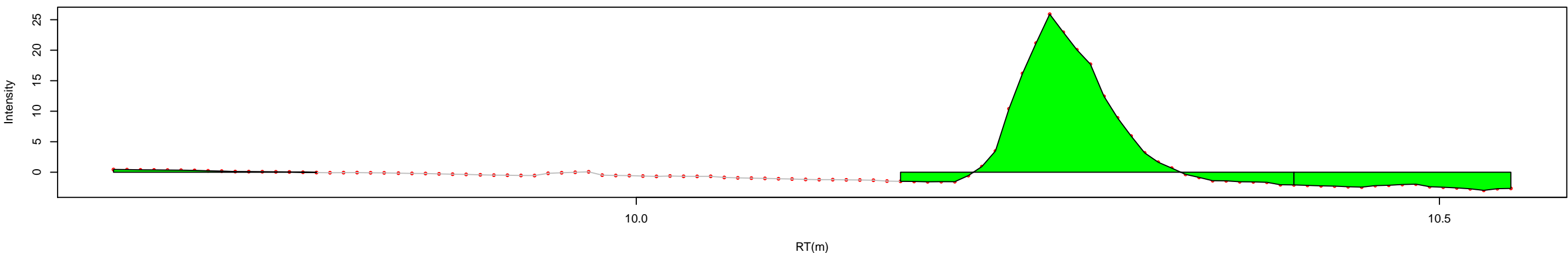
raw chromatogram | batch: 1 sample: std-8 conc: 50 function: 278 mass: 548 > 142.8



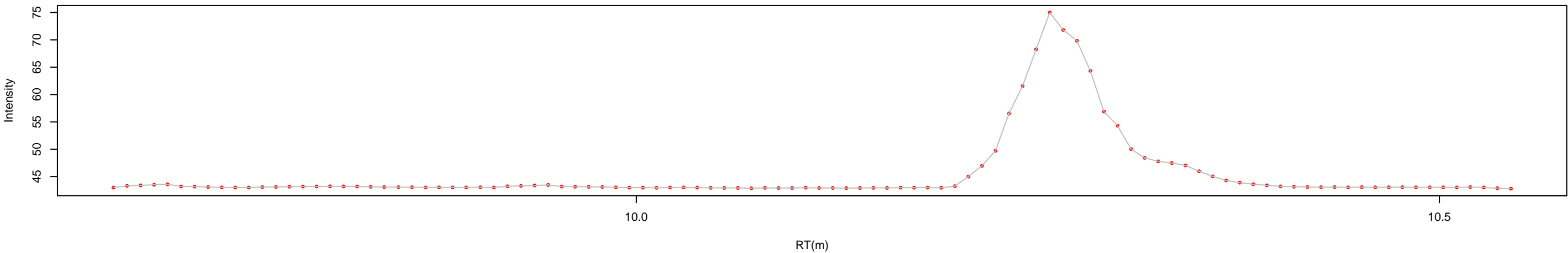
peak picking | window size: 19 iteration: 11 lp: 2 rp: 2 snr: 5 peak location: all noise: 0.11 BLine: yes



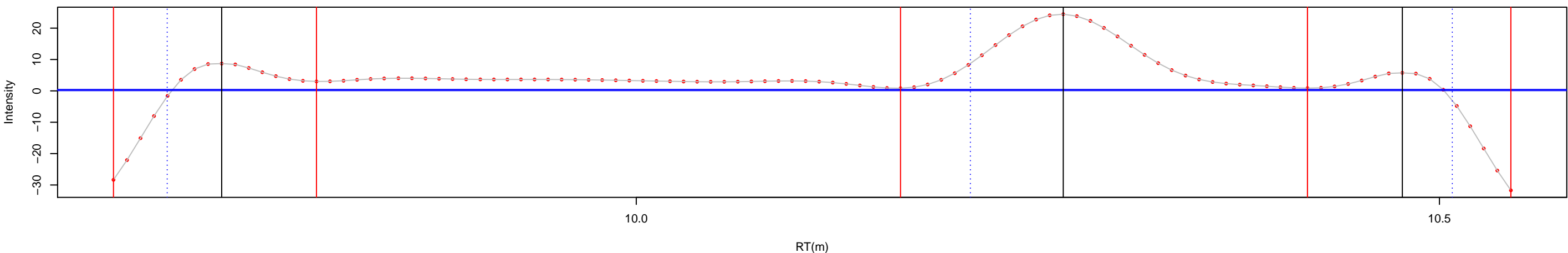
peak area | window size:3 BLine: yes



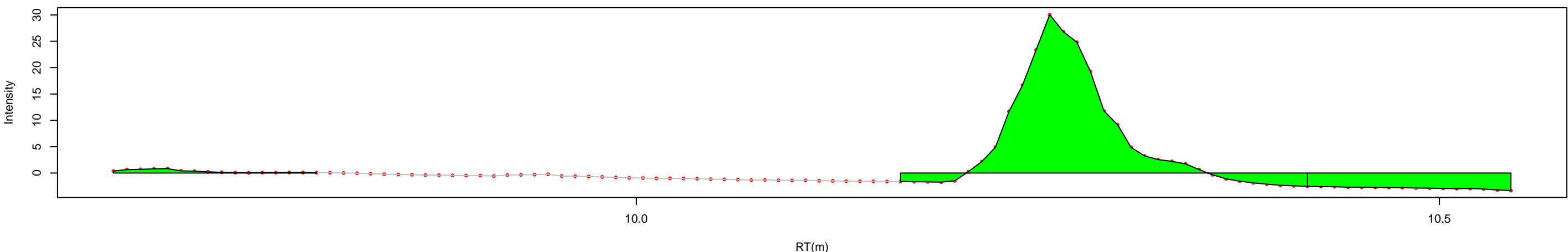
raw chromatogram | batch: 1 sample: std-9 conc: 50 function: 278 mass: 548 > 142.8



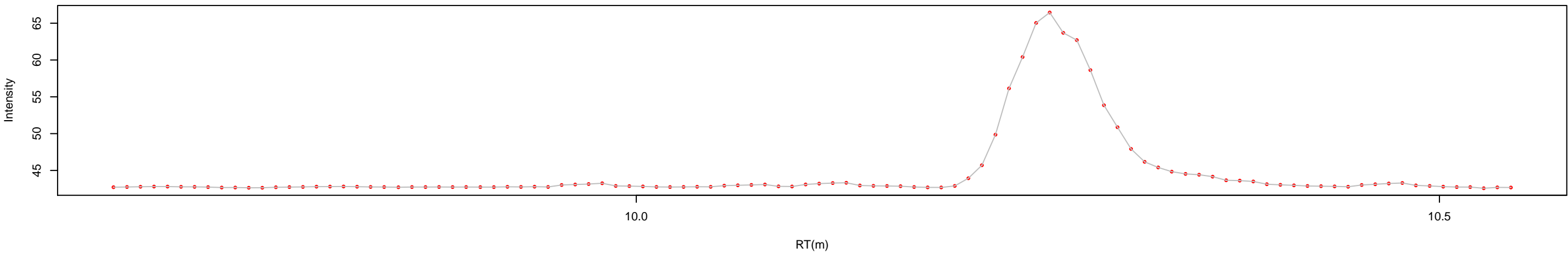
peak picking | window size: 19 iteration: 11 lp: 2 rp: 2 snr: 5 peak location: all noise: 0.0878 BLine: yes



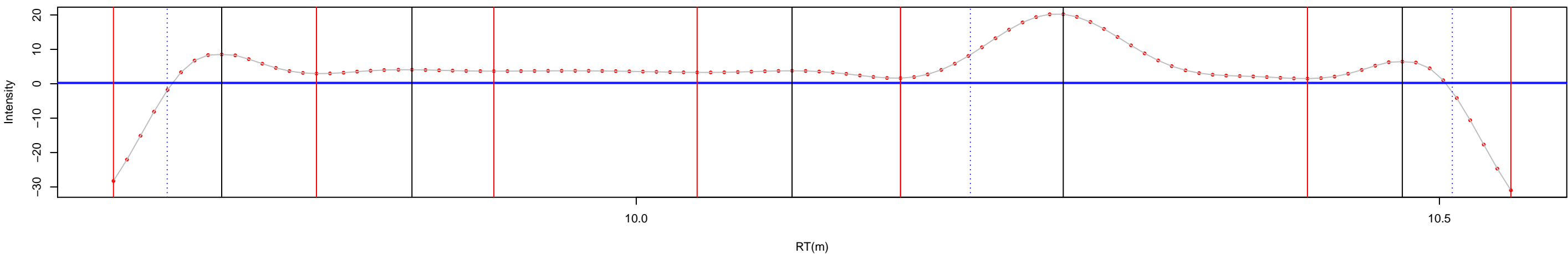
peak area | window size:3 BLine: yes



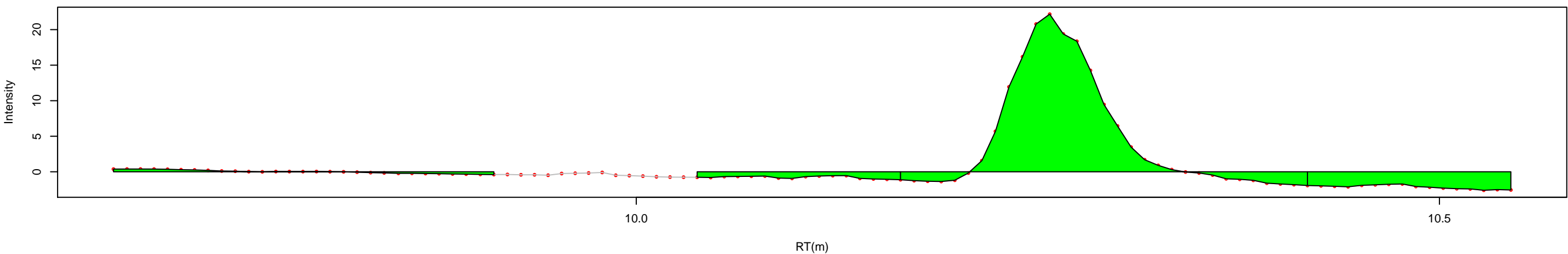
raw chromatogram | batch: 1   sample: std-10   conc: 50   function: 278   mass: 548 > 142.8



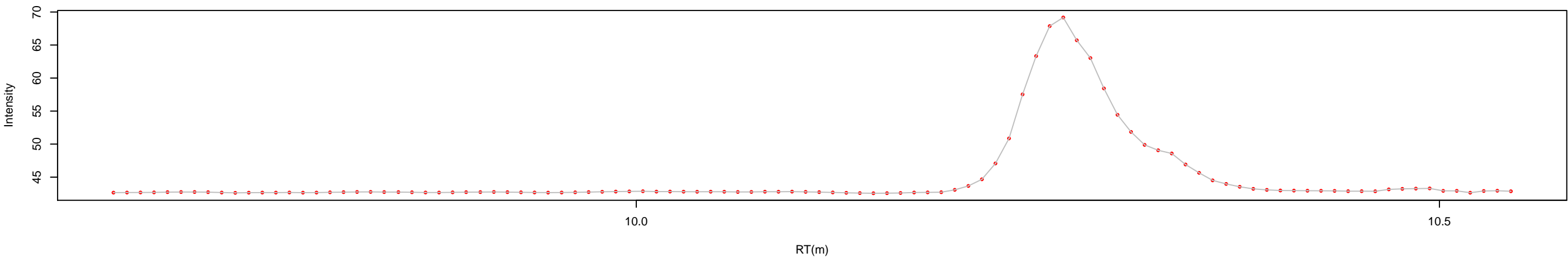
peak picking | window size: 19   iteration: 11   lp: 2   rp: 2   snr: 5   peak location: all   noise: 0.0805   BLine: yes



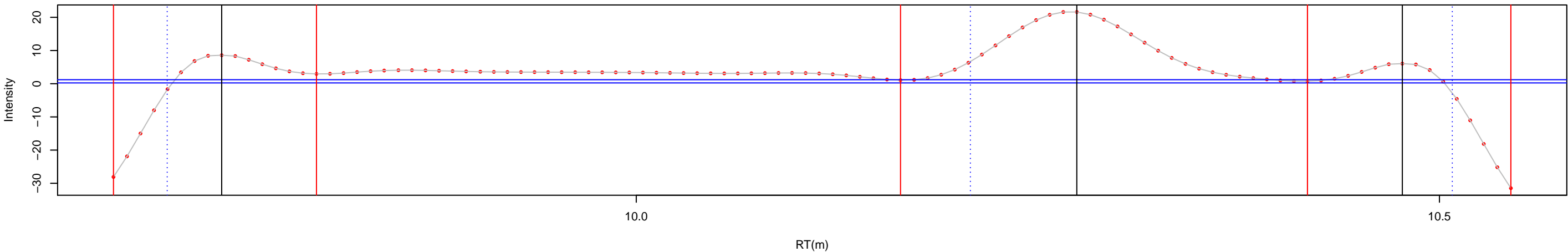
peak area | window size:3   BLine: yes



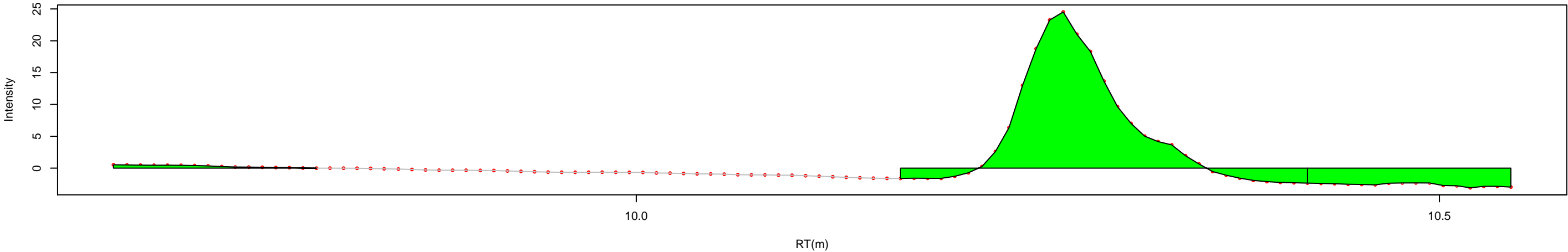
raw chromatogram | batch: 1   sample: std-11   conc: 50   function: 278   mass: 548 > 142.8



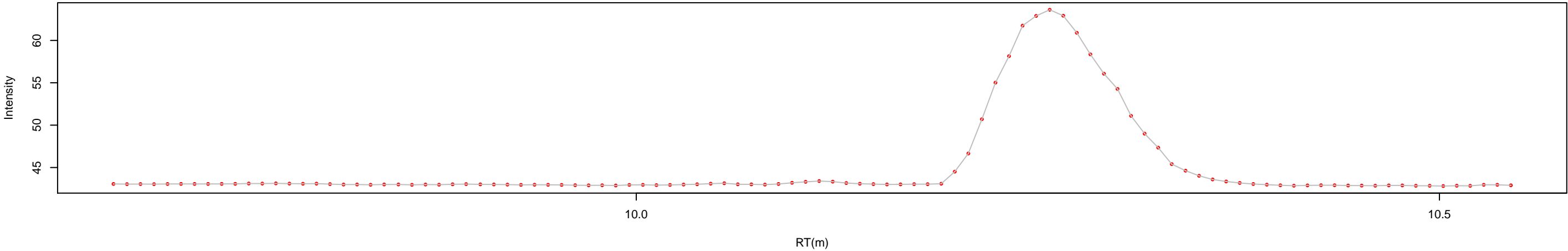
peak picking | window size: 19   iteration: 11   lp: 2   rp: 2   snr: 5   peak location: all   noise: 0.241   BLine: yes



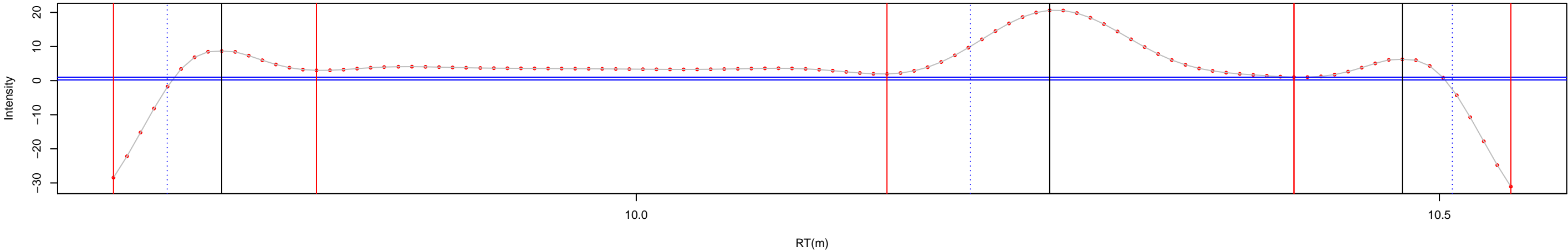
peak area | window size:3   BLine: yes



raw chromatogram | batch: 1   sample: std-12   conc: 50   function: 278   mass: 548 > 142.8



peak picking | window size: 19   iteration: 11   lp: 2   rp: 2   snr: 5   peak location: all   noise: 0.202   BLine: yes



peak area | window size:3   BLine: yes

