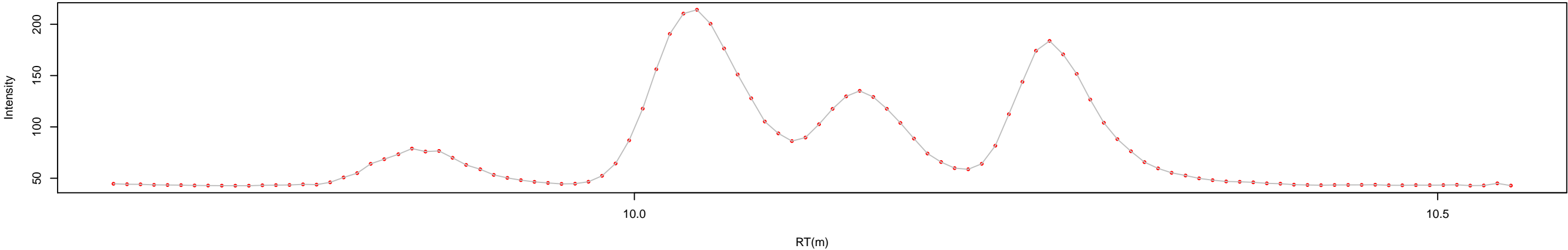
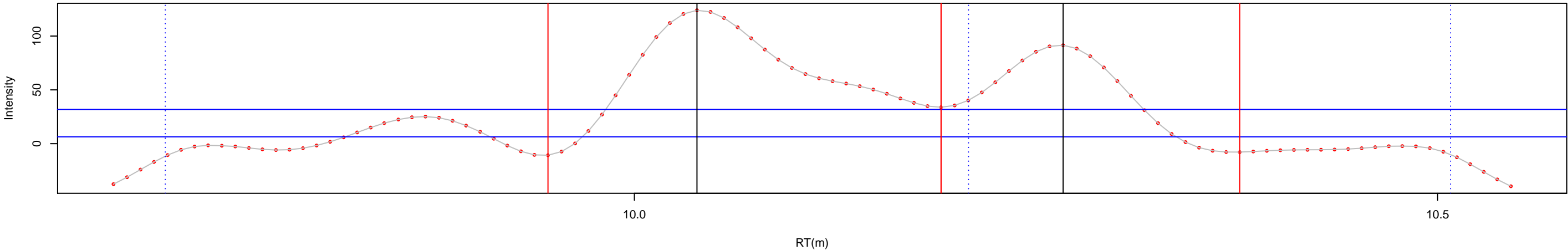


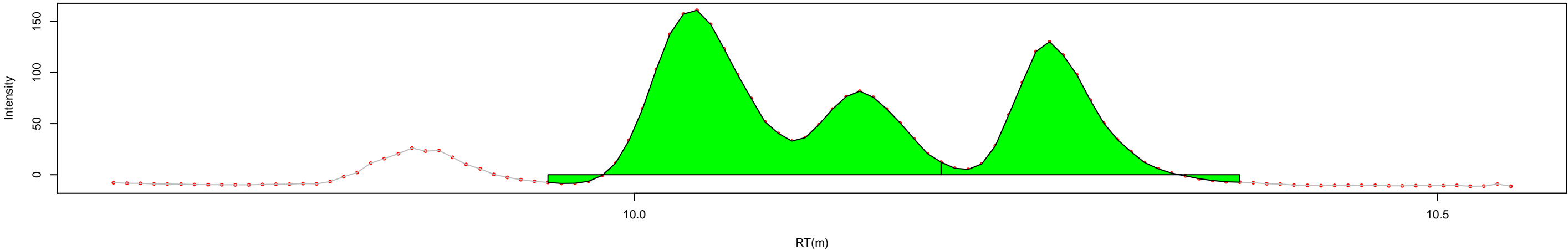
raw chromatogram | batch: 1   sample: female-y-1   conc: NA   function: 272   mass: 542 > 136.8



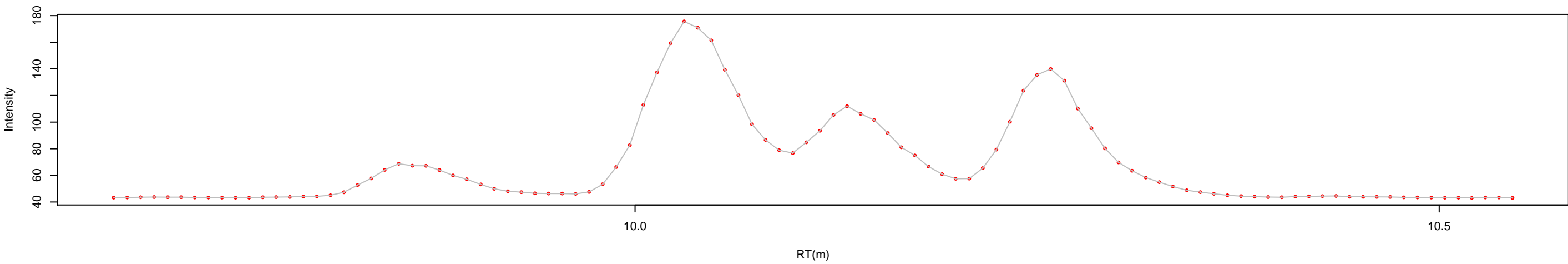
peak picking | window size: 19   iteration: 11   lp: 2   rp: 2   snr: 5   peak location: all   noise: 6.36   BLine: yes



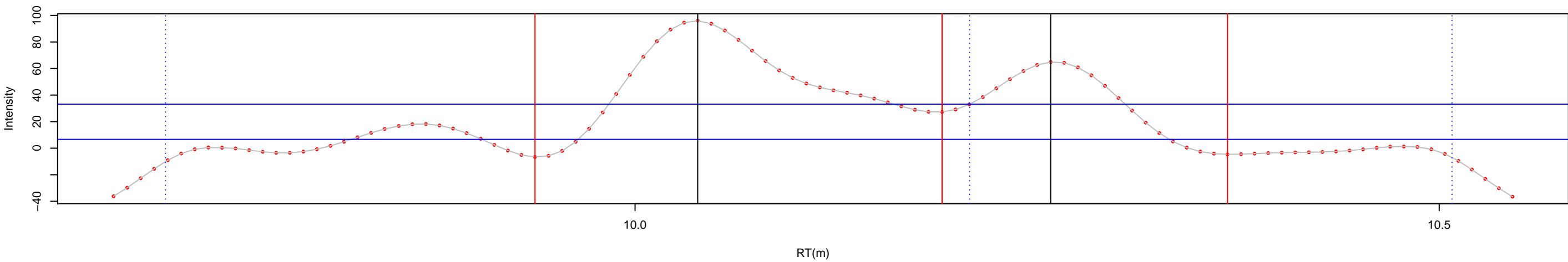
peak area | window size:3   BLine: yes



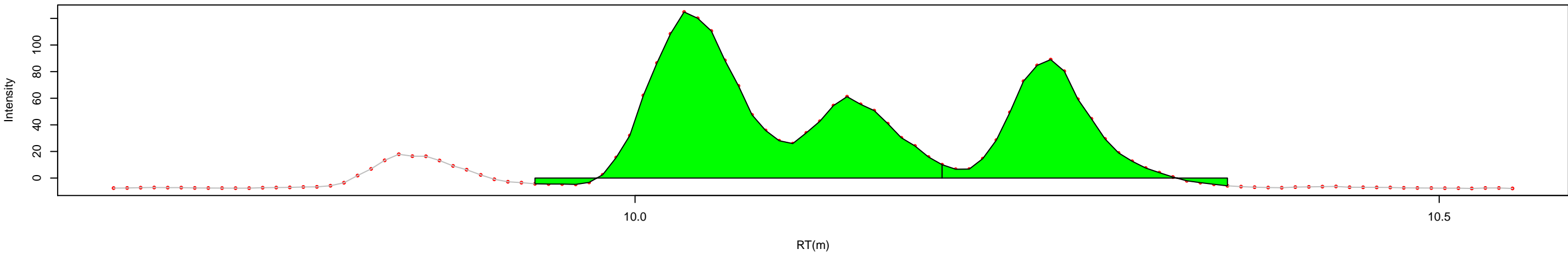
raw chromatogram | batch: 1 sample: female-y-m-7 conc: NA function: 272 mass: 542 > 136.8



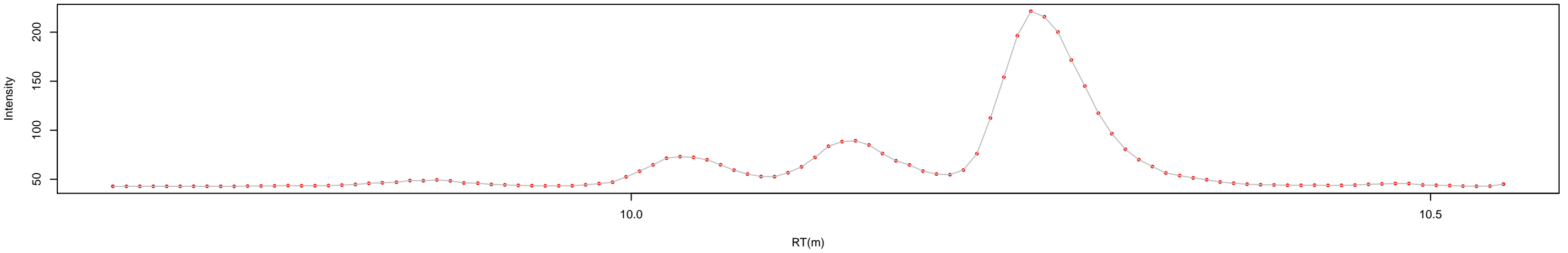
peak picking | window size: 19 iteration: 11 lp: 2 rp: 2 snr: 5 peak location: all noise: 6.63 BLine: yes



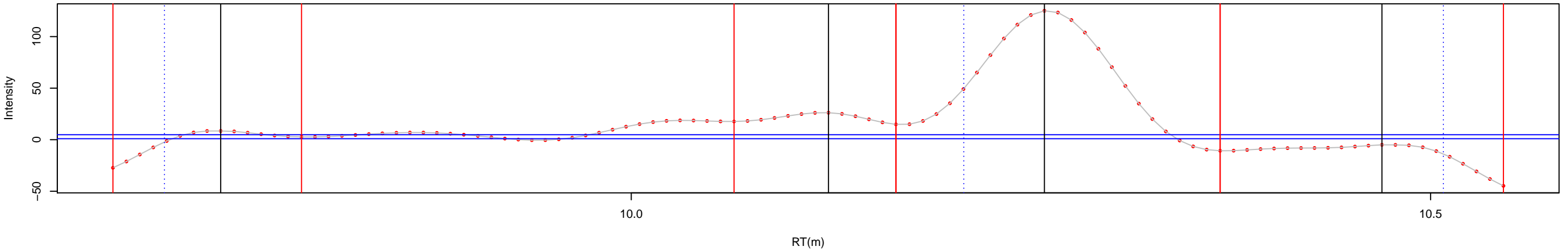
peak area | window size:3 BLine: yes



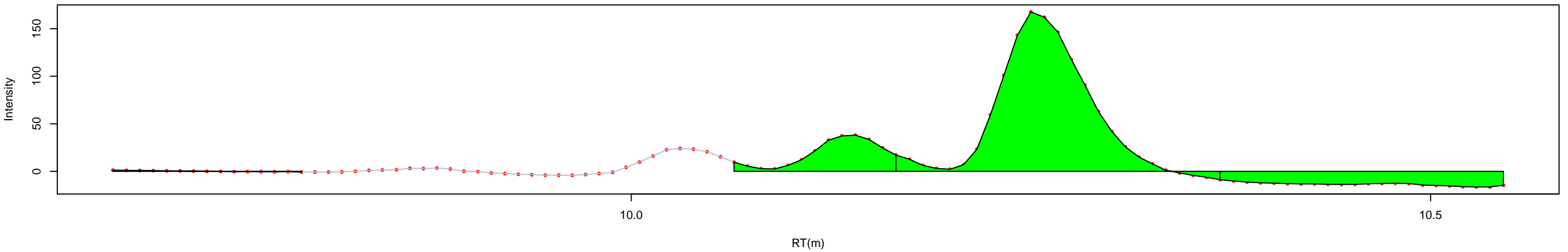
raw chromatogram | batch: 1 sample: female-o-13 conc: NA function: 272 mass: 542 > 136.8



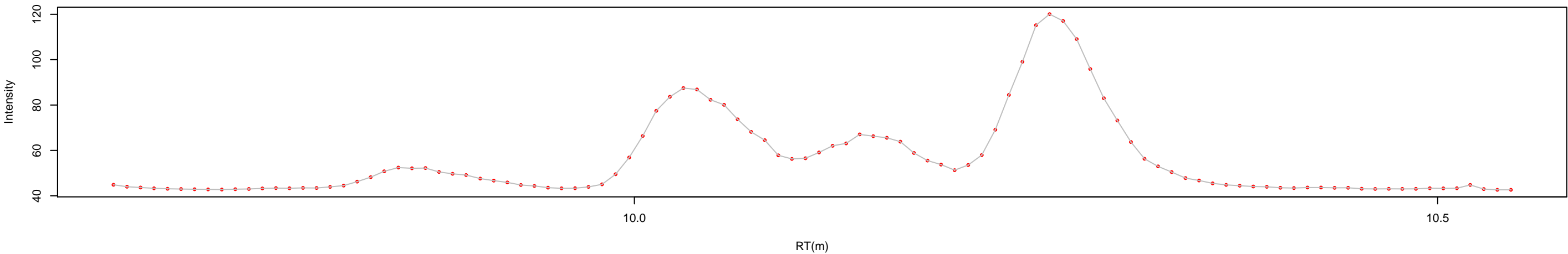
peak picking | window size: 19 iteration: 11 lp: 2 rp: 2 snr: 5 peak location: all noise: 0.966 BLine: yes



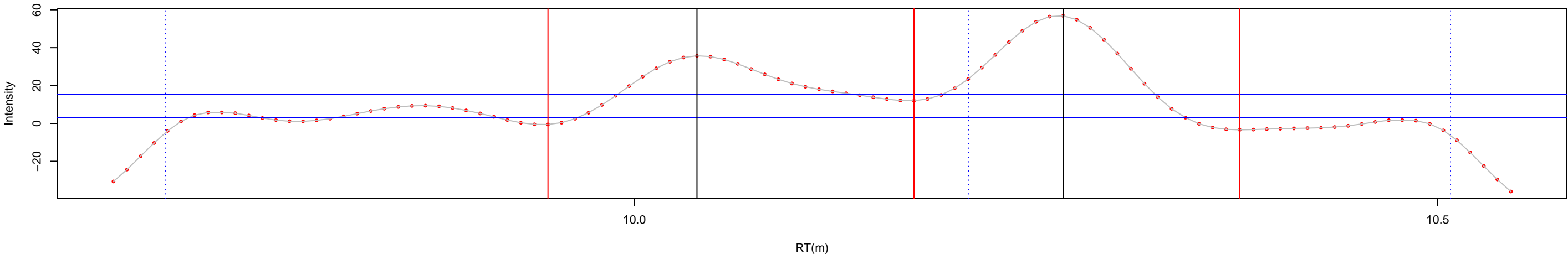
peak area | window size:3 BLine: yes



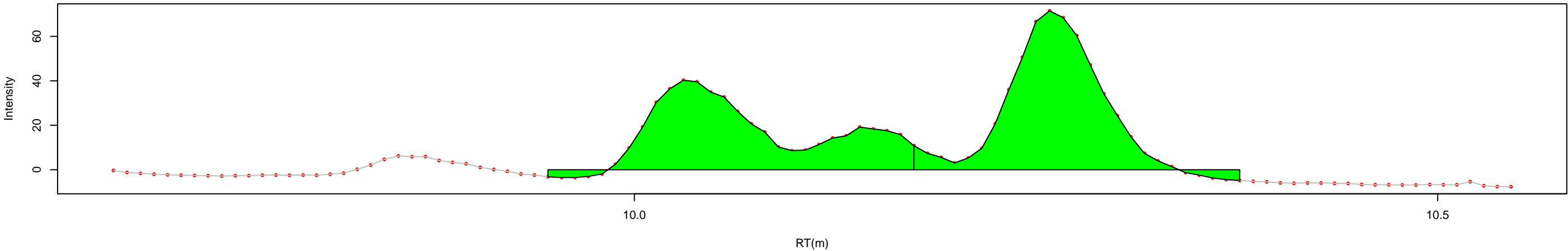
raw chromatogram | batch: 1   sample: female-o-m-20   conc: NA   function: 272   mass: 542 > 136.8



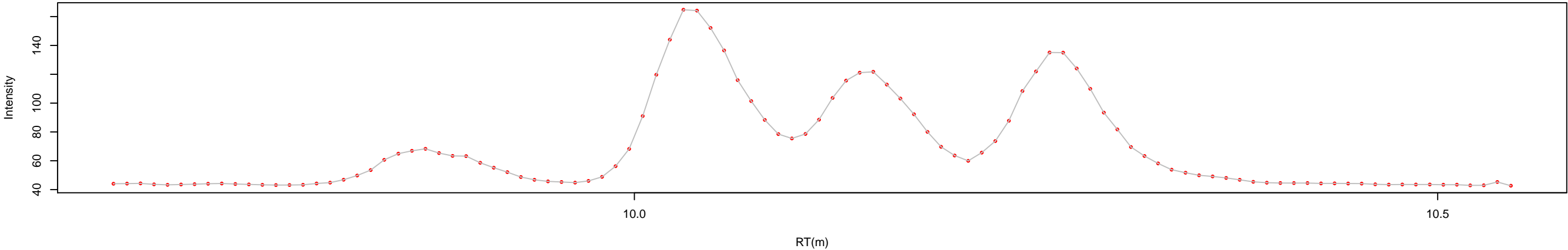
peak picking | window size: 19   iteration: 11   lp: 2   rp: 2   snr: 5   peak location: all   noise: 3.06   BLine: yes



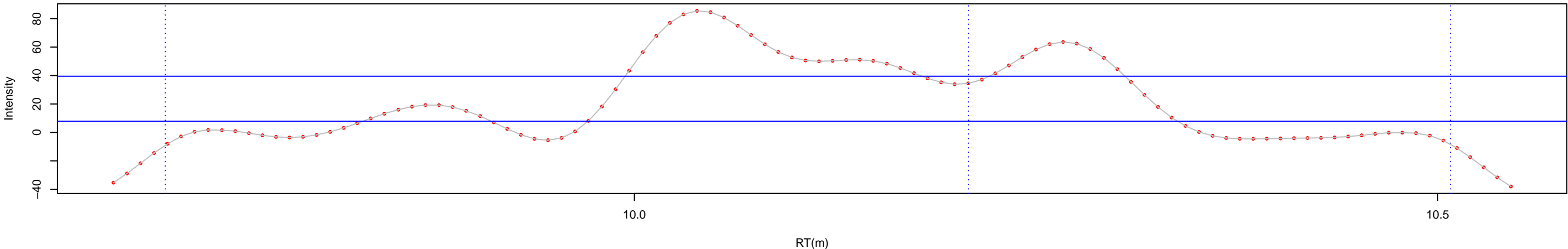
peak area | window size:3   BLine: yes



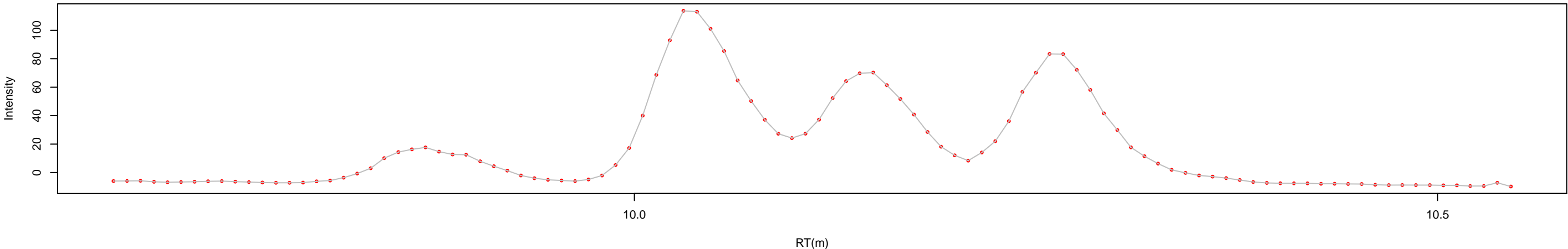
raw chromatogram | batch: 1 sample: female-y-2 conc: NA function: 272 mass: 542 > 136.8



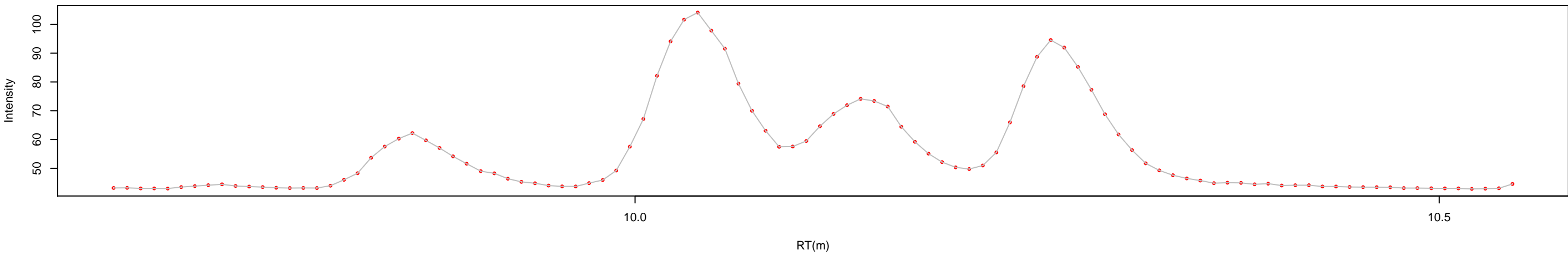
peak picking | window size: 19 iteration: 11 lp: 2 rp: 2 snr: 5 peak location: all noise: 7.9 BLine: yes



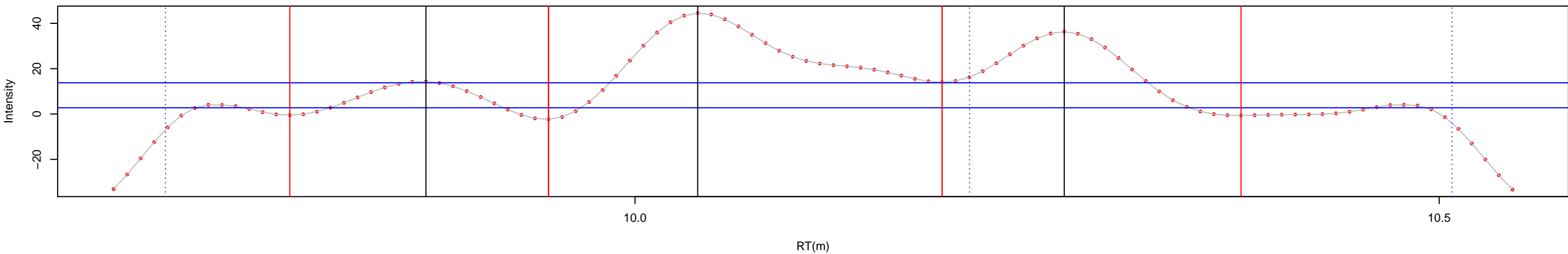
peak area | window size:3 BLine: yes



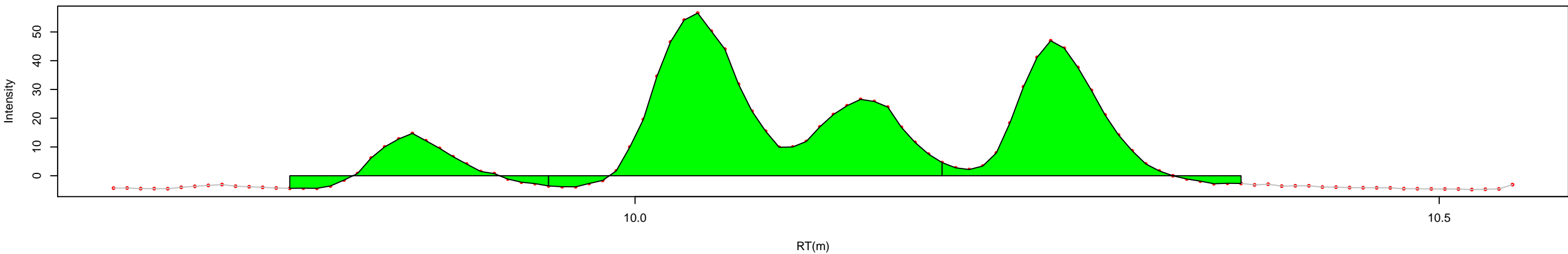
raw chromatogram | batch: 1 sample: female-y-m-8 conc: NA function: 272 mass: 542 > 136.8



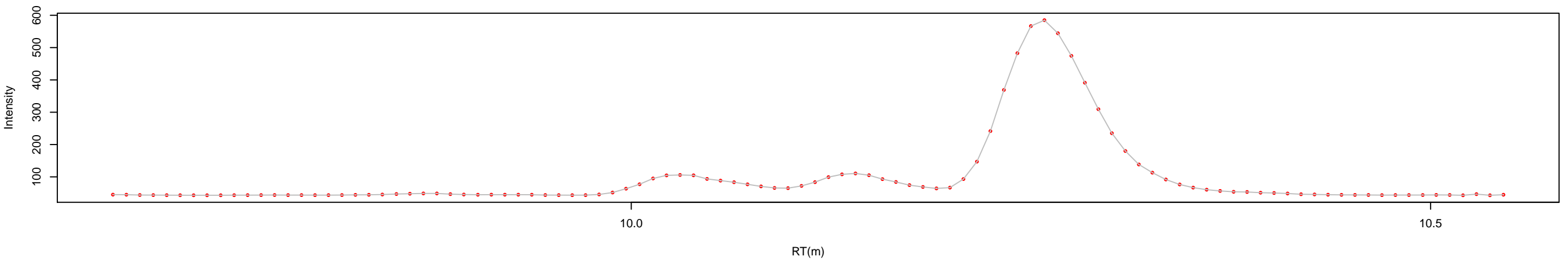
peak picking | window size: 19 iteration: 11 lp: 2 rp: 2 snr: 5 peak location: all noise: 2.75 BLine: yes



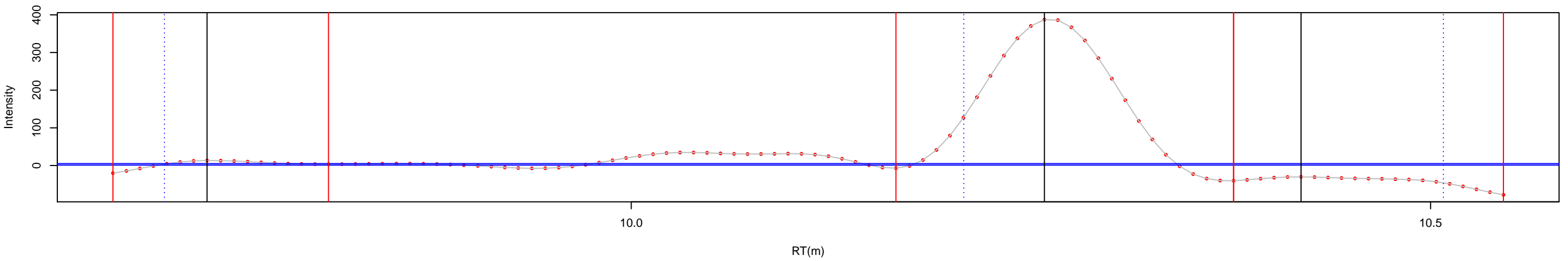
peak area | window size:3 BLine: yes



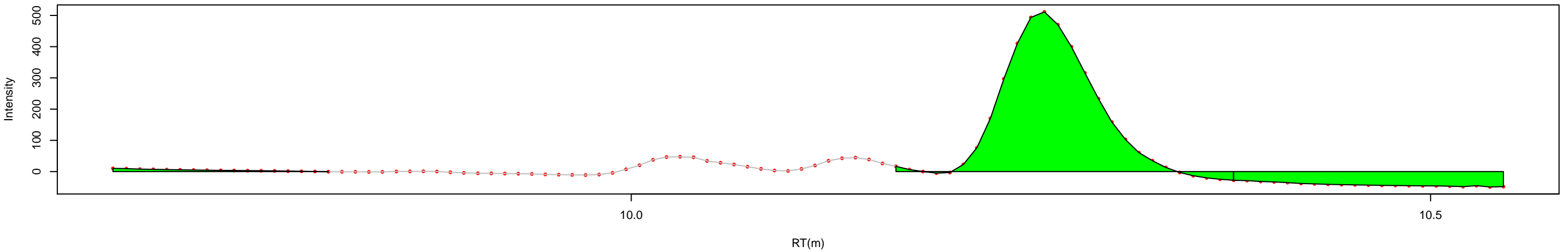
raw chromatogram | batch: 1   sample: female-o-14   conc: NA   function: 272   mass: 542 > 136.8



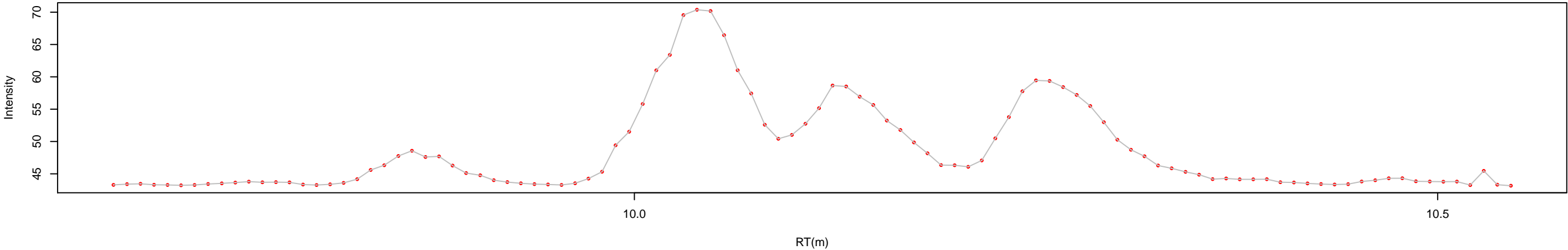
peak picking | window size: 19   iteration: 11   lp: 2   rp: 2   snr: 5   peak location: all   noise: 1.01   BLine: yes



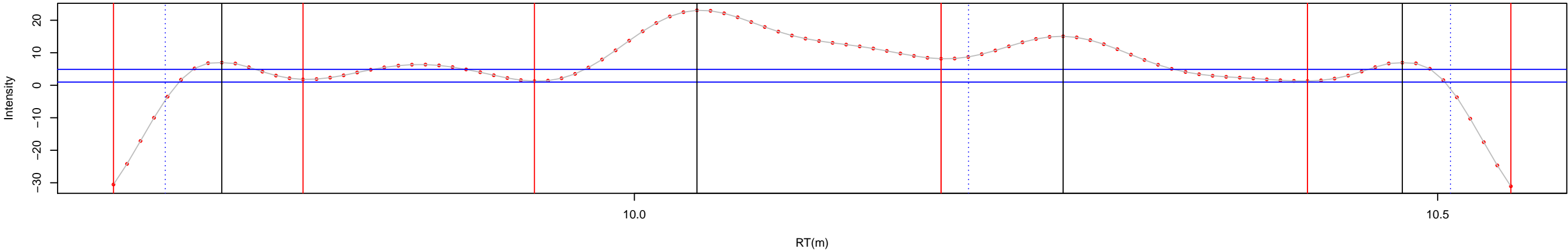
peak area | window size:3   BLine: yes



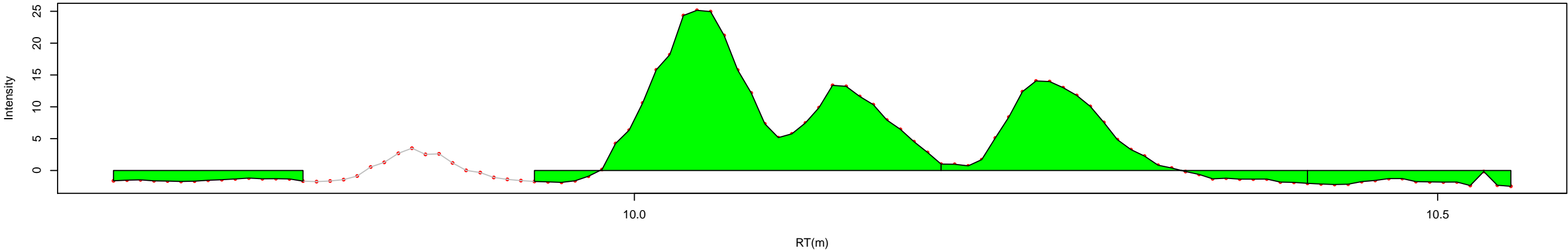
raw chromatogram | batch: 1   sample: female-o-m-21   conc: NA   function: 272   mass: 542 > 136.8



peak picking | window size: 19   iteration: 11   lp: 2   rp: 2   snr: 5   peak location: all   noise: 0.976   BLine: yes

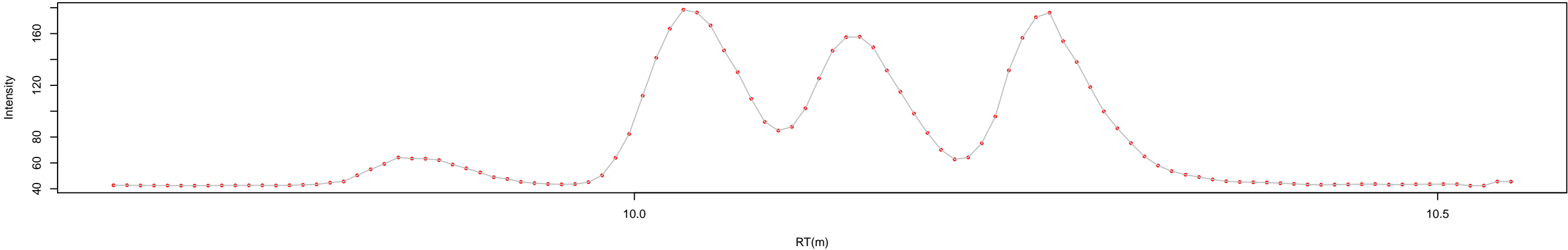


peak area | window size:3   BLine: yes

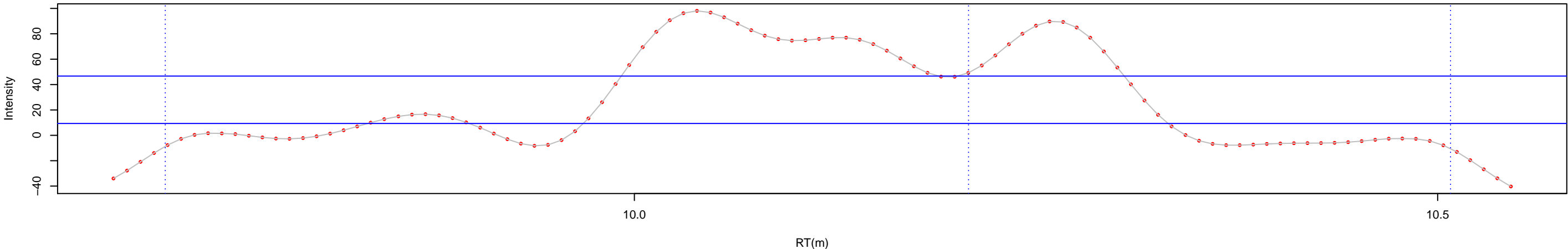




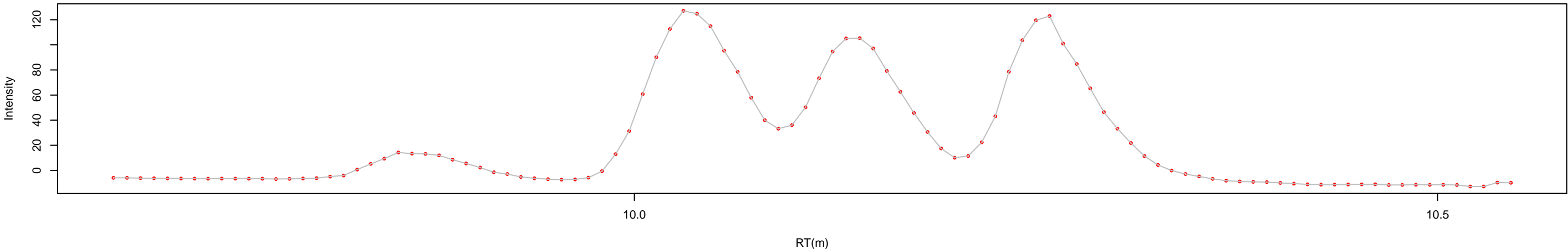
raw chromatogram | batch: 1 sample: female-y-3 conc: NA function: 272 mass: 542 > 136.8



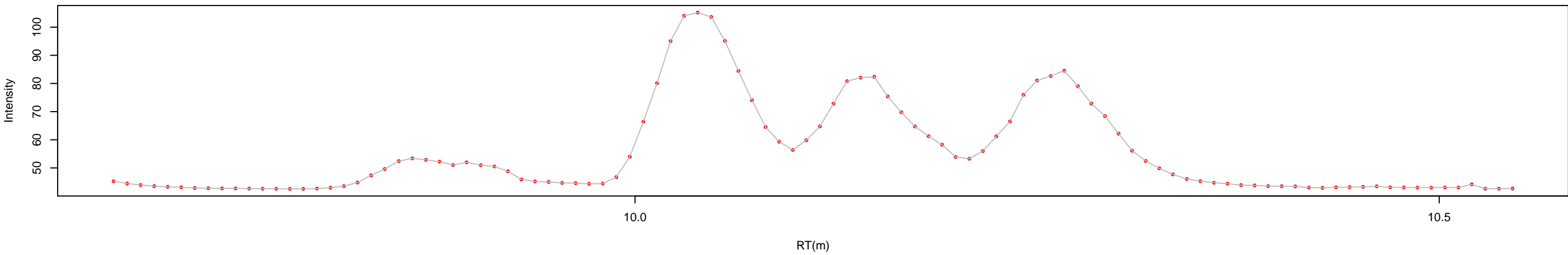
peak picking | window size: 19 iteration: 11 lp: 2 rp: 2 snr: 5 peak location: all noise: 9.34 BLine: yes



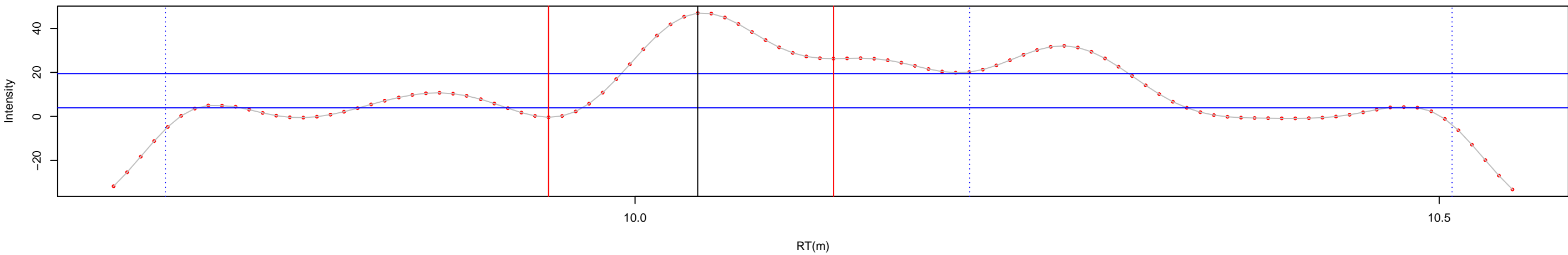
peak area | window size:3 BLine: yes



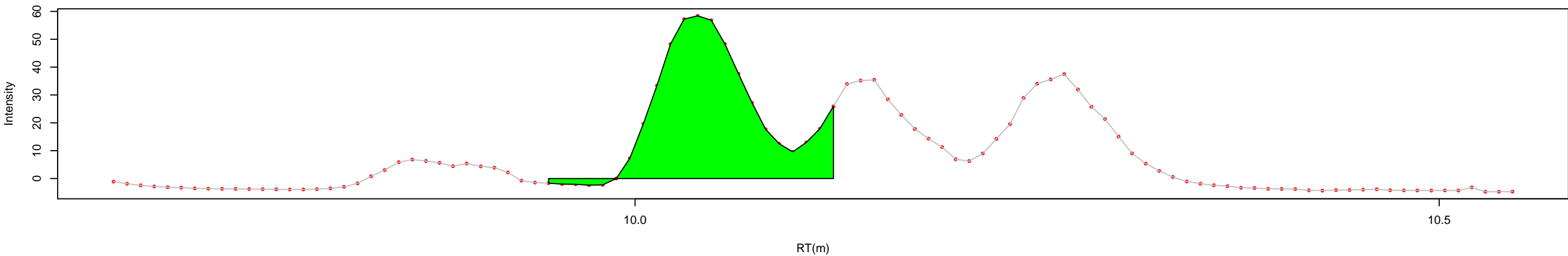
raw chromatogram | batch: 1 sample: female-y-m-9 conc: NA function: 272 mass: 542 > 136.8



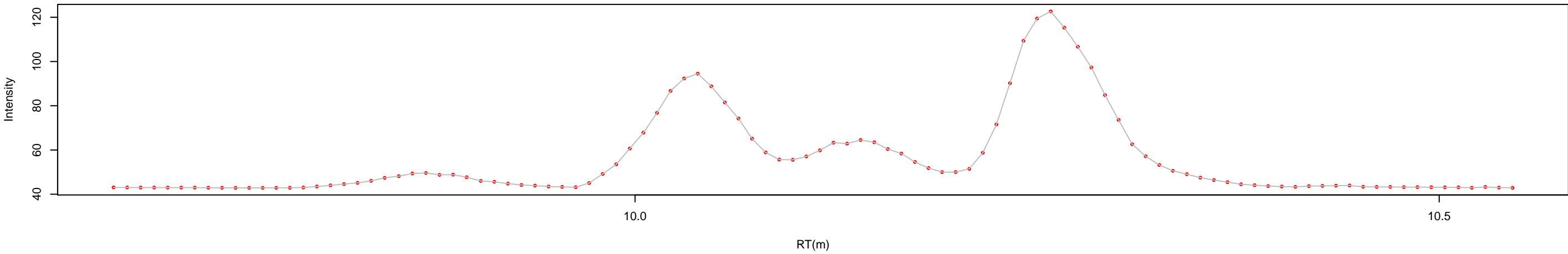
peak picking | window size: 19 iteration: 11 lp: 2 rp: 2 snr: 5 peak location: all noise: 3.89 BLine: yes



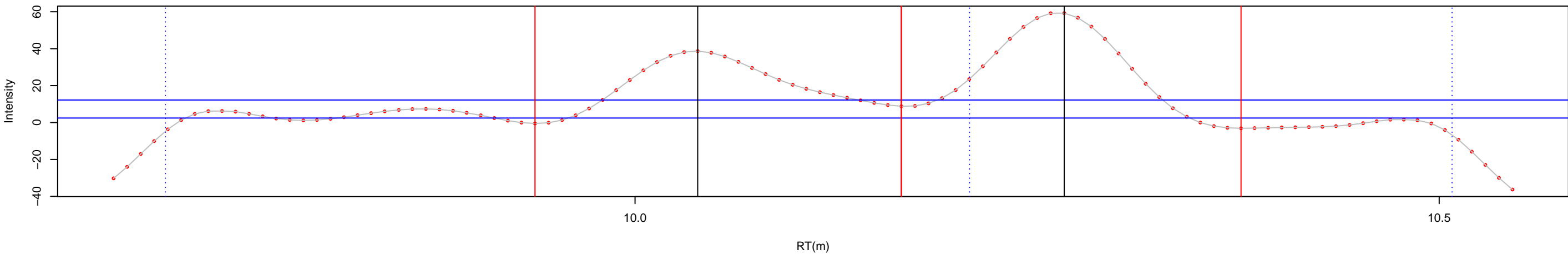
peak area | window size:3 BLine: yes



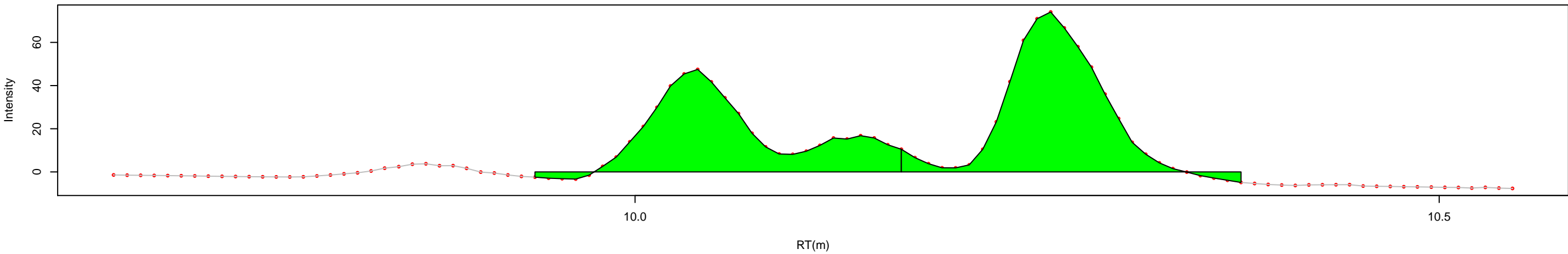
raw chromatogram | batch: 1 sample: female-o-15 conc: NA function: 272 mass: 542 > 136.8



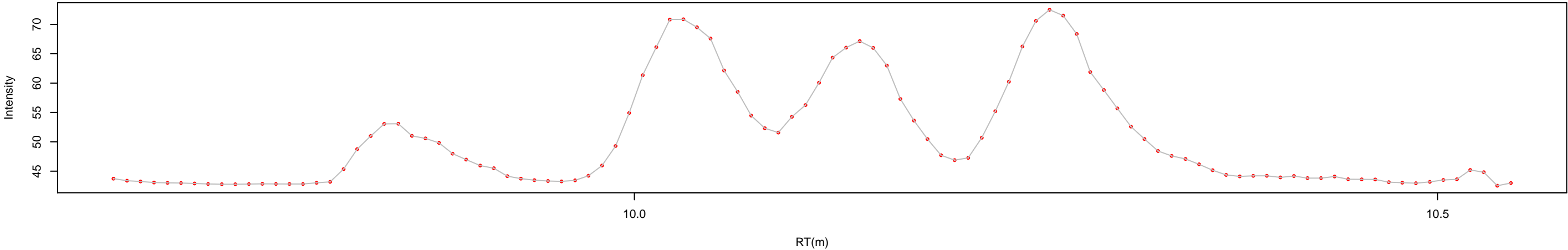
peak picking | window size: 19 iteration: 11 lp: 2 rp: 2 snr: 5 peak location: all noise: 2.44 BLine: yes



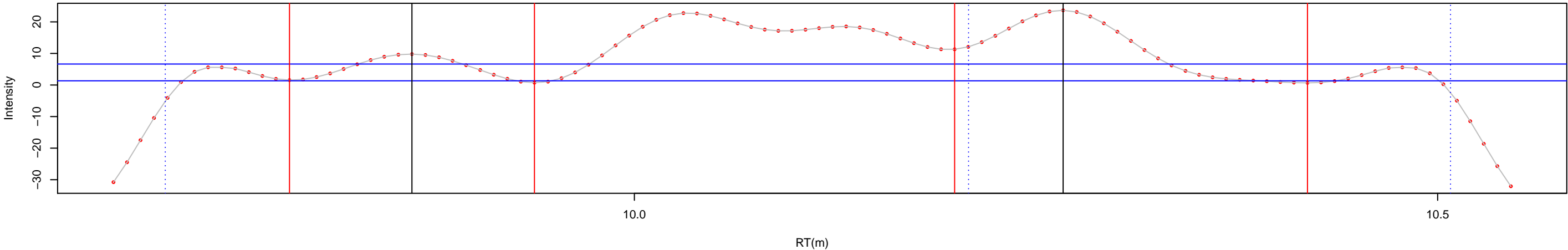
peak area | window size:3 BLine: yes



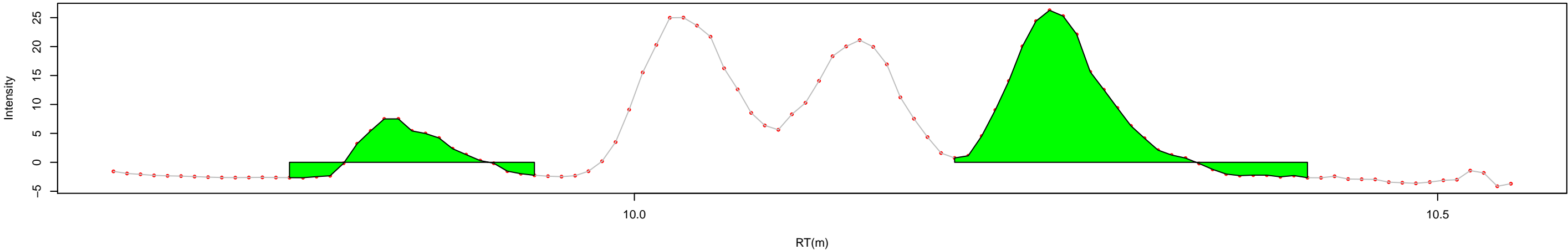
raw chromatogram | batch: 1   sample: female-o-m-22   conc: NA   function: 272   mass: 542 > 136.8



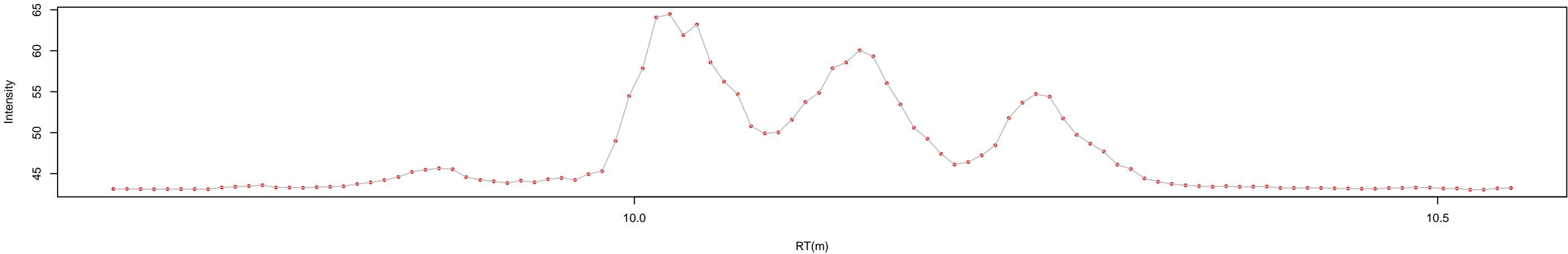
peak picking | window size: 19   iteration: 11   lp: 2   rp: 2   snr: 5   peak location: all   noise: 1.33   BLine: yes



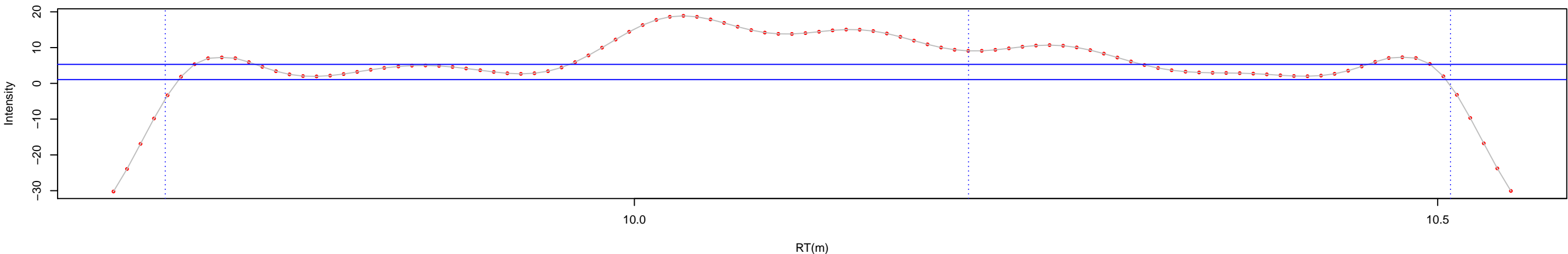
peak area | window size:3   BLine: yes



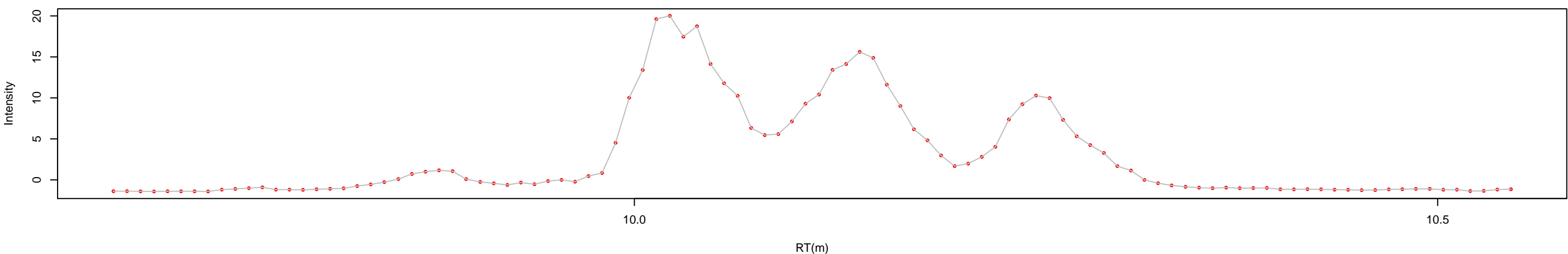
raw chromatogram | batch: 1   sample: female-y-4   conc: NA   function: 272   mass: 542 > 136.8



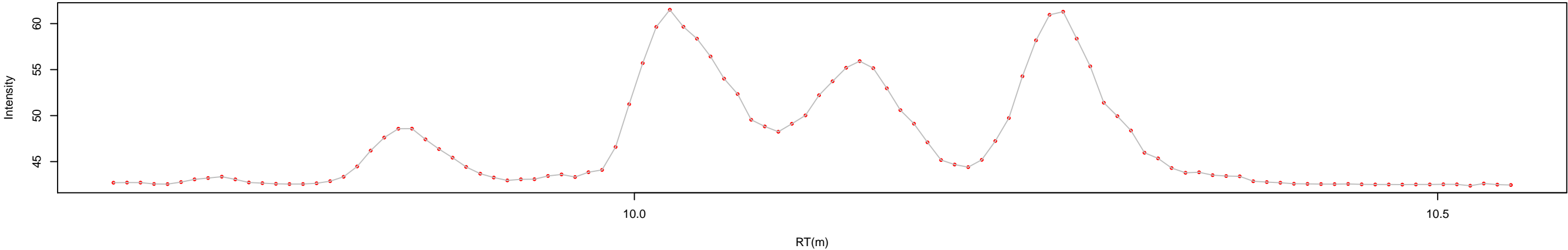
peak picking | window size: 19   iteration: 11   lp: 2   rp: 2   snr: 5   peak location: all   noise: 1.06   BLine: yes



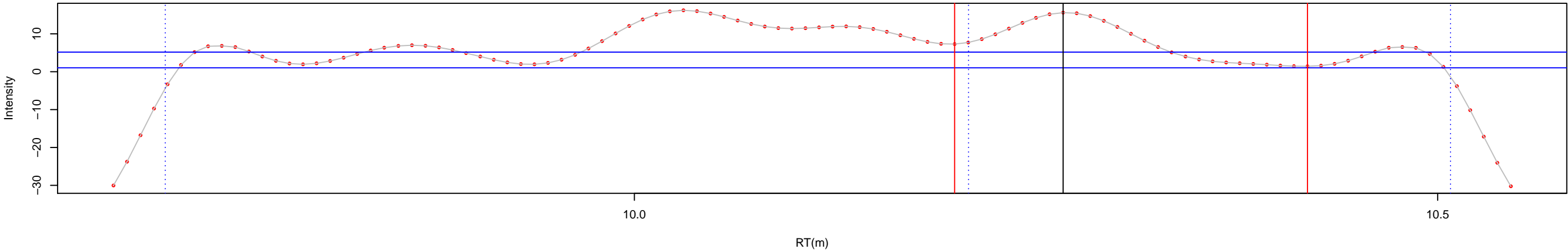
peak area | window size:3   BLine: yes



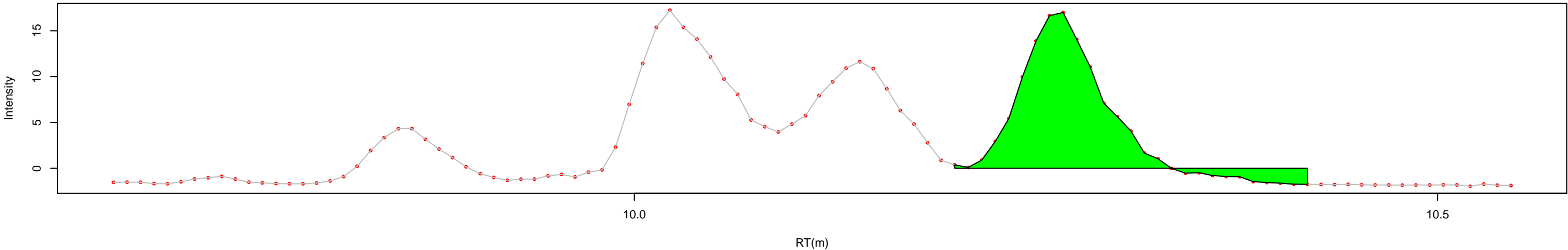
raw chromatogram | batch: 1   sample: female-y-m-10   conc: NA   function: 272   mass: 542 > 136.8



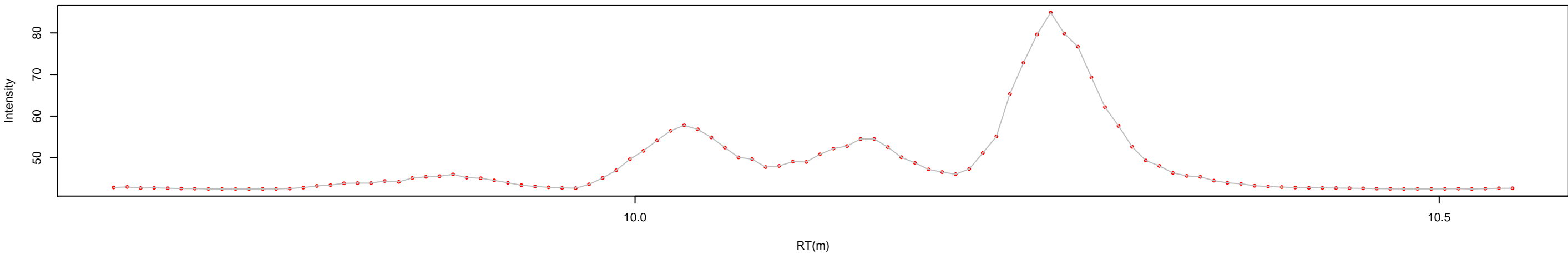
peak picking | window size: 19   iteration: 11   lp: 2   rp: 2   snr: 5   peak location: all   noise: 1.04   BLine: yes



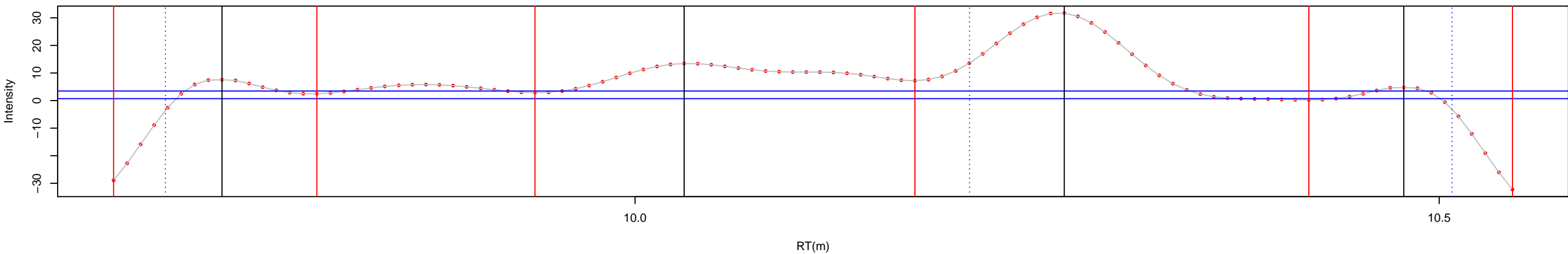
peak area | window size:3   BLine: yes



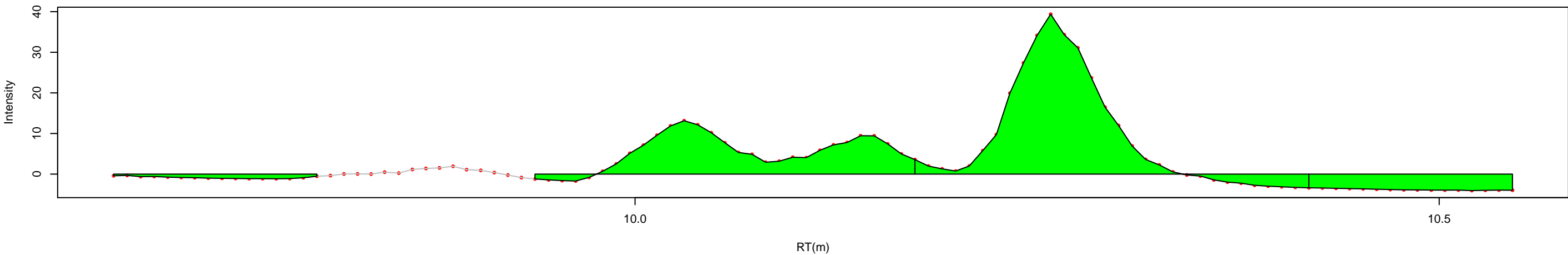
raw chromatogram | batch: 1 sample: female-o-16 conc: NA function: 272 mass: 542 > 136.8



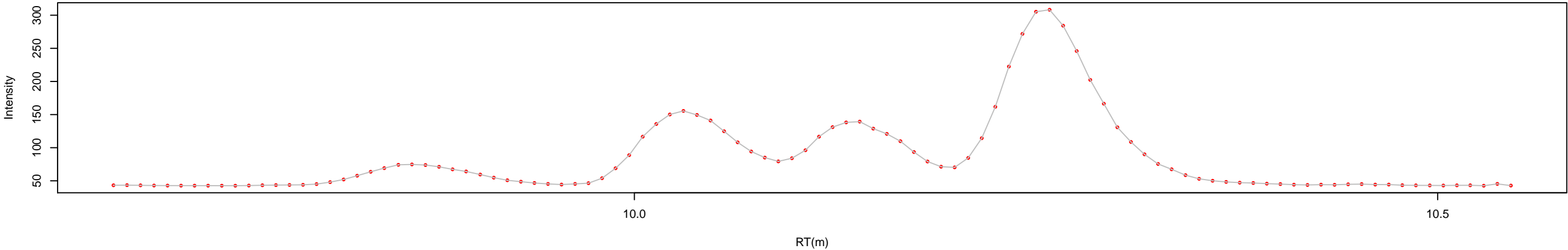
peak picking | window size: 19 iteration: 11 lp: 2 rp: 2 snr: 5 peak location: all noise: 0.695 BLine: yes



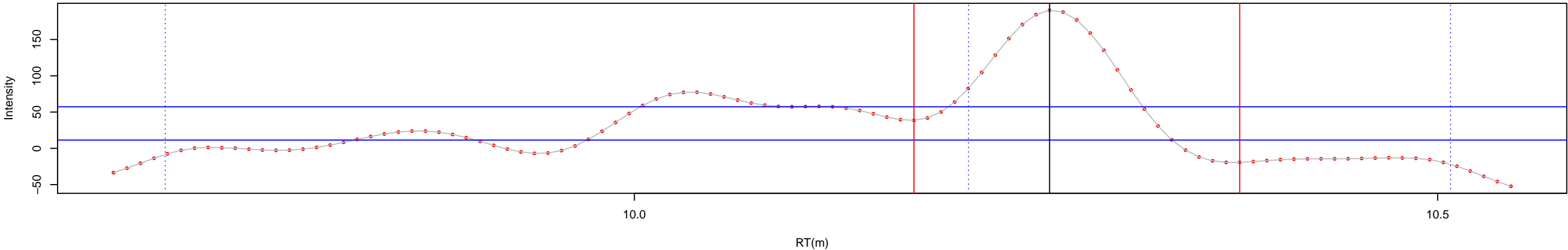
peak area | window size:3 BLine: yes



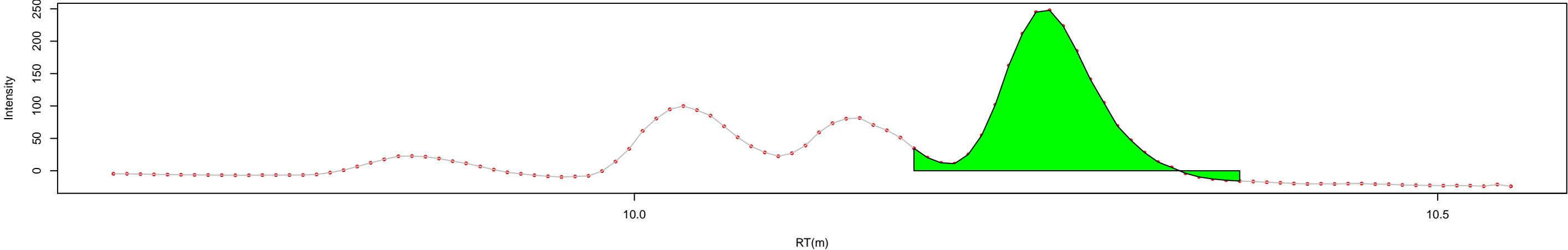
raw chromatogram | batch: 1   sample: female-o-m-23   conc: NA   function: 272   mass: 542 > 136.8



peak picking | window size: 19   iteration: 11   lp: 2   rp: 2   snr: 5   peak location: all   noise: 11.5   BLine: yes

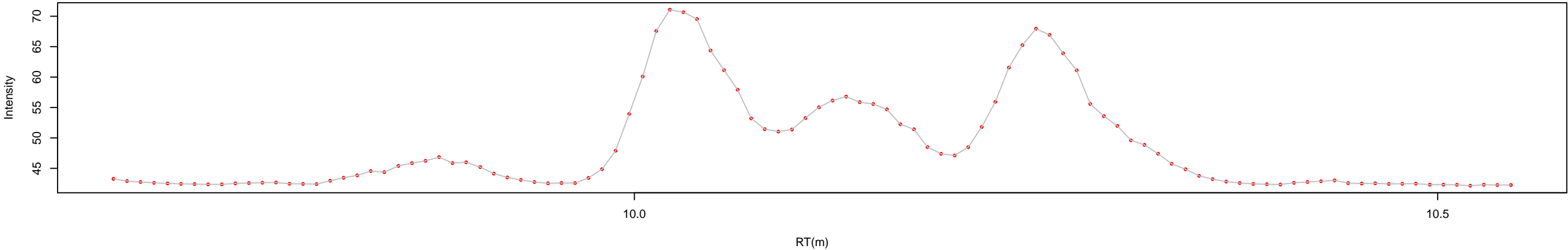


peak area | window size:3   BLine: yes

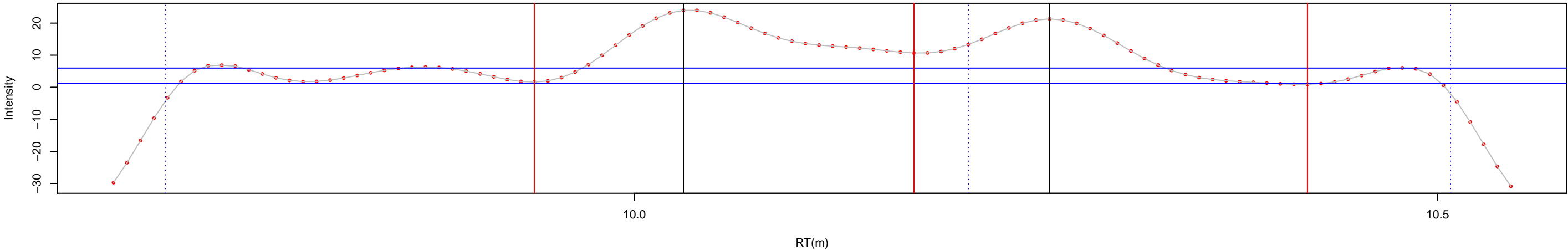




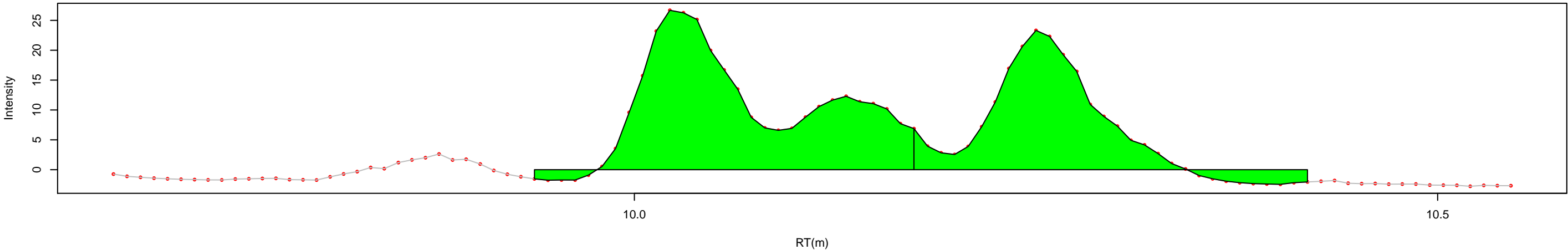
raw chromatogram | batch: 1   sample: female-y-5   conc: NA   function: 272   mass: 542 > 136.8



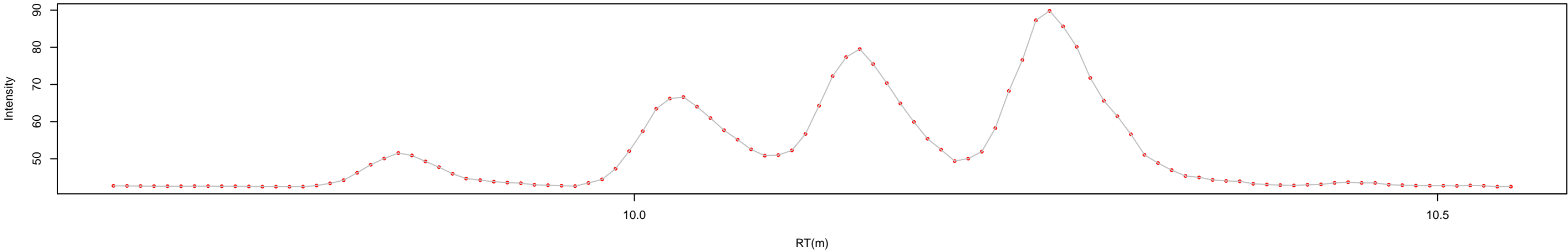
peak picking | window size: 19   iteration: 11   lp: 2   rp: 2   snr: 5   peak location: all   noise: 1.19   BLine: yes



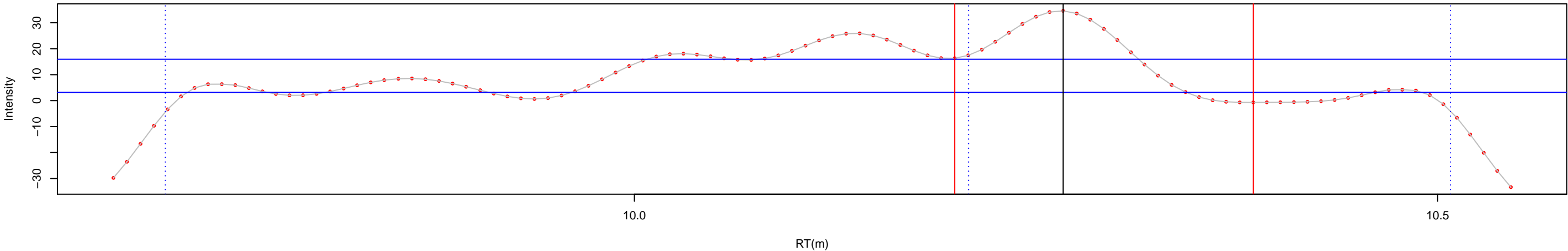
peak area | window size:3   BLine: yes



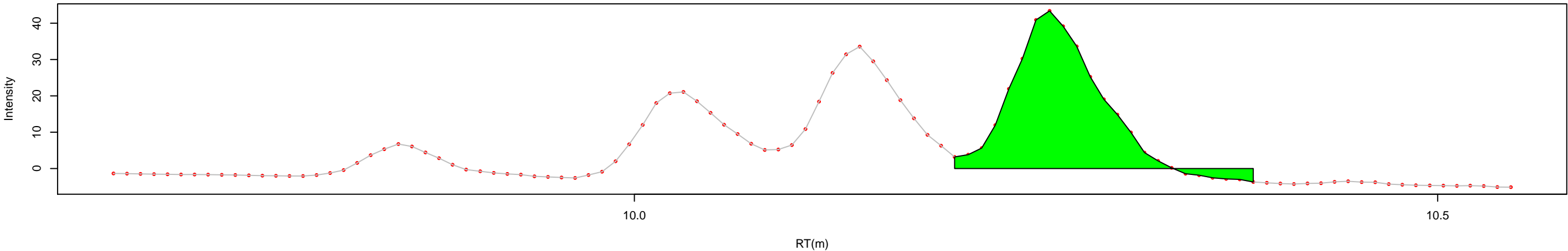
raw chromatogram | batch: 1   sample: female-y-m-11   conc: NA   function: 272   mass: 542 > 136.8



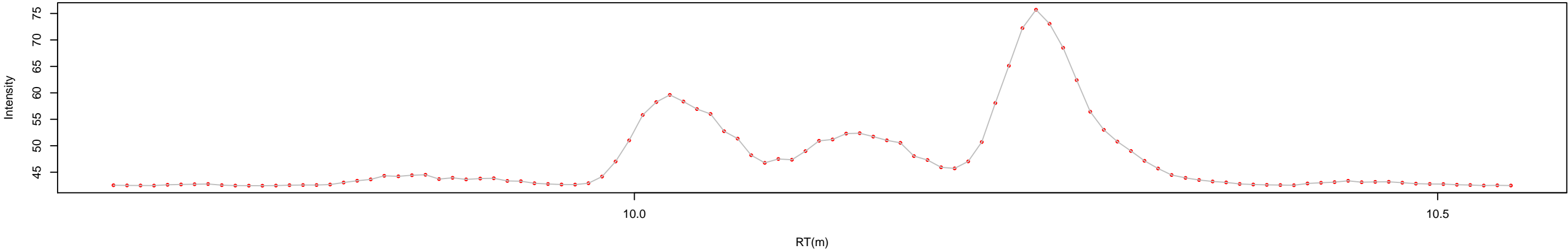
peak picking | window size: 19   iteration: 11   lp: 2   rp: 2   snr: 5   peak location: all   noise: 3.19   BLine: yes



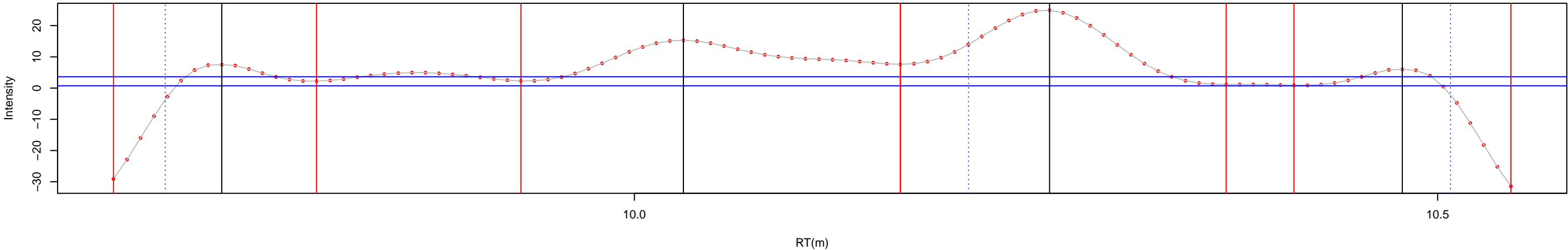
peak area | window size:3   BLine: yes



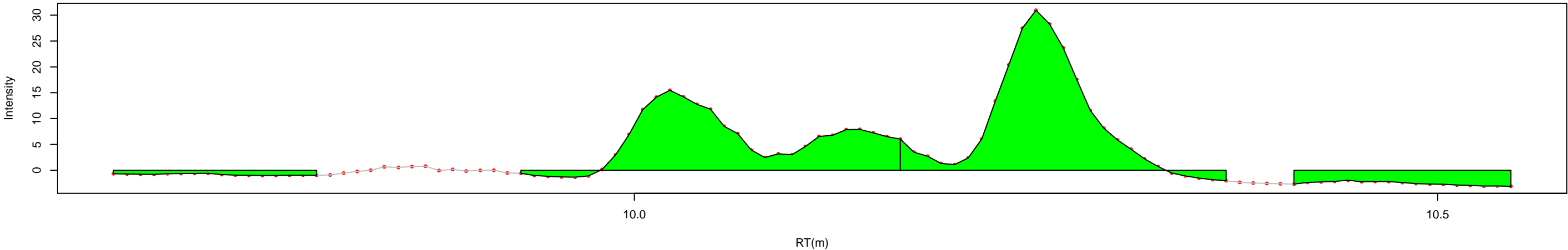
raw chromatogram | batch: 1 sample: female-o-17 conc: NA function: 272 mass: 542 > 136.8



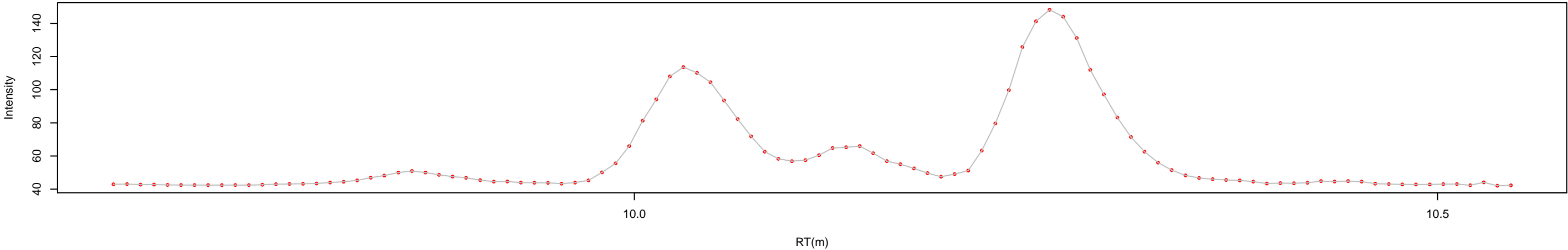
peak picking | window size: 19 iteration: 11 lp: 2 rp: 2 snr: 5 peak location: all noise: 0.724 BLine: yes



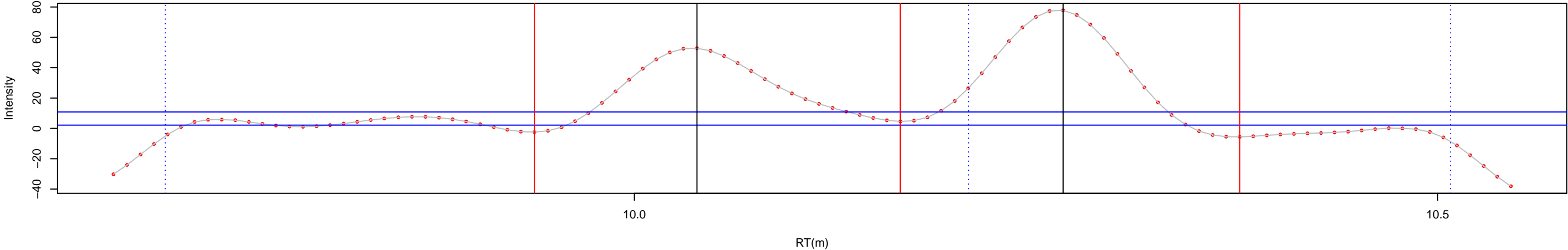
peak area | window size:3 BLine: yes



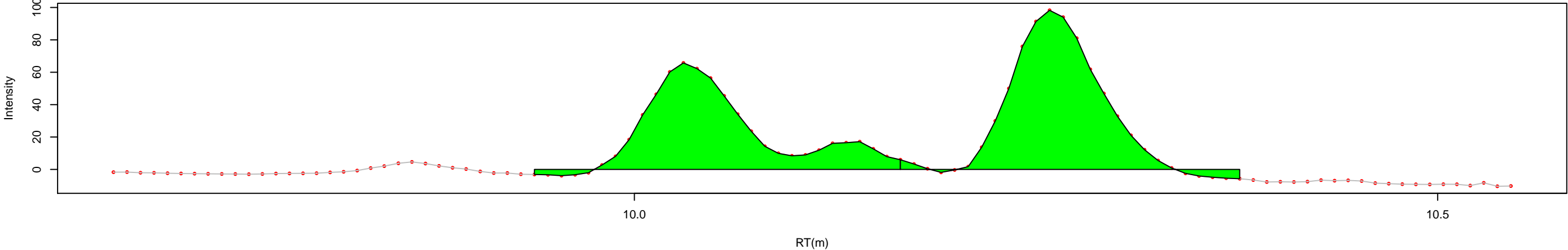
raw chromatogram | batch: 1   sample: female-o-m-24   conc: NA   function: 272   mass: 542 > 136.8



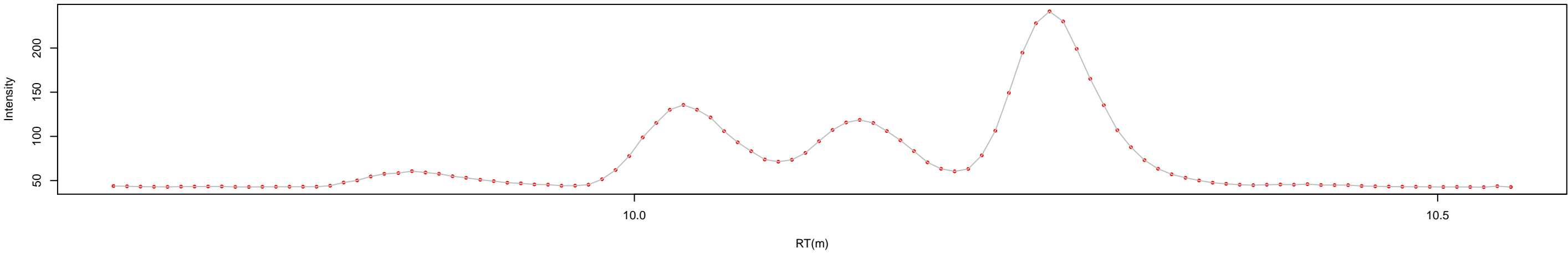
peak picking | window size: 19   iteration: 11   lp: 2   rp: 2   snr: 5   peak location: all   noise: 2.17   BLine: yes



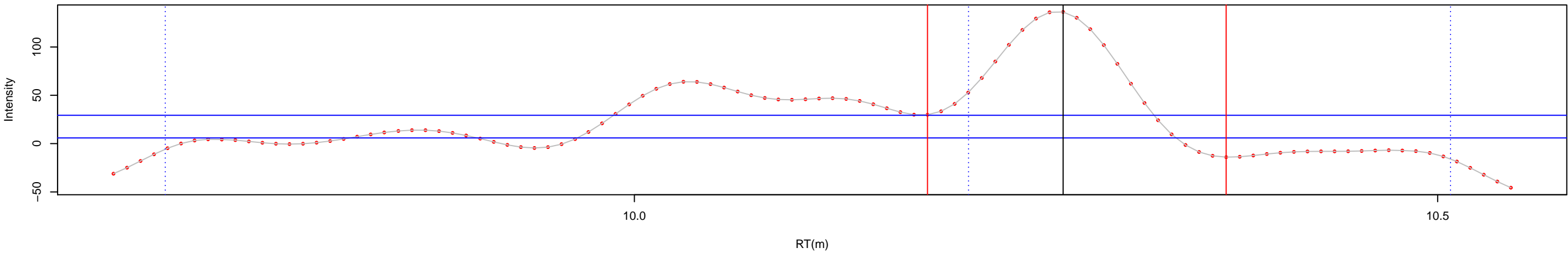
peak area | window size:3   BLine: yes



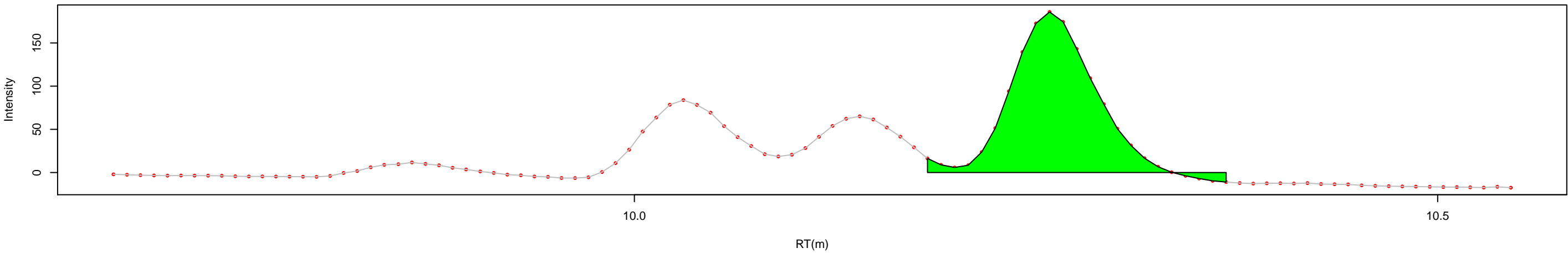
raw chromatogram | batch: 1 sample: female-o-18 conc: NA function: 272 mass: 542 > 136.8



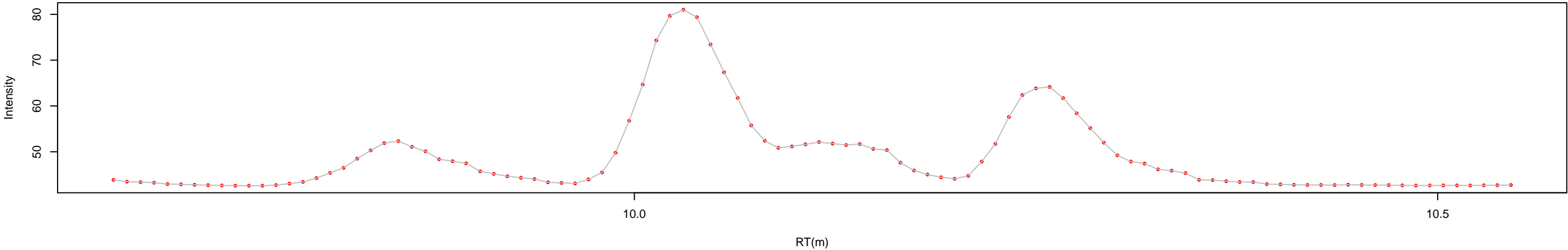
peak picking | window size: 19 iteration: 11 lp: 2 rp: 2 snr: 5 peak location: all noise: 5.86 BLine: yes



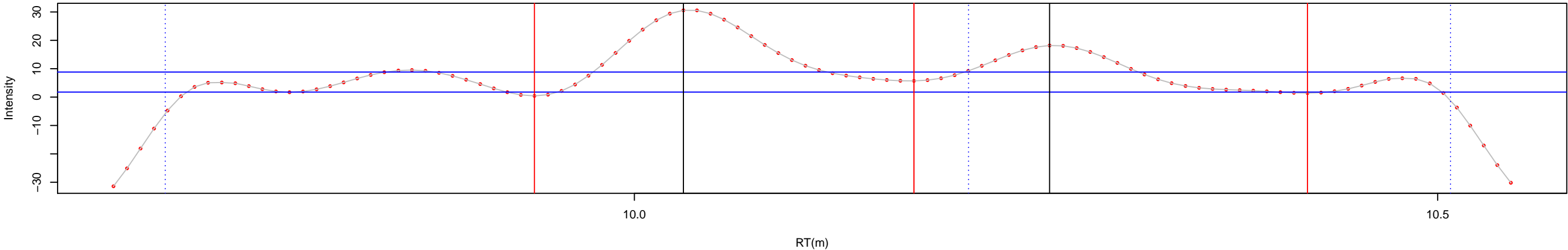
peak area | window size:3 BLine: yes



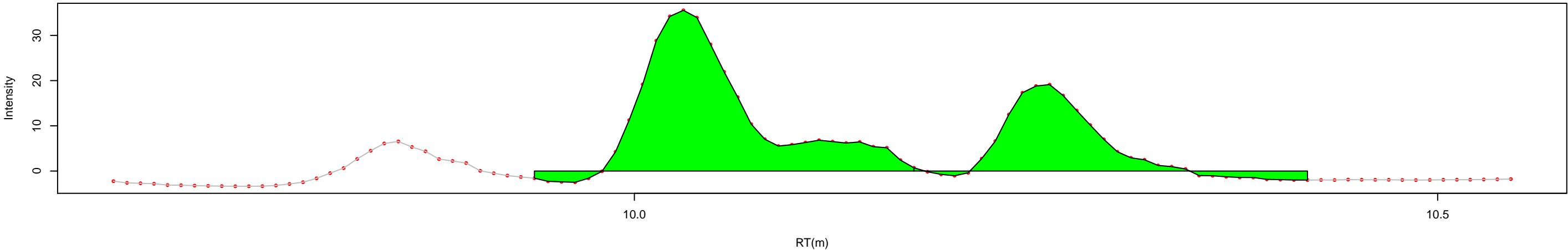
raw chromatogram | batch: 1   sample: female-o-m-25   conc: NA   function: 272   mass: 542 > 136.8



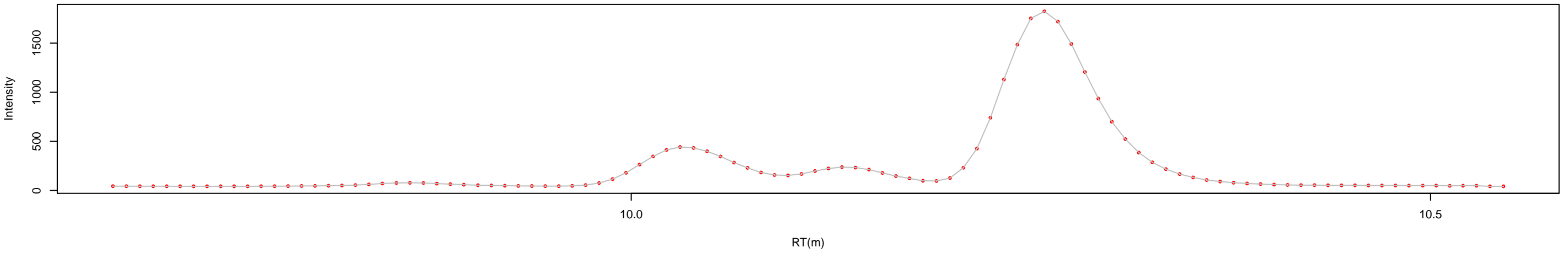
peak picking | window size: 19   iteration: 11   lp: 2   rp: 2   snr: 5   peak location: all   noise: 1.77   BLine: yes



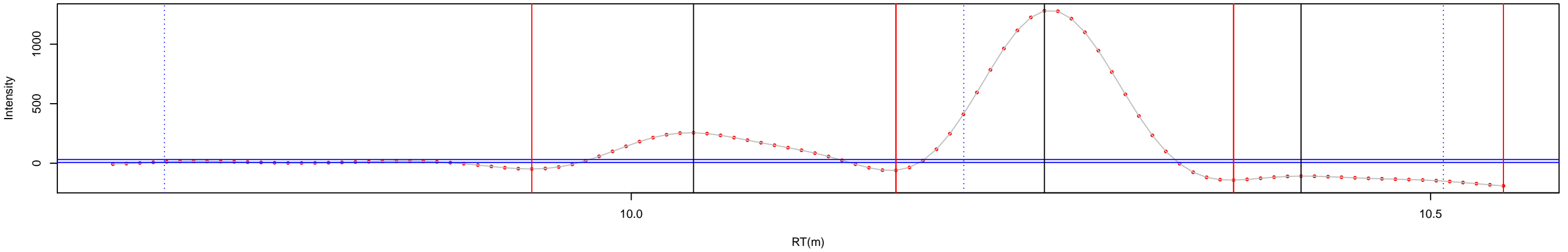
peak area | window size:3   BLine: yes



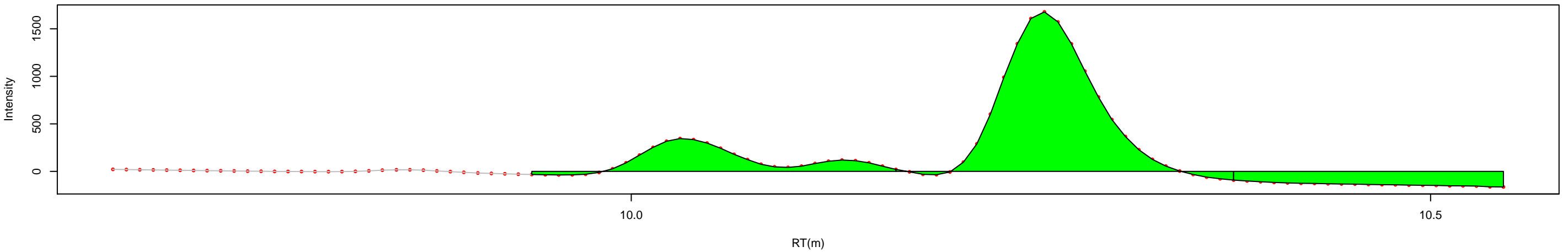
raw chromatogram | batch: 1 sample: female-o-19 conc: NA function: 272 mass: 542 > 136.8



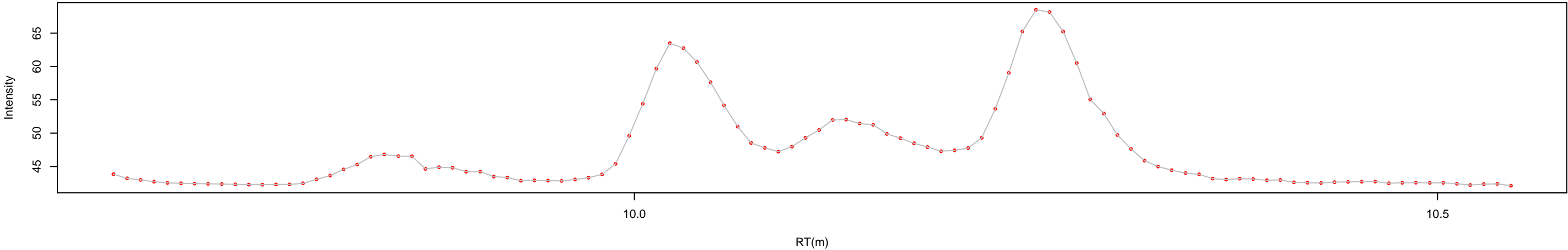
peak picking | window size: 19 iteration: 11 lp: 2 rp: 2 snr: 5 peak location: all noise: 6.15 BLine: yes



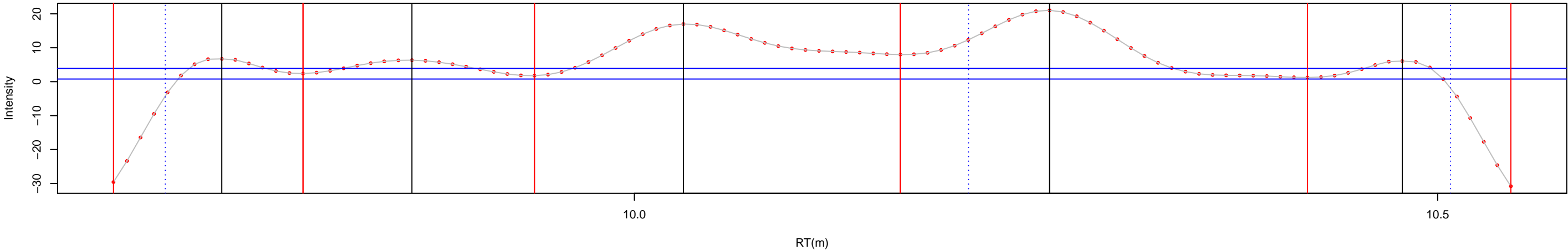
peak area | window size:3 BLine: yes



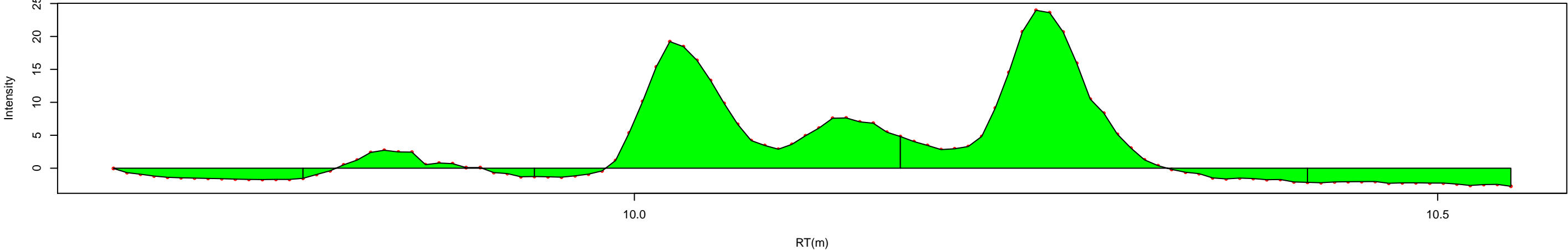
raw chromatogram | batch: 1   sample: female-o-m-26   conc: NA   function: 272   mass: 542 > 136.8



peak picking | window size: 19   iteration: 11   lp: 2   rp: 2   snr: 5   peak location: all   noise: 0.782   BLine: yes

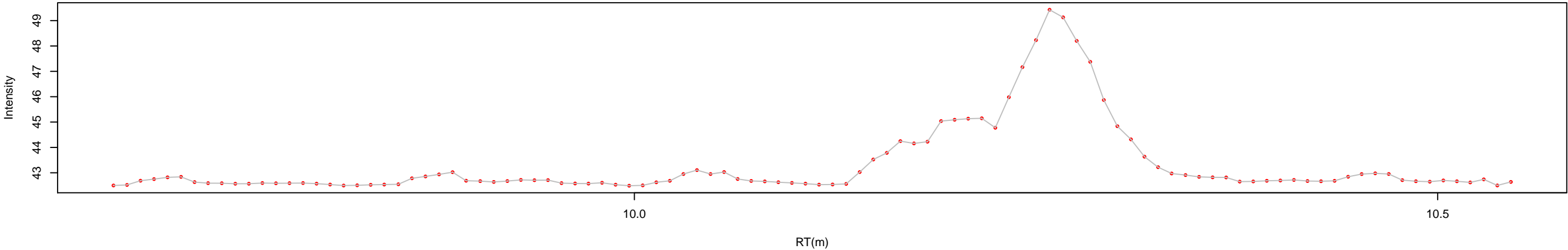


peak area | window size:3   BLine: yes

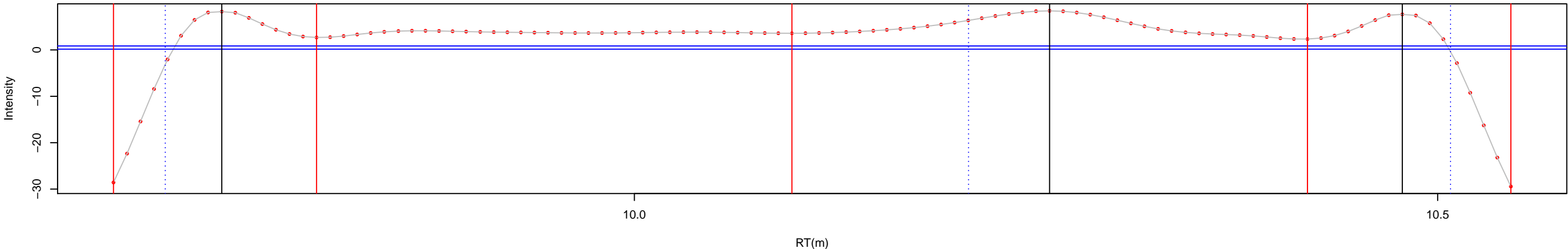




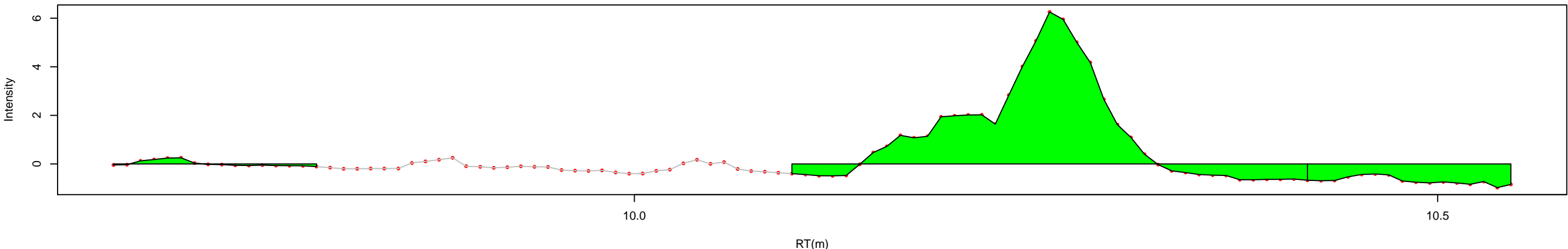
raw chromatogram | batch: 1 sample: std-1 conc: 100 function: 272 mass: 542 > 136.8



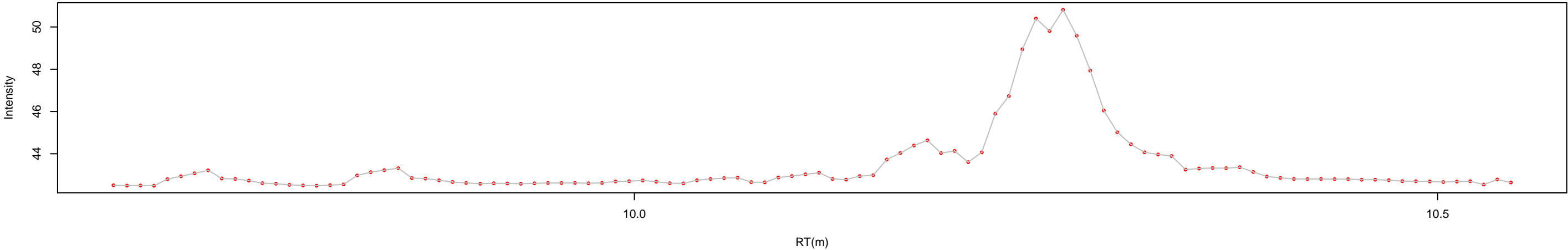
peak picking | window size: 19 iteration: 11 lp: 2 rp: 2 snr: 5 peak location: all noise: 0.171 BLine: yes



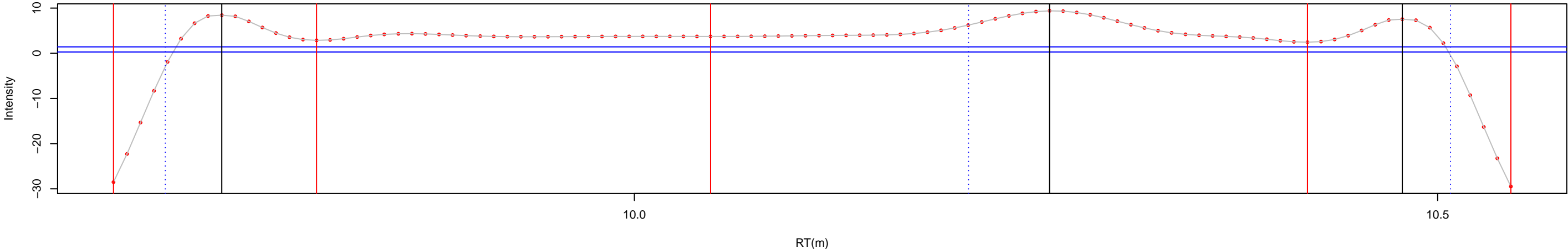
peak area | window size:3 BLine: yes



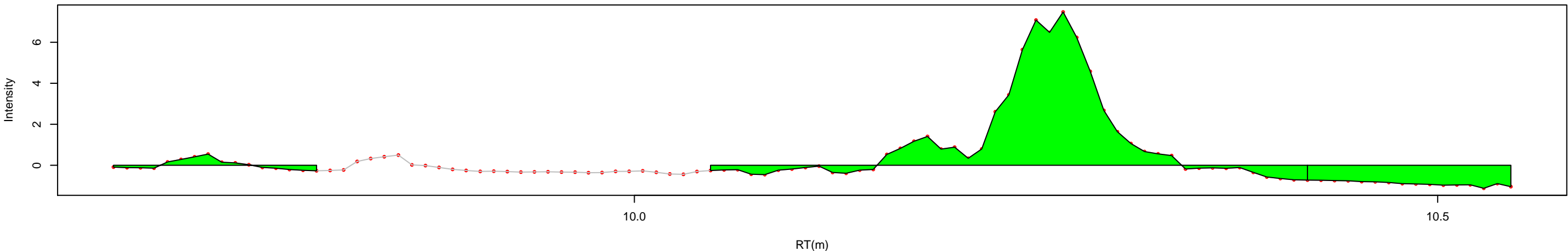
raw chromatogram | batch: 1   sample: std-2   conc: 200   function: 272   mass: 542 > 136.8



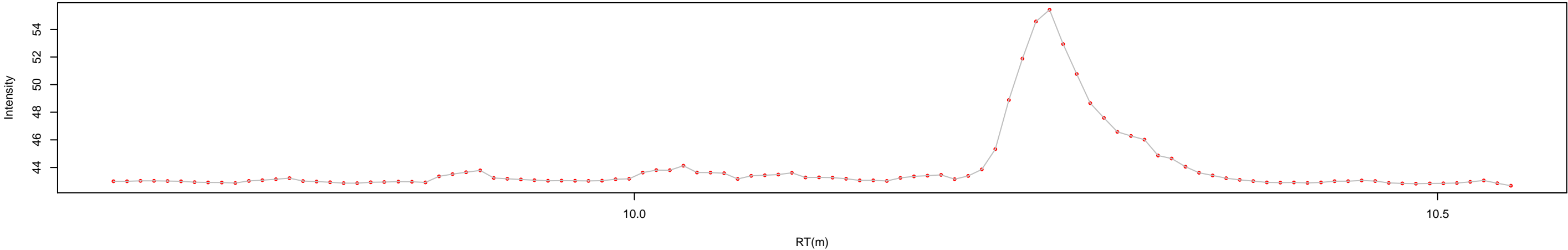
peak picking | window size: 19   iteration: 11   lp: 2   rp: 2   snr: 5   peak location: all   noise: 0.284   BLine: yes



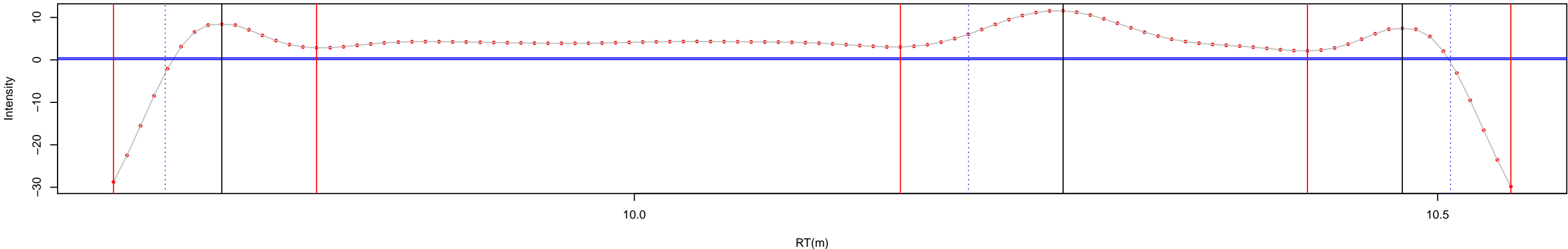
peak area | window size:3   BLine: yes



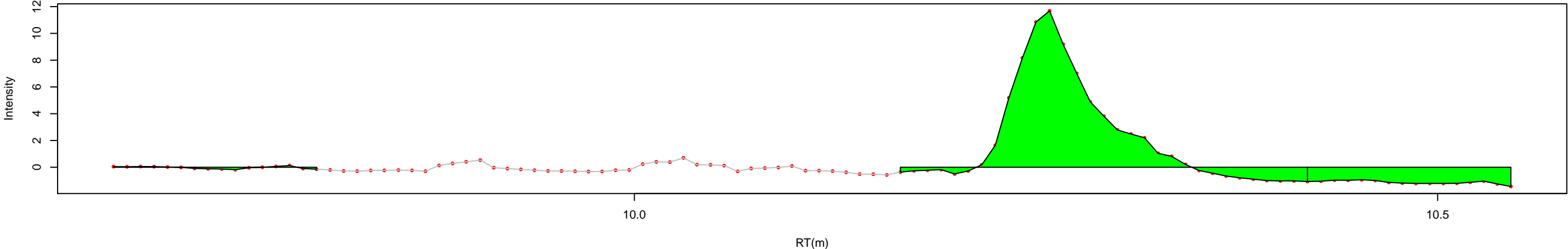
raw chromatogram | batch: 1   sample: std-3   conc: 400   function: 272   mass: 542 > 136.8



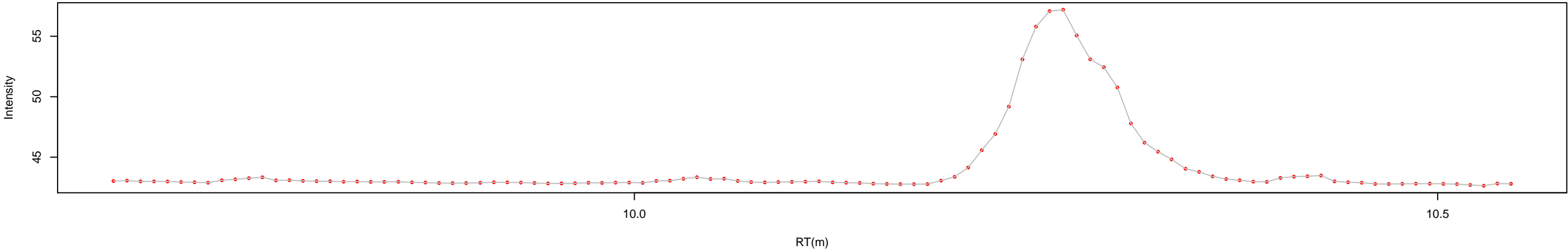
peak picking | window size: 19   iteration: 11   lp: 2   rp: 2   snr: 5   peak location: all   noise: 0.0958   BLine: yes



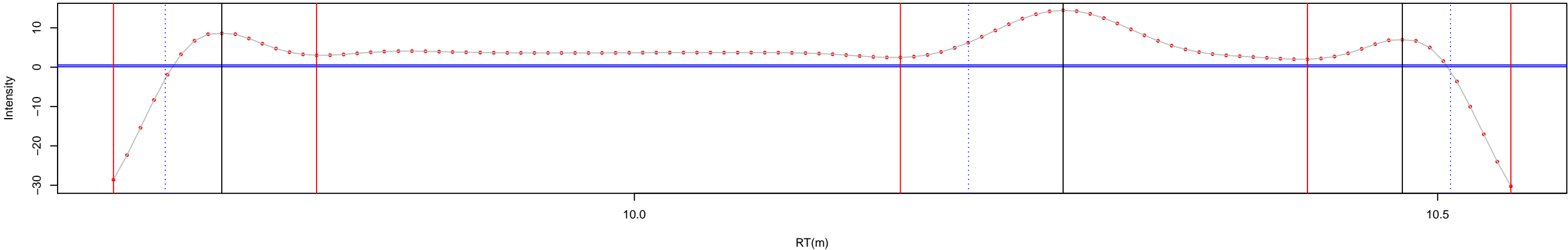
peak area | window size:3   BLine: yes



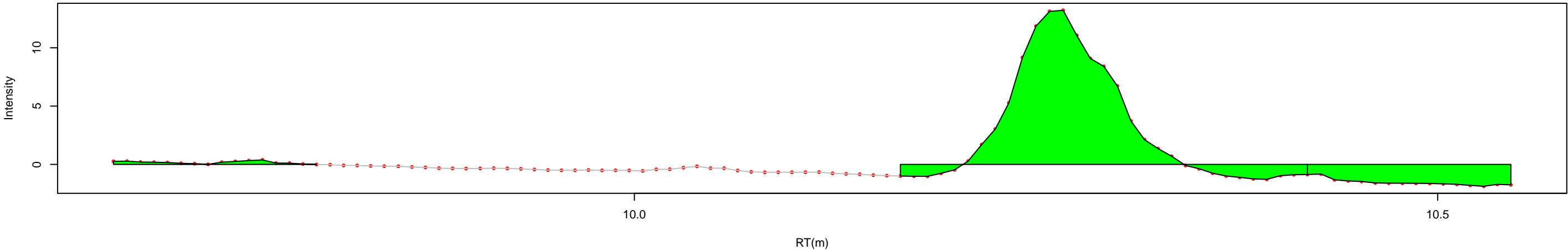
raw chromatogram | batch: 1   sample: std-4   conc: 1000   function: 272   mass: 542 > 136.8



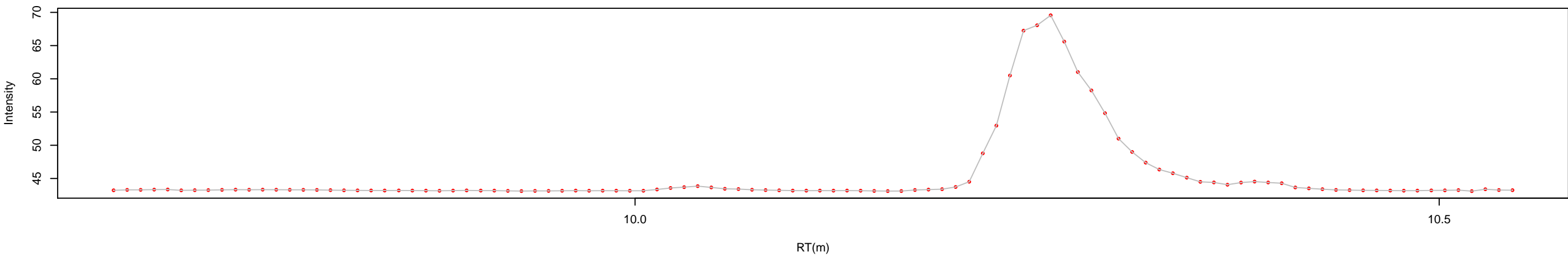
peak picking | window size: 19   iteration: 11   lp: 2   rp: 2   snr: 5   peak location: all   noise: 0.112   BLine: yes



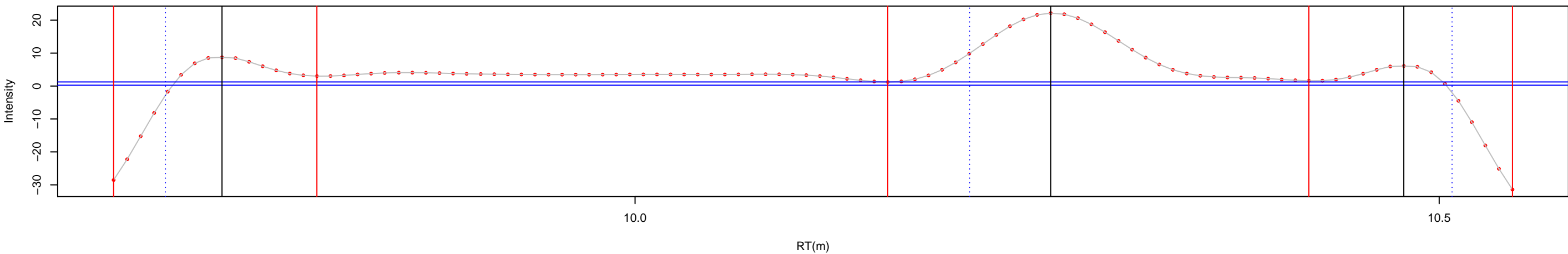
peak area | window size:3   BLine: yes



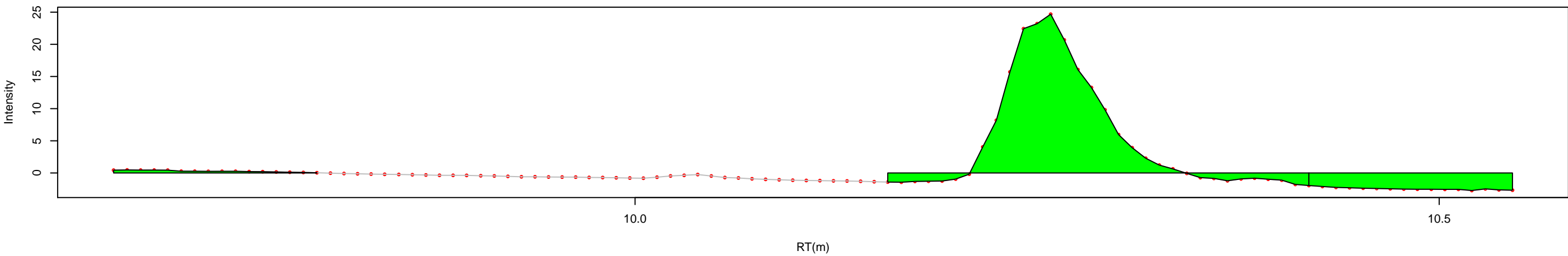
raw chromatogram | batch: 1 sample: std-5 conc: 2000 function: 272 mass: 542 > 136.8



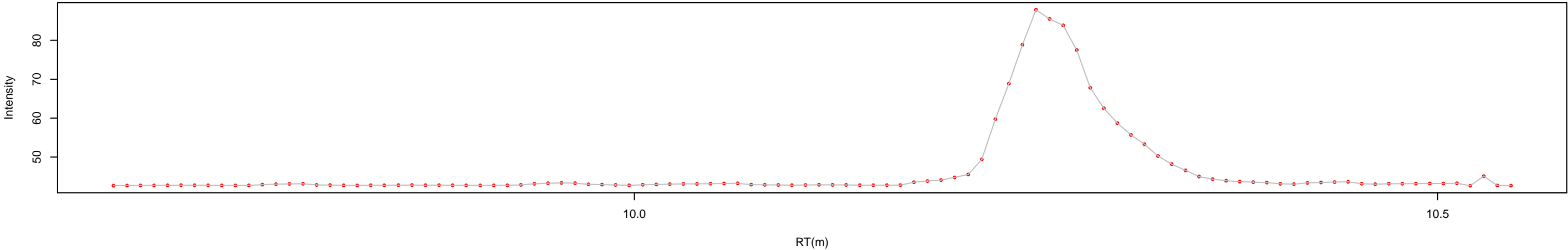
peak picking | window size: 19 iteration: 11 lp: 2 rp: 2 snr: 5 peak location: all noise: 0.249 BLine: yes



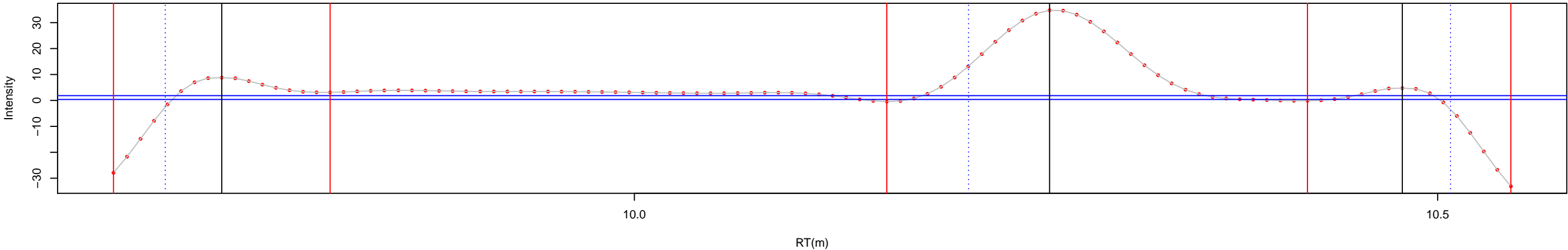
peak area | window size:3 BLine: yes



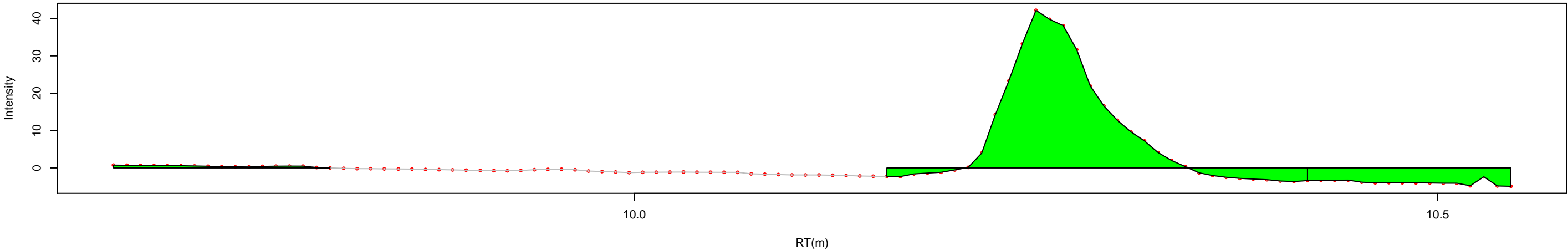
raw chromatogram | batch: 1   sample: std-6   conc: 4000   function: 272   mass: 542 > 136.8



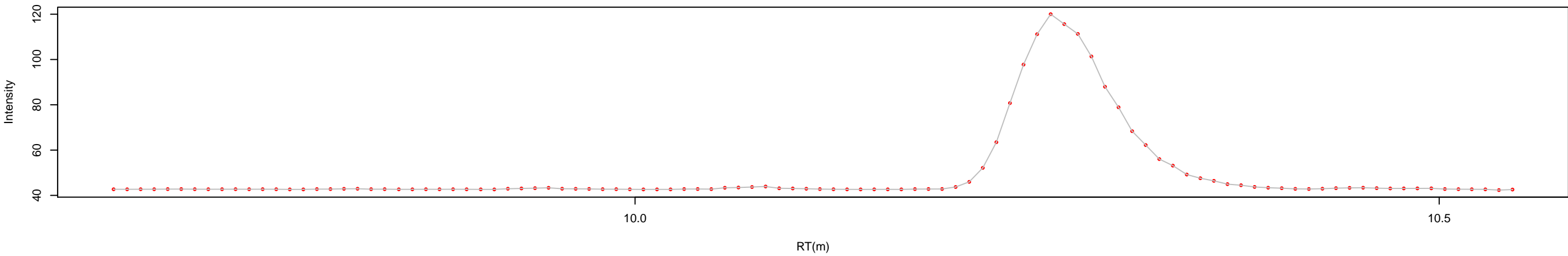
peak picking | window size: 19   iteration: 11   lp: 2   rp: 2   snr: 5   peak location: all   noise: 0.369   BLine: yes



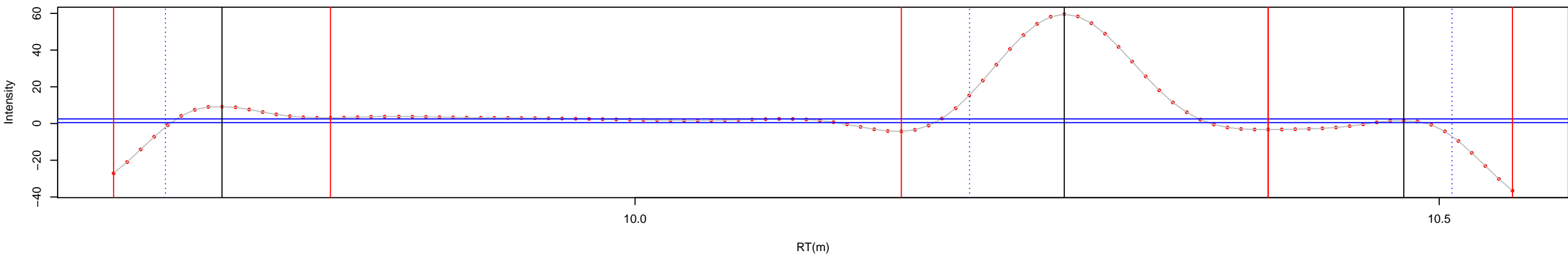
peak area | window size:3   BLine: yes



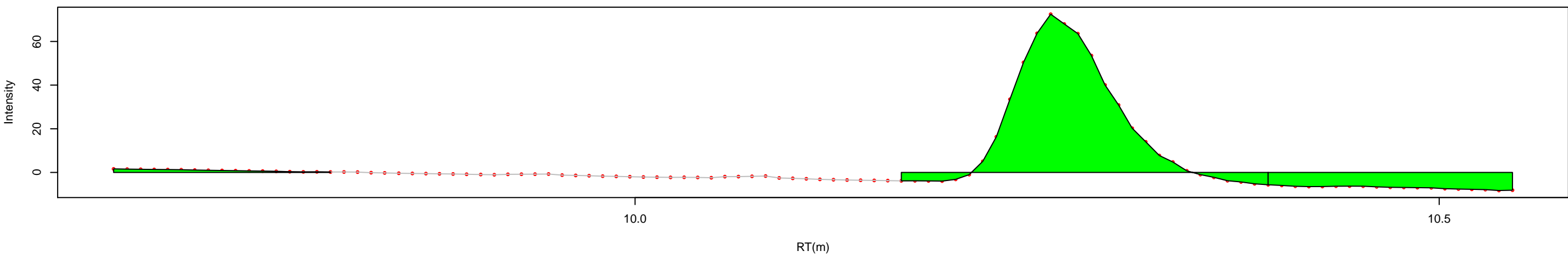
raw chromatogram | batch: 1 sample: std-7 conc: 8000 function: 272 mass: 542 > 136.8



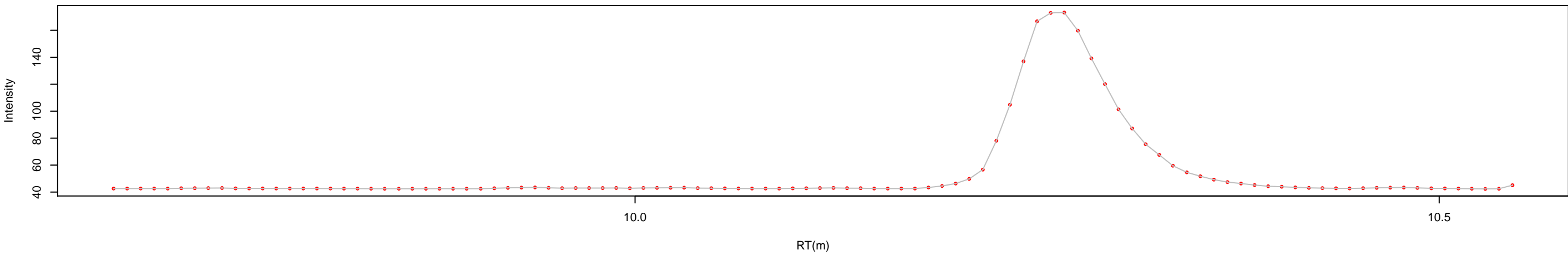
peak picking | window size: 19 iteration: 11 lp: 2 rp: 2 snr: 5 peak location: all noise: 0.5 BLine: yes



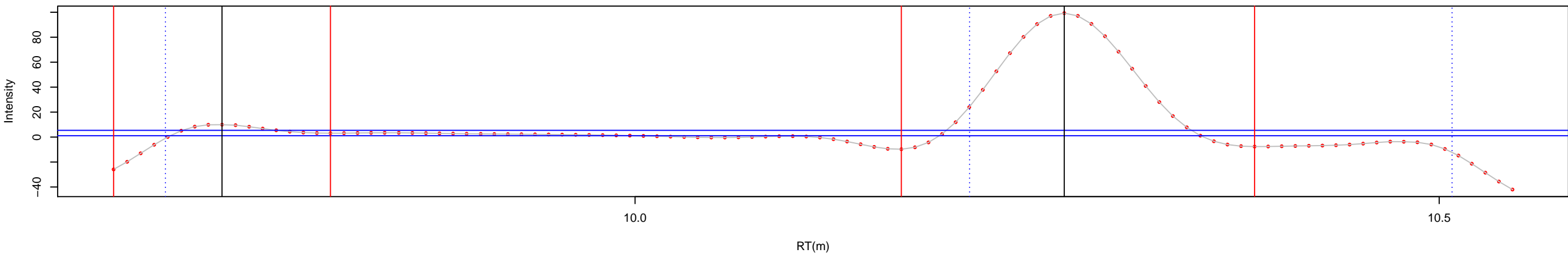
peak area | window size:3 BLine: yes



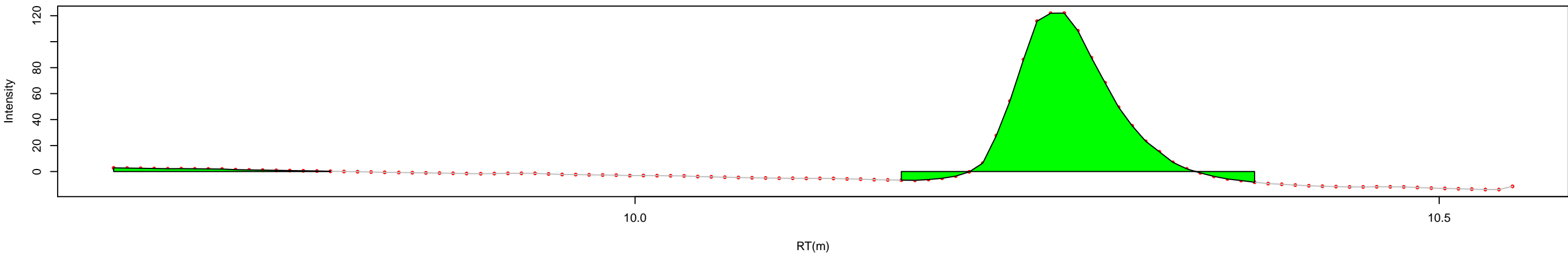
raw chromatogram | batch: 1 sample: std-8 conc: 16000 function: 272 mass: 542 > 136.8



peak picking | window size: 19 iteration: 11 lp: 2 rp: 2 snr: 5 peak location: all noise: 1.08 BLine: yes

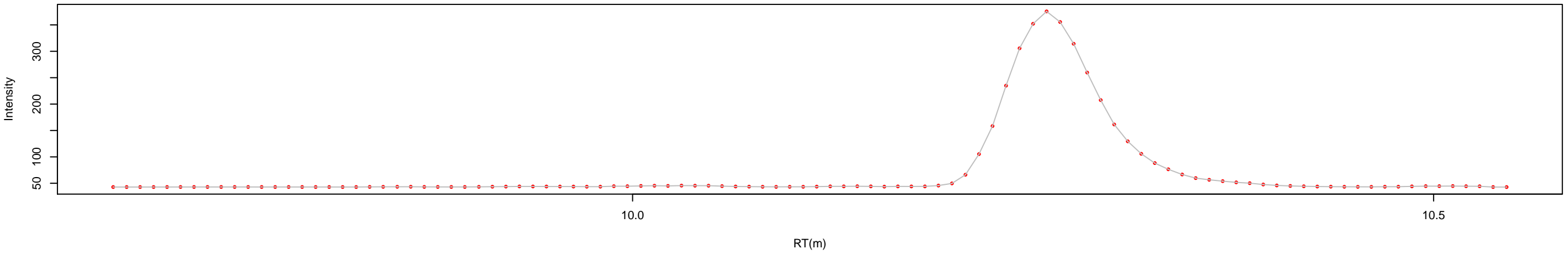


peak area | window size:3 BLine: yes

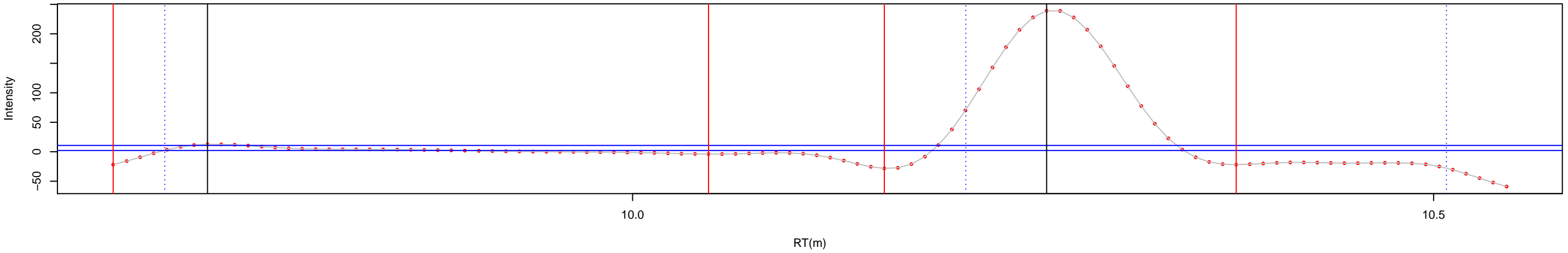




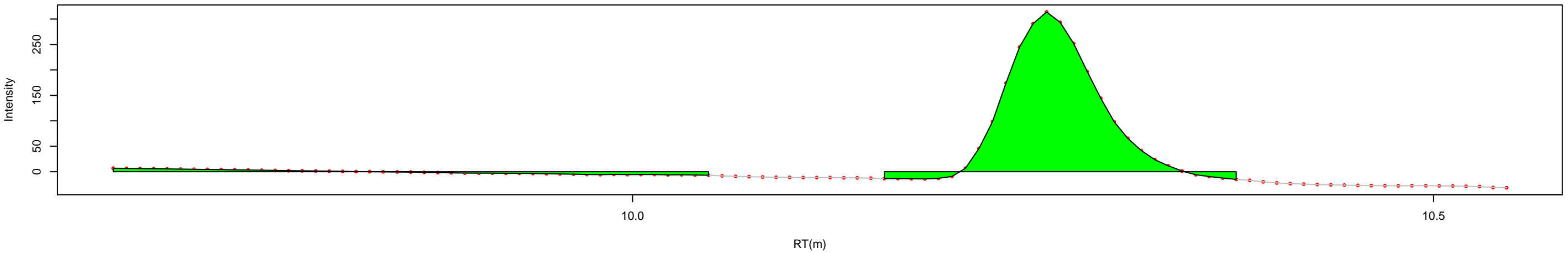
raw chromatogram | batch: 1   sample: std-9   conc: 40000   function: 272   mass: 542 > 136.8



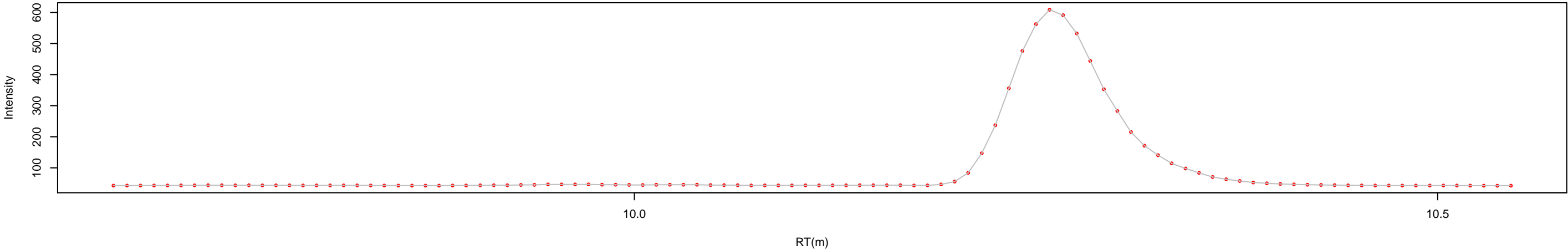
peak picking | window size: 19   iteration: 11   lp: 2   rp: 2   snr: 5   peak location: all   noise: 2.14   BLine: yes



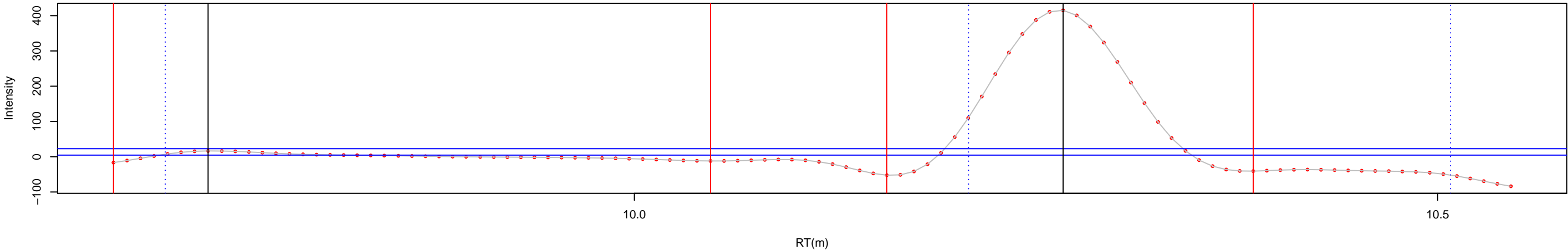
peak area | window size:3   BLine: yes



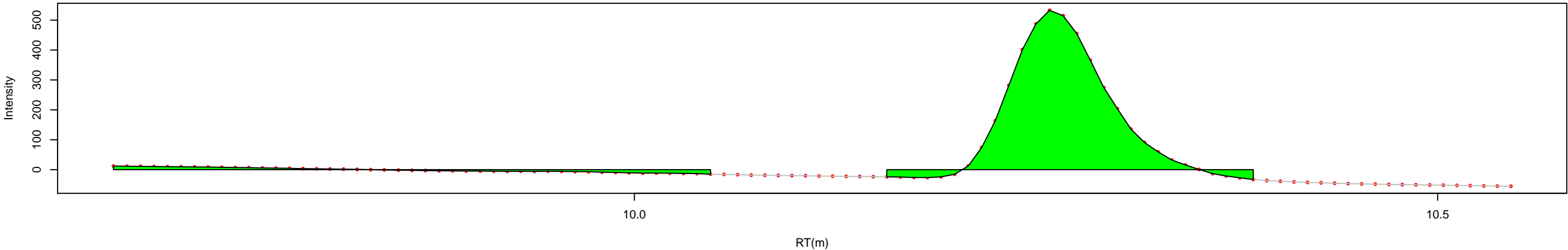
raw chromatogram | batch: 1   sample: std-10   conc: 80000   function: 272   mass: 542 > 136.8



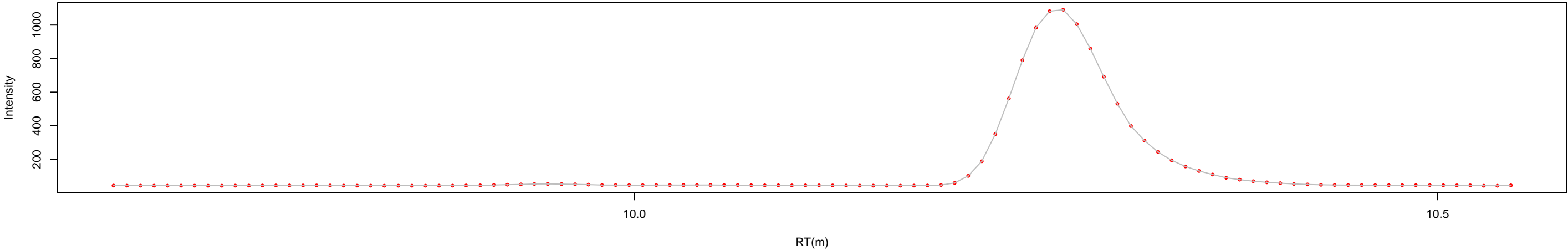
peak picking | window size: 19   iteration: 11   lp: 2   rp: 2   snr: 5   peak location: all   noise: 4.55   BLine: yes



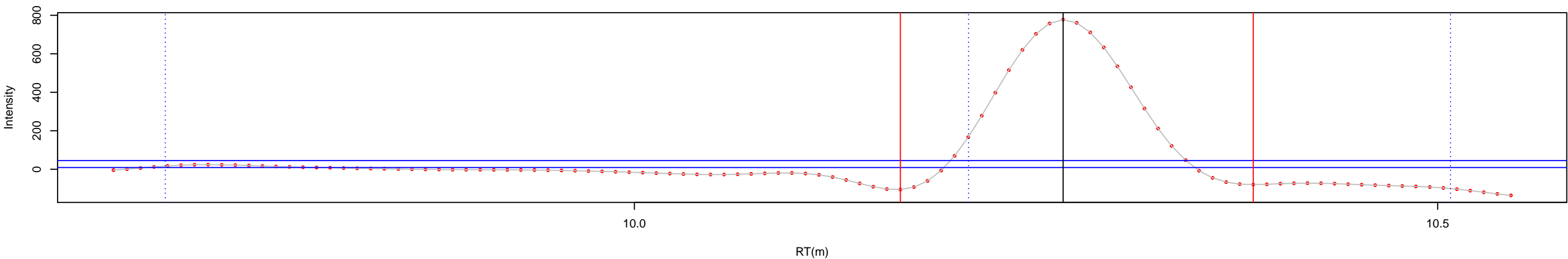
peak area | window size:3   BLine: yes



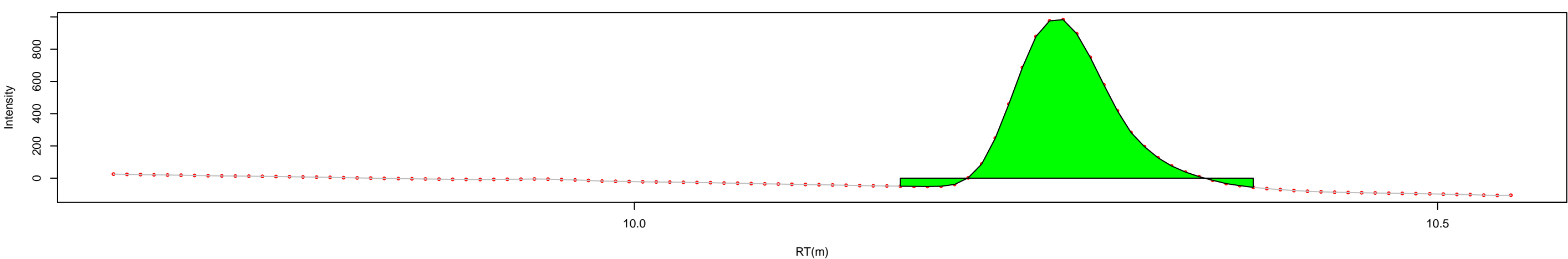
raw chromatogram | batch: 1   sample: std-11   conc: 2e+05   function: 272   mass: 542 > 136.8



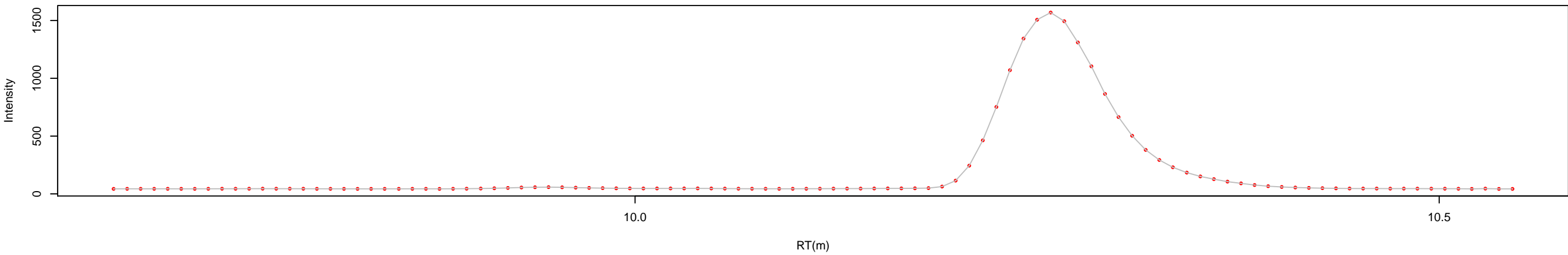
peak picking | window size: 19   iteration: 11   lp: 2   rp: 2   snr: 5   peak location: all   noise: 9.02   BLine: yes



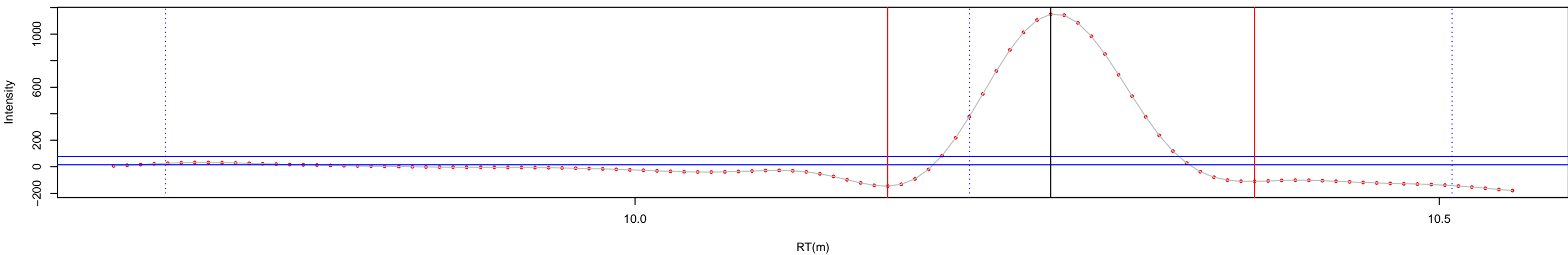
peak area | window size:3   BLine: yes



raw chromatogram | batch: 1 sample: std-12 conc: 4e+05 function: 272 mass: 542 > 136.8



peak picking | window size: 19 iteration: 11 lp: 2 rp: 2 snr: 5 peak location: all noise: 15.3 BLine: yes



peak area | window size:3 BLine: yes

