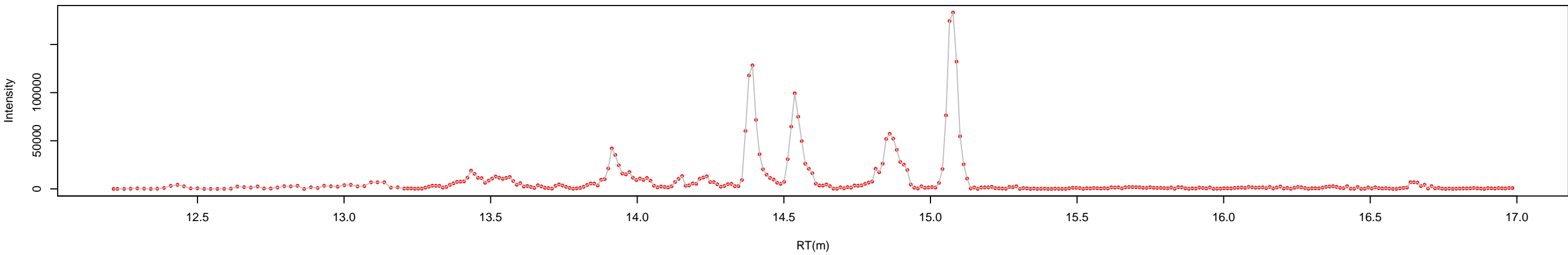
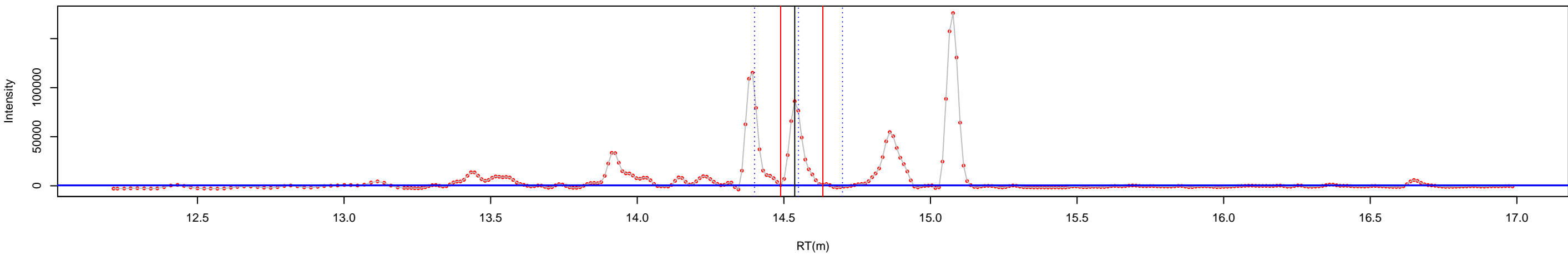


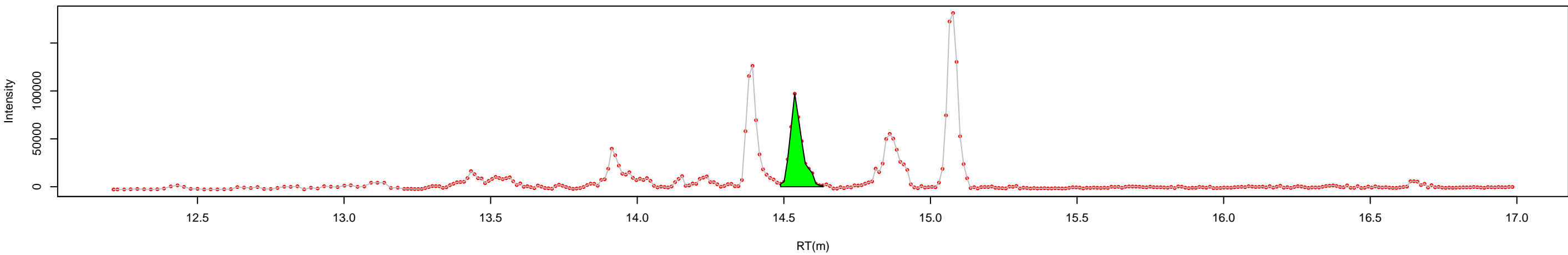
raw chromatogram | batch: 1 sample: coth10 conc: NA function: 1 mass: 389.35>389.35



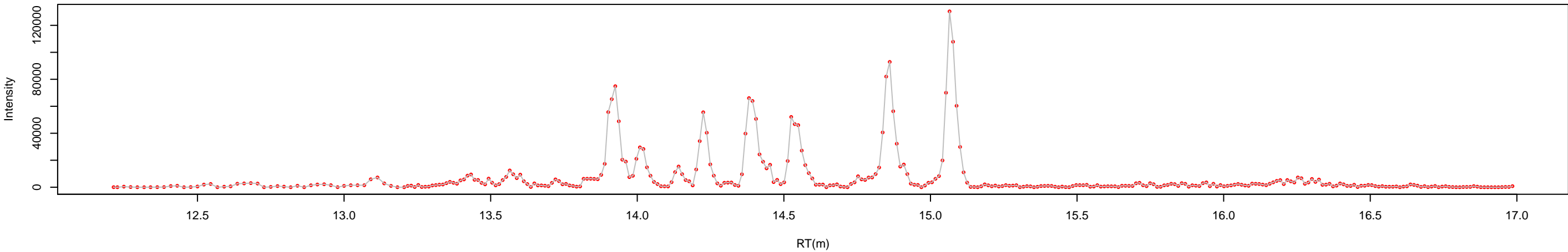
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 80.5 BLine: yes



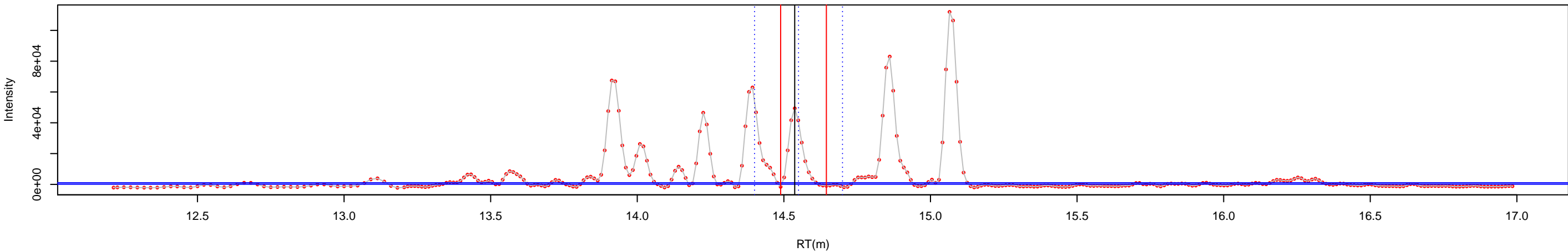
peak area | window size:3 BLine: yes



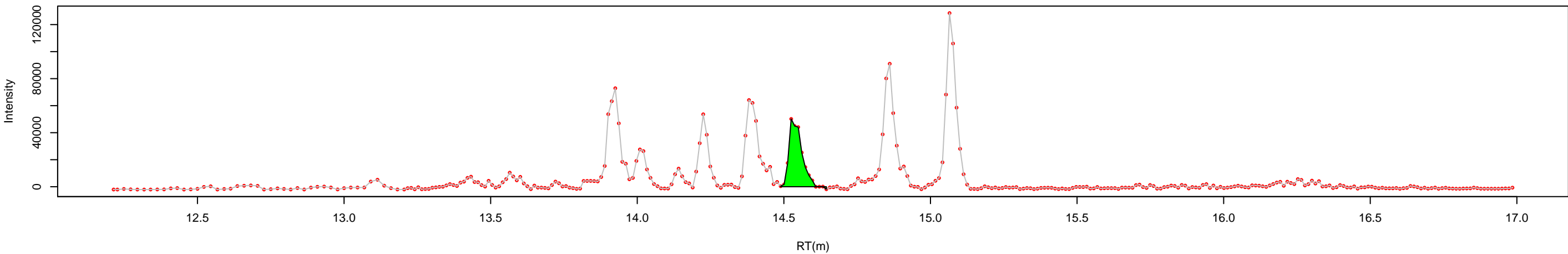
raw chromatogram | batch: 1 sample: cotn19 conc: NA function: 1 mass: 389.35>389.35



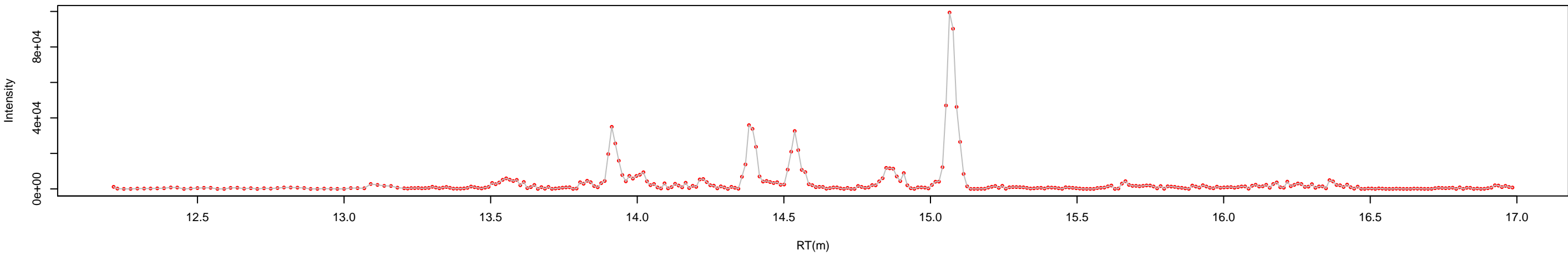
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 102 BLine: yes



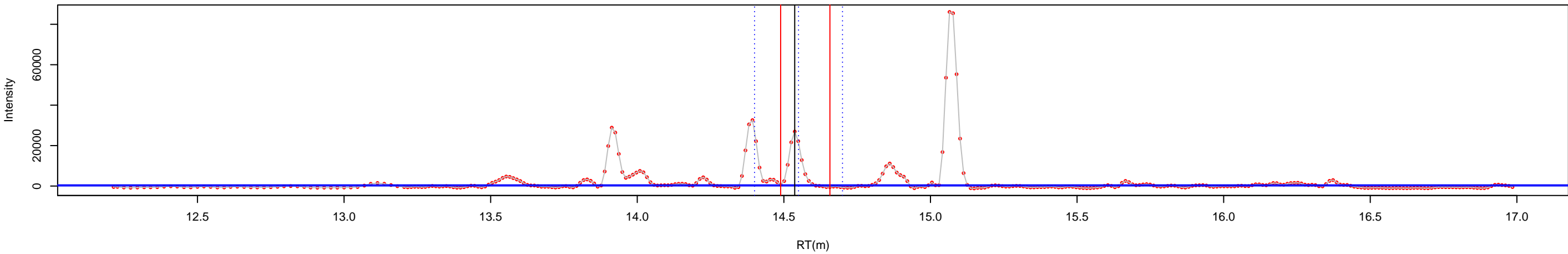
peak area | window size:3 BLine: yes



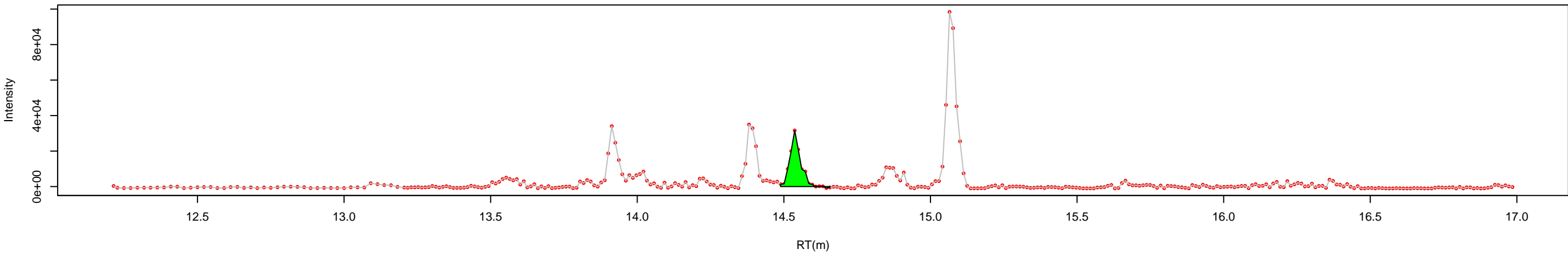
raw chromatogram | batch: 1 sample: coth11 conc: NA function: 1 mass: 389.35>389.35



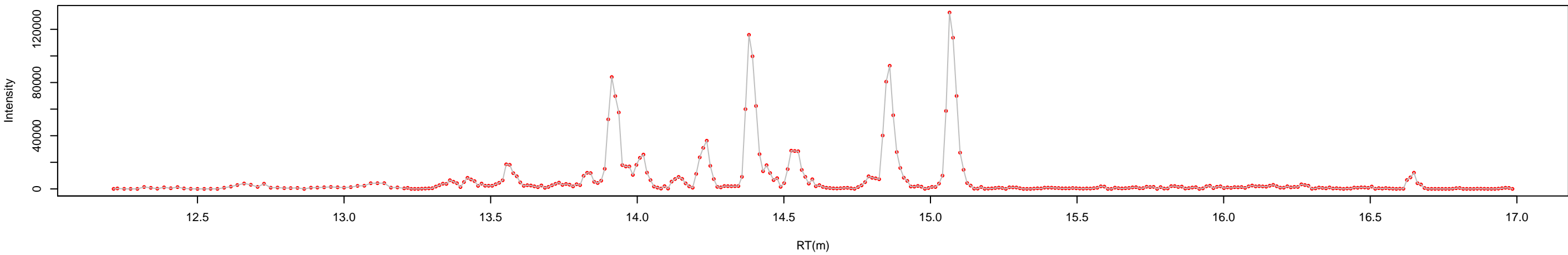
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 57.5 BLine: yes



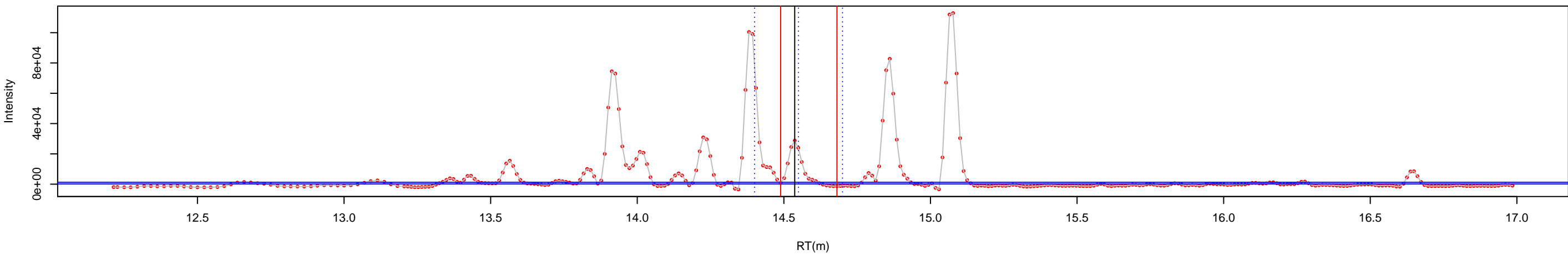
peak area | window size:3 BLine: yes



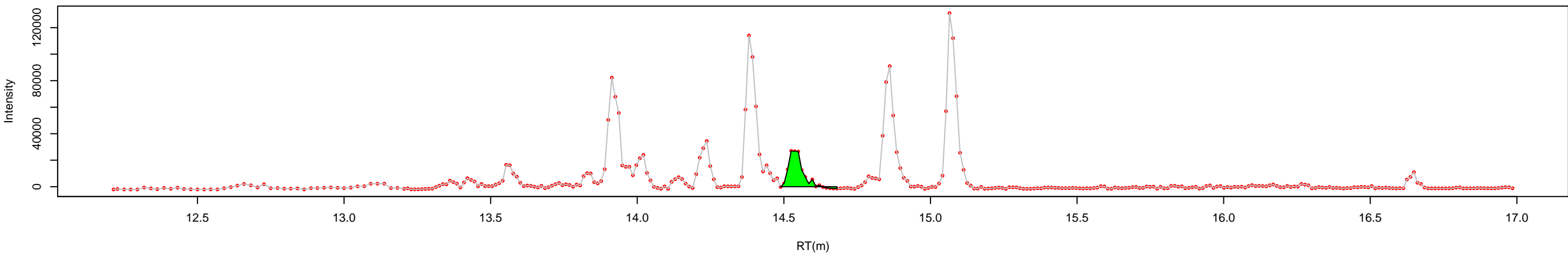
raw chromatogram | batch: 1 sample: cotn20 conc: NA function: 1 mass: 389.35>389.35



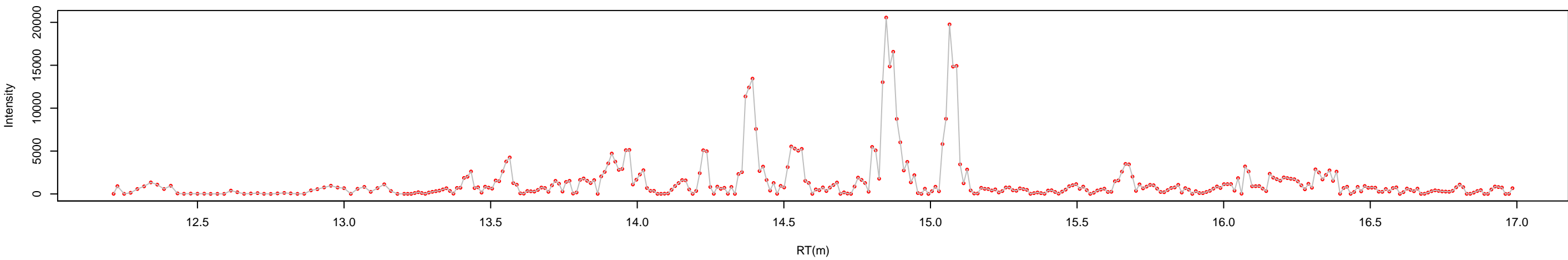
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 123 BLine: yes



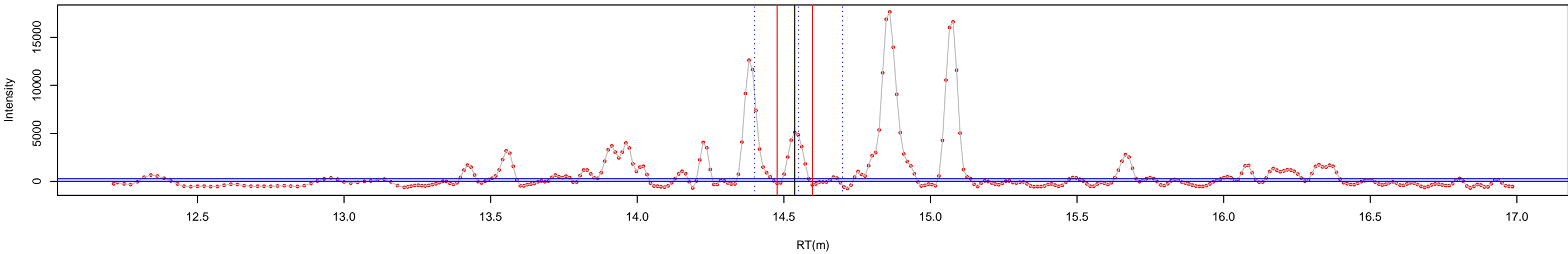
peak area | window size:3 BLine: yes



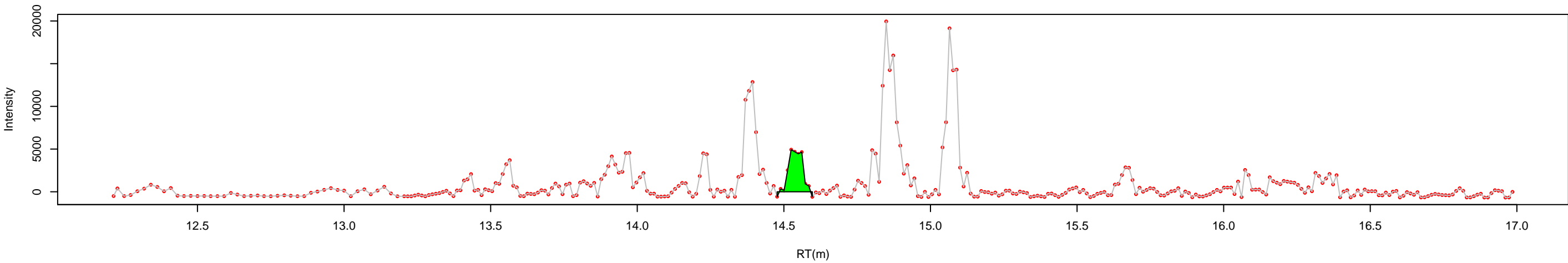
raw chromatogram | batch: 1 sample: coth12 conc: NA function: 1 mass: 389.35>389.35



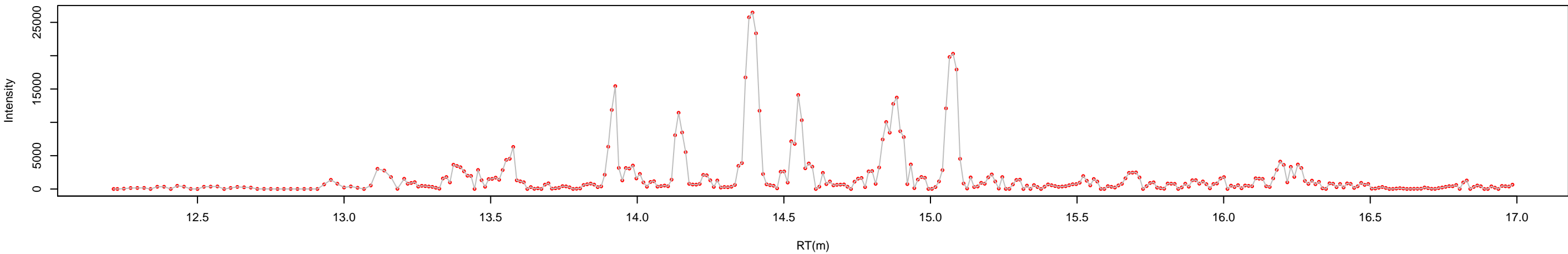
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 28.8 BLine: yes



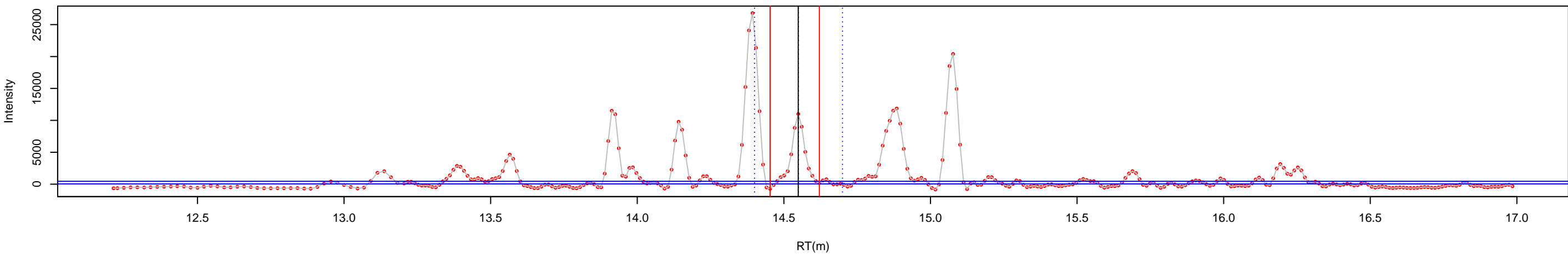
peak area | window size:3 BLine: yes



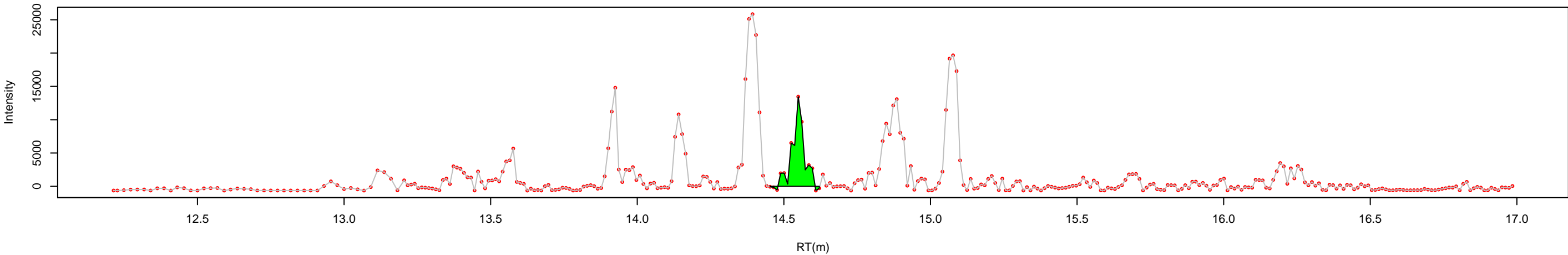
raw chromatogram | batch: 1 sample: cotn21 conc: NA function: 1 mass: 389.35>389.35



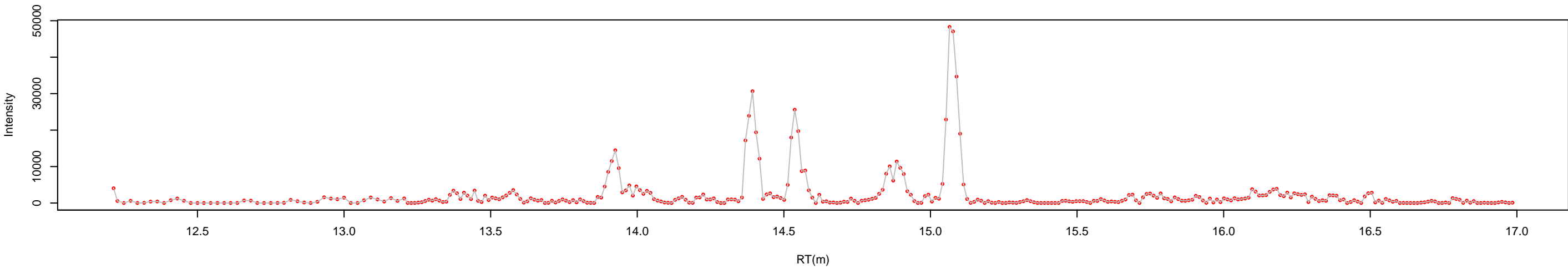
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 45.3 BLine: yes



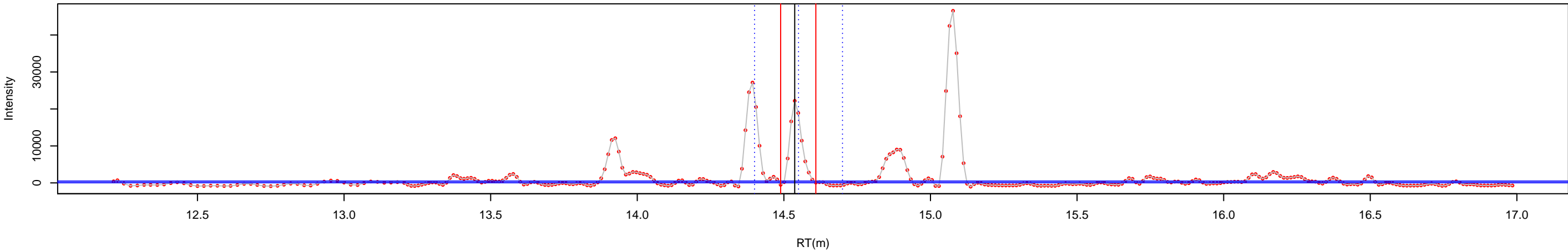
peak area | window size:3 BLine: yes



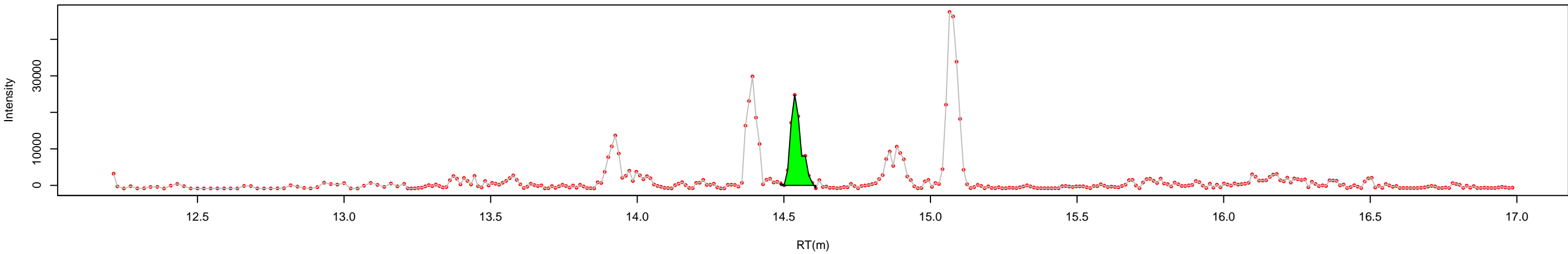
raw chromatogram | batch: 1 sample: coth13 conc: NA function: 1 mass: 389.35>389.35



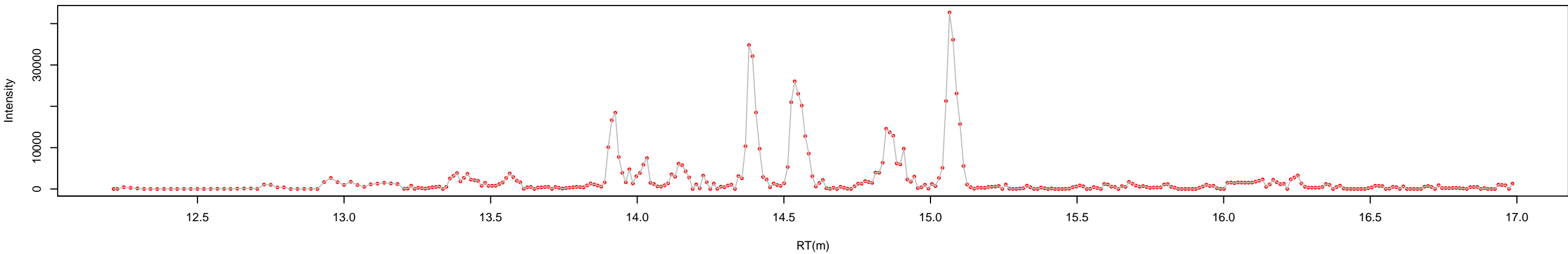
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 47.8 BLine: yes



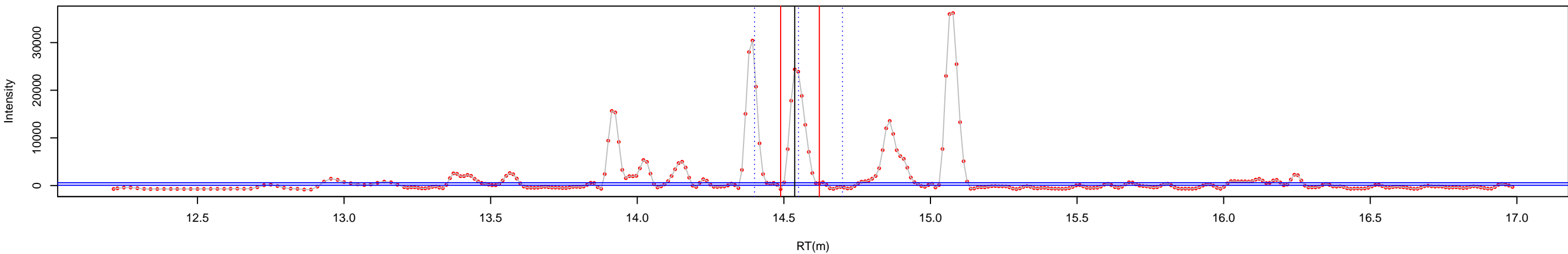
peak area | window size:3 BLine: yes



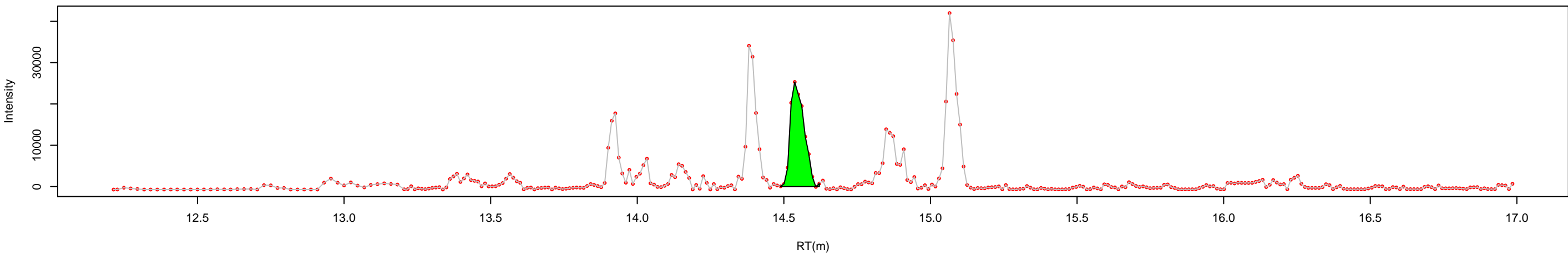
raw chromatogram | batch: 1 sample: cotn22 conc: NA function: 1 mass: 389.35>389.35



peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 58.8 BLine: yes

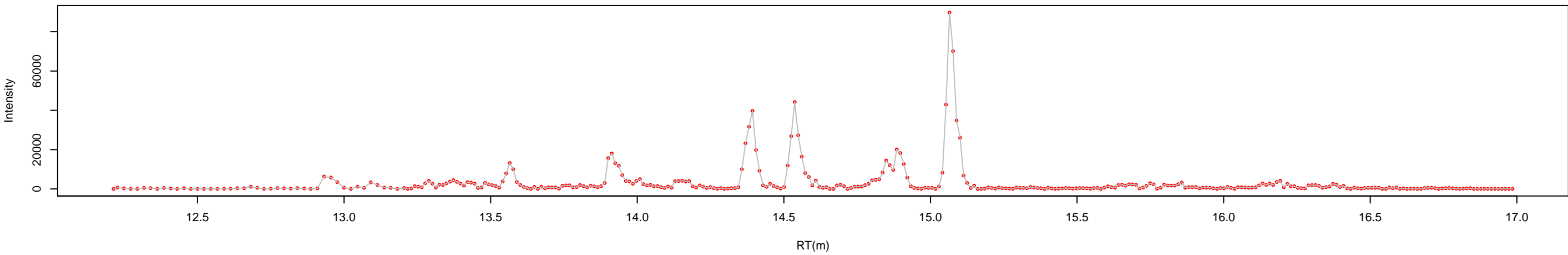


peak area | window size:3 BLine: yes

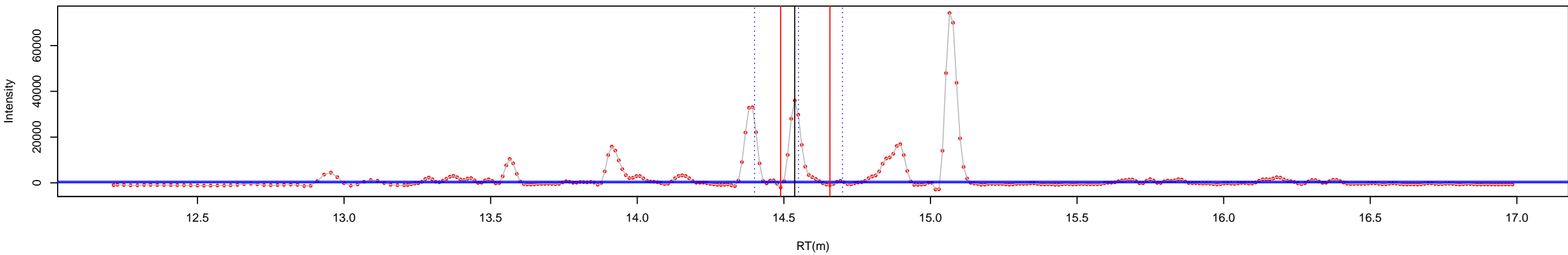




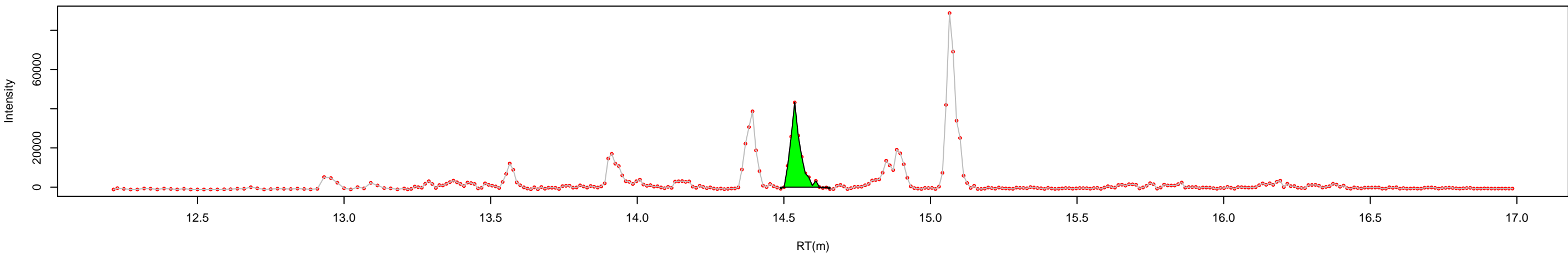
raw chromatogram | batch: 1 sample: coth14 conc: NA function: 1 mass: 389.35>389.35



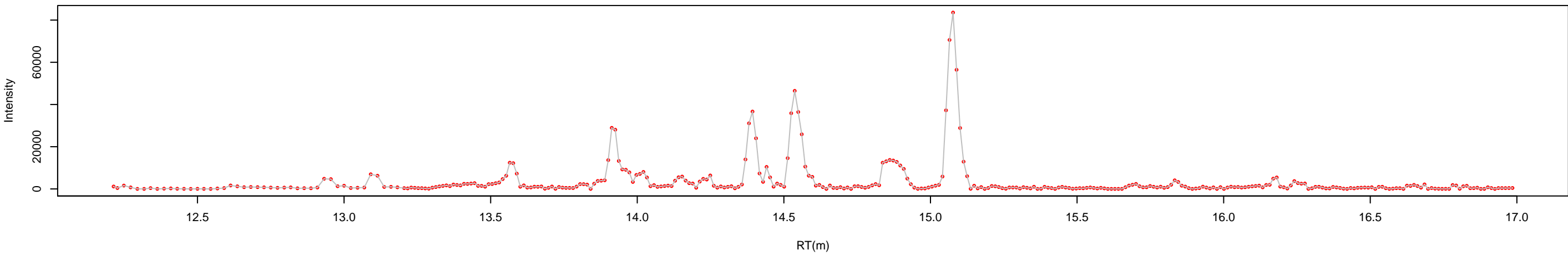
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 66 BLine: yes



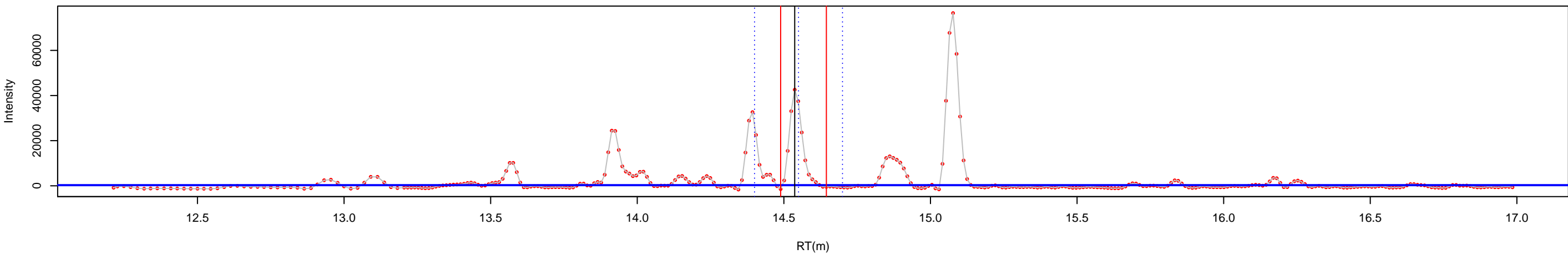
peak area | window size:3 BLine: yes



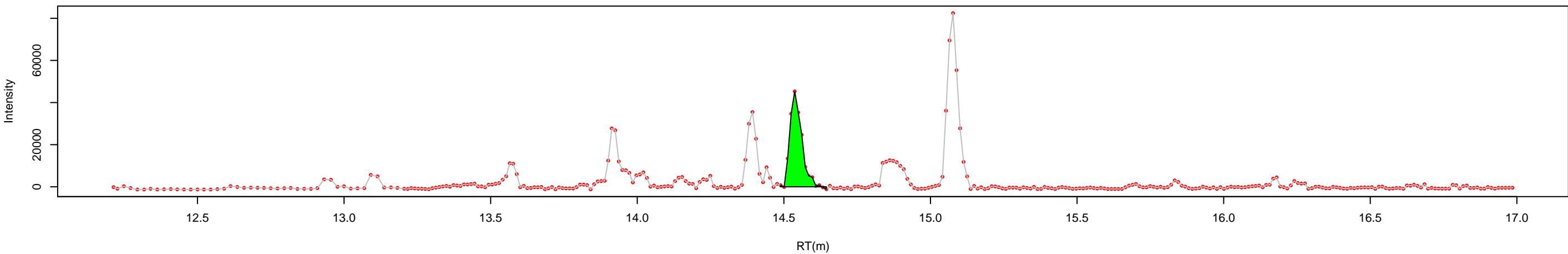
raw chromatogram | batch: 1 sample: cotn23 conc: NA function: 1 mass: 389.35>389.35



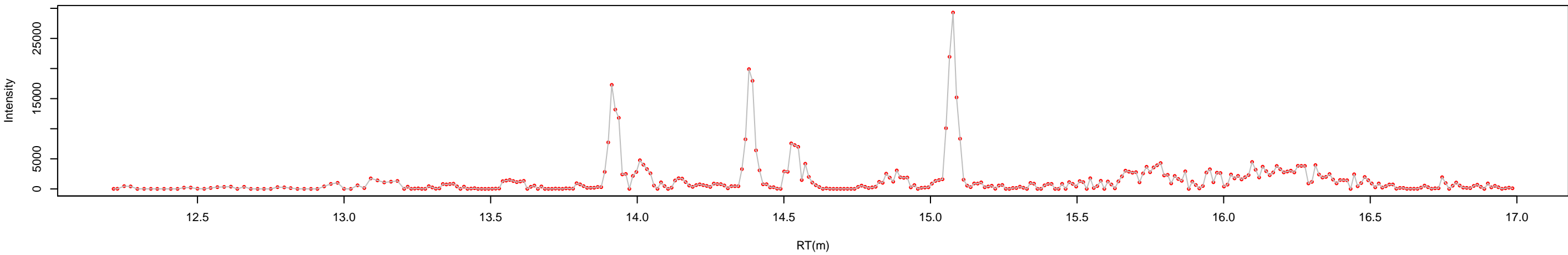
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 51.5 BLine: yes



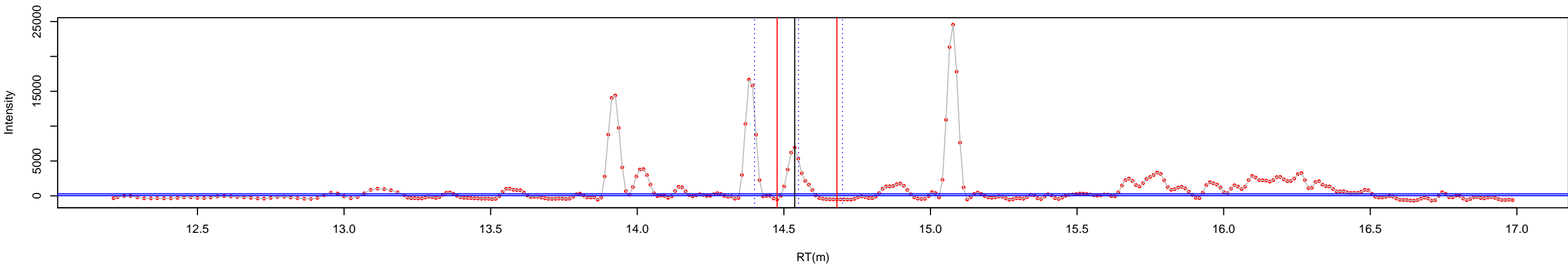
peak area | window size:3 BLine: yes



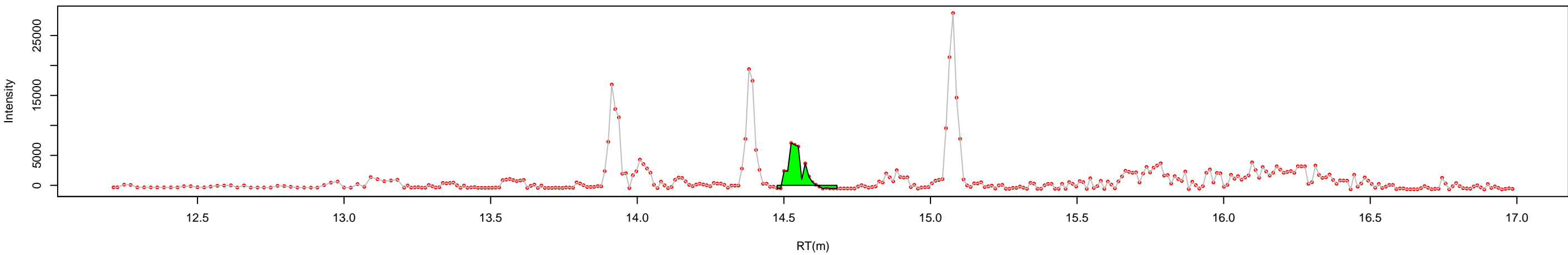
raw chromatogram | batch: 1 sample: coth15 conc: NA function: 1 mass: 389.35>389.35



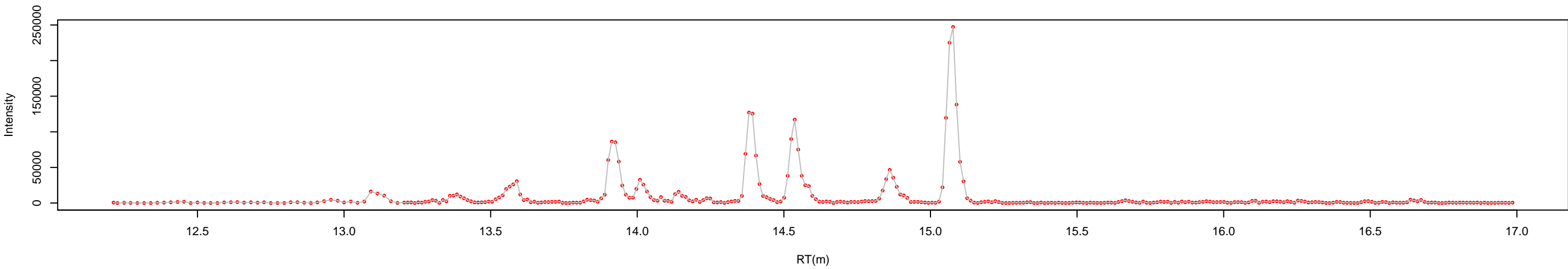
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 28.9 BLine: yes



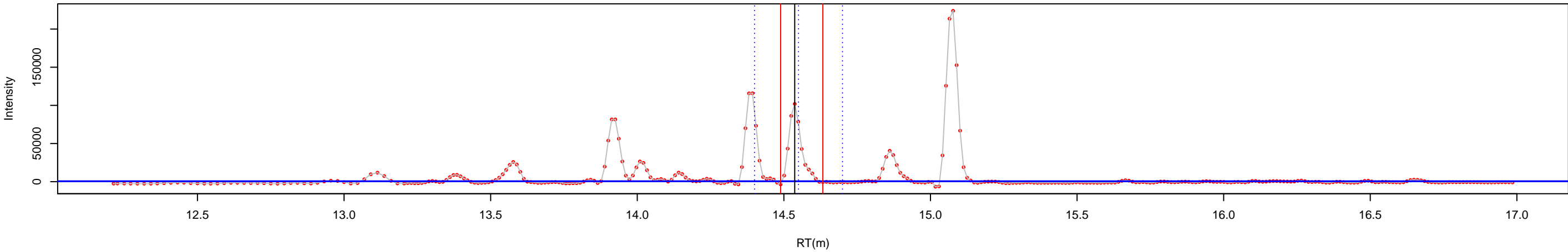
peak area | window size:3 BLine: yes



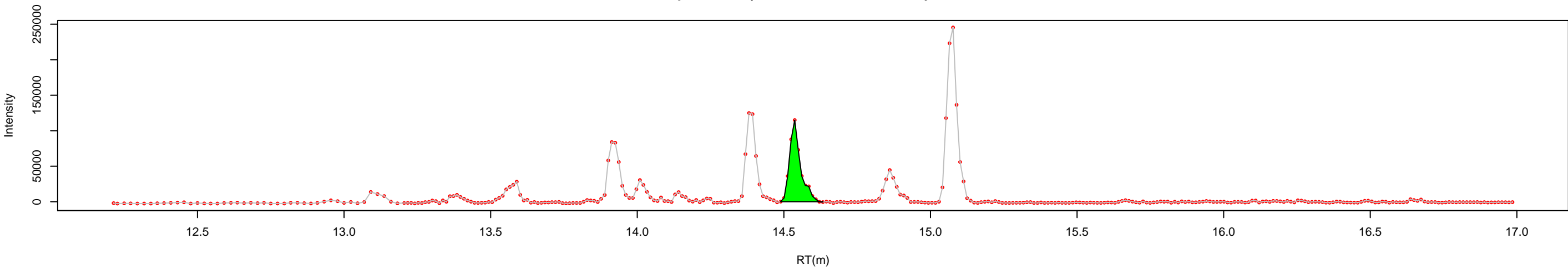
raw chromatogram | batch: 1 sample: cotn24 conc: NA function: 1 mass: 389.35>389.35



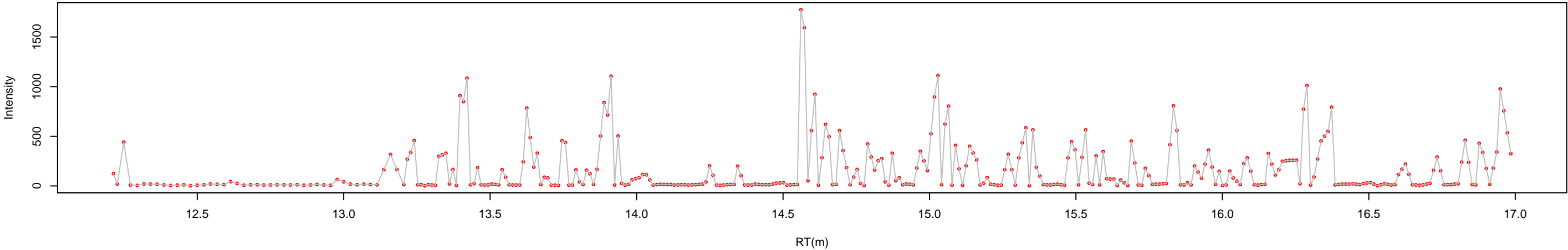
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 103 BLine: yes



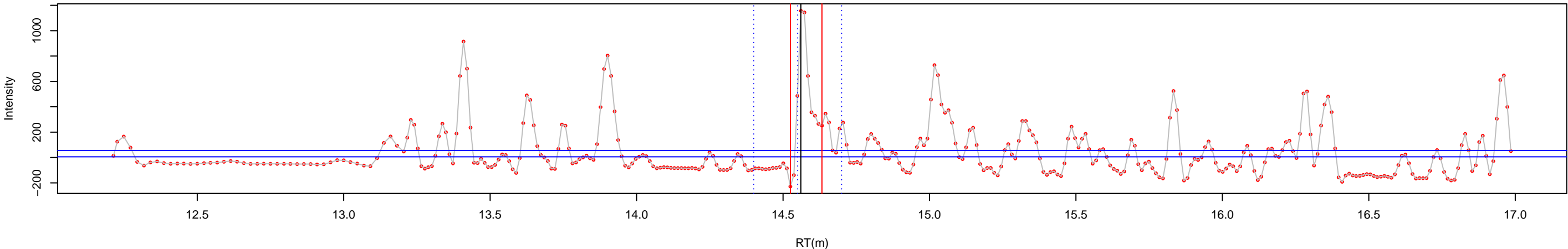
peak area | window size:3 BLine: yes



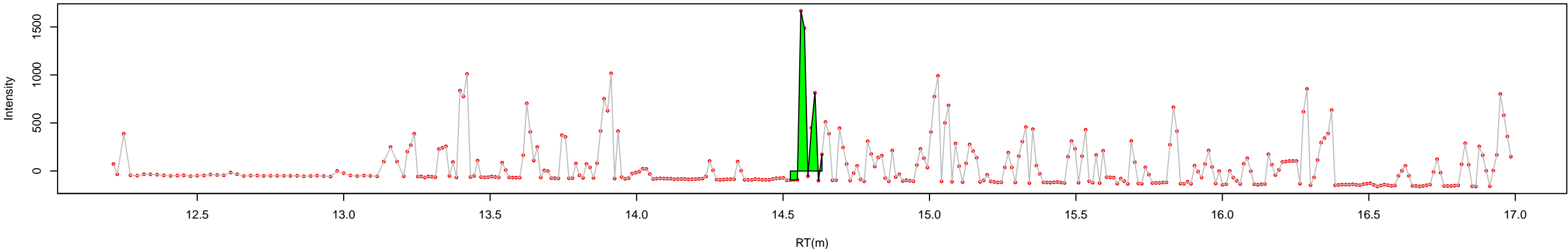
raw chromatogram | batch: 1   sample: std0-10ul-1   conc: 0.001   function: 1   mass: 389.35>389.35



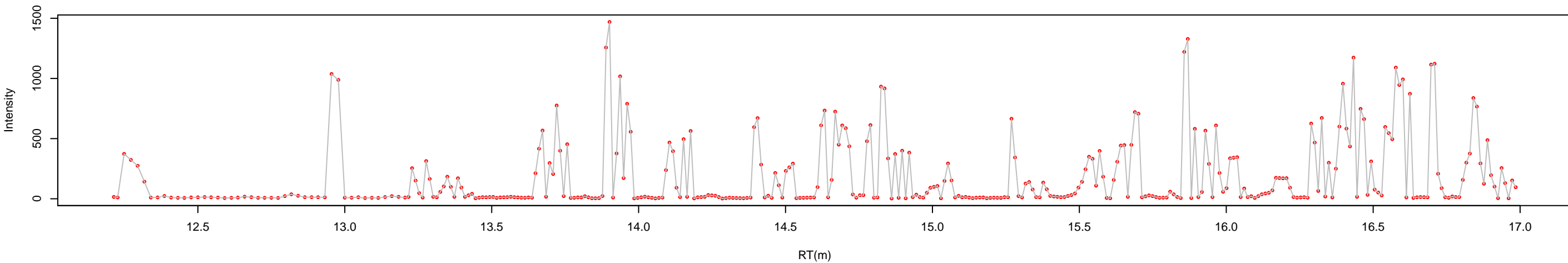
peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 5.57   BLine: yes



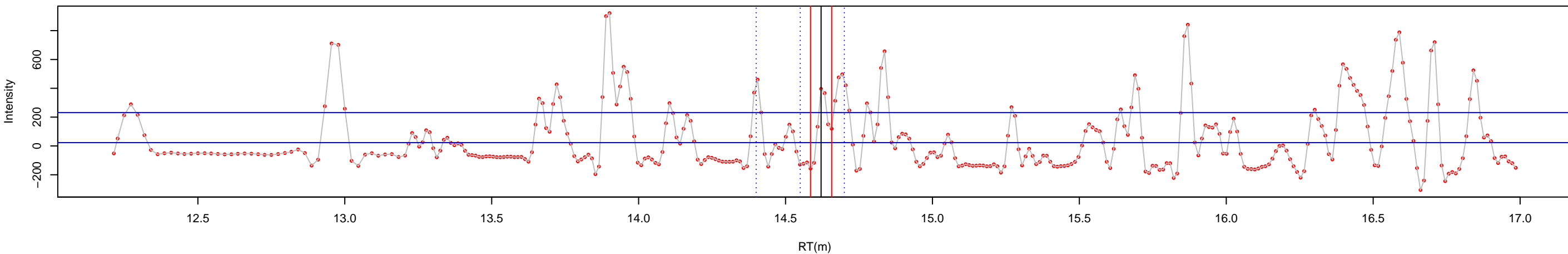
peak area | window size:3   BLine: yes



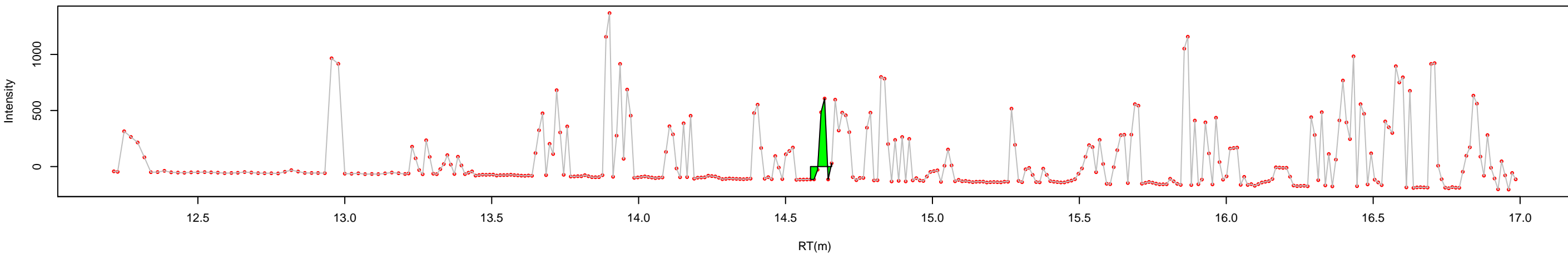
raw chromatogram | batch: 1 sample: std1-10ul-1 conc: 0.002 function: 1 mass: 389.35>389.35



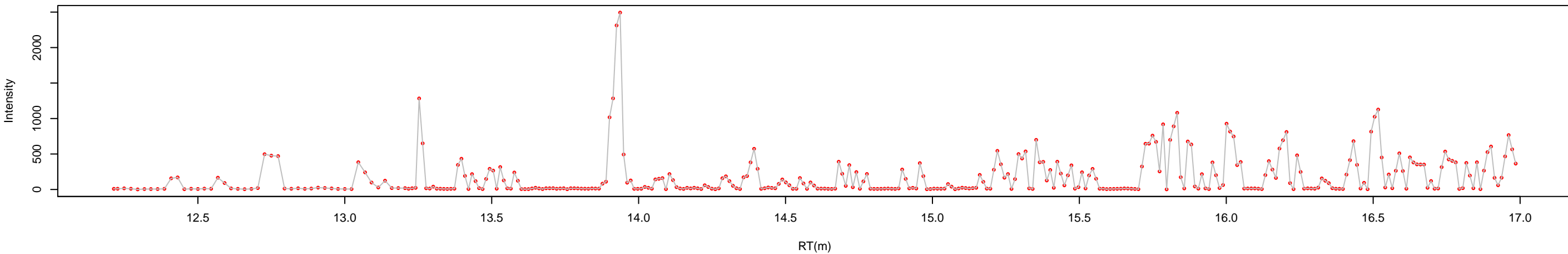
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 23.1 BLine: yes



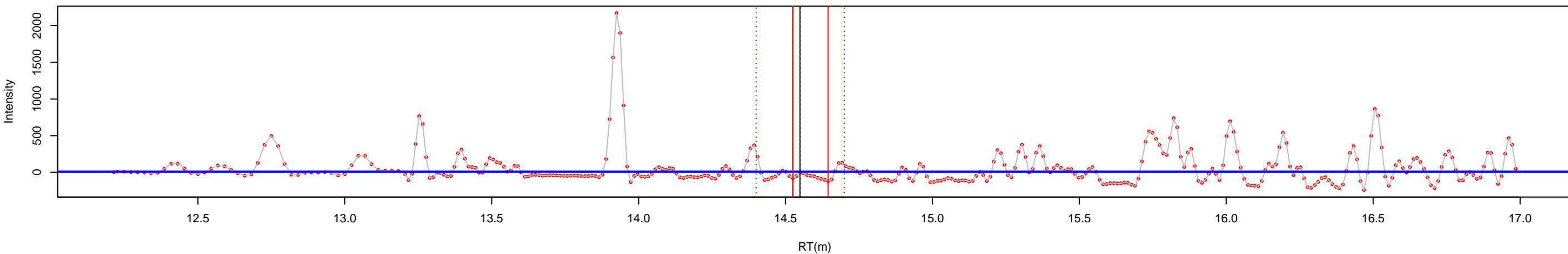
peak area | window size:3 BLine: yes



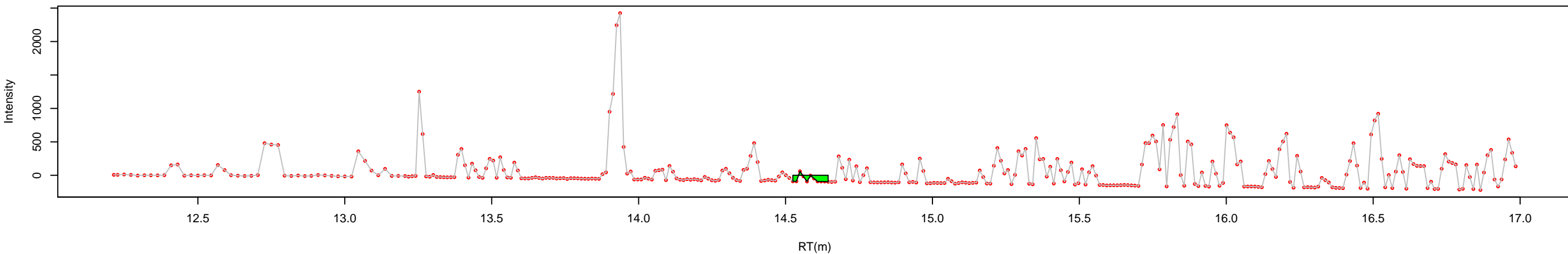
raw chromatogram | batch: 1 sample: std2-10ul-1 conc: 0.005 function: 1 mass: 389.35>389.35



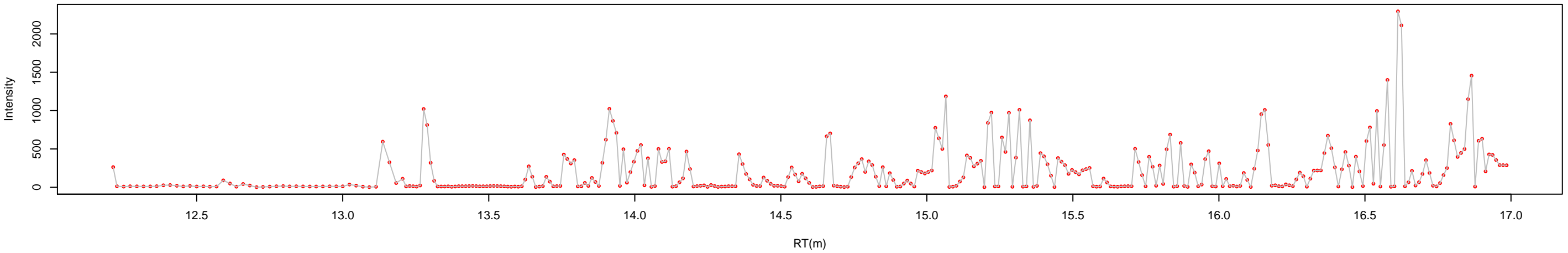
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 1.61 BLine: yes



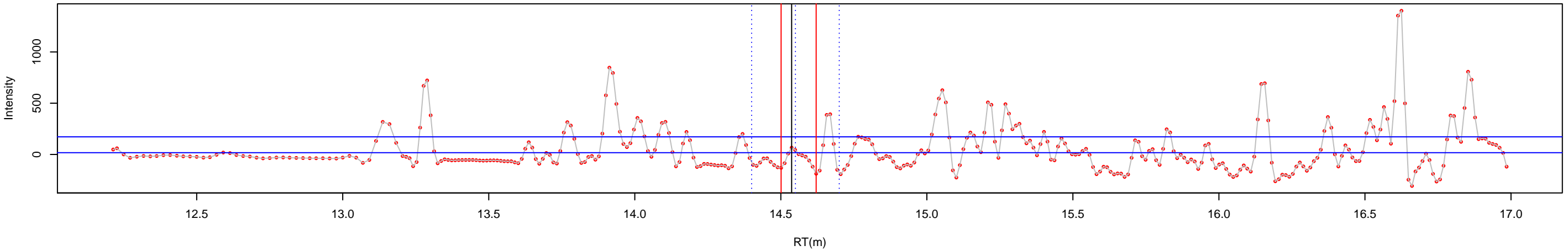
peak area | window size:3 BLine: yes



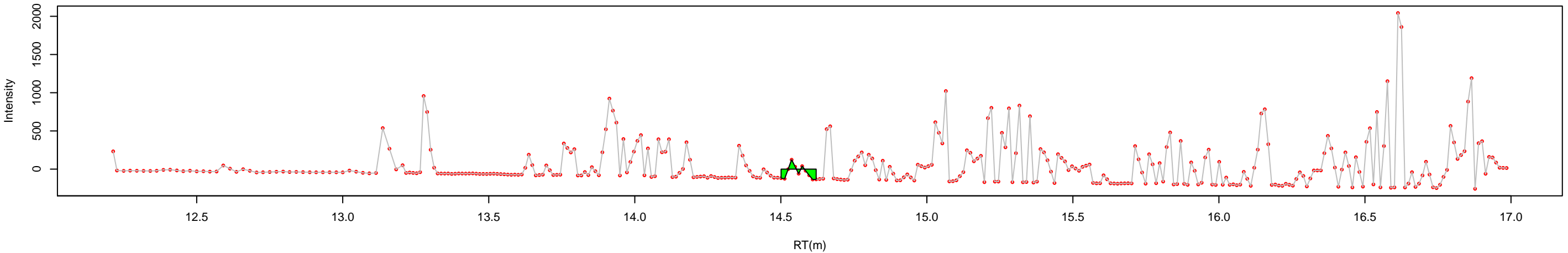
raw chromatogram | batch: 1 sample: std3-10ul-1 conc: 0.01 function: 1 mass: 389.35>389.35



peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 17.2 BLine: yes

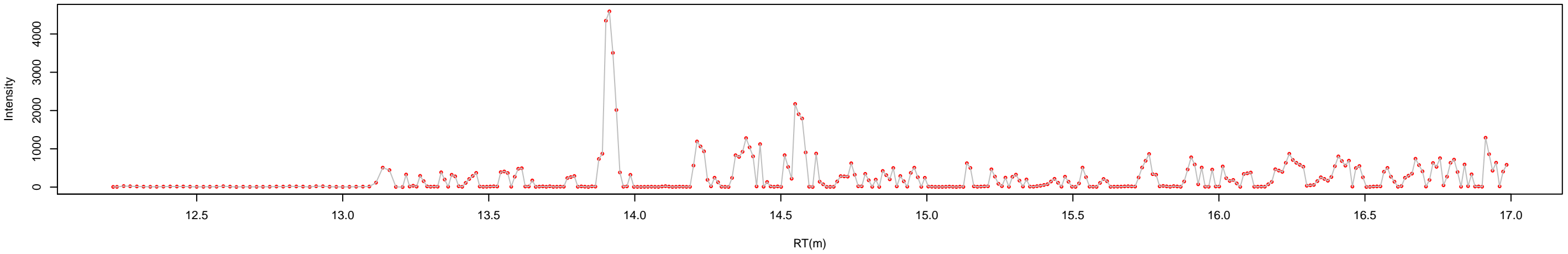


peak area | window size:3 BLine: yes

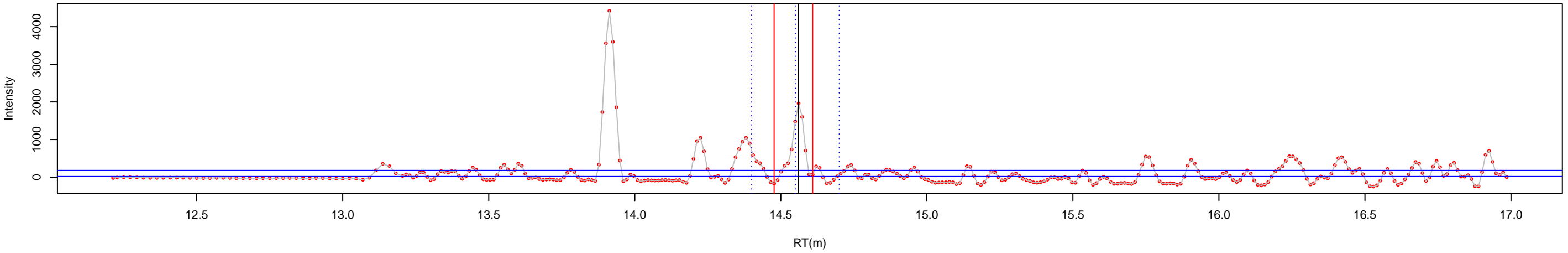




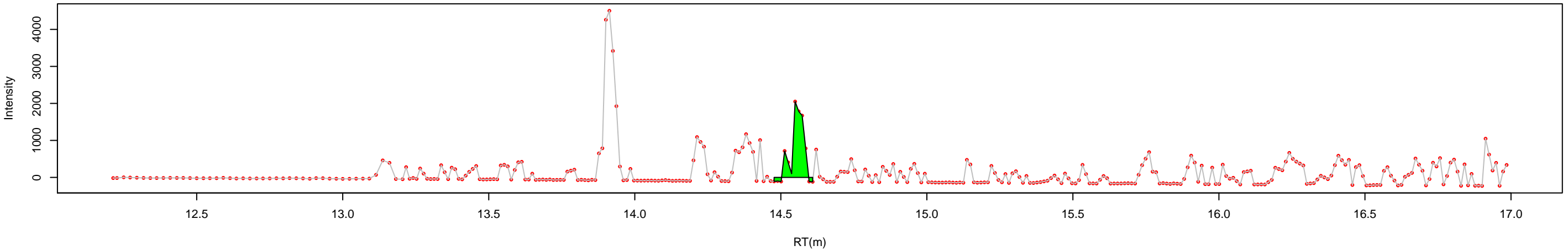
raw chromatogram | batch: 1 sample: std4-10ul-1 conc: 0.02 function: 1 mass: 389.35>389.35



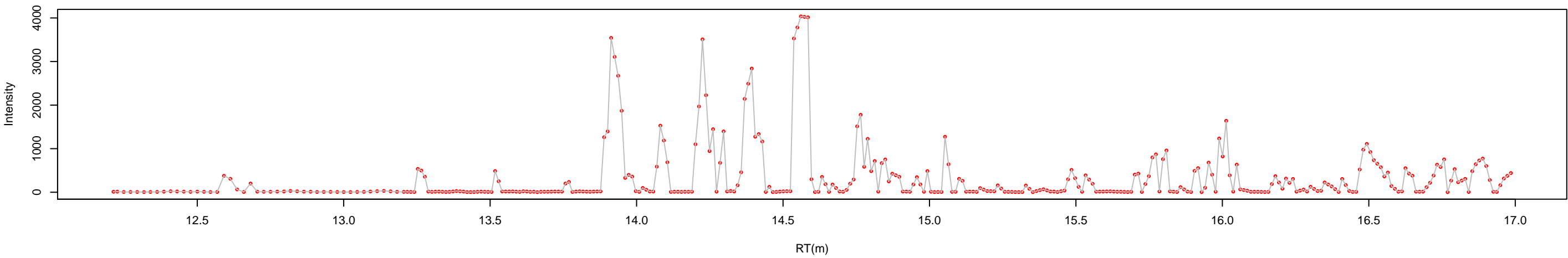
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 18 BLine: yes



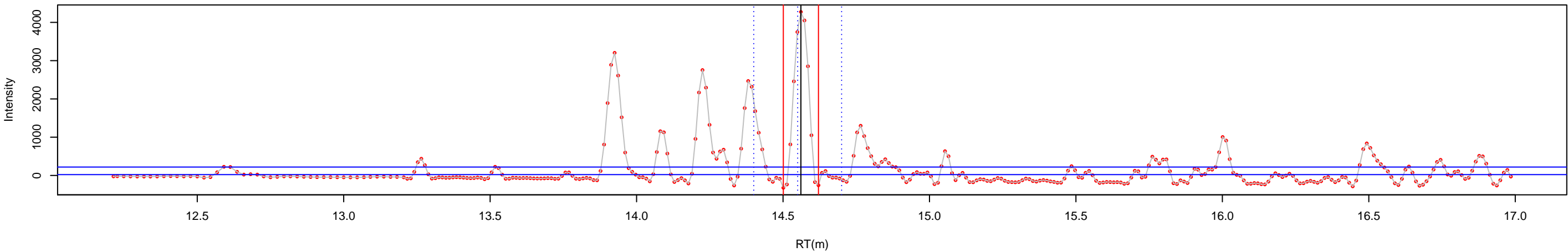
peak area | window size:3 BLine: yes



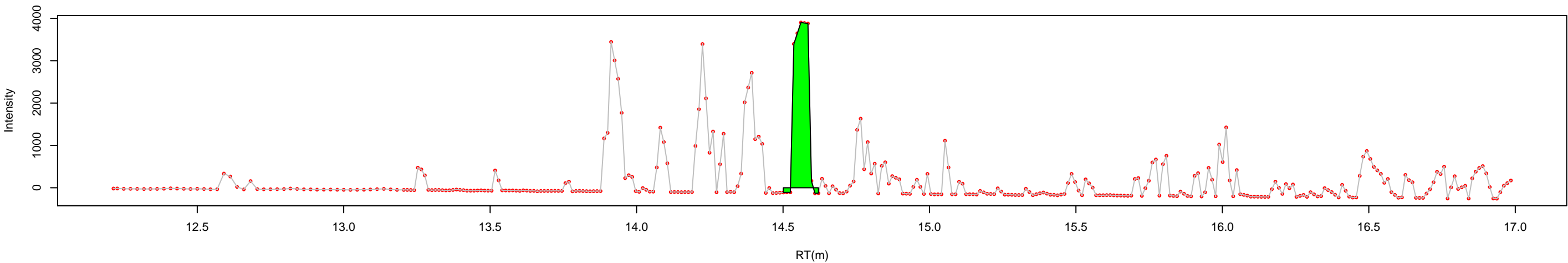
raw chromatogram | batch: 1 sample: std5-10ul-1 conc: 0.05 function: 1 mass: 389.35>389.35



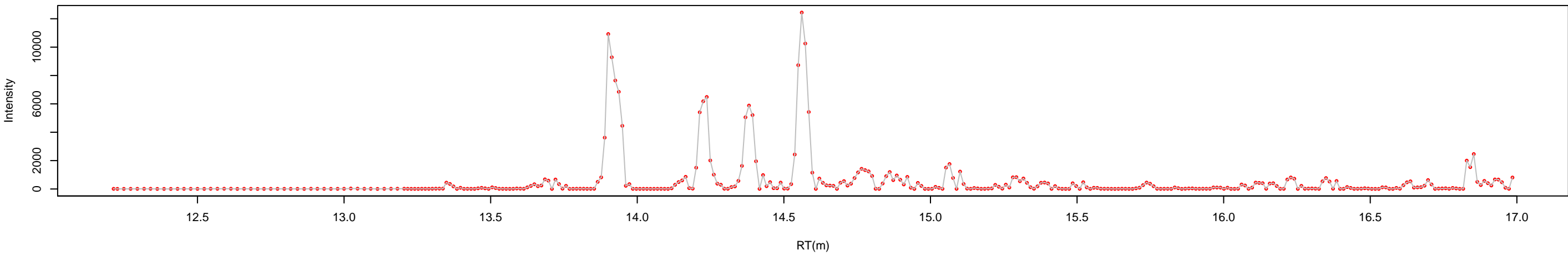
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 22 BLine: yes



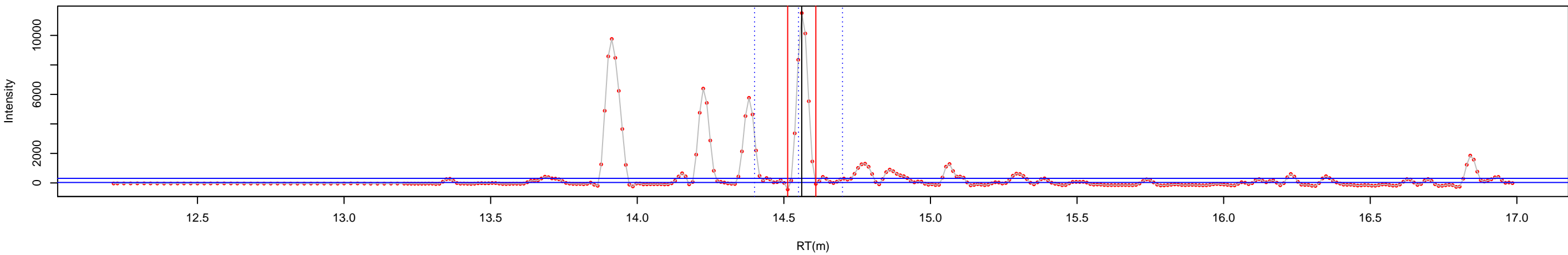
peak area | window size:3 BLine: yes



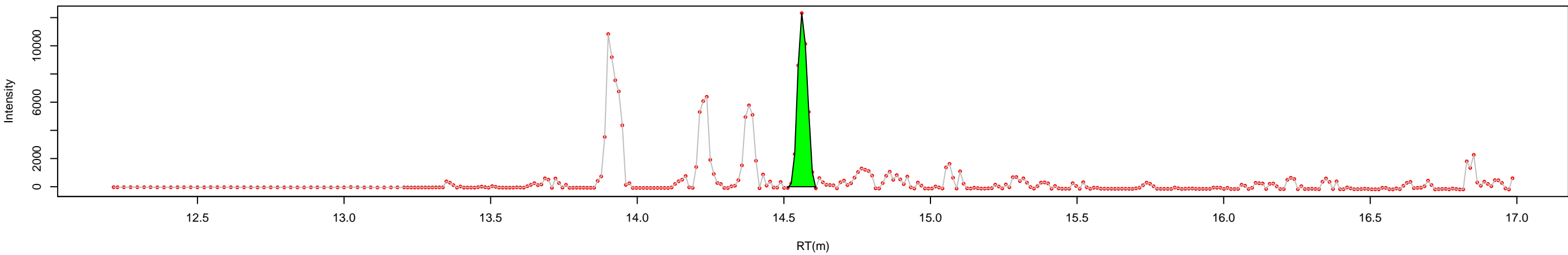
raw chromatogram | batch: 1 sample: std6-10ul-1 conc: 0.1 function: 1 mass: 389.35>389.35



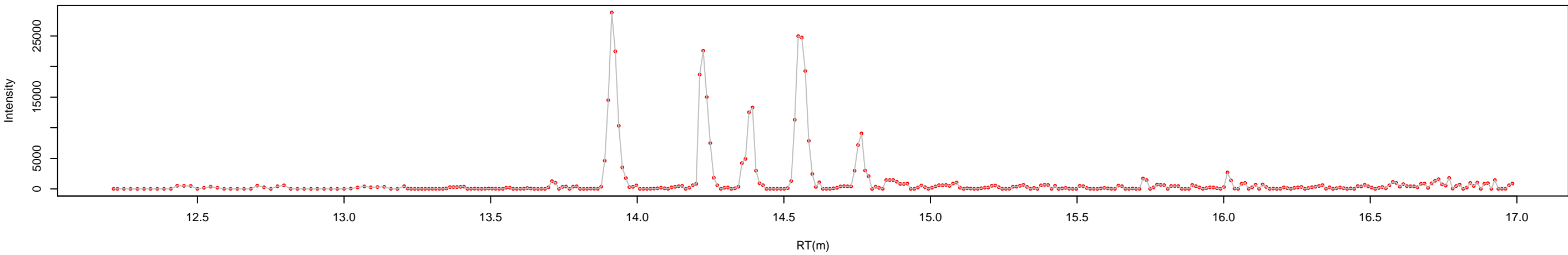
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 31 BLine: yes



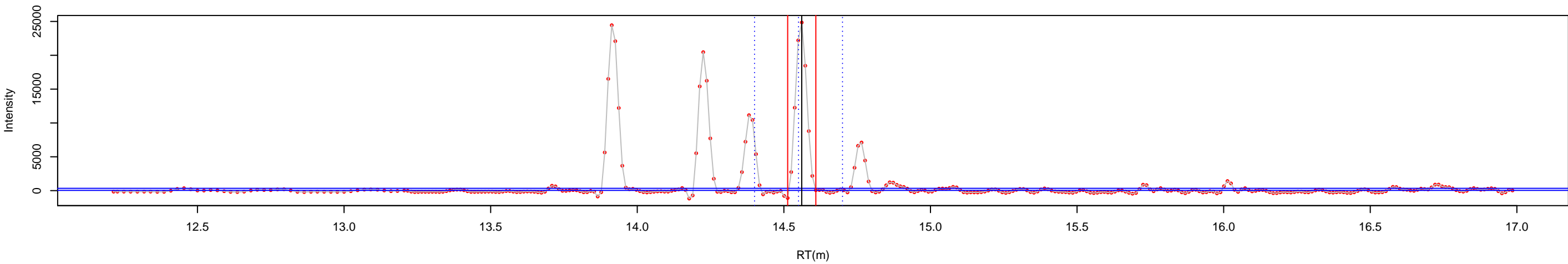
peak area | window size:3 BLine: yes



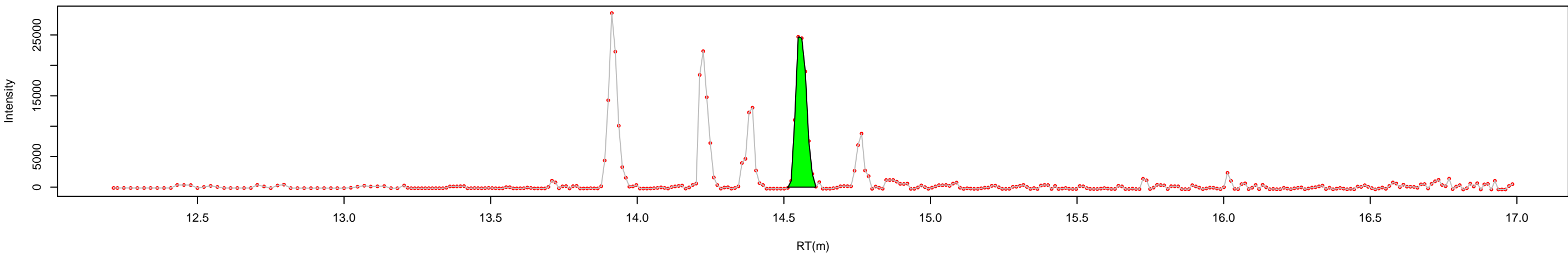
raw chromatogram | batch: 1 sample: std7-10ul-1 conc: 0.2 function: 1 mass: 389.35>389.35



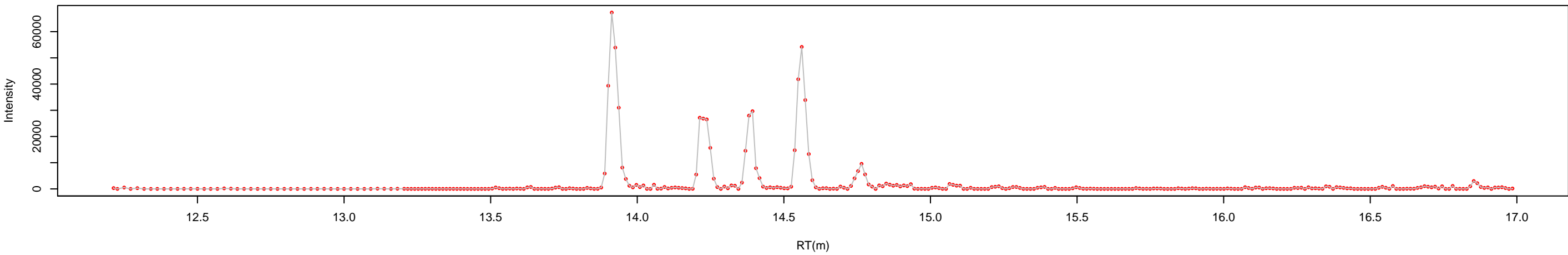
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 33.7 BLine: yes



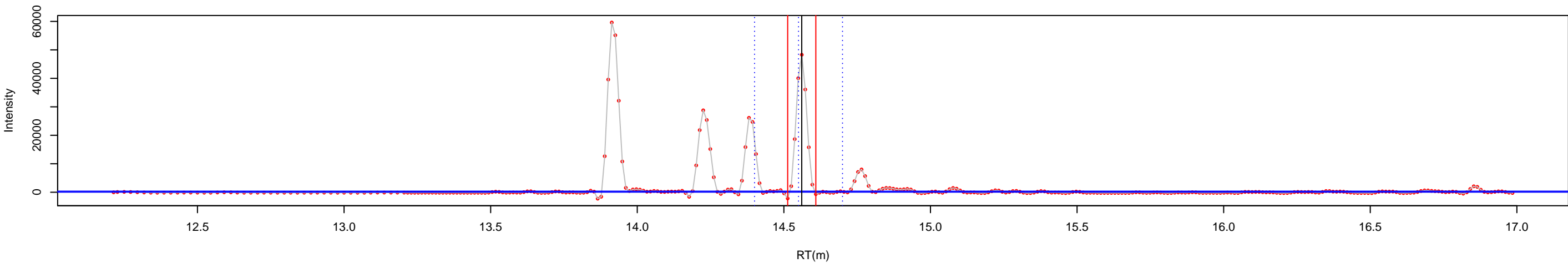
peak area | window size:3 BLine: yes



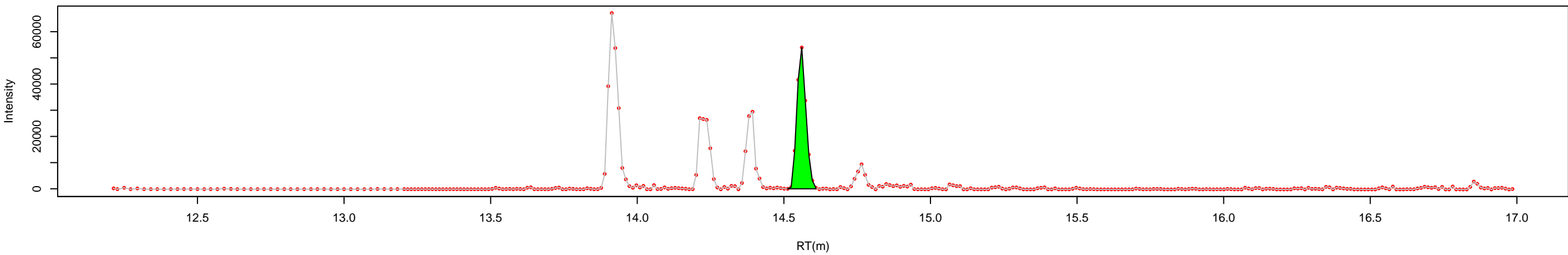
raw chromatogram | batch: 1 sample: std8-10ul-1 conc: 0.5 function: 1 mass: 389.35>389.35



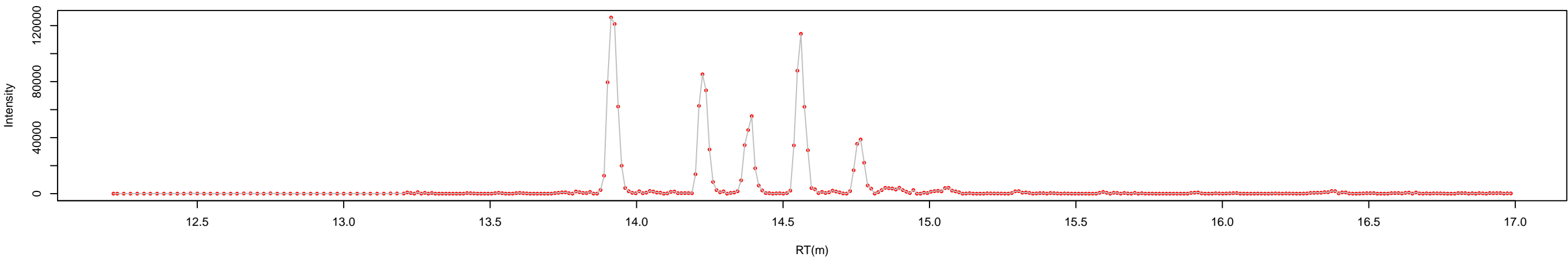
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 36.8 BLine: yes



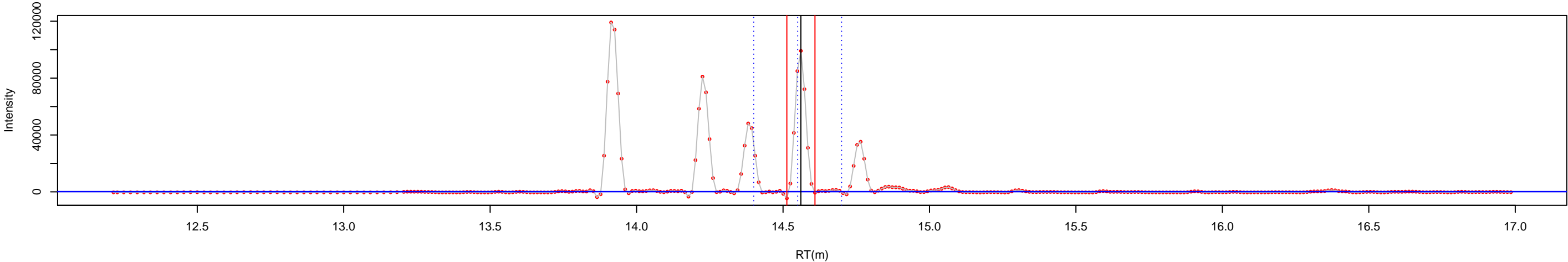
peak area | window size:3 BLine: yes



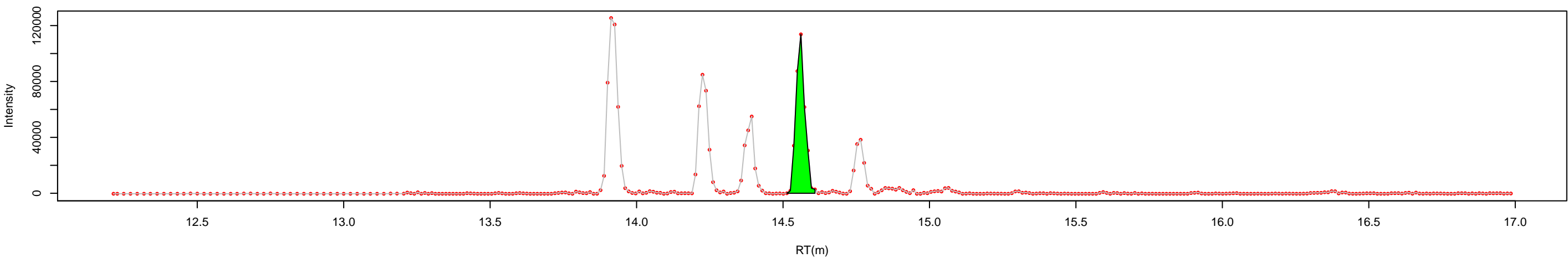
raw chromatogram | batch: 1 sample: std9-10ul-1 conc: 1 function: 1 mass: 389.35>389.35



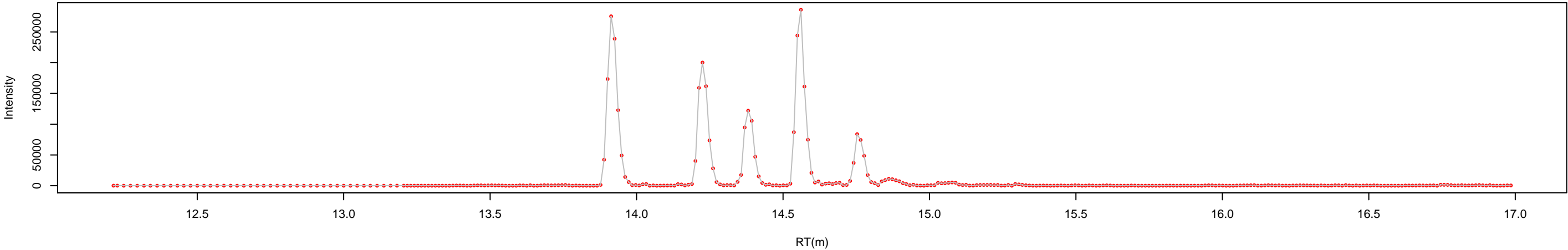
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 22.5 BLine: yes



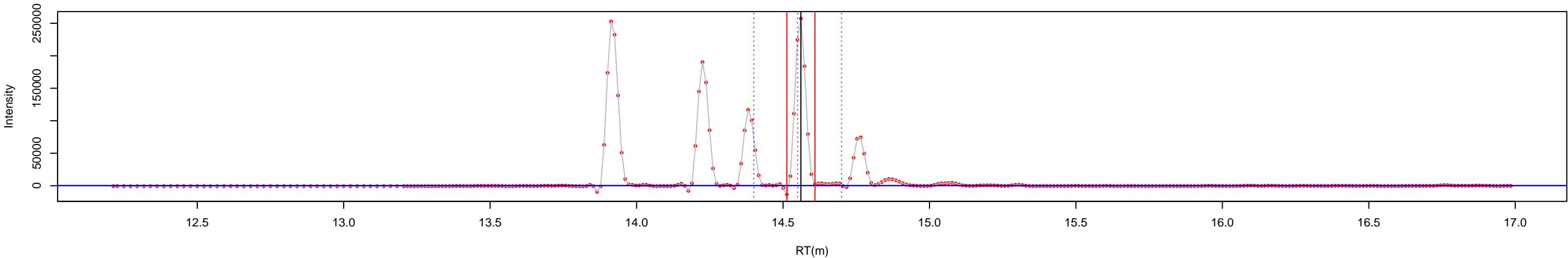
peak area | window size:3 BLine: yes



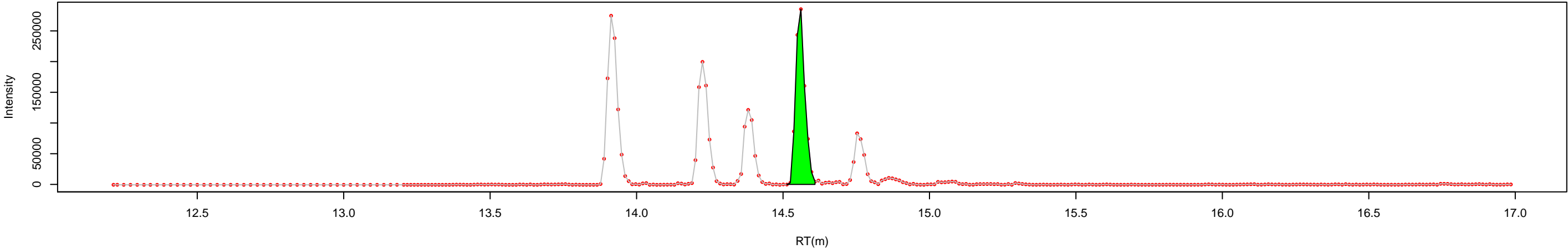
raw chromatogram | batch: 1   sample: std10-10ul-1   conc: 2   function: 1   mass: 389.35>389.35



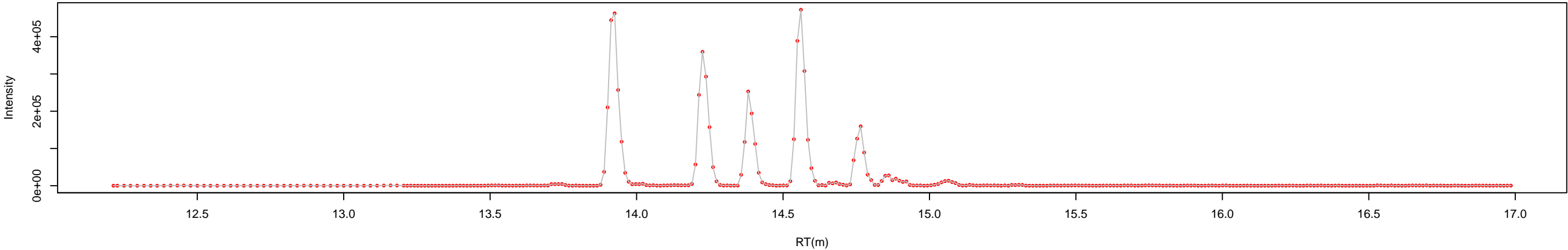
peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 44.6   BLine: yes



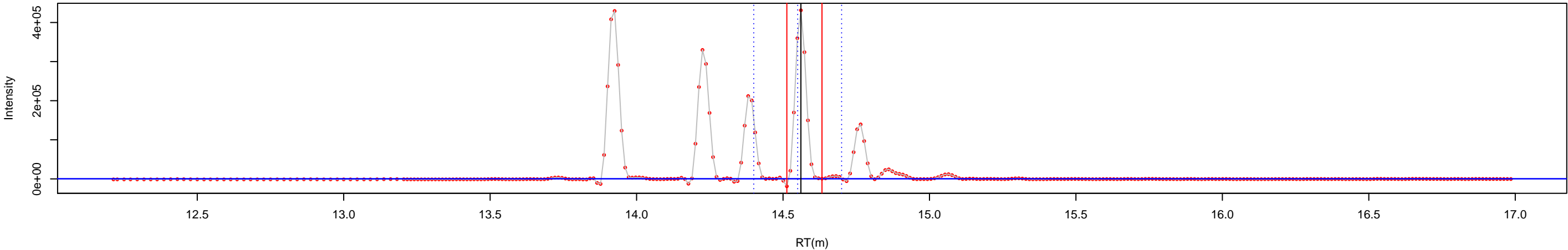
peak area | window size:3   BLine: yes



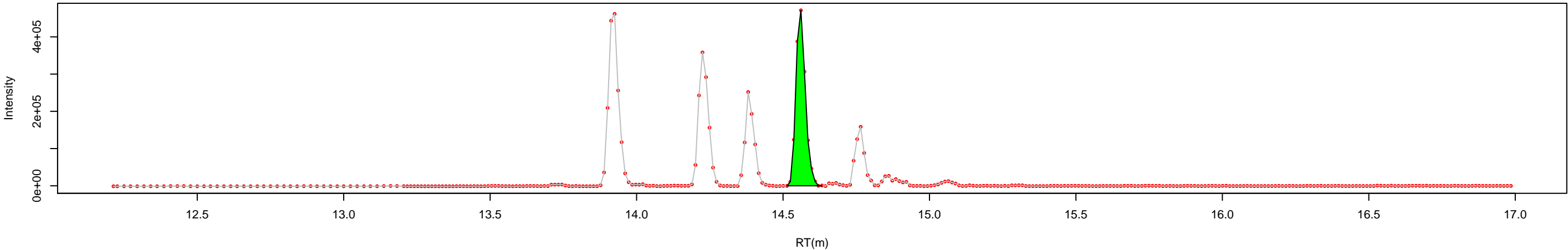
raw chromatogram | batch: 1   sample: std11-10ul-1   conc: 5   function: 1   mass: 389.35>389.35



peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 56.7   BLine: yes

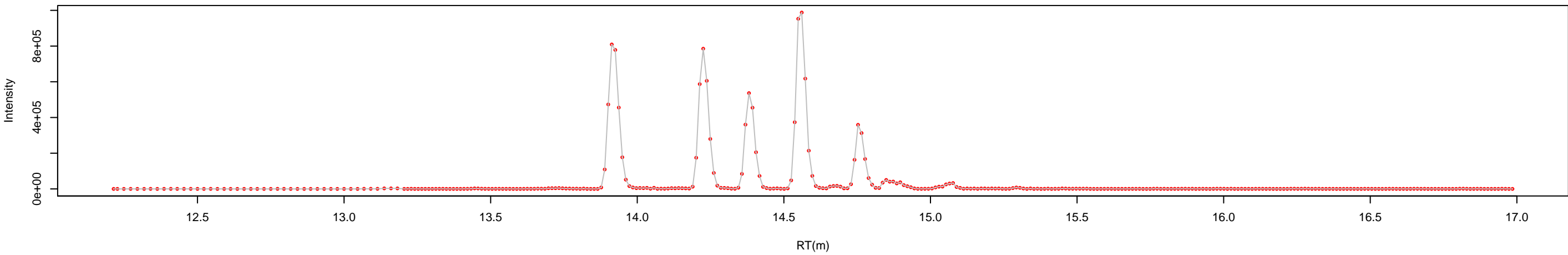


peak area | window size:3   BLine: yes

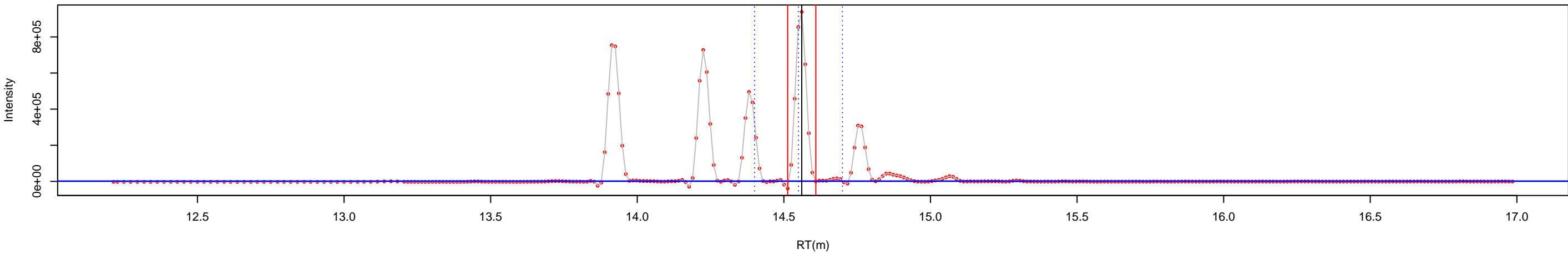




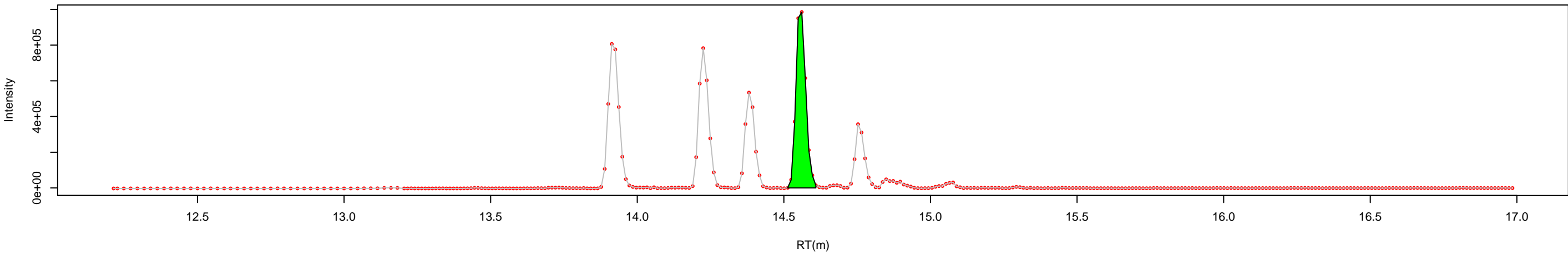
raw chromatogram | batch: 1 sample: std12-10ul-1 conc: 10 function: 1 mass: 389.35>389.35



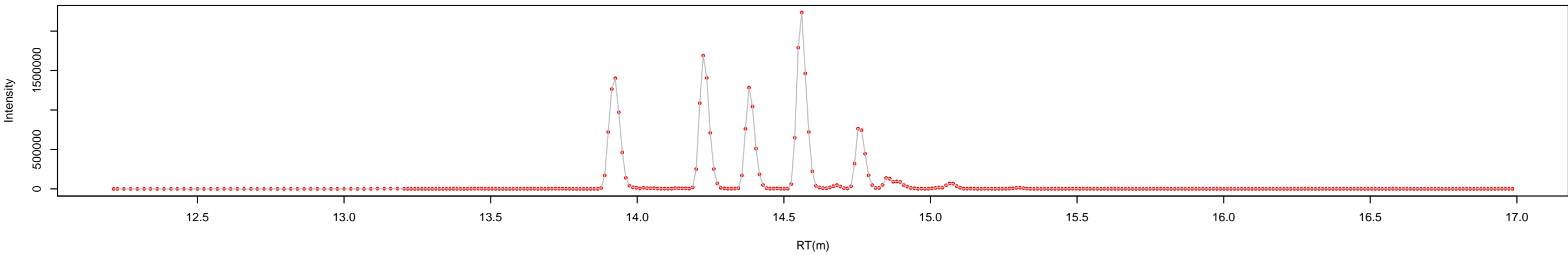
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 254 BLine: yes



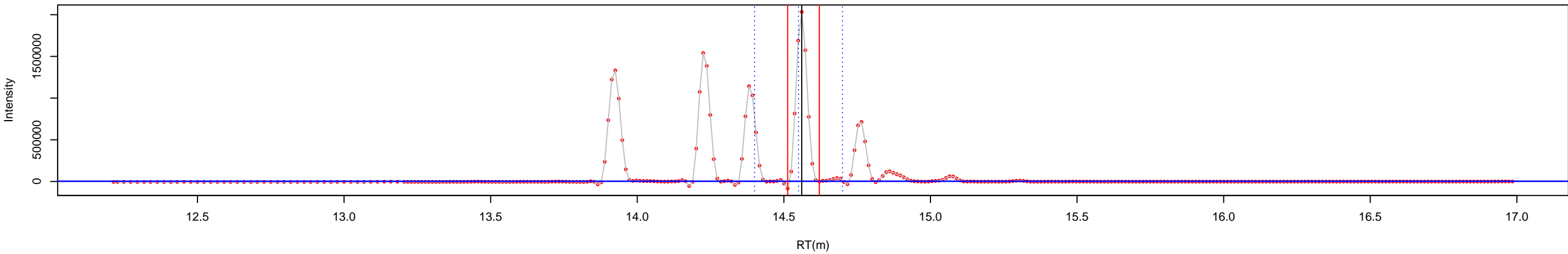
peak area | window size:3 BLine: yes



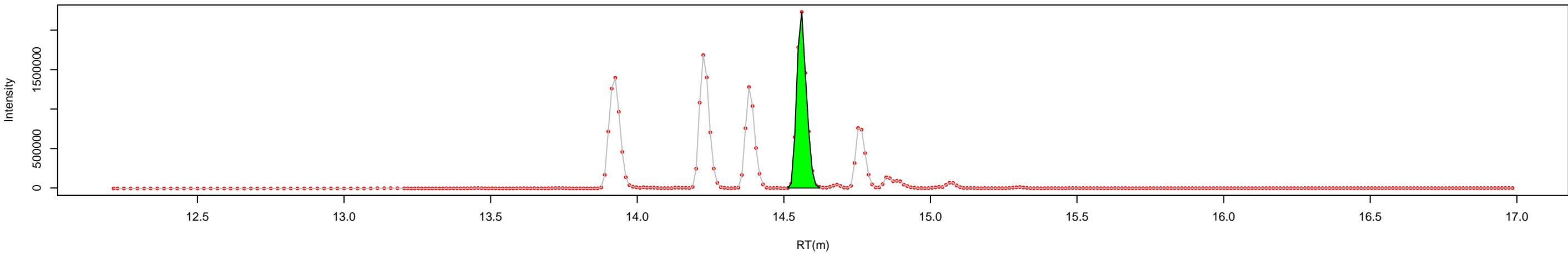
raw chromatogram | batch: 1 sample: std13-10ul-1 conc: 20 function: 1 mass: 389.35>389.35



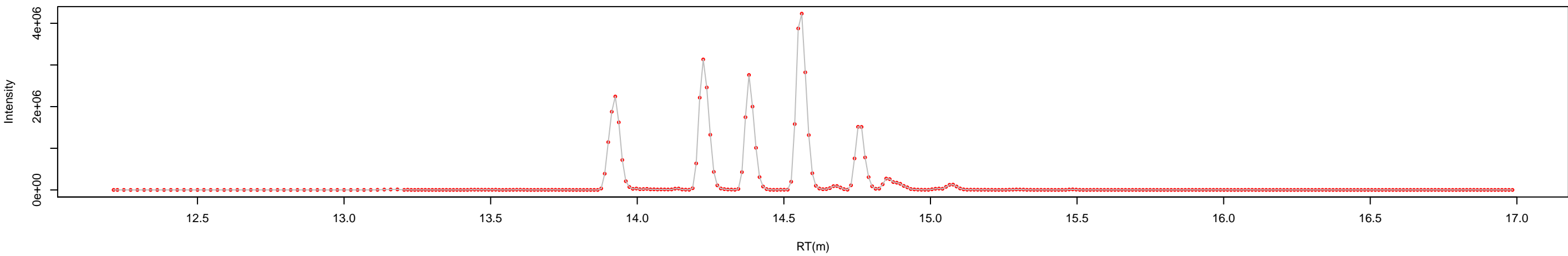
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 521 BLine: yes



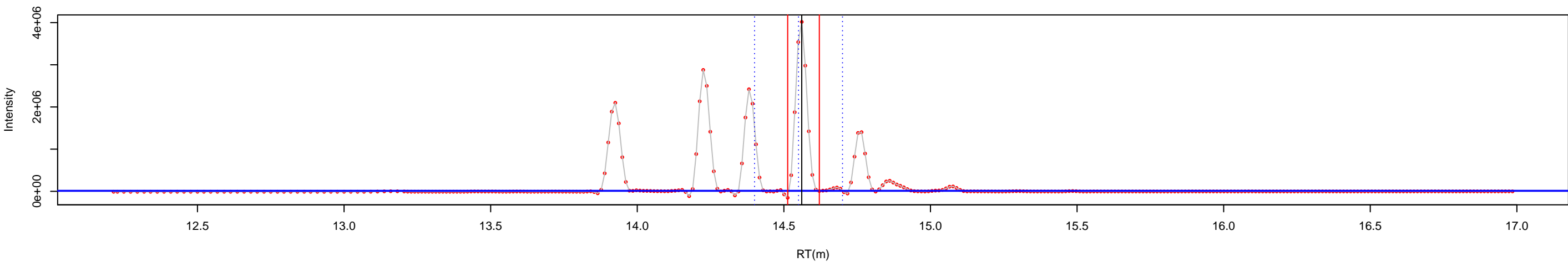
peak area | window size:3 BLine: yes



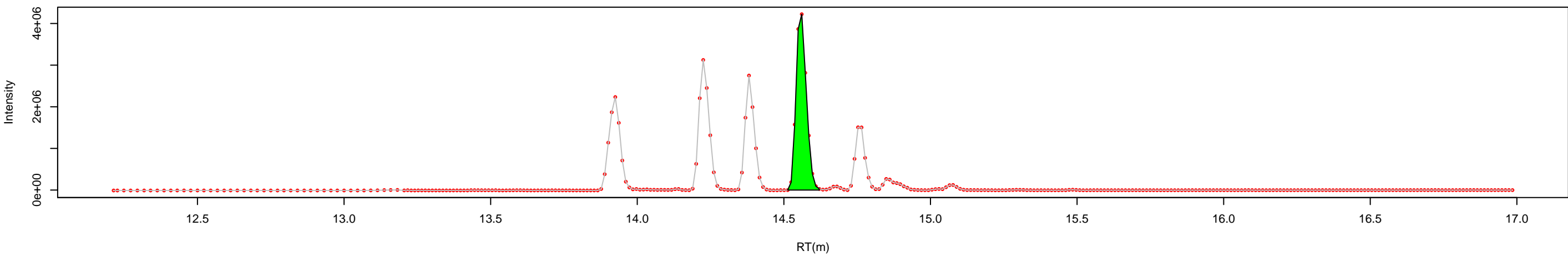
raw chromatogram | batch: 1 sample: std14-10ul-1 conc: 50 function: 1 mass: 389.35>389.35



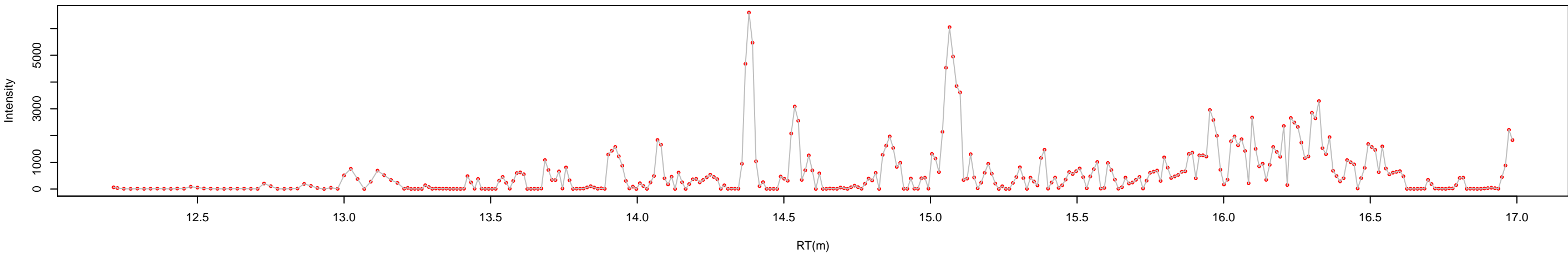
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 2220 BLine: yes



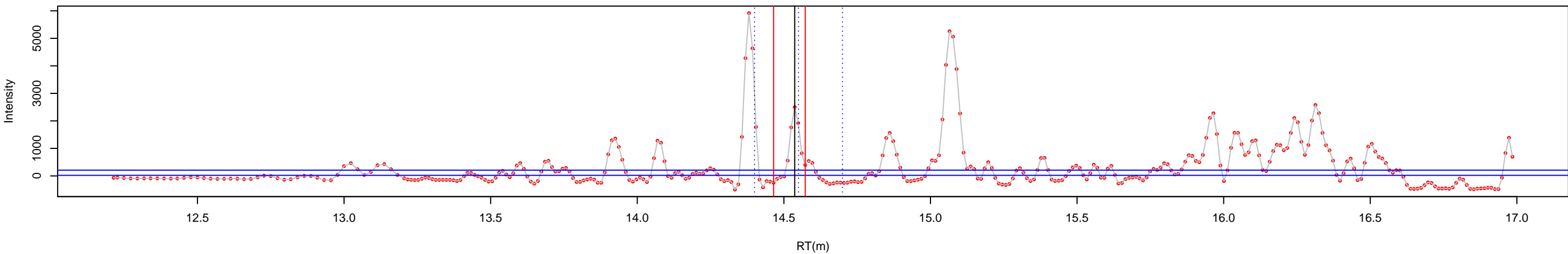
peak area | window size:3 BLine: yes



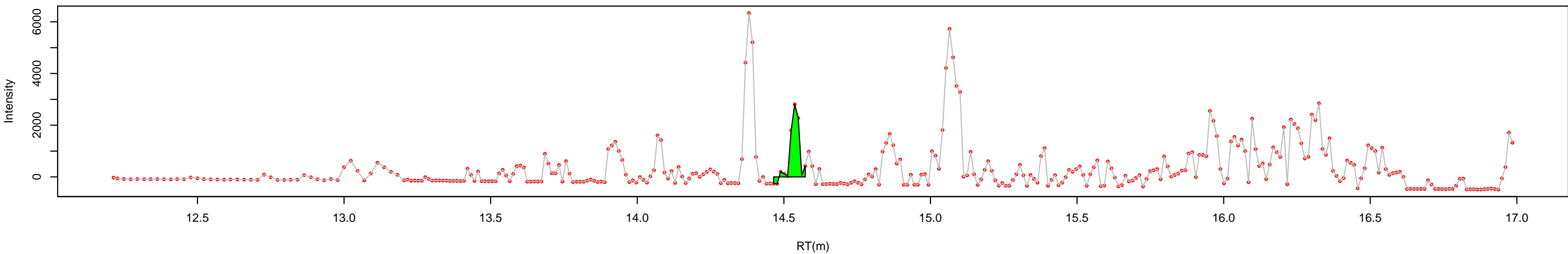
raw chromatogram | batch: 2 sample: coth45 conc: NA function: 1 mass: 389.35>389.35



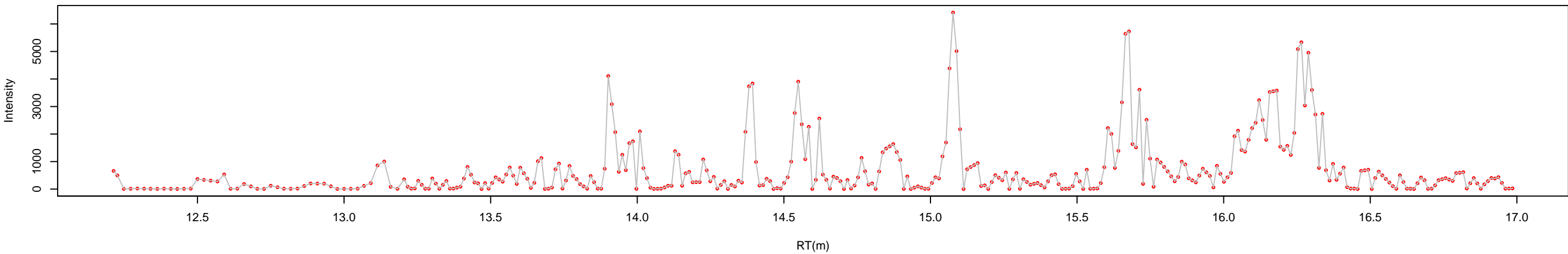
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 20.9 BLine: yes



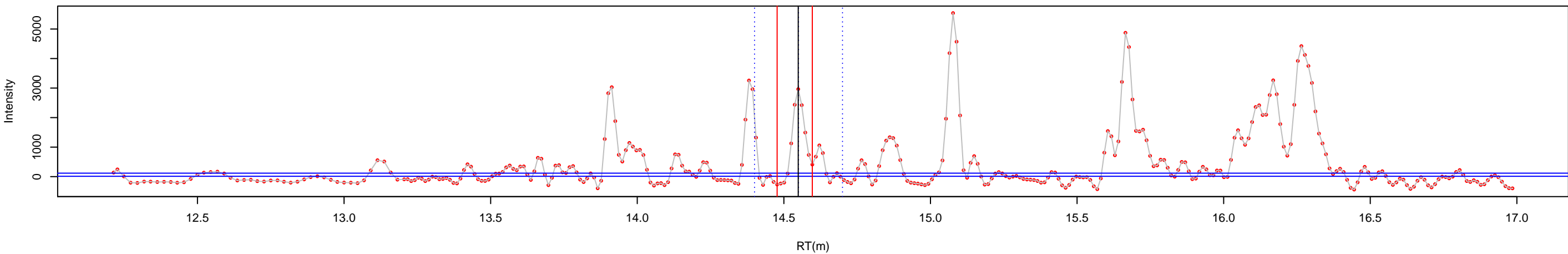
peak area | window size:3 BLine: yes



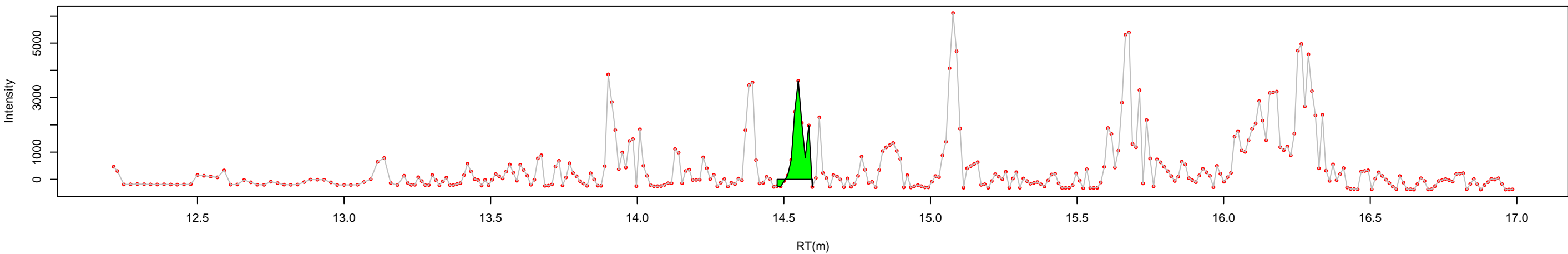
raw chromatogram | batch: 2 sample: coth46 conc: NA function: 1 mass: 389.35>389.35



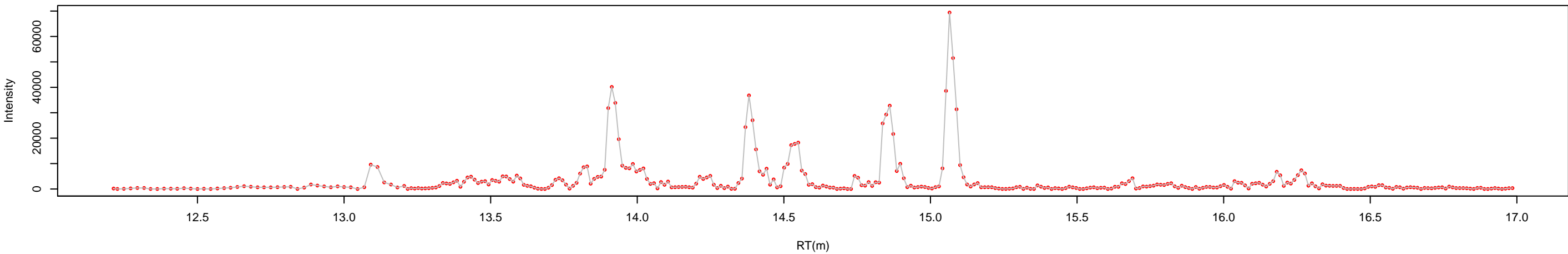
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 11.7 BLine: yes



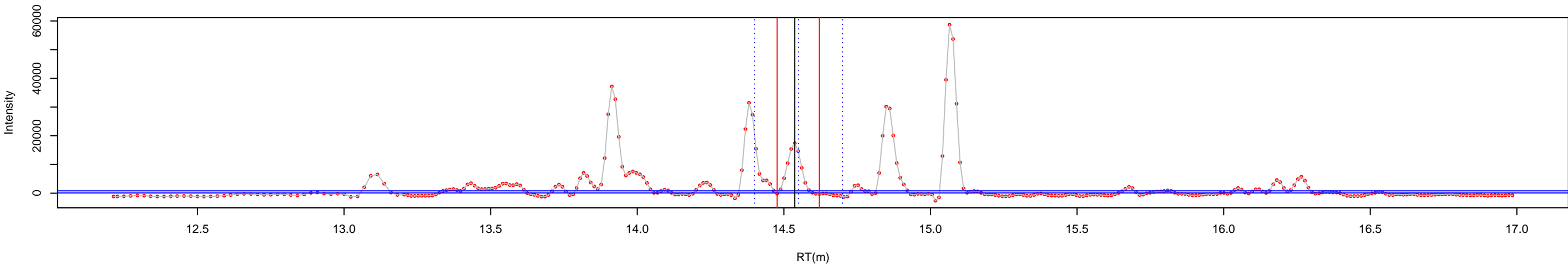
peak area | window size:3 BLine: yes



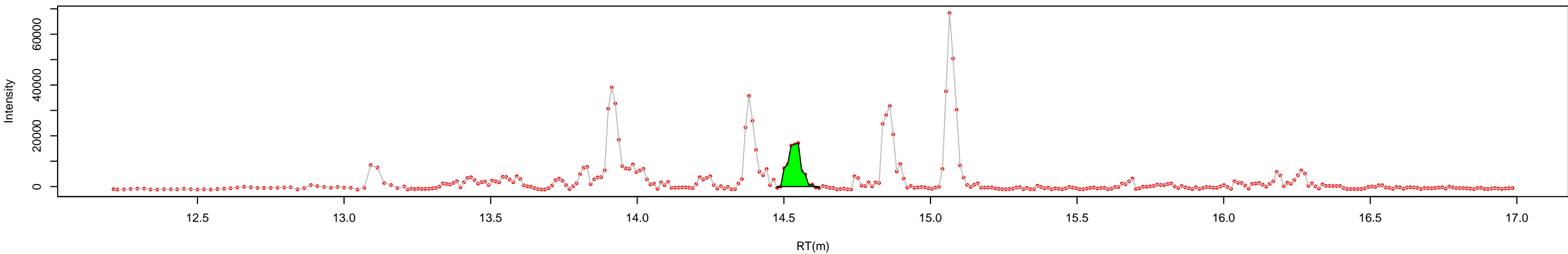
raw chromatogram | batch: 2 sample: coth47 conc: NA function: 1 mass: 389.35>389.35



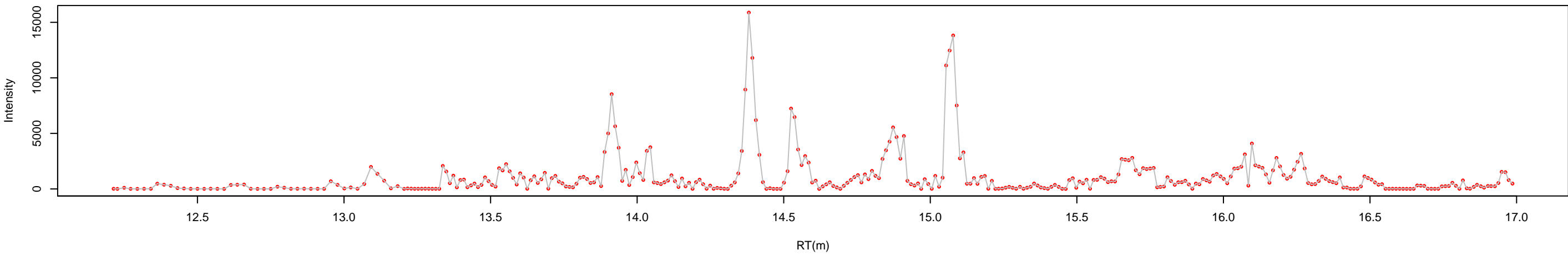
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 82.5 BLine: yes



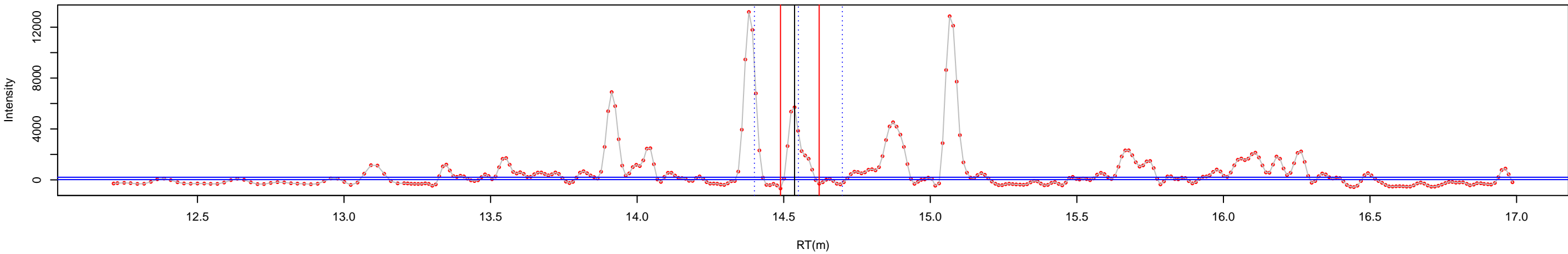
peak area | window size:3 BLine: yes



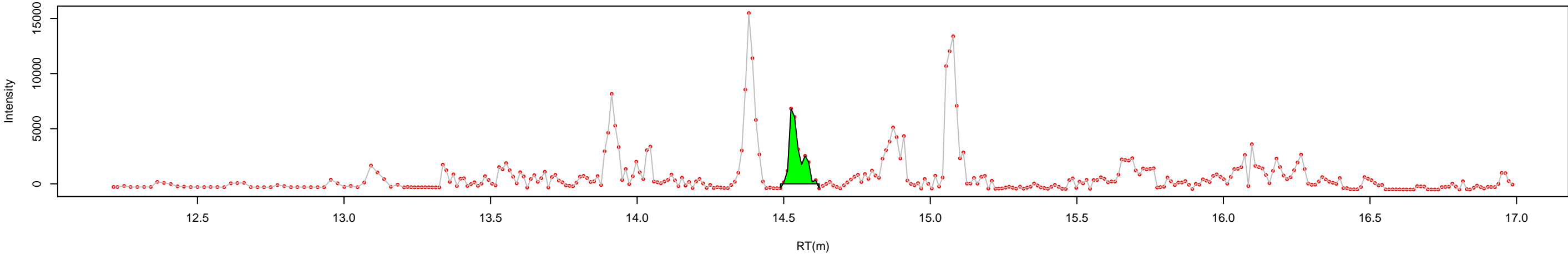
raw chromatogram | batch: 2 sample: coth48 conc: NA function: 1 mass: 389.35>389.35



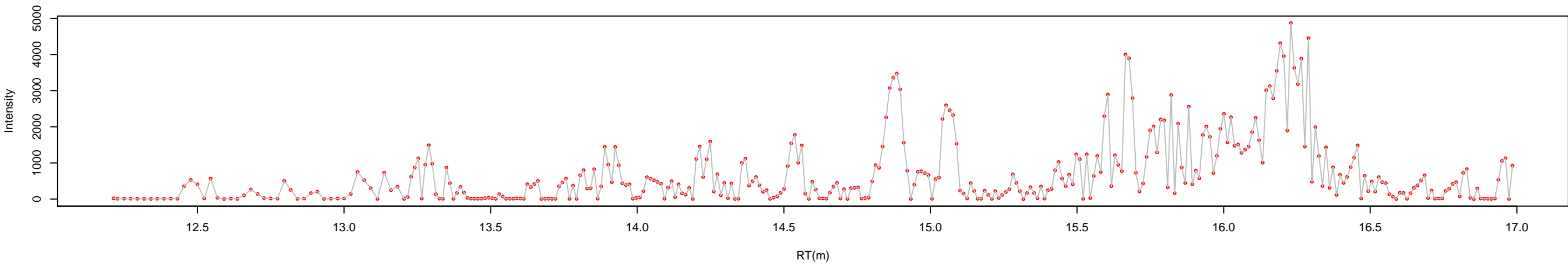
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 20.5 BLine: yes



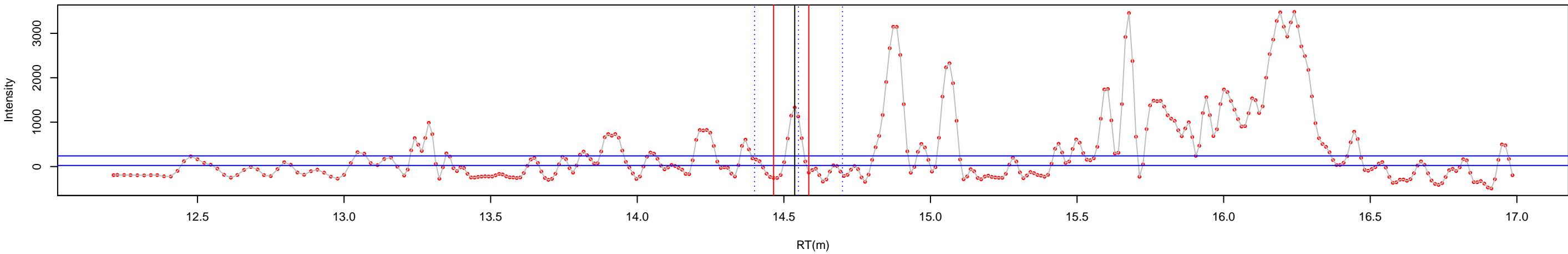
peak area | window size:3 BLine: yes



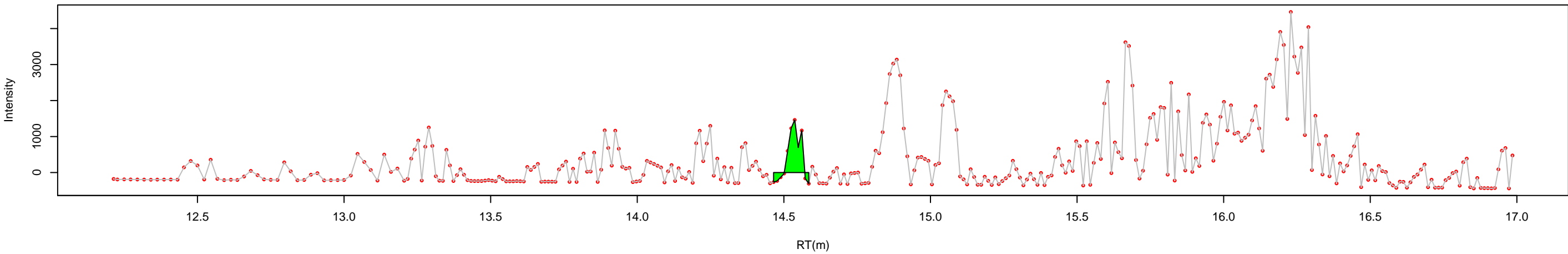
raw chromatogram | batch: 2 sample: coth49 conc: NA function: 1 mass: 389.35>389.35



peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 24 BLine: yes

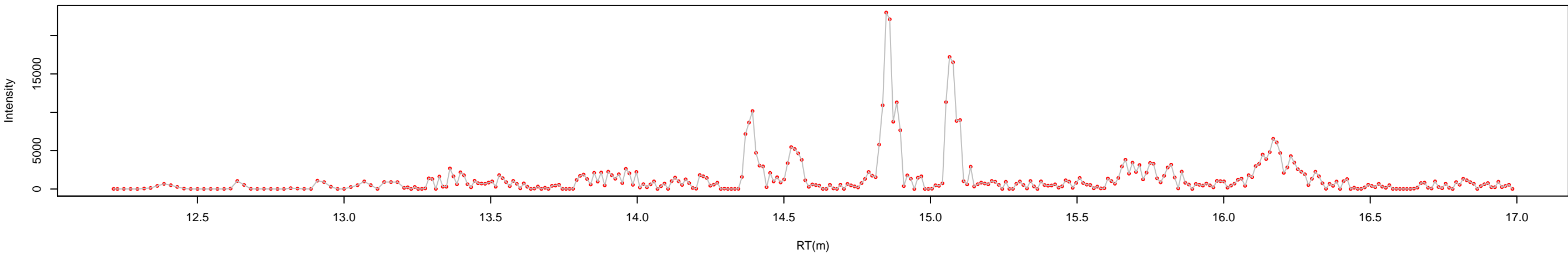


peak area | window size:3 BLine: yes

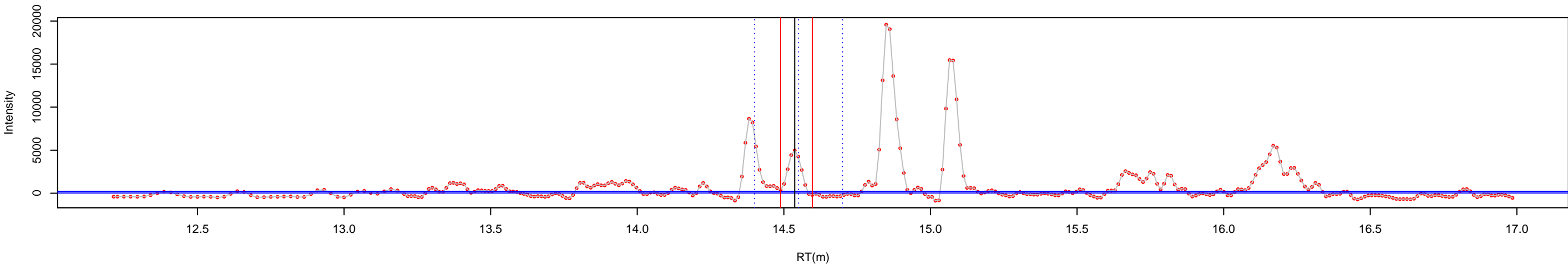




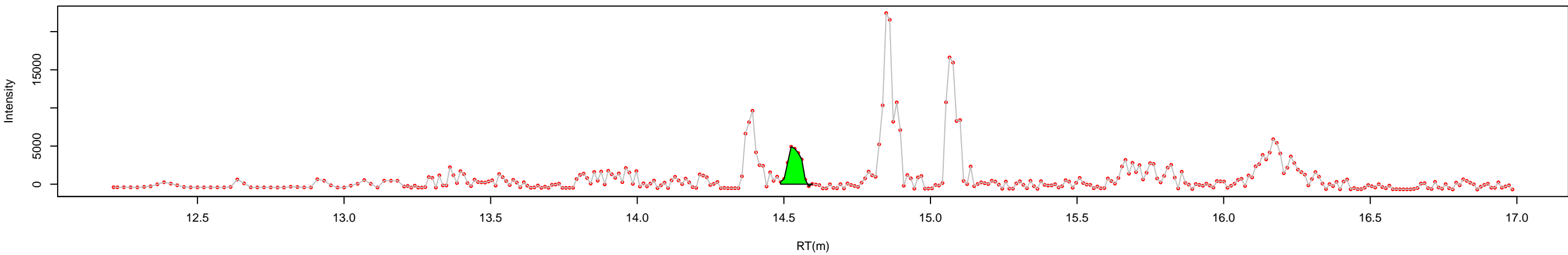
raw chromatogram | batch: 2 sample: coth50 conc: NA function: 1 mass: 389.35>389.35



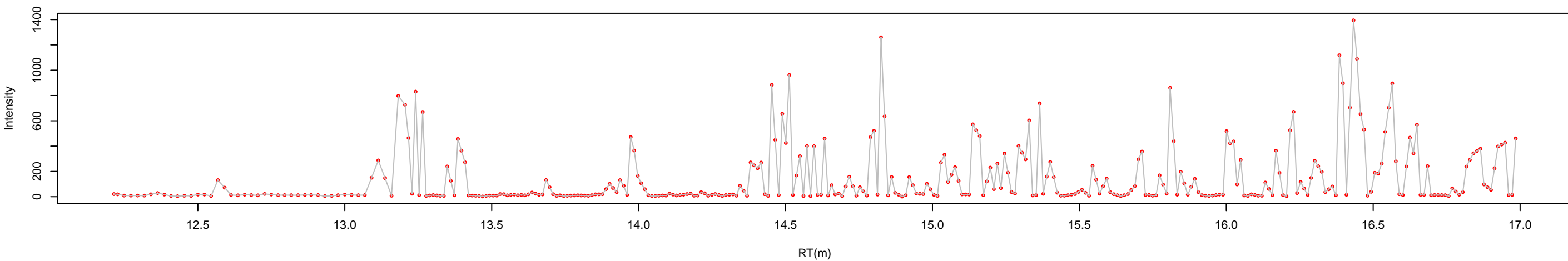
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 22.2 BLine: yes



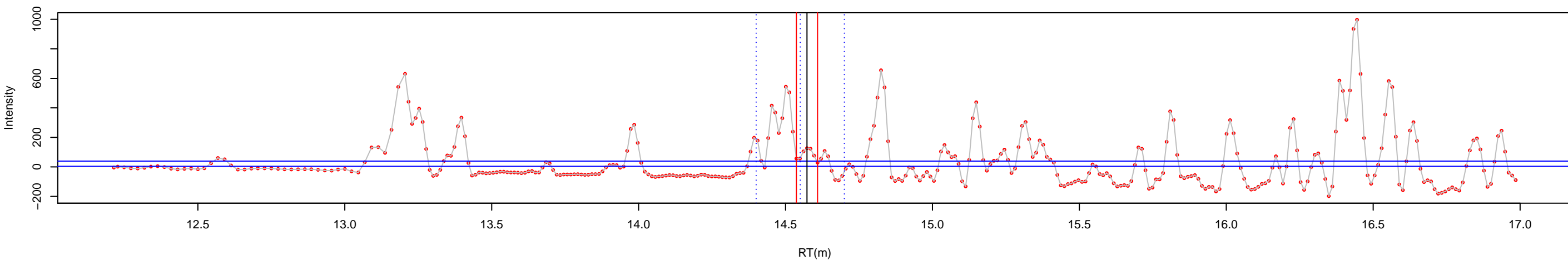
peak area | window size:3 BLine: yes



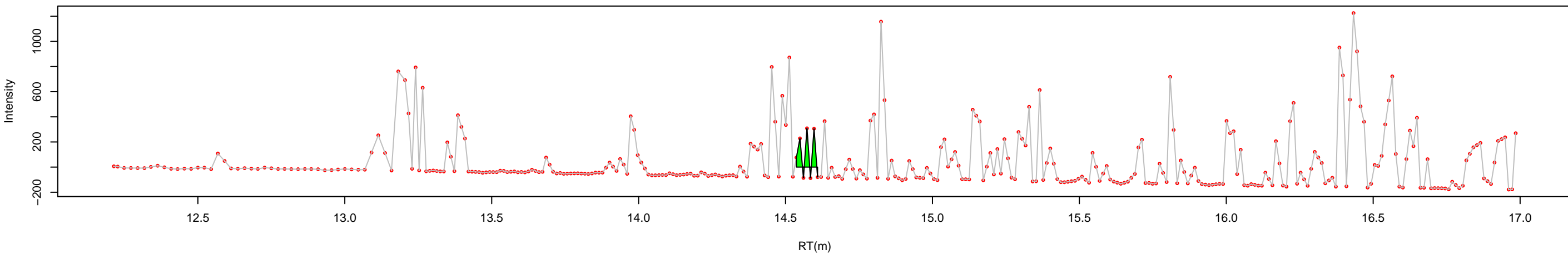
raw chromatogram | batch: 2 sample: std0-10ul-2 conc: 0.001 function: 1 mass: 389.35>389.35



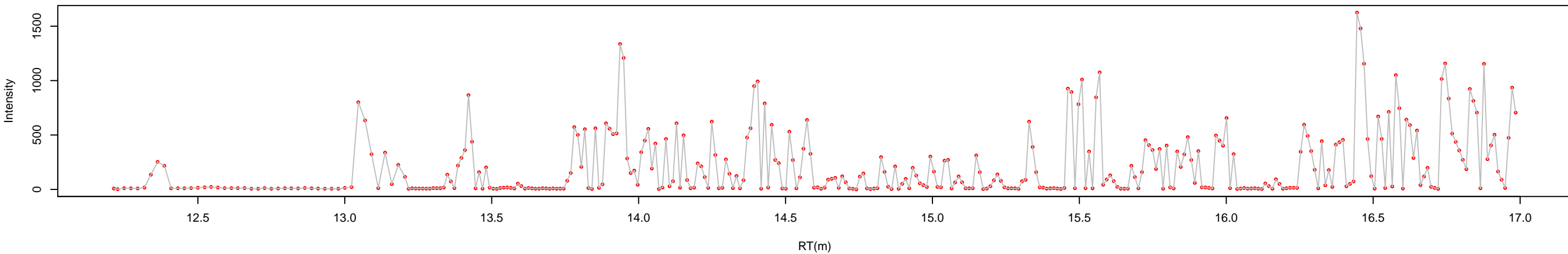
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 3.92 BLine: yes



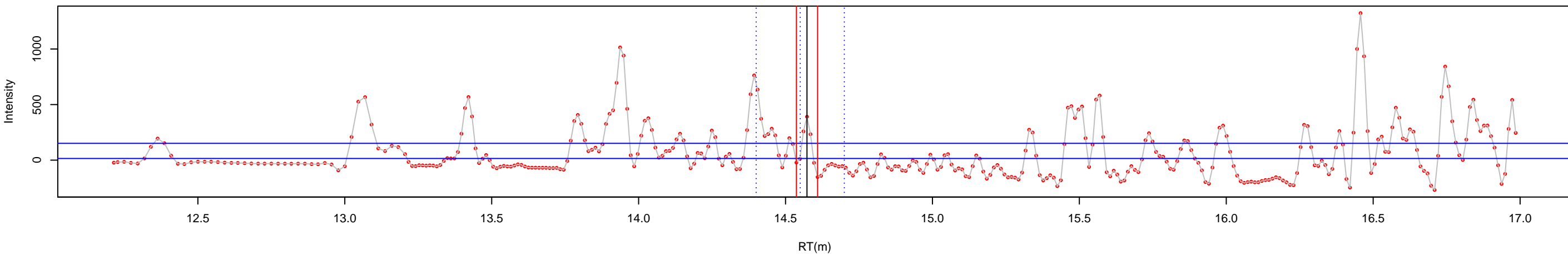
peak area | window size:3 BLine: yes



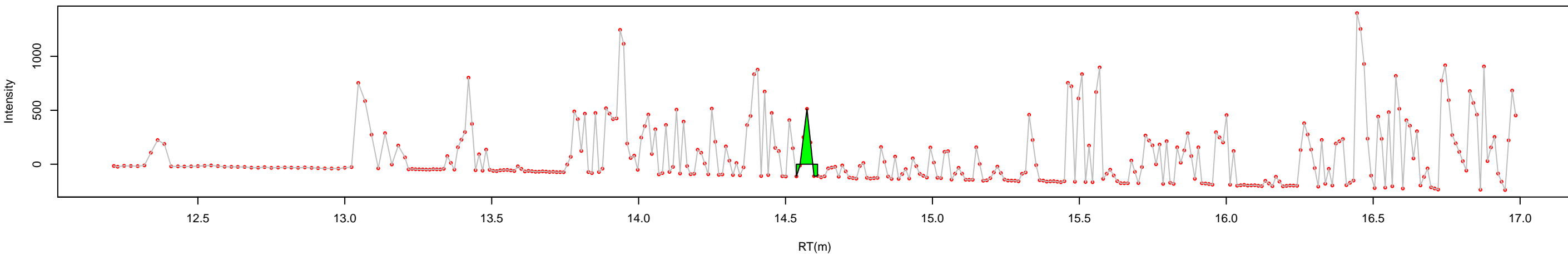
raw chromatogram | batch: 2 sample: std1-10ul-2 conc: 0.002 function: 1 mass: 389.35>389.35



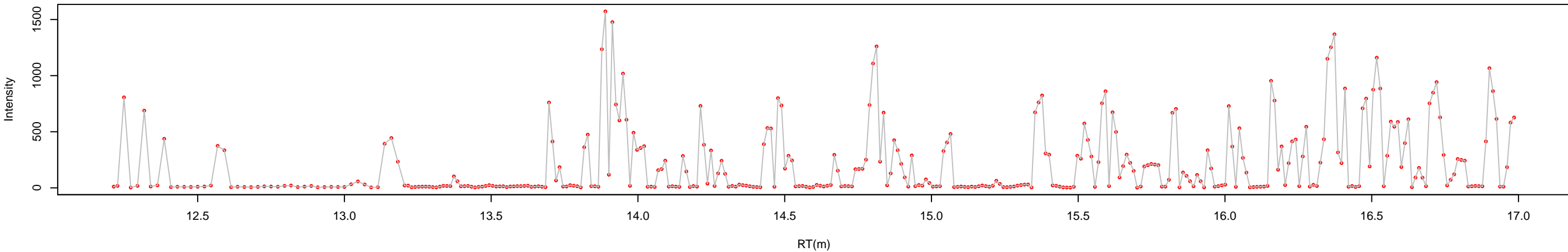
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 15.1 BLine: yes



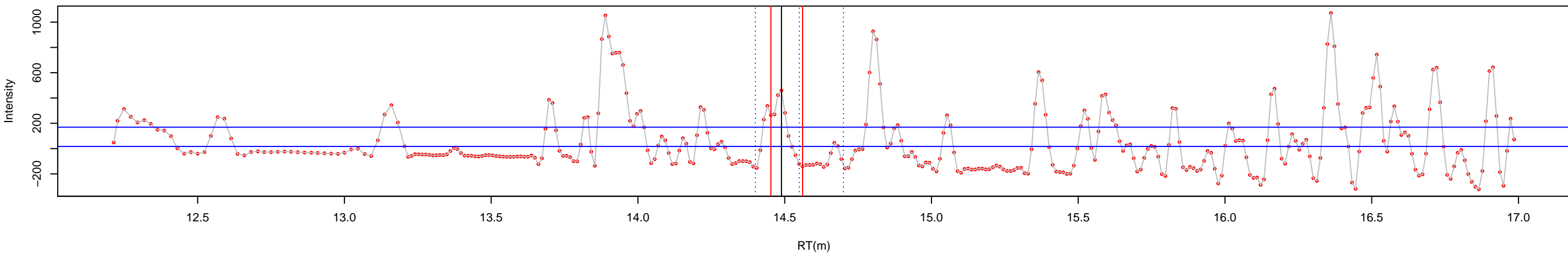
peak area | window size:3 BLine: yes



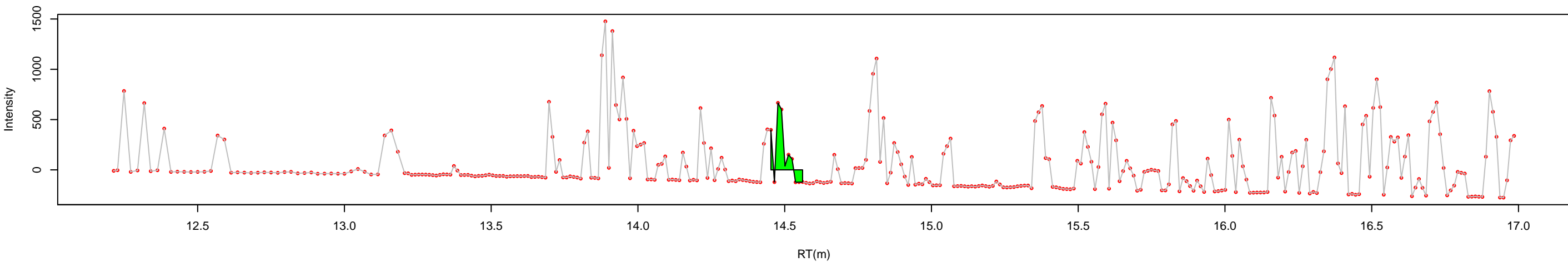
raw chromatogram | batch: 2 sample: std2-10ul-2 conc: 0.005 function: 1 mass: 389.35>389.35



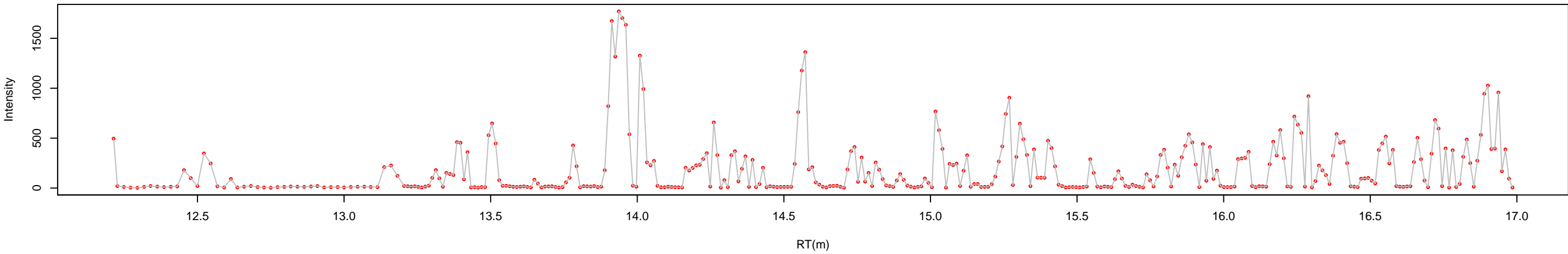
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 16.9 BLine: yes



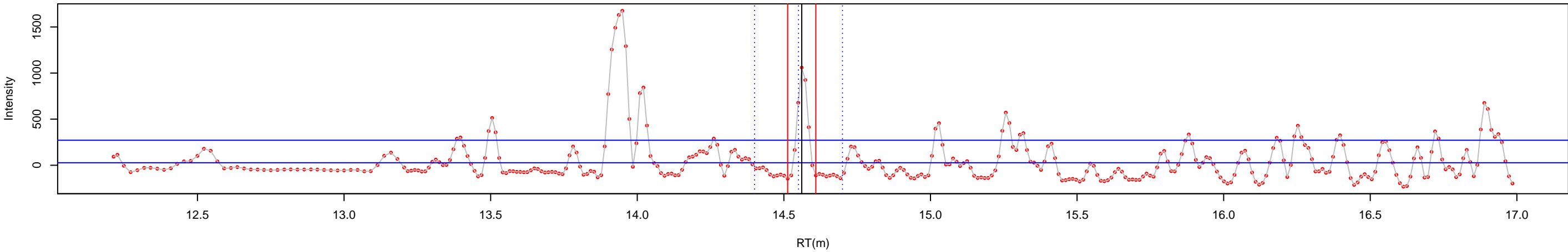
peak area | window size:3 BLine: yes



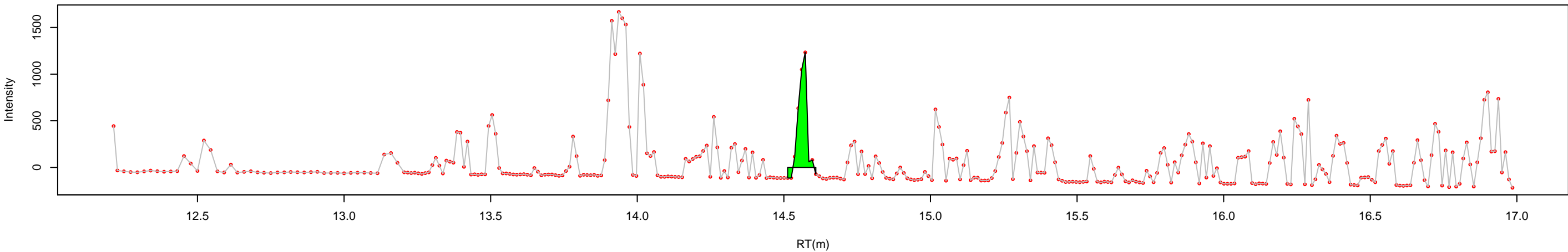
raw chromatogram | batch: 2 sample: std3-10ul-2 conc: 0.01 function: 1 mass: 389.35>389.35



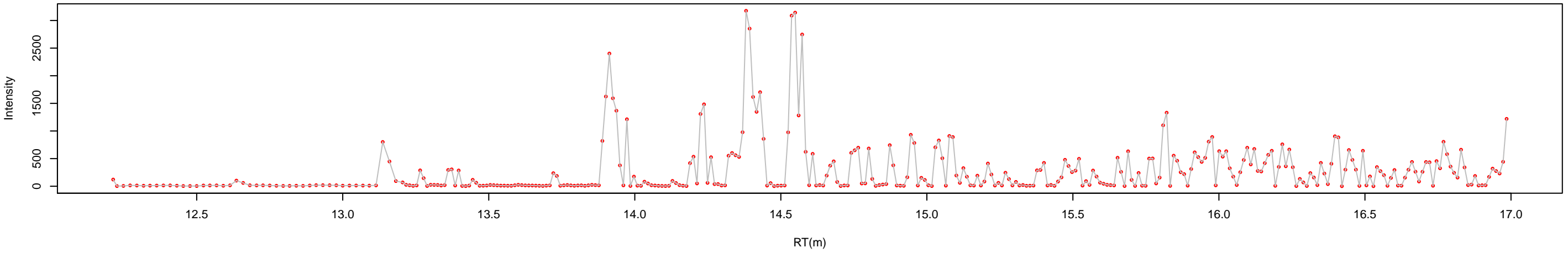
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 27.1 BLine: yes



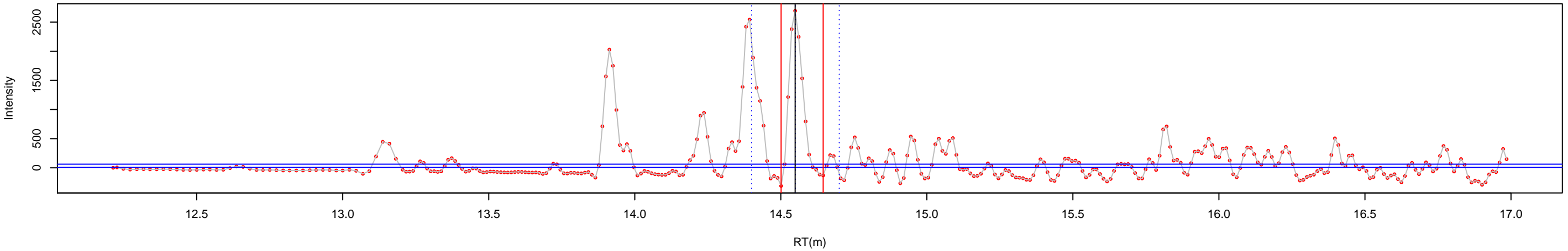
peak area | window size:3 BLine: yes



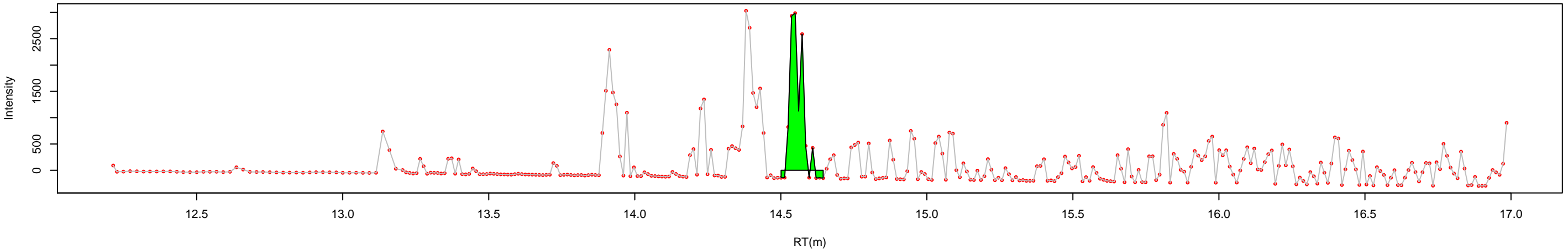
raw chromatogram | batch: 2   sample: std4-10ul-2   conc: 0.02   function: 1   mass: 389.35>389.35



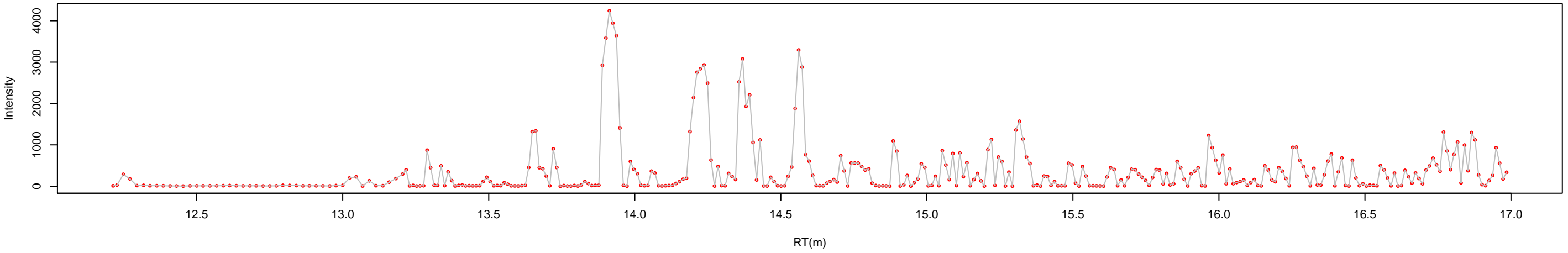
peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 6.26   BLine: yes



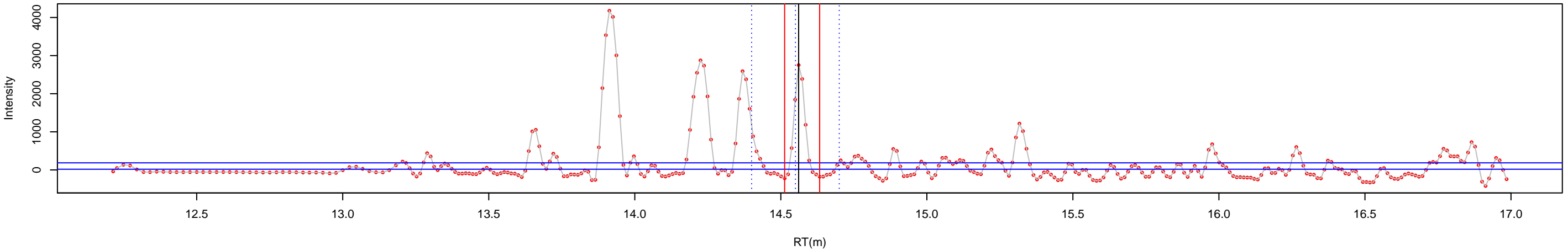
peak area | window size:3   BLine: yes



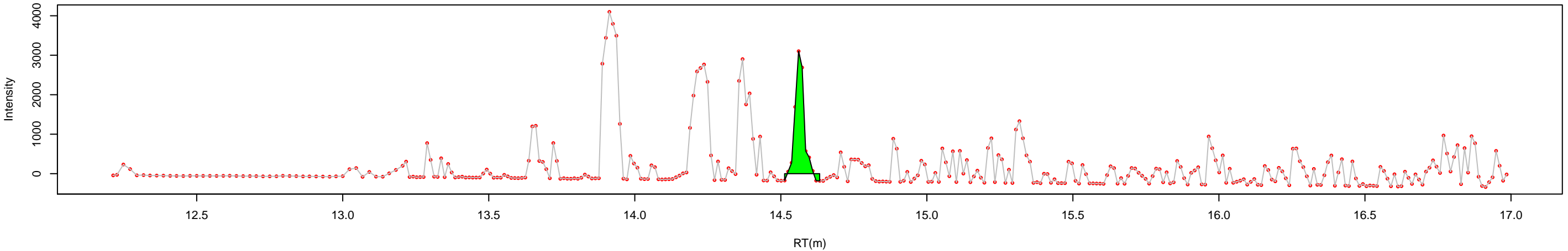
raw chromatogram | batch: 2   sample: std5-10ul-2   conc: 0.05   function: 1   mass: 389.35>389.35



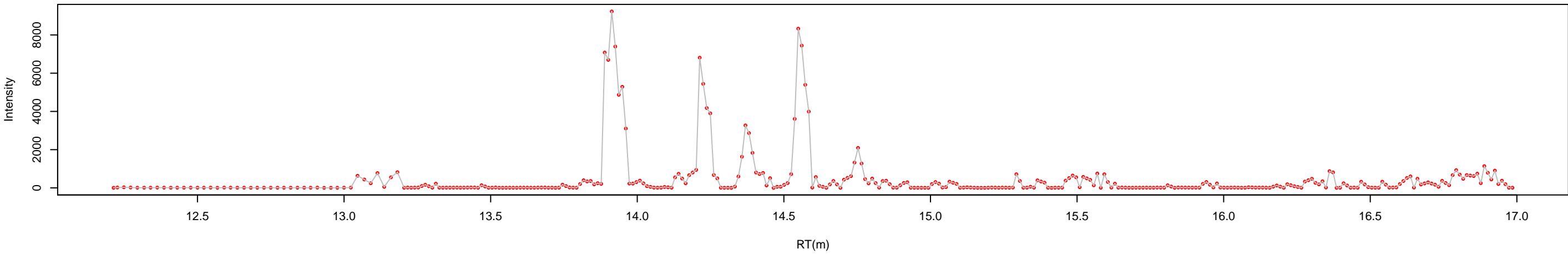
peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 18.6   BLine: yes



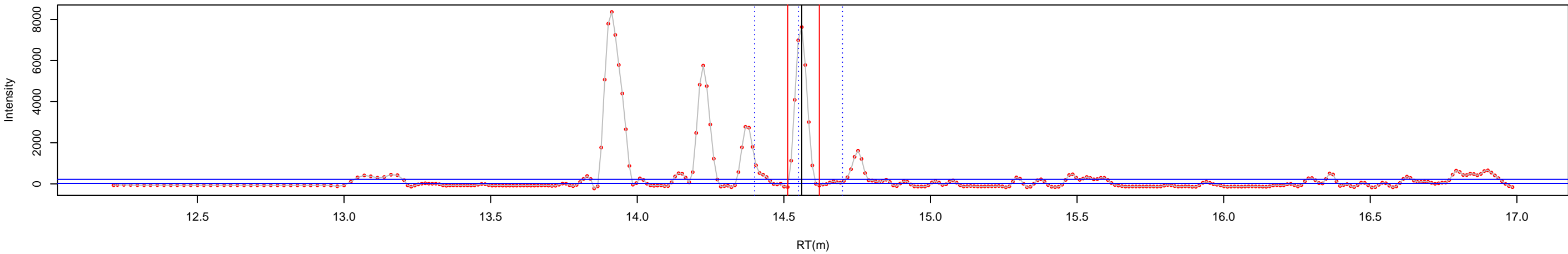
peak area | window size:3   BLine: yes



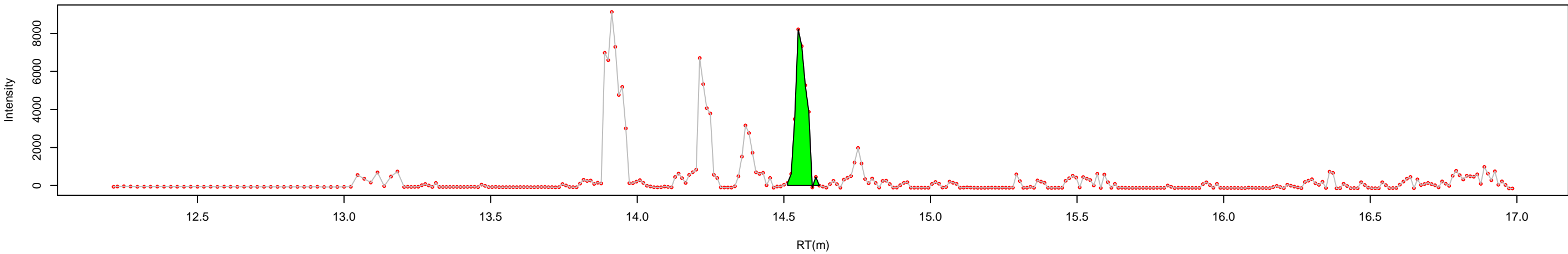
raw chromatogram | batch: 2 sample: std6-10ul-2 conc: 0.1 function: 1 mass: 389.35>389.35



peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 21.8 BLine: yes

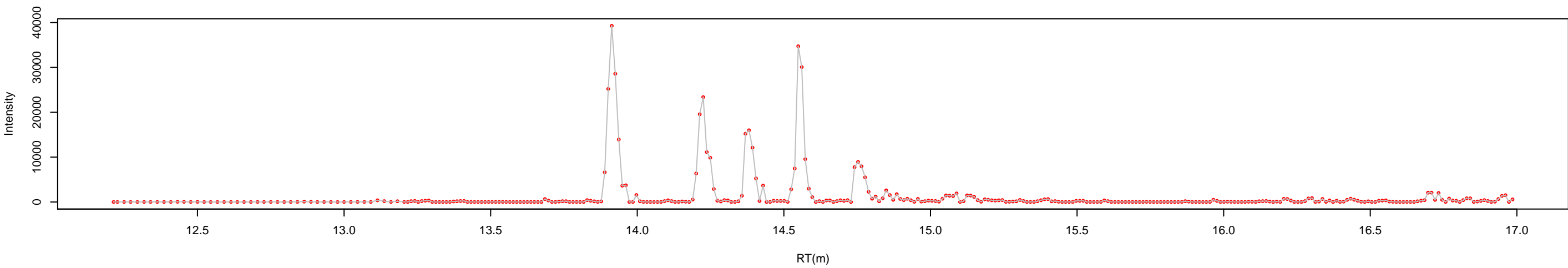


peak area | window size:3 BLine: yes

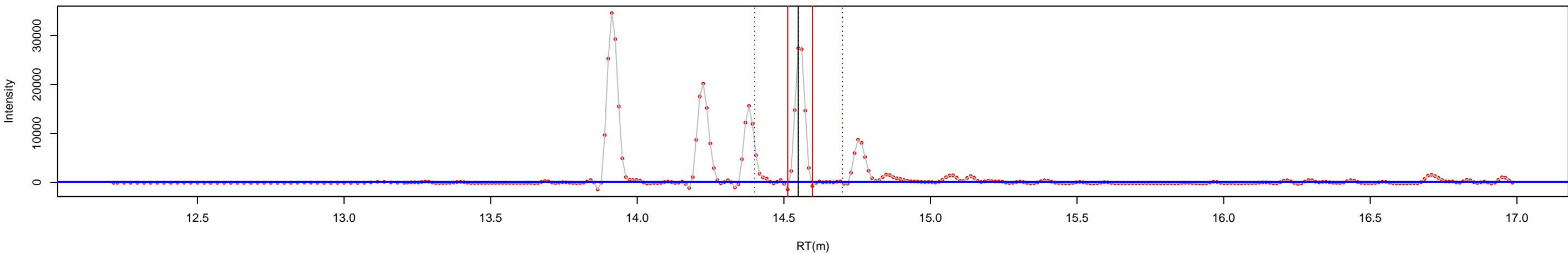




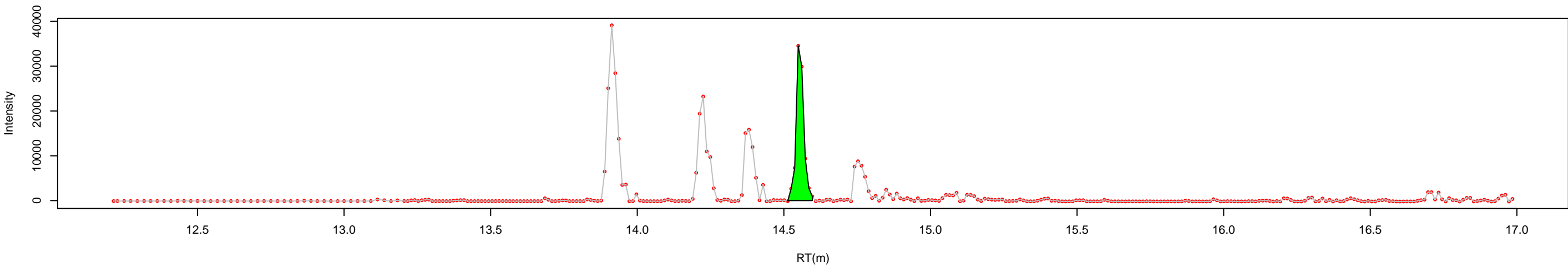
raw chromatogram | batch: 2 sample: std7-10ul-2 conc: 0.2 function: 1 mass: 389.35>389.35



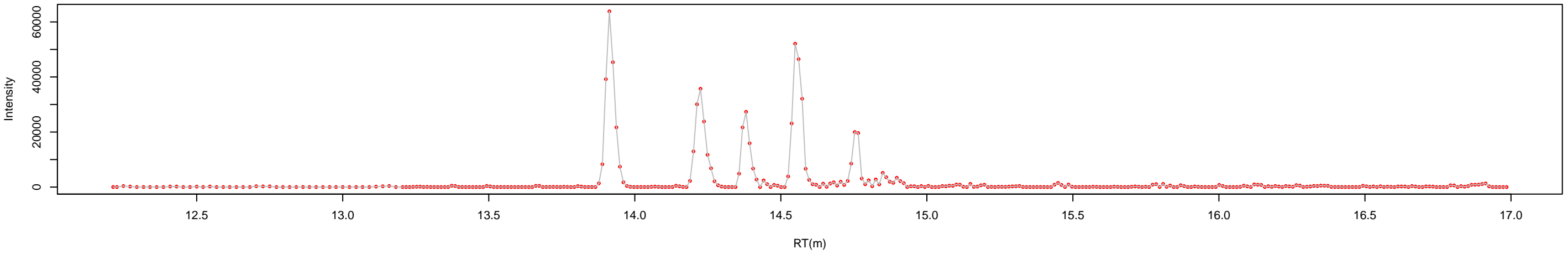
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 17.2 BLine: yes



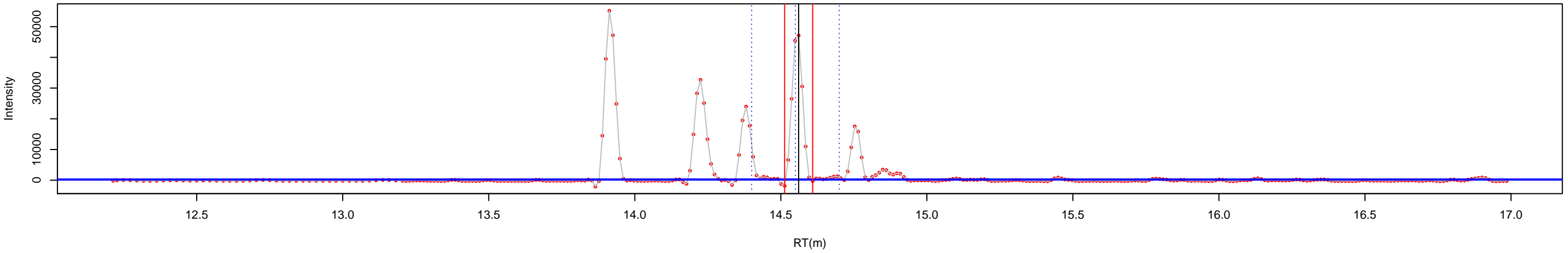
peak area | window size:3 BLine: yes



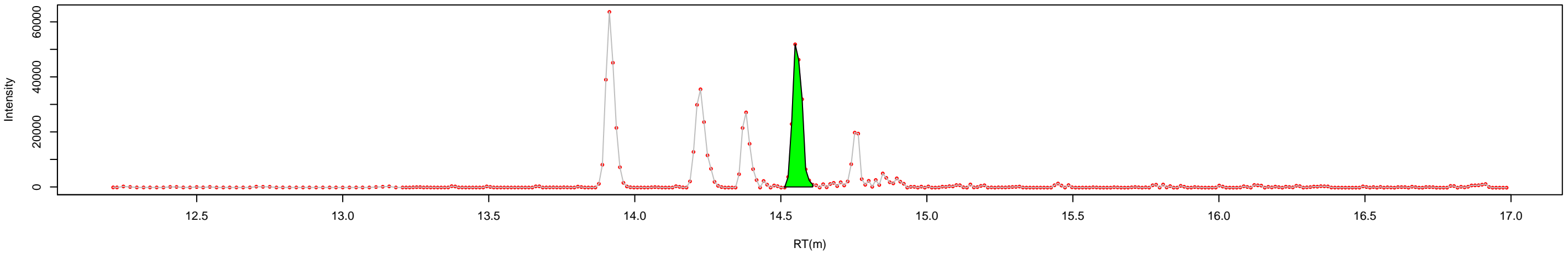
raw chromatogram | batch: 2 sample: std8-10ul-2 conc: 0.5 function: 1 mass: 389.35>389.35



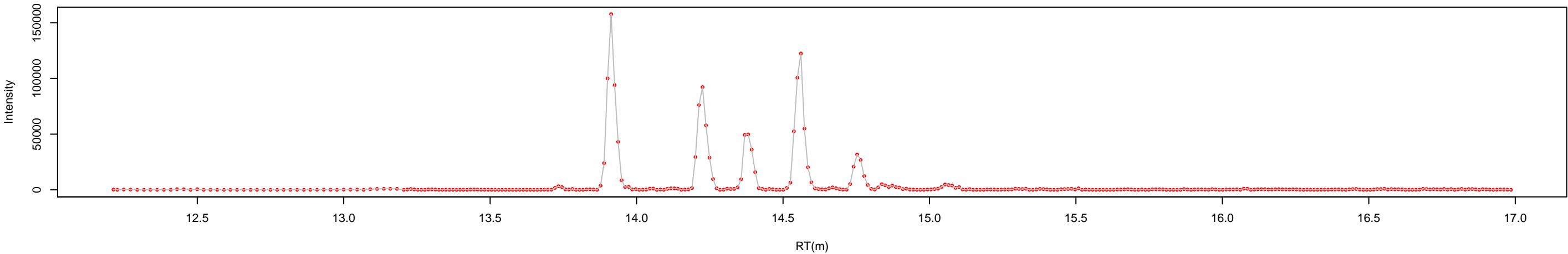
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 39.3 BLine: yes



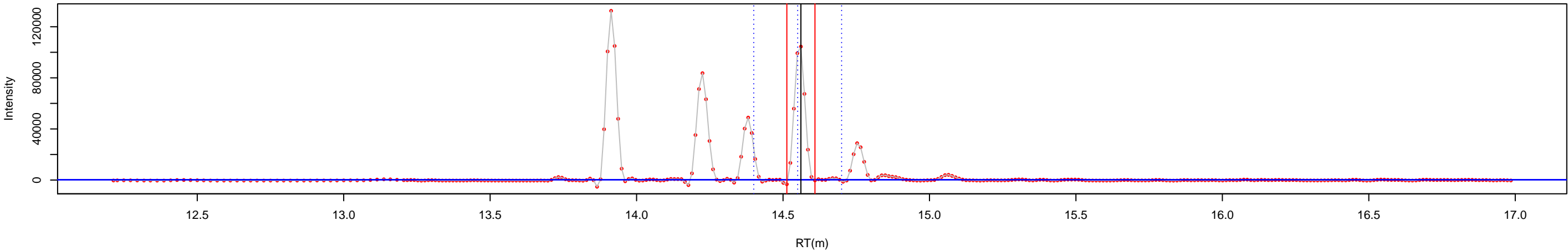
peak area | window size:3 BLine: yes



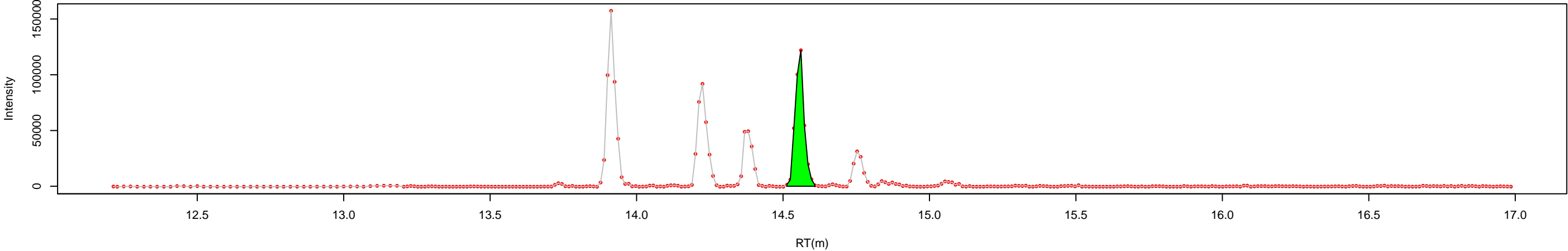
raw chromatogram | batch: 2   sample: std9-10ul-2   conc: 1   function: 1   mass: 389.35>389.35



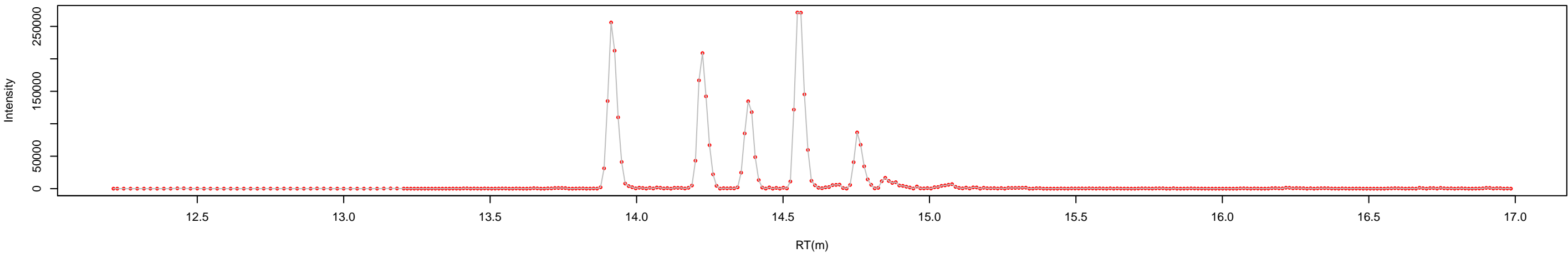
peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 37.9   BLine: yes



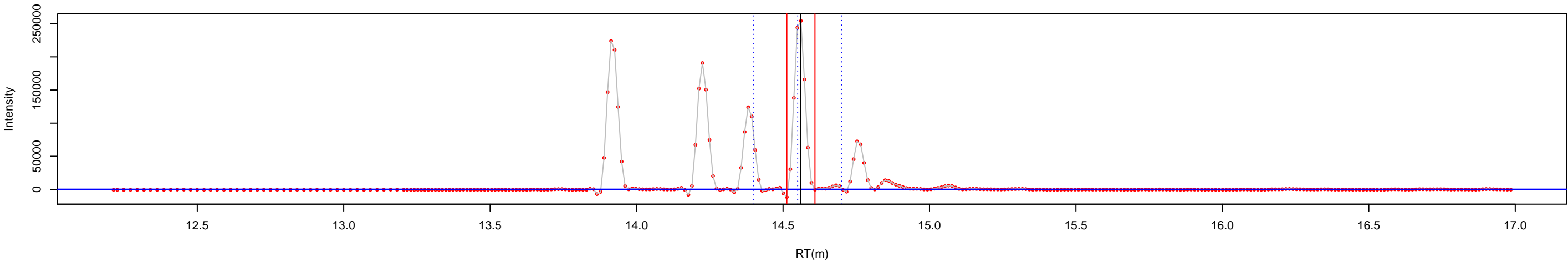
peak area | window size:3   BLine: yes



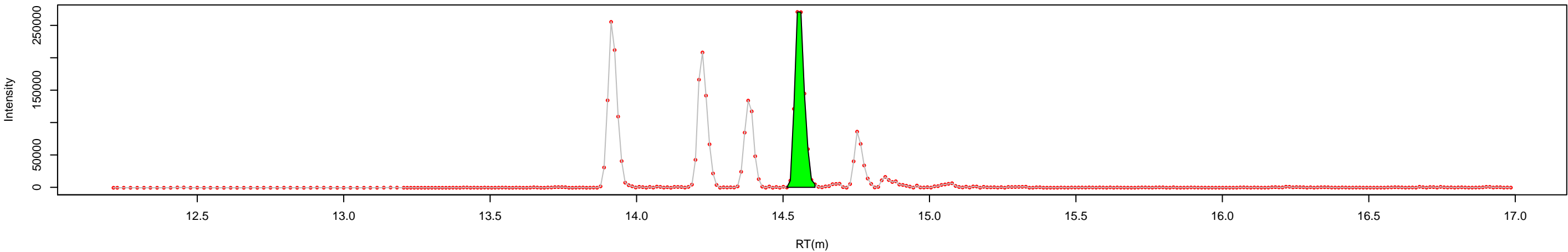
raw chromatogram | batch: 2 sample: std10-10ul-2 conc: 2 function: 1 mass: 389.35>389.35



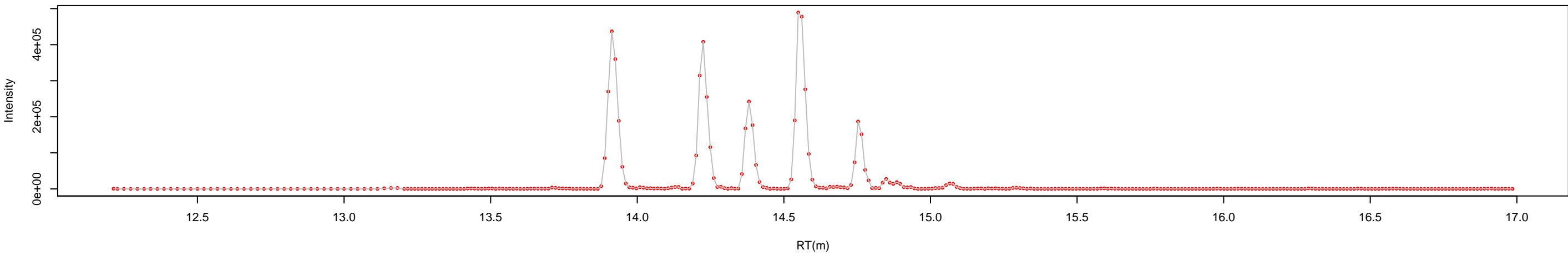
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 36 BLine: yes



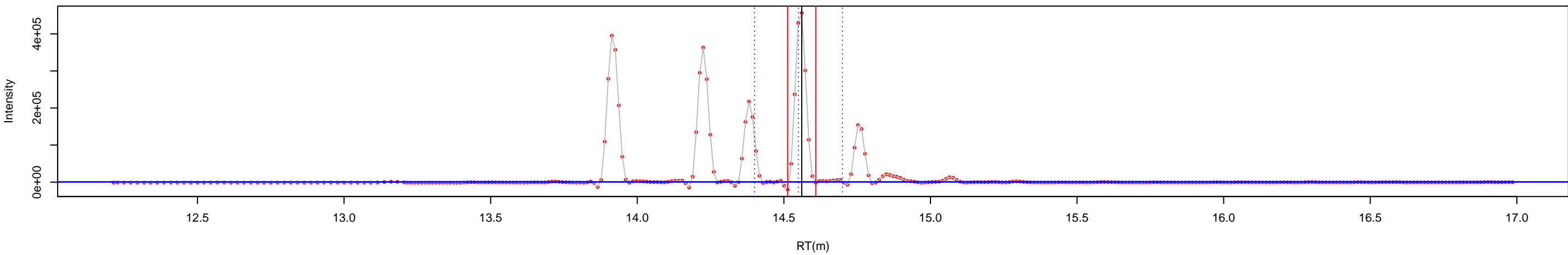
peak area | window size:3 BLine: yes



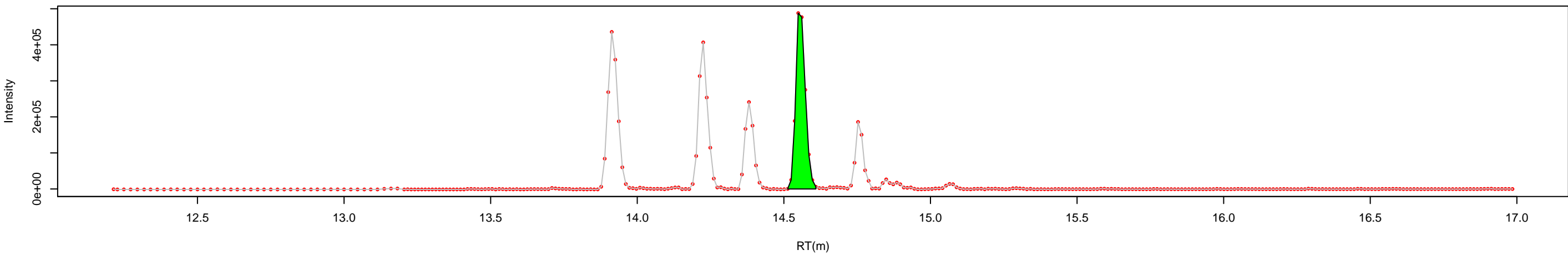
raw chromatogram | batch: 2   sample: std11-10ul-2-1   conc: 5   function: 1   mass: 389.35>389.35



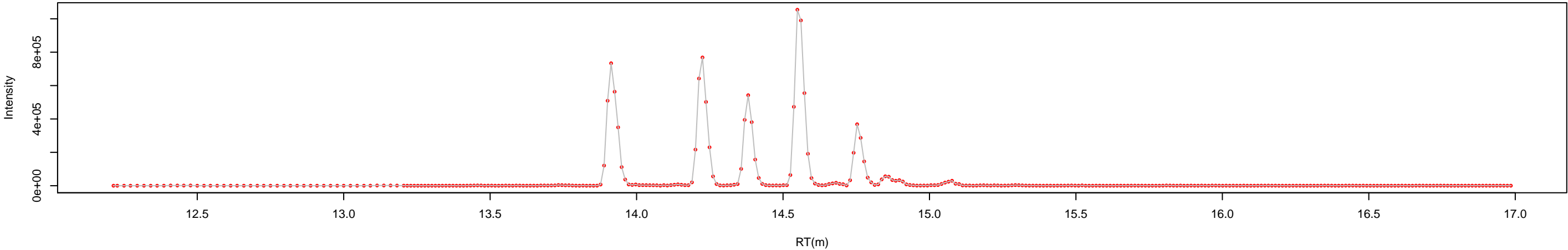
peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 109   BLine: yes



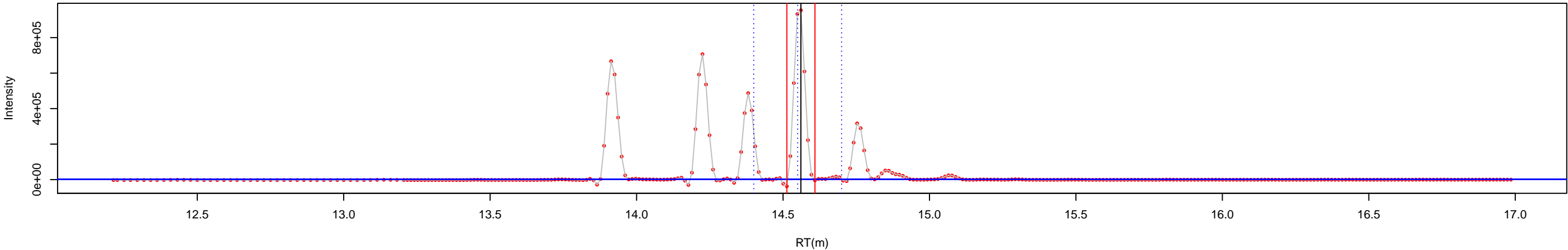
peak area | window size:3   BLine: yes



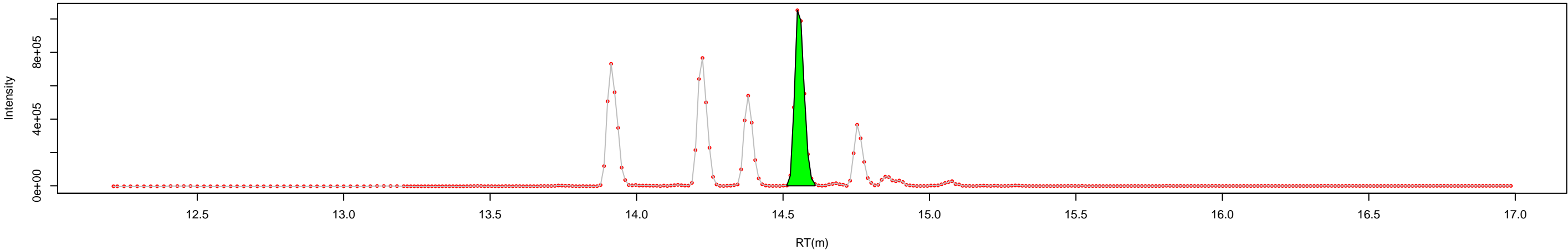
raw chromatogram | batch: 2   sample: std12-10ul-2-1   conc: 10   function: 1   mass: 389.35>389.35



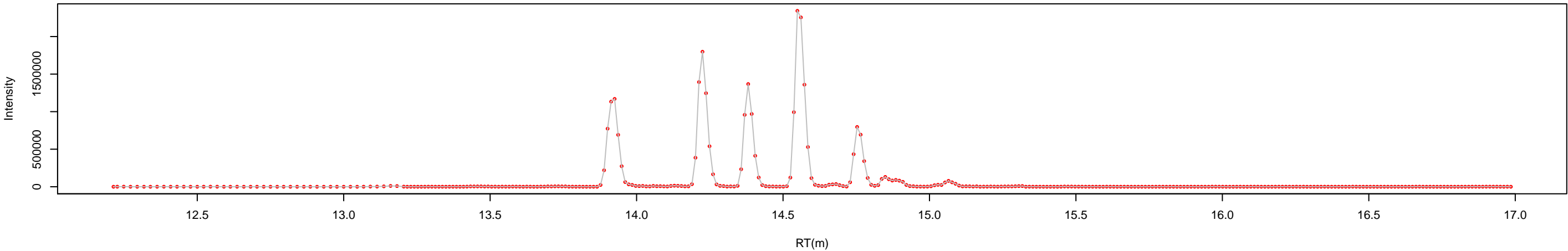
peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 318   BLine: yes



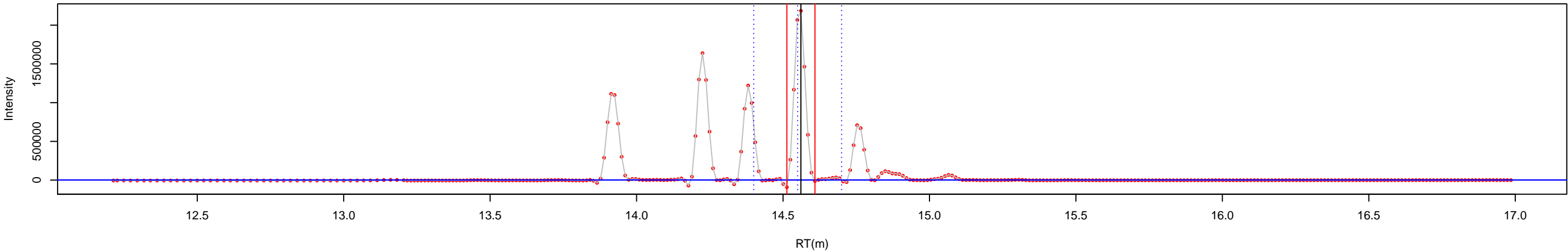
peak area | window size:3   BLine: yes



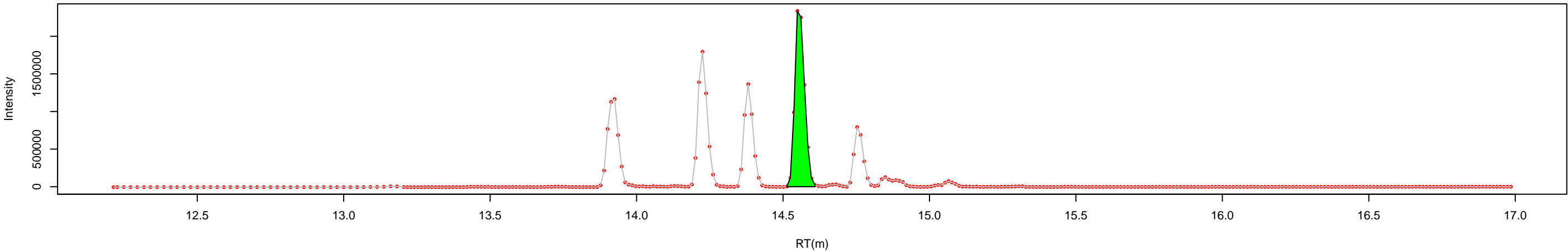
raw chromatogram | batch: 2   sample: std13-10ul-2-1   conc: 20   function: 1   mass: 389.35>389.35



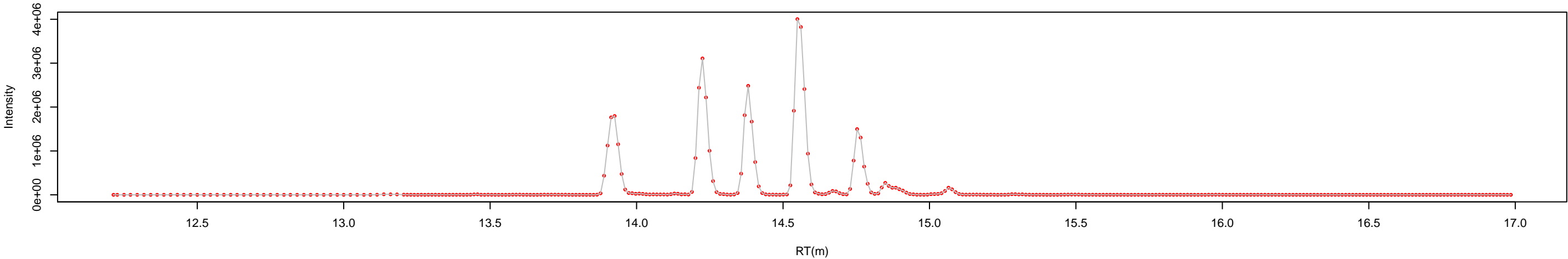
peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 269   BLine: yes



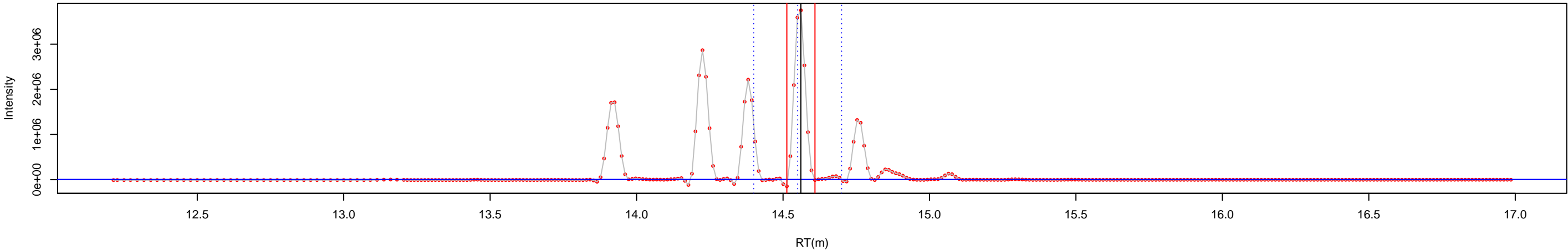
peak area | window size:3   BLine: yes



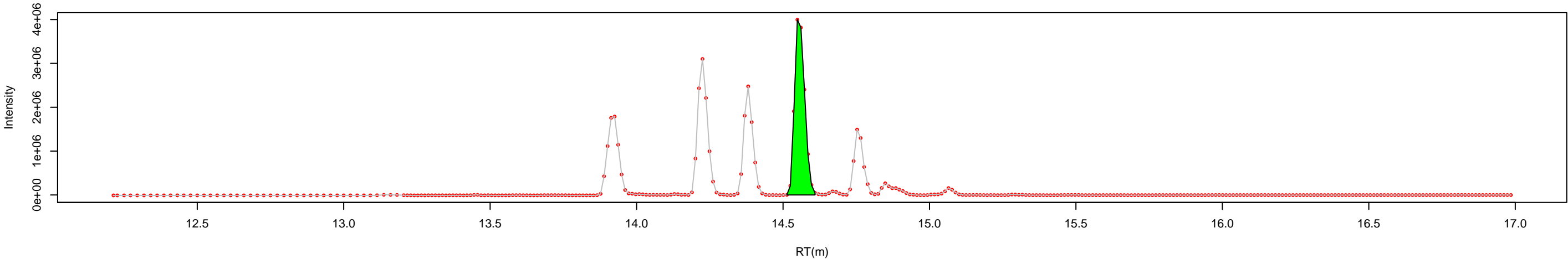
raw chromatogram | batch: 2   sample: std14-10ul-2-1   conc: 50   function: 1   mass: 389.35>389.35



peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 529   BLine: yes

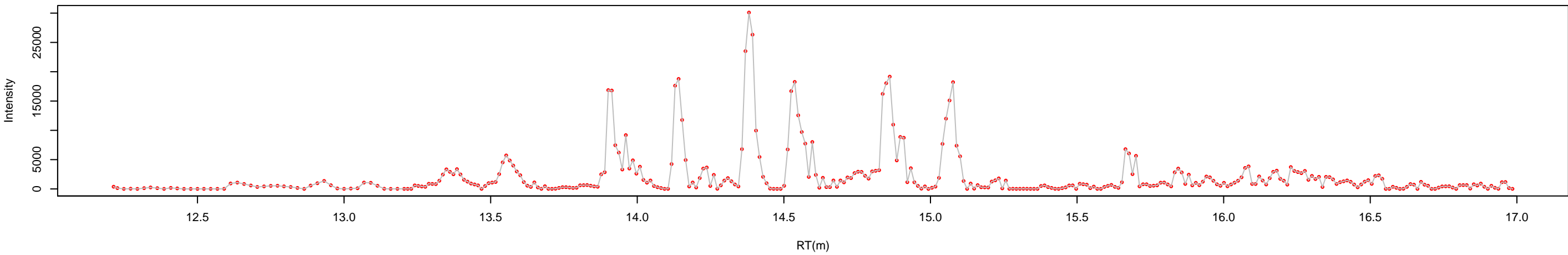


peak area | window size:3   BLine: yes

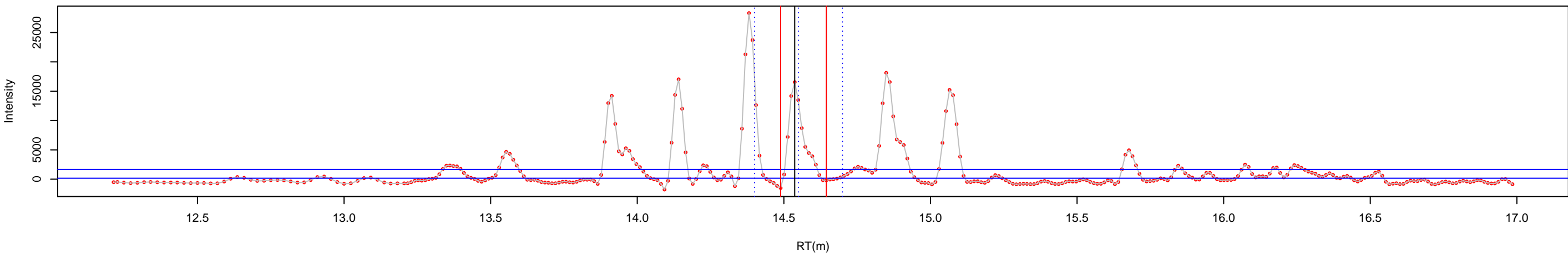




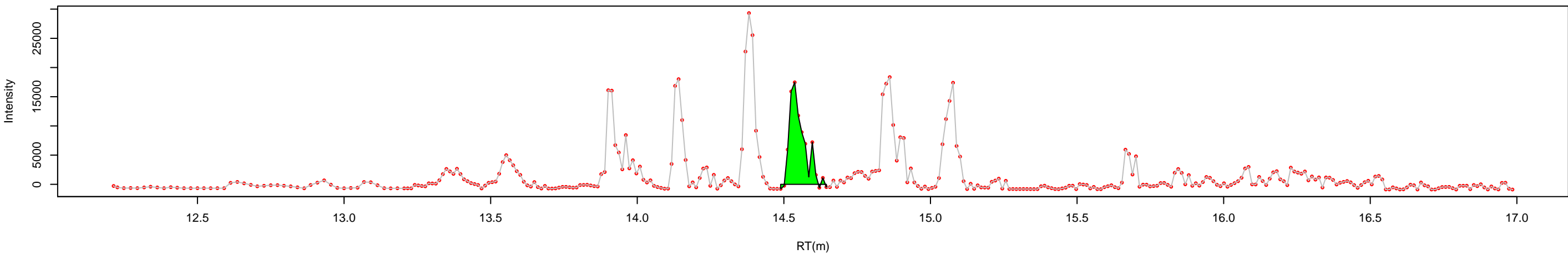
raw chromatogram | batch: 3 sample: cotn65 conc: NA function: 1 mass: 389.35>389.35



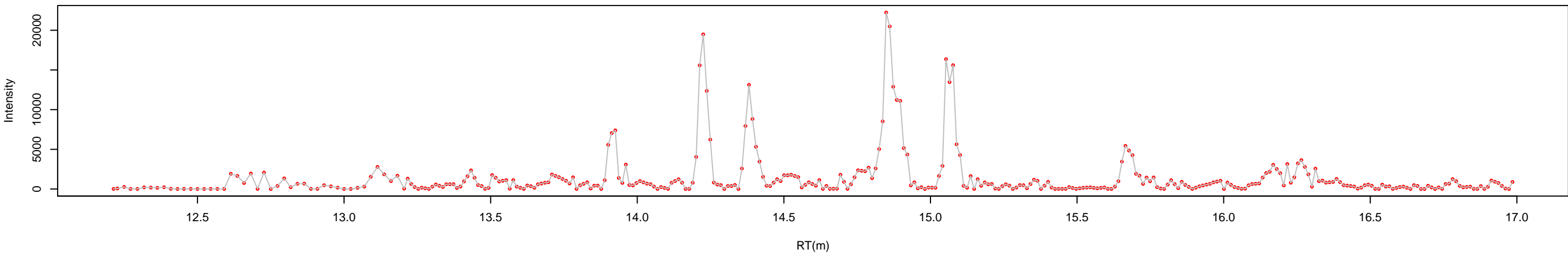
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 166 BLine: yes



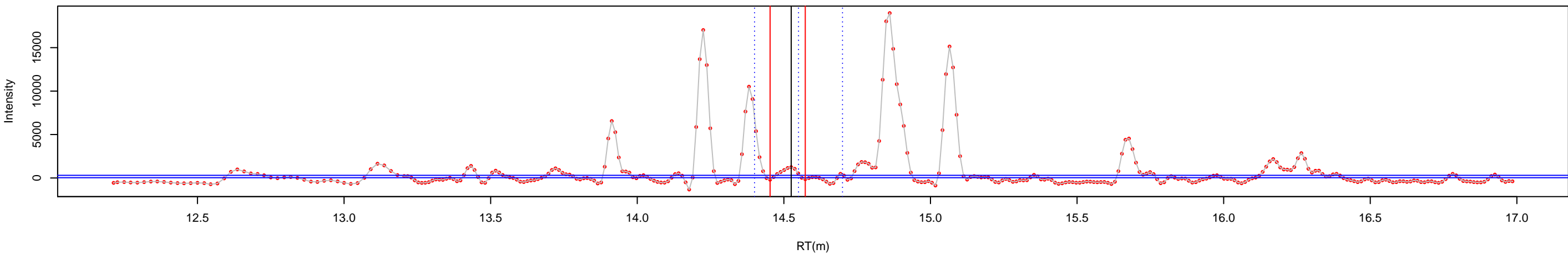
peak area | window size:3 BLine: yes



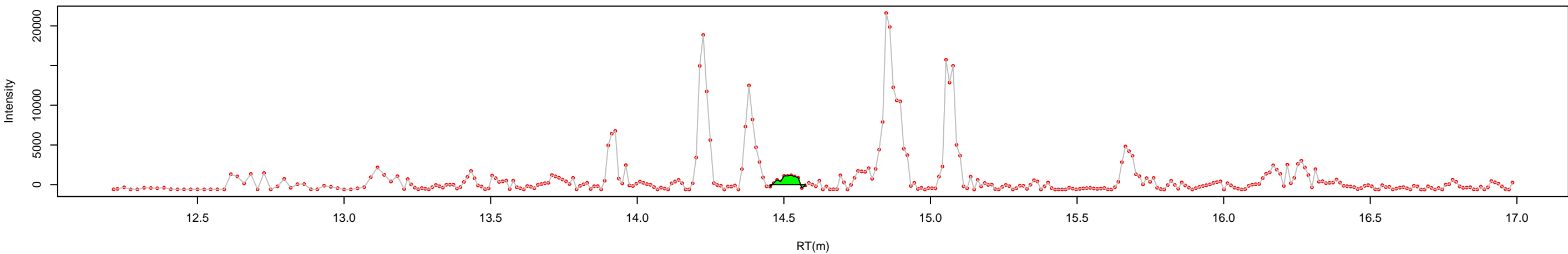
raw chromatogram | batch: 3 sample: cotn66 conc: NA function: 1 mass: 389.35>389.35



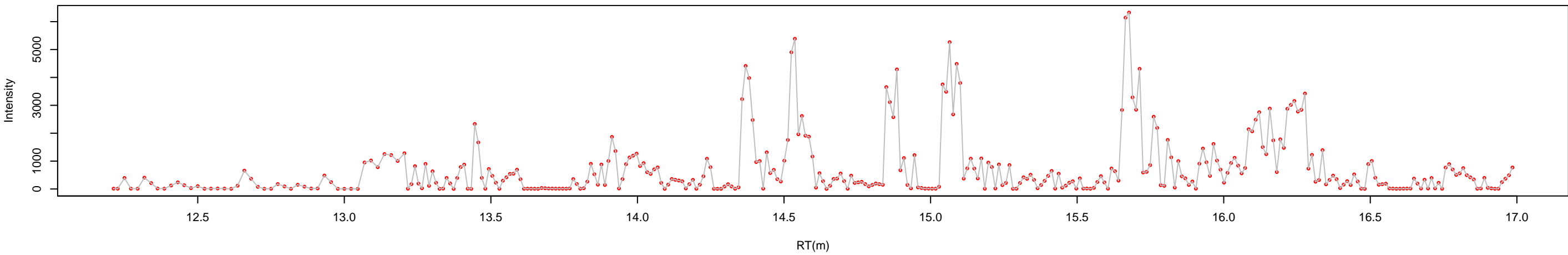
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 30.5 BLine: yes



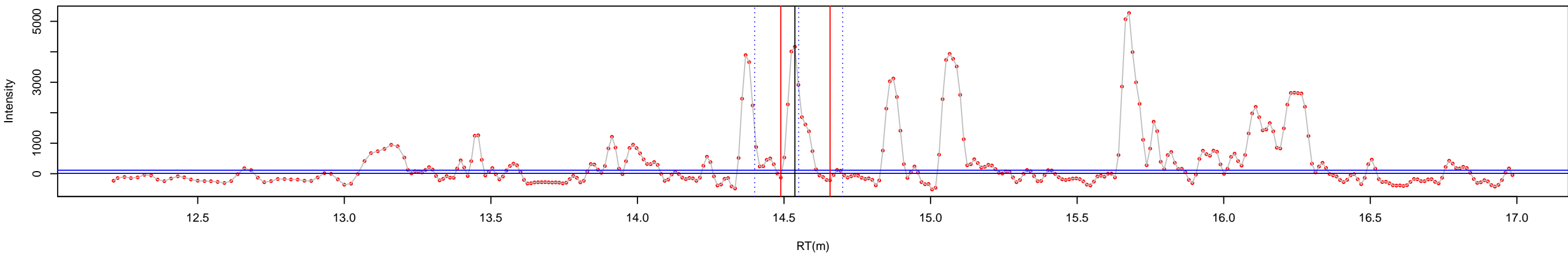
peak area | window size:3 BLine: yes



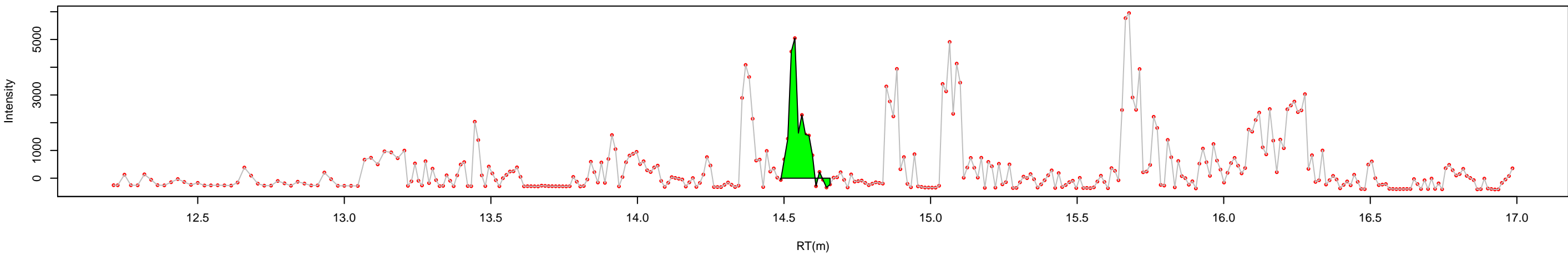
raw chromatogram | batch: 3 sample: cotn67 conc: NA function: 1 mass: 389.35>389.35



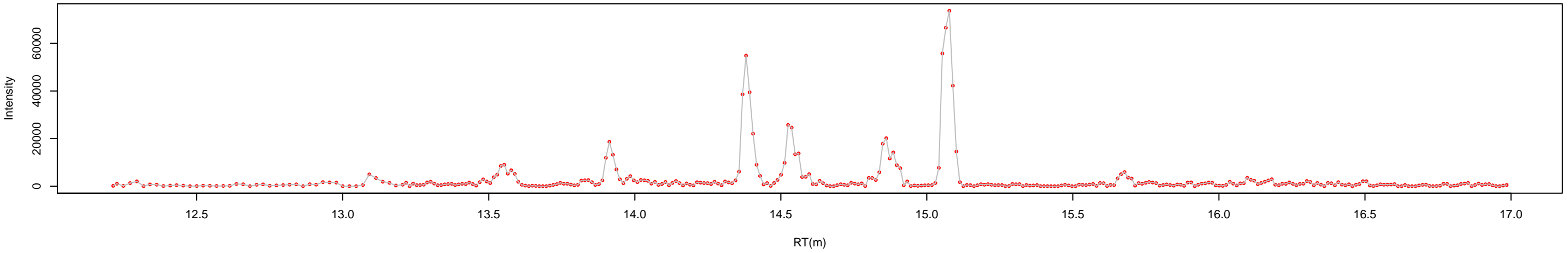
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 11.3 BLine: yes



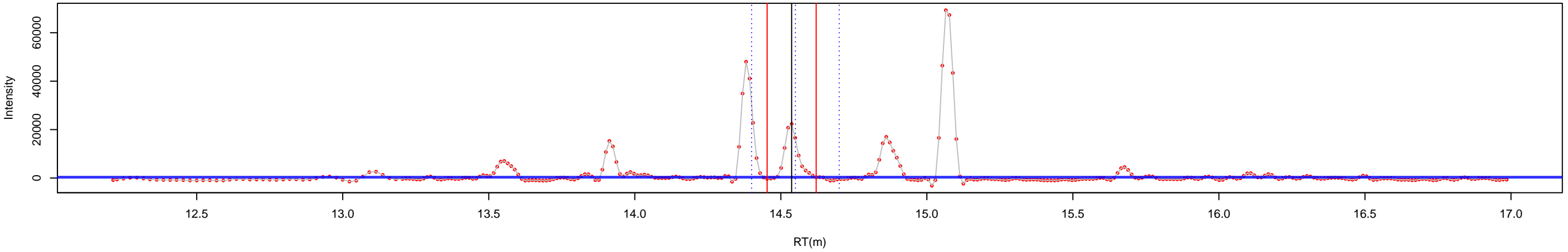
peak area | window size:3 BLine: yes



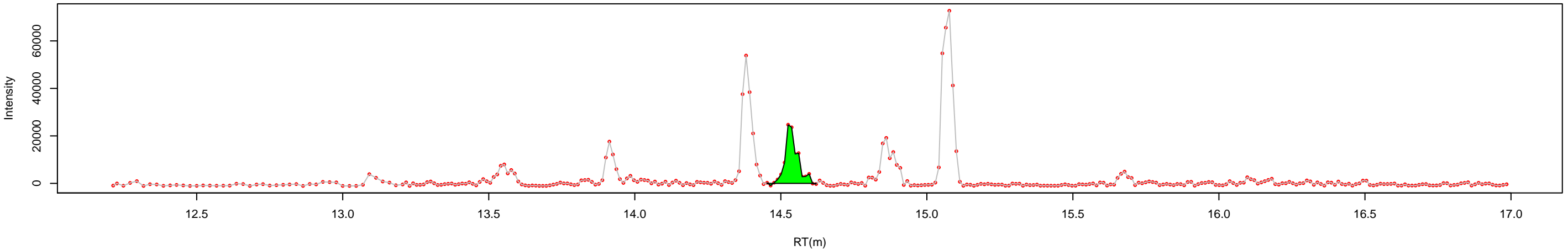
raw chromatogram | batch: 3 sample: cotn195 conc: NA function: 1 mass: 389.35>389.35



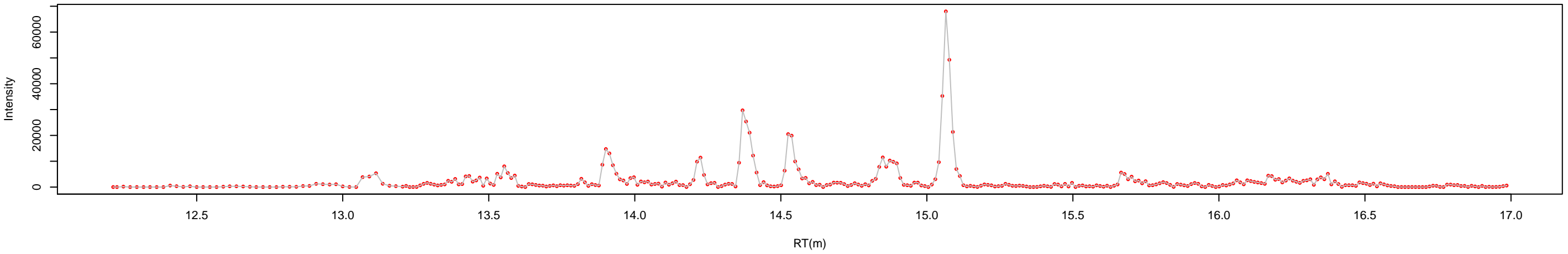
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 62.7 BLine: yes



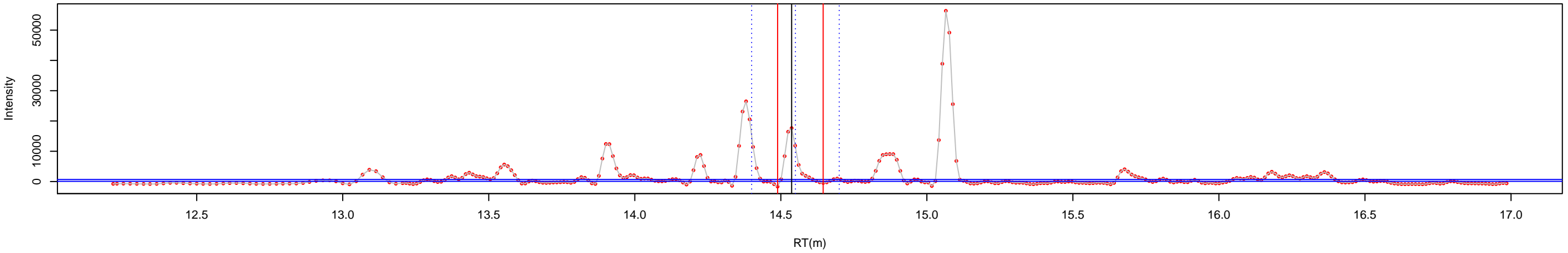
peak area | window size:3 BLine: yes



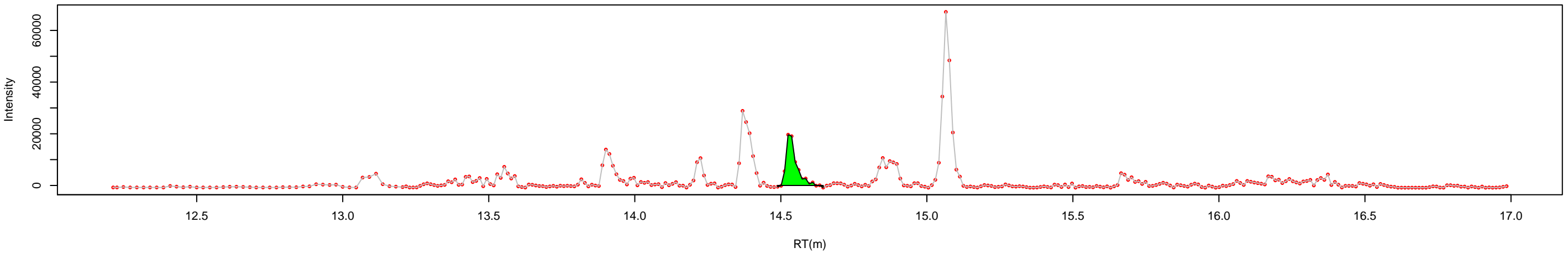
raw chromatogram | batch: 3 sample: cotn196 conc: NA function: 1 mass: 389.35>389.35



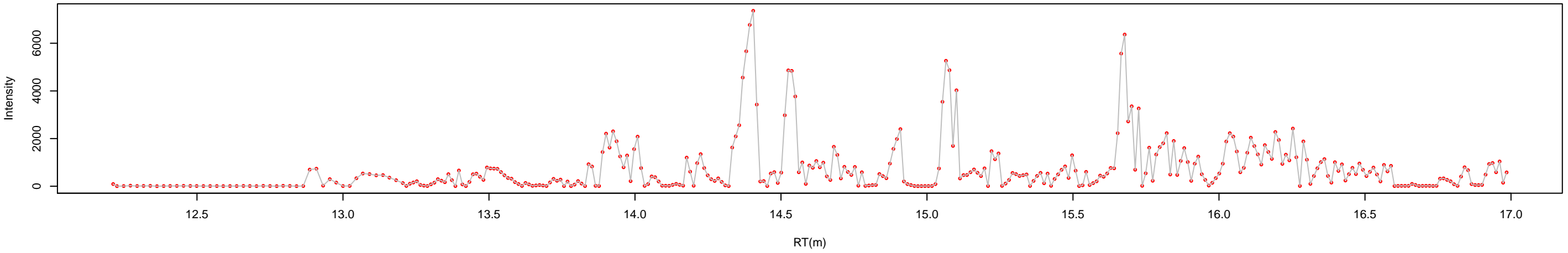
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 68 BLine: yes



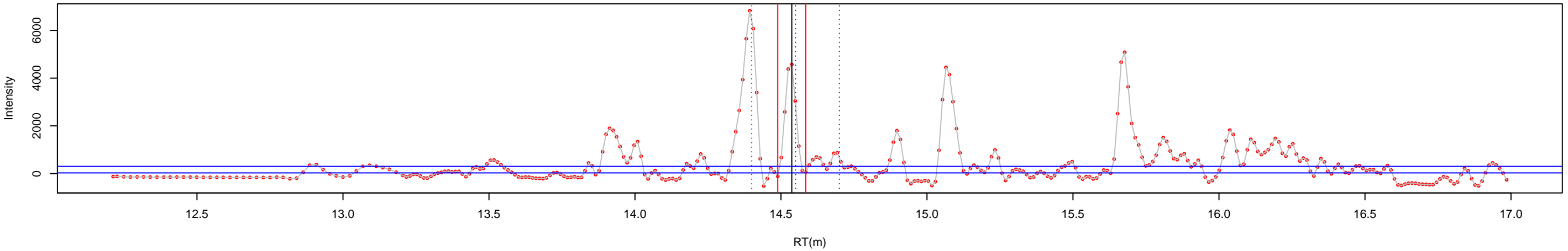
peak area | window size:3 BLine: yes



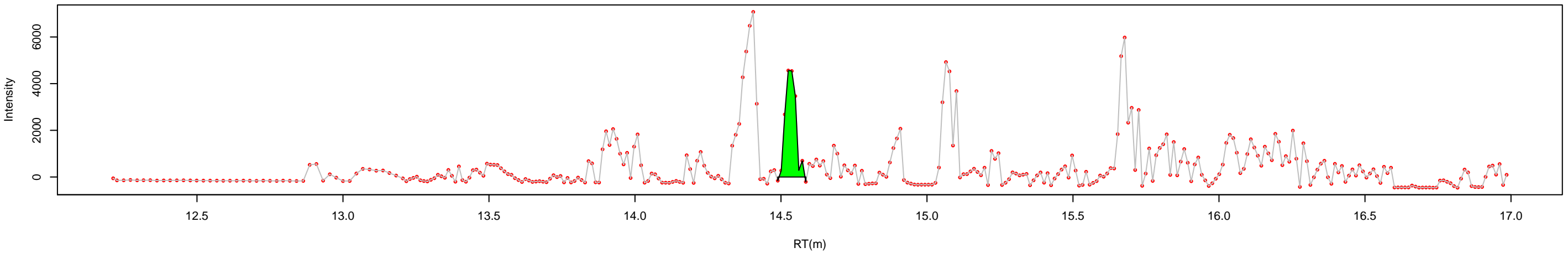
raw chromatogram | batch: 3 sample: cotn197 conc: NA function: 1 mass: 389.35>389.35



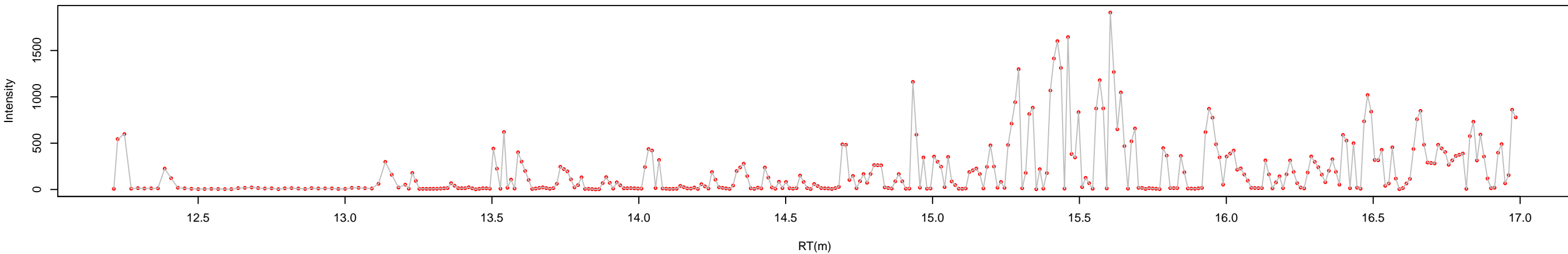
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 30.4 BLine: yes



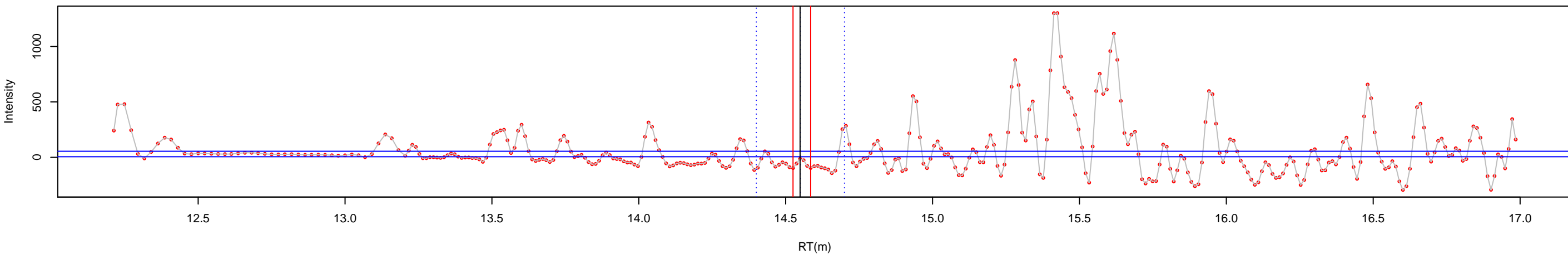
peak area | window size:3 BLine: yes



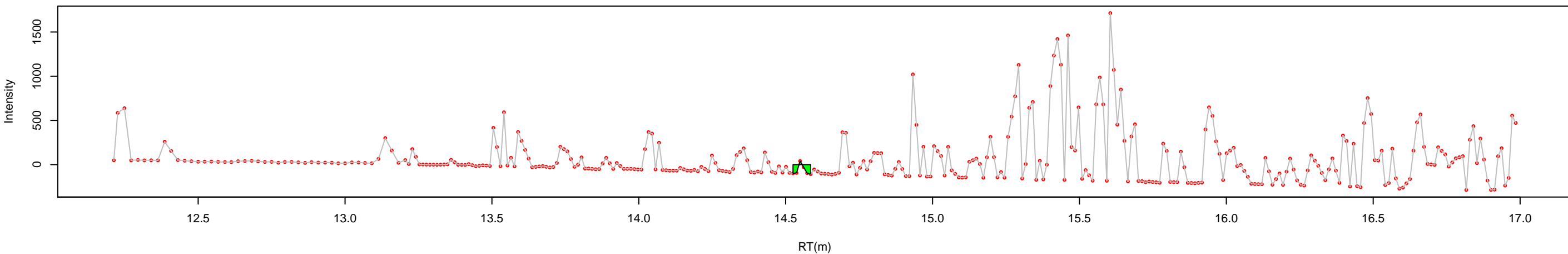
raw chromatogram | batch: 3 sample: std0-10ul-3 conc: 0.001 function: 1 mass: 389.35>389.35



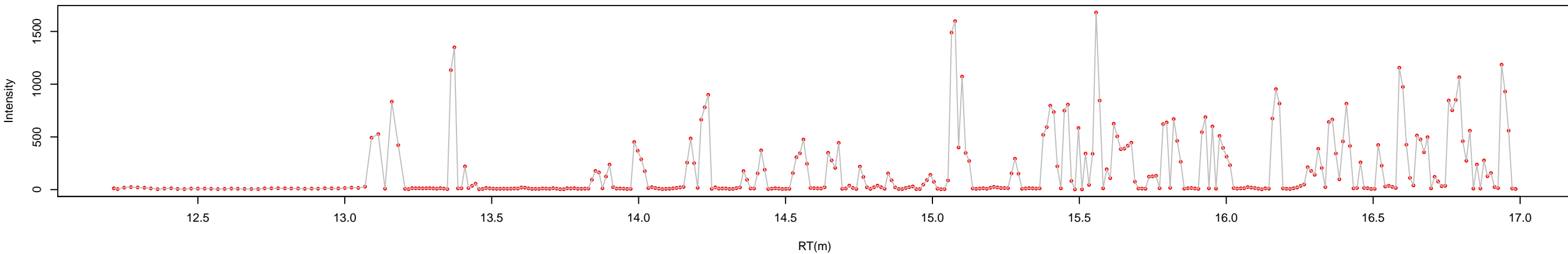
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 5.48 BLine: yes



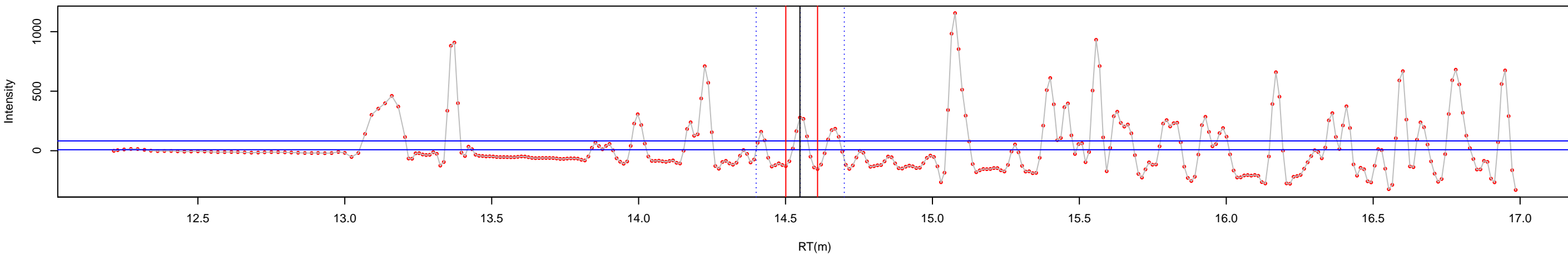
peak area | window size:3 BLine: yes



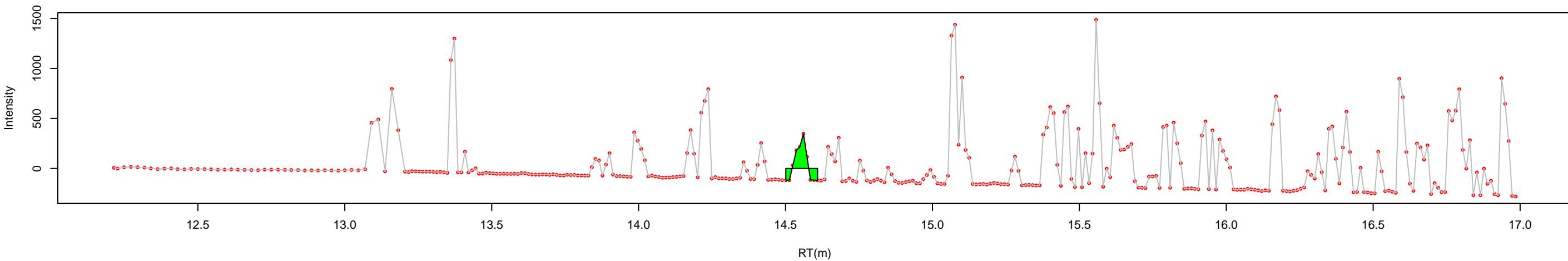
raw chromatogram | batch: 3 sample: std1-10ul-3 conc: 0.002 function: 1 mass: 389.35>389.35



peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 8.22 BLine: yes

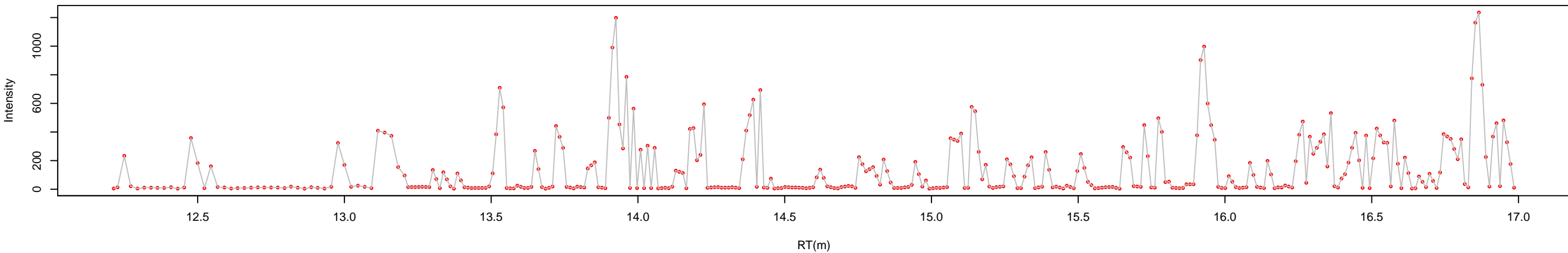


peak area | window size:3 BLine: yes

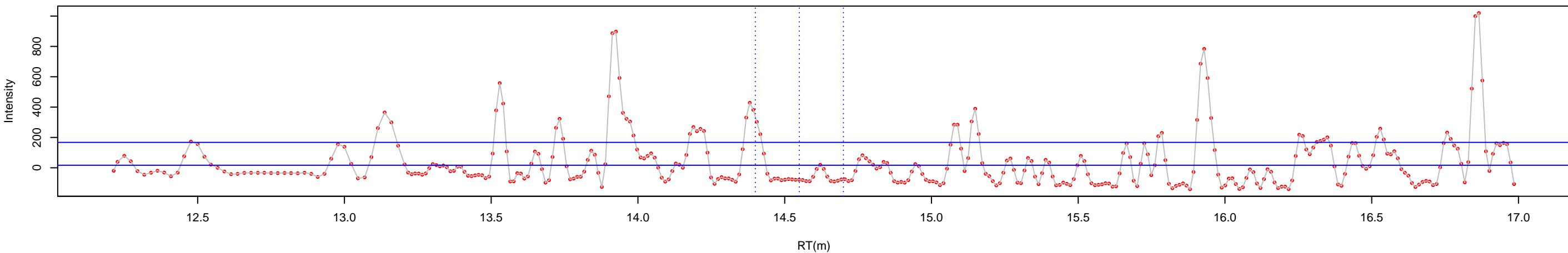




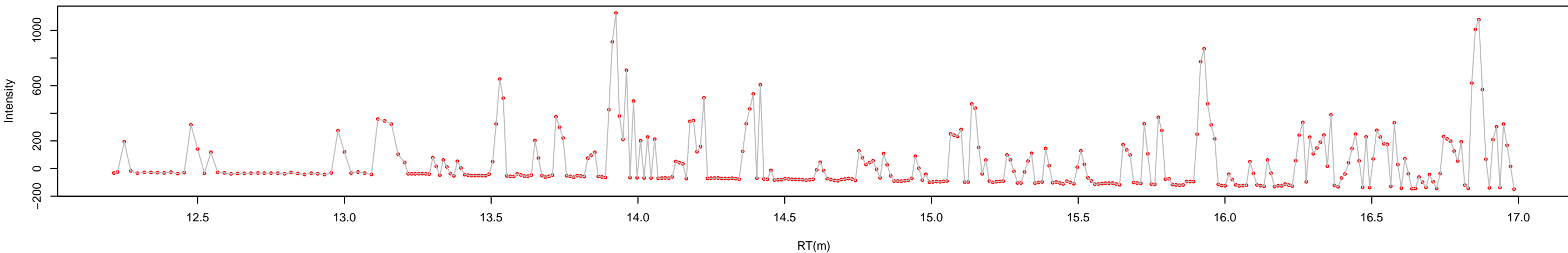
raw chromatogram | batch: 3 sample: std2-10ul-3 conc: 0.005 function: 1 mass: 389.35>389.35



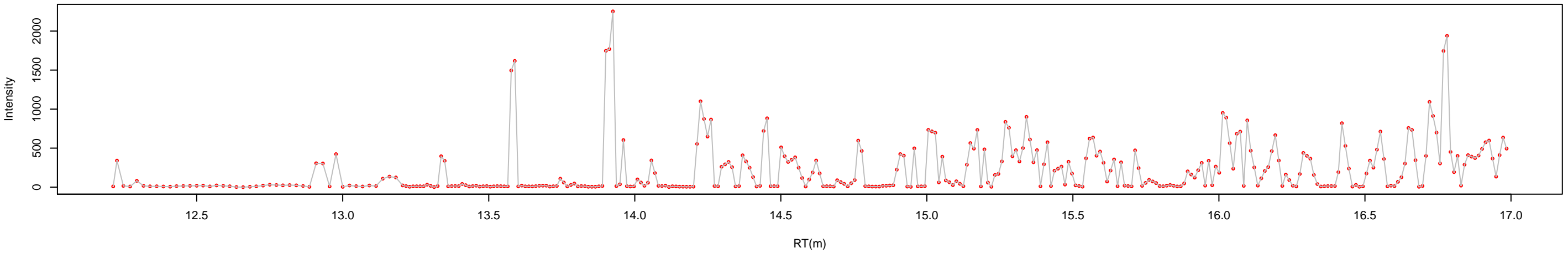
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 16.7 BLine: yes



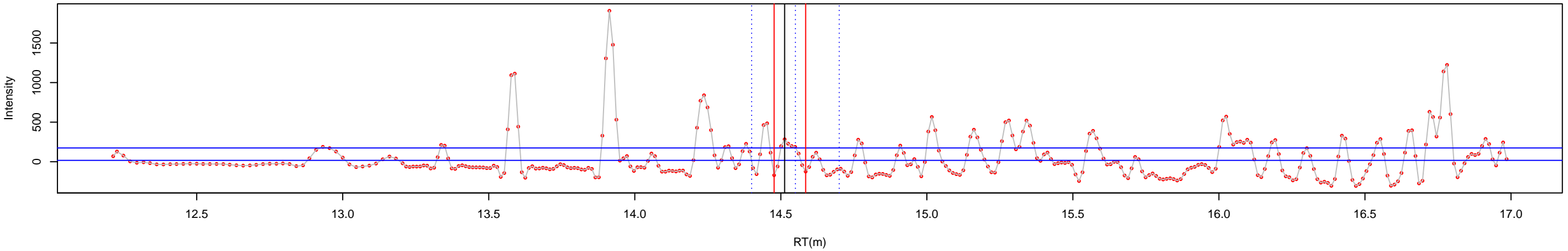
peak area | window size:3 BLine: yes



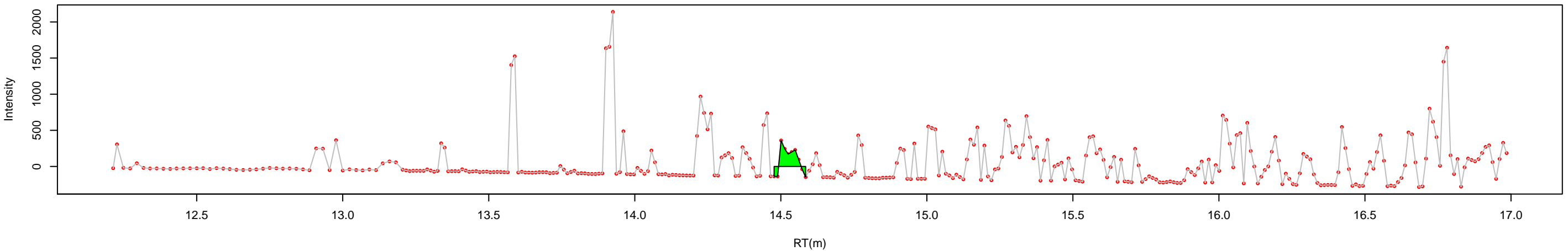
raw chromatogram | batch: 3 sample: std3-10ul-3 conc: 0.01 function: 1 mass: 389.35>389.35



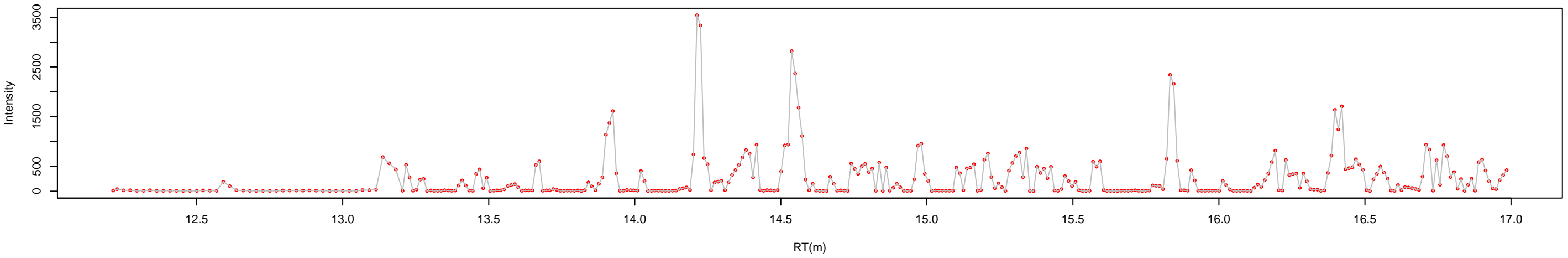
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 17.4 BLine: yes



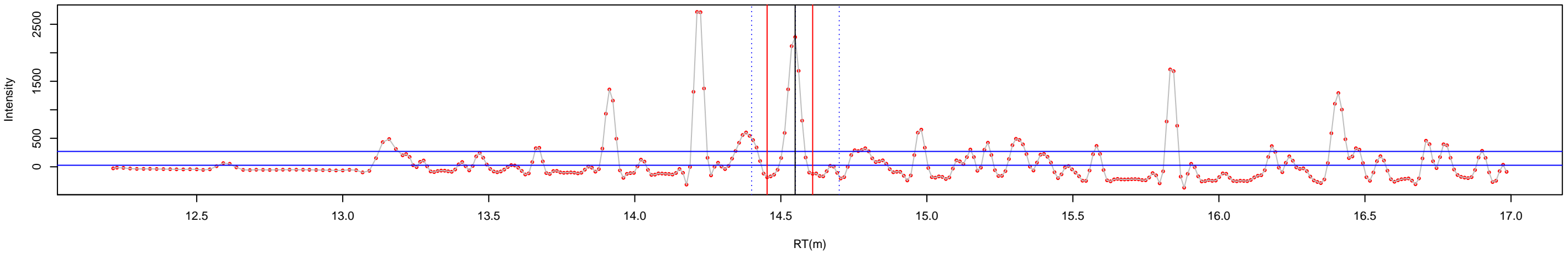
peak area | window size:3 BLine: yes



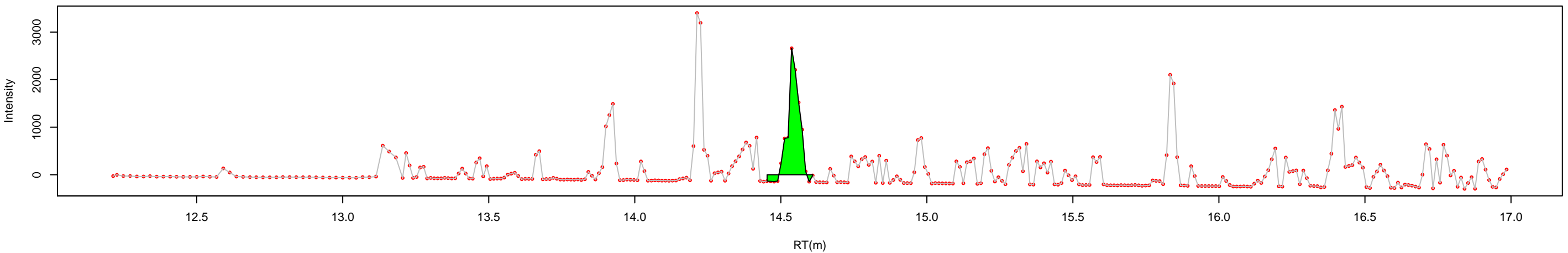
raw chromatogram | batch: 3 sample: std4-10ul-3 conc: 0.02 function: 1 mass: 389.35>389.35



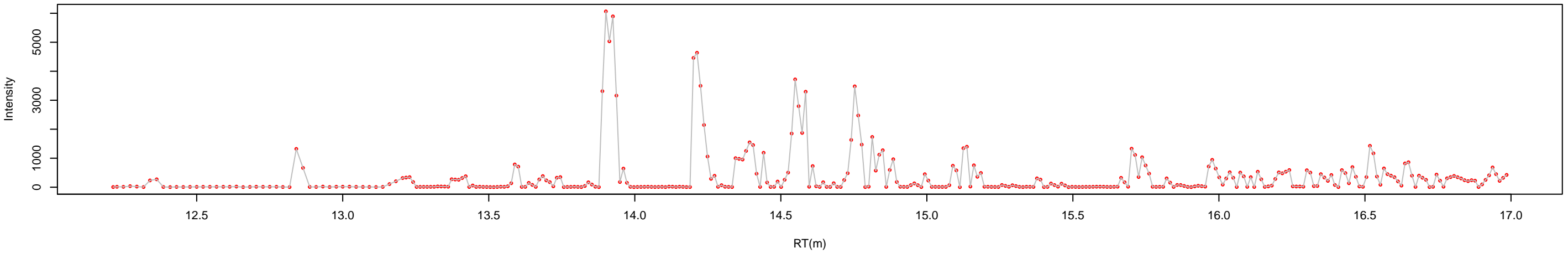
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 26.9 BLine: yes



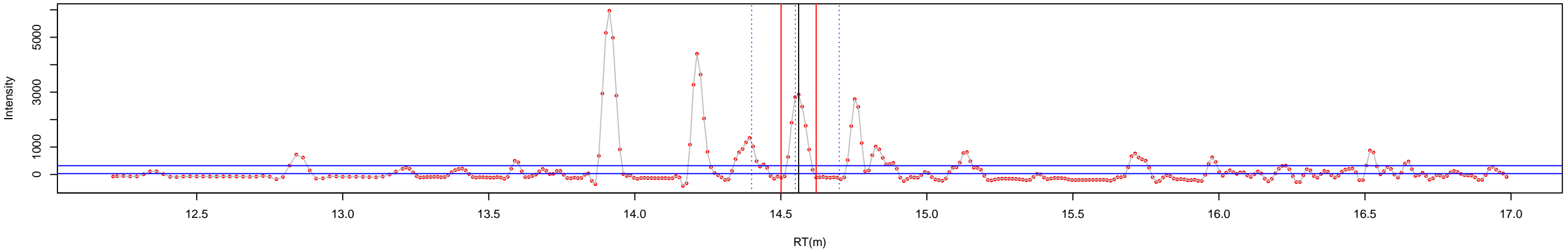
peak area | window size:3 BLine: yes



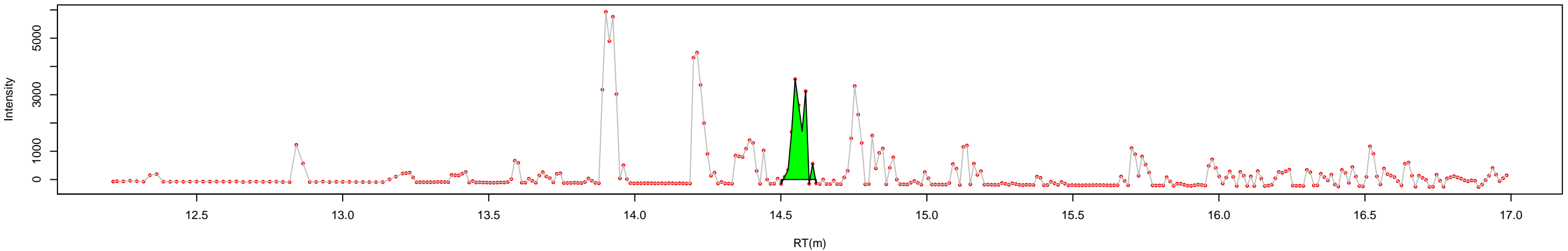
raw chromatogram | batch: 3 sample: std5-10ul-3 conc: 0.05 function: 1 mass: 389.35>389.35



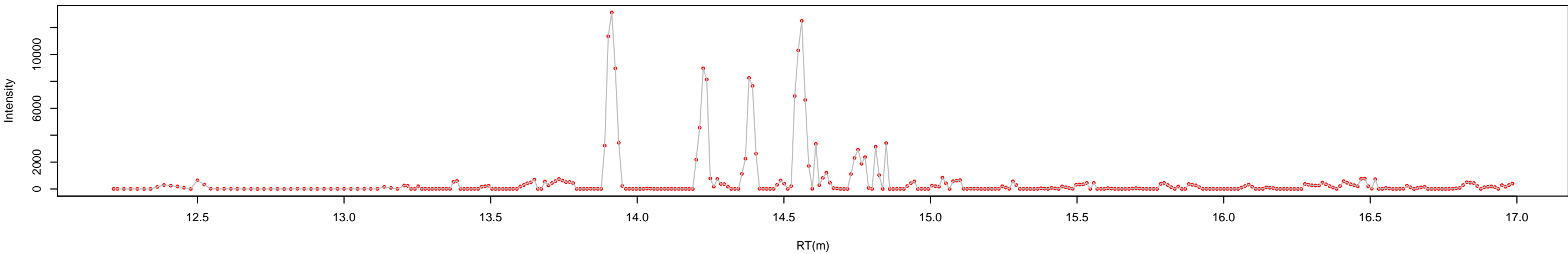
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 32.1 BLine: yes



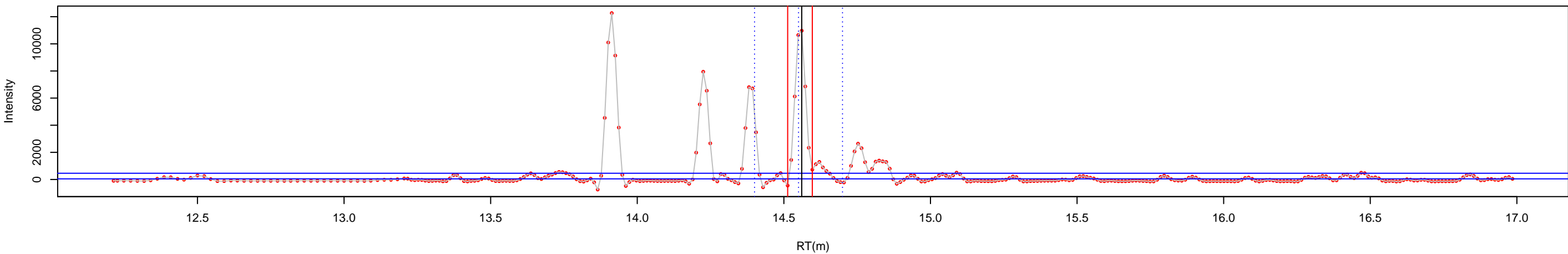
peak area | window size:3 BLine: yes



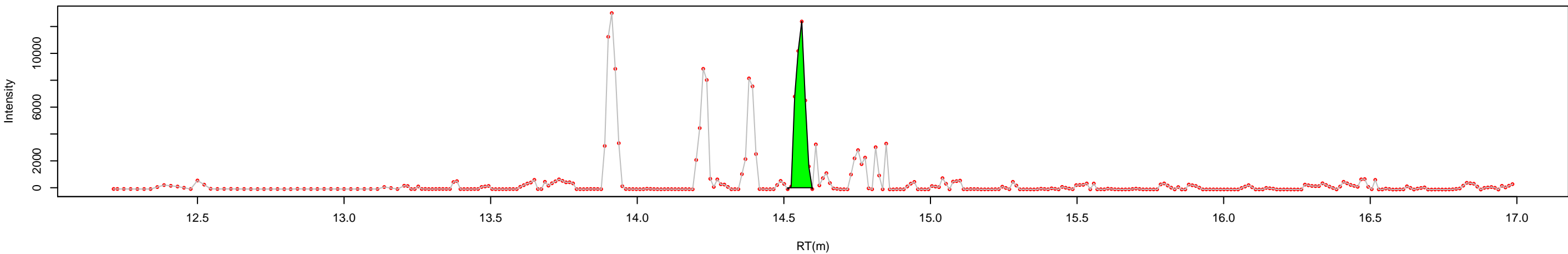
raw chromatogram | batch: 3 sample: std6-10ul-3 conc: 0.1 function: 1 mass: 389.35>389.35



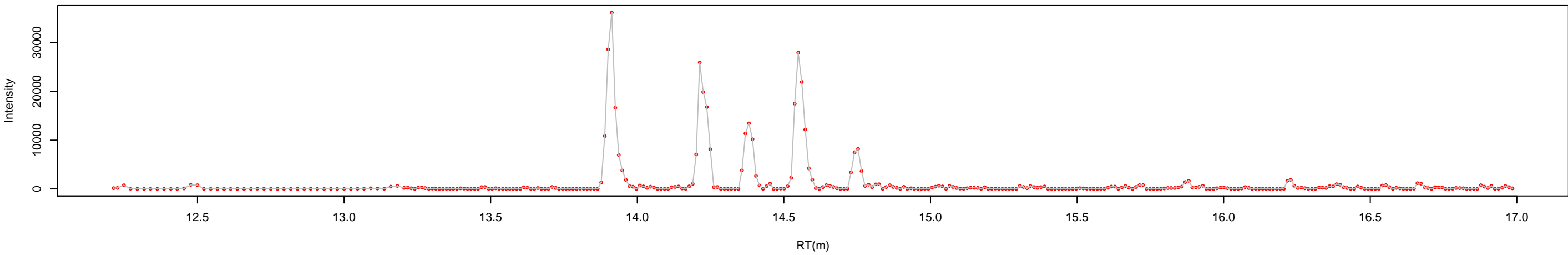
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 45.9 BLine: yes



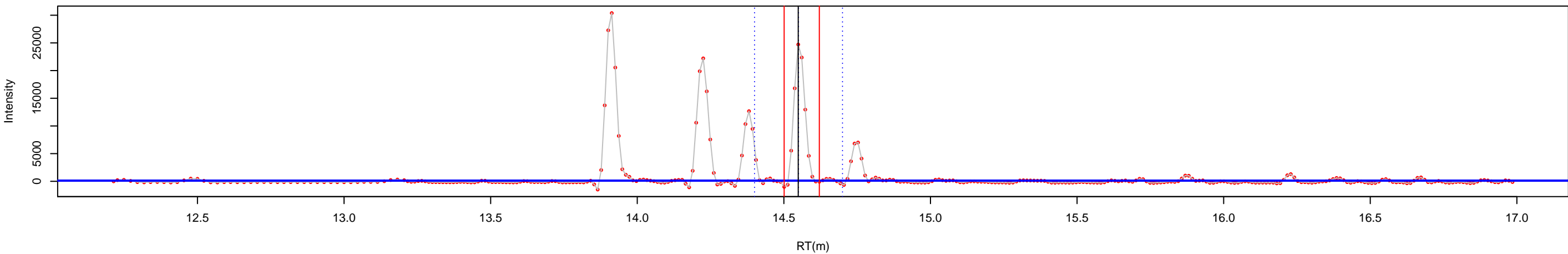
peak area | window size:3 BLine: yes



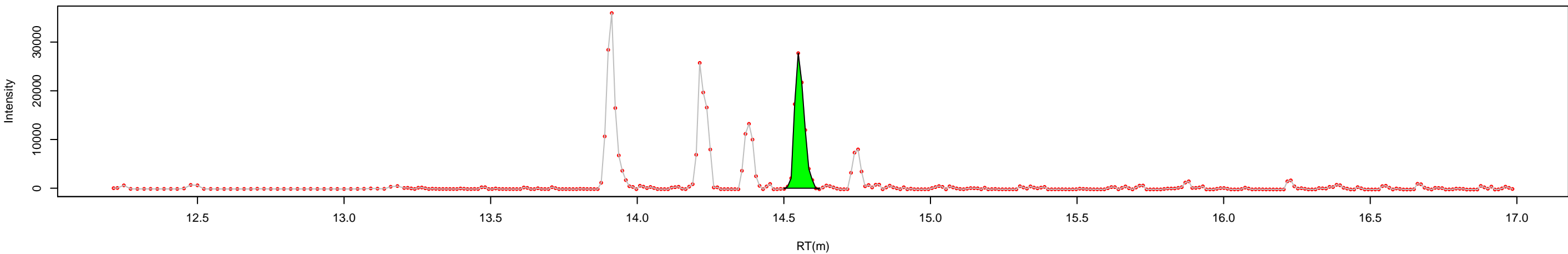
raw chromatogram | batch: 3 sample: std7-10ul-3 conc: 0.2 function: 1 mass: 389.35>389.35



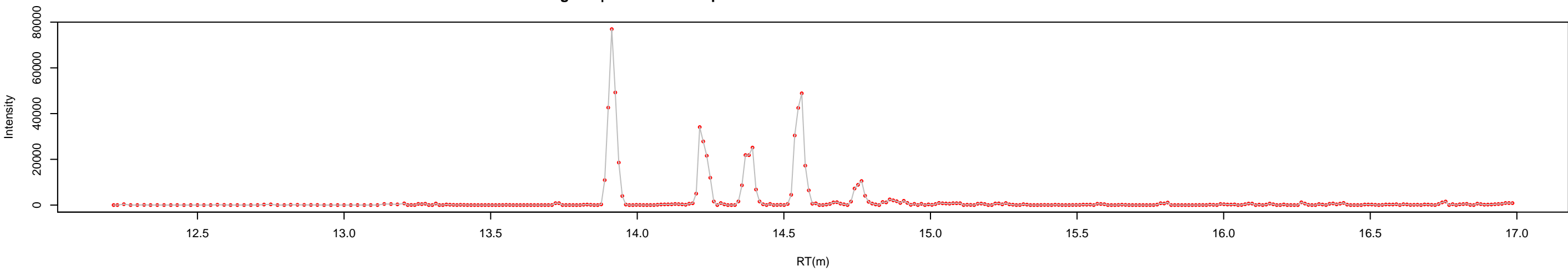
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 22.5 BLine: yes



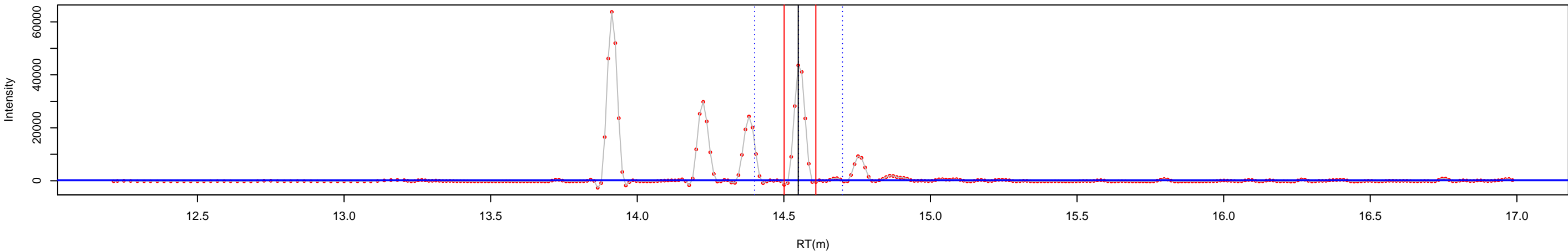
peak area | window size:3 BLine: yes



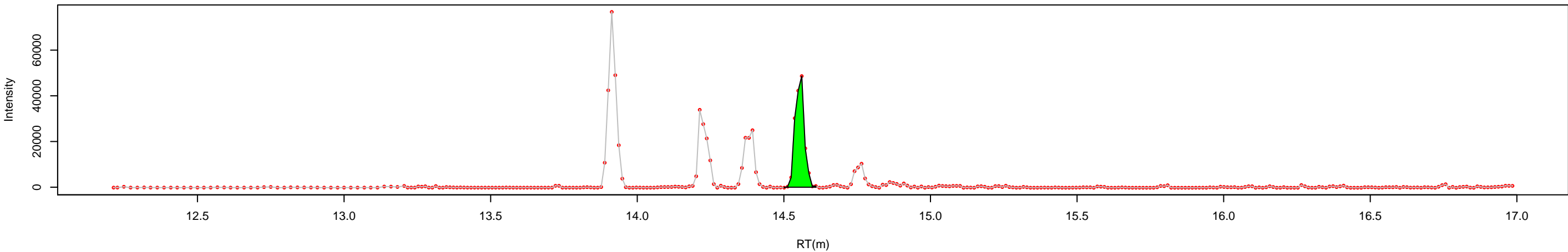
raw chromatogram | batch: 3 sample: std8-10ul-3 conc: 0.5 function: 1 mass: 389.35>389.35



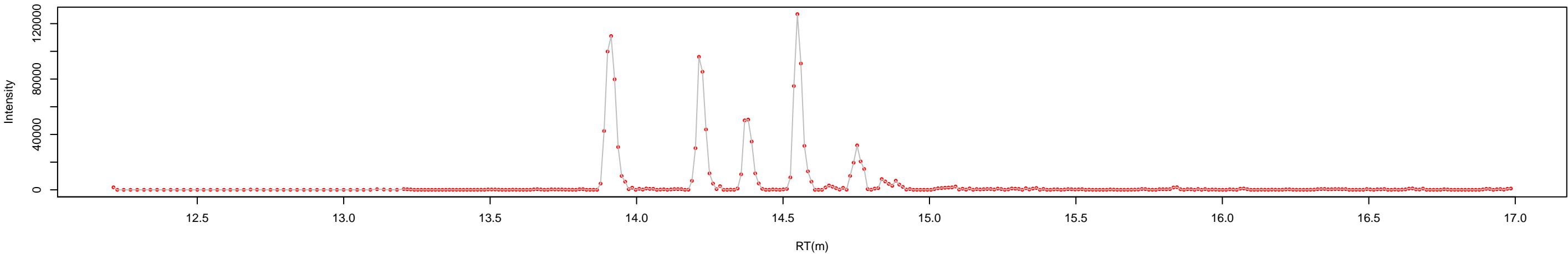
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 35.8 BLine: yes



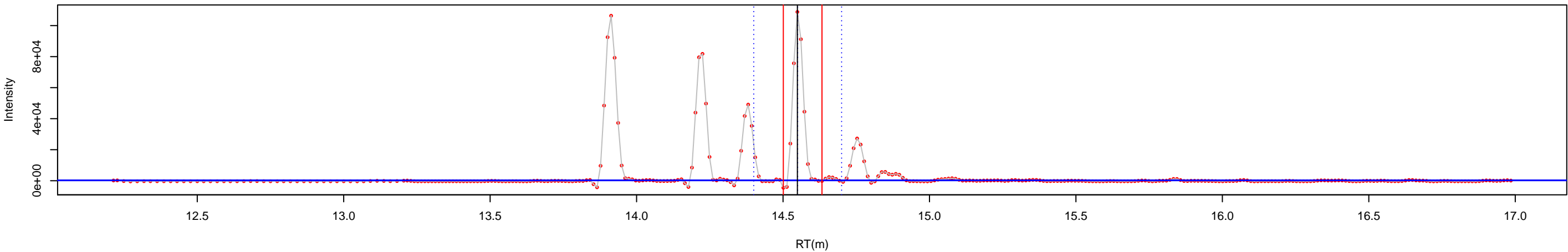
peak area | window size:3 BLine: yes



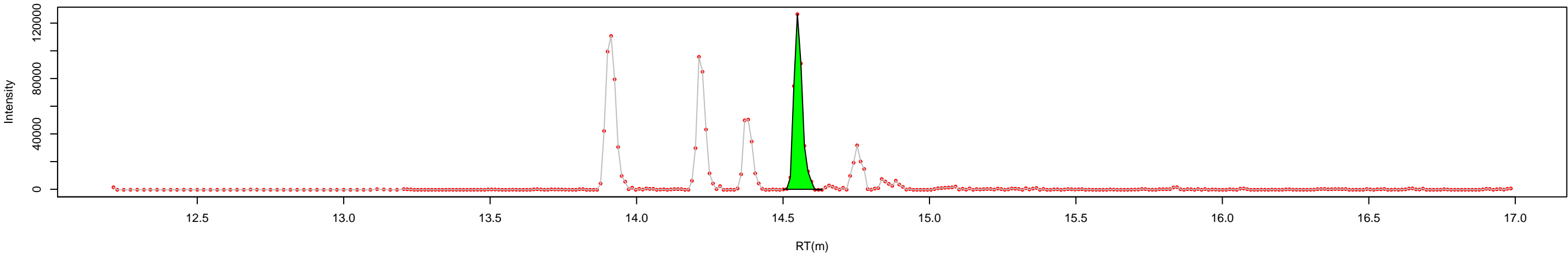
raw chromatogram | batch: 3 sample: std9-10ul-3 conc: 1 function: 1 mass: 389.35>389.35



peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 43.3 BLine: yes

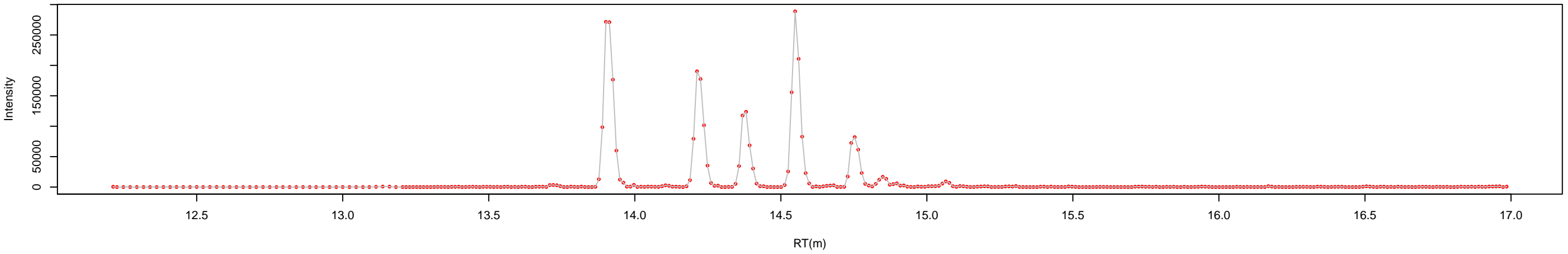


peak area | window size:3 BLine: yes

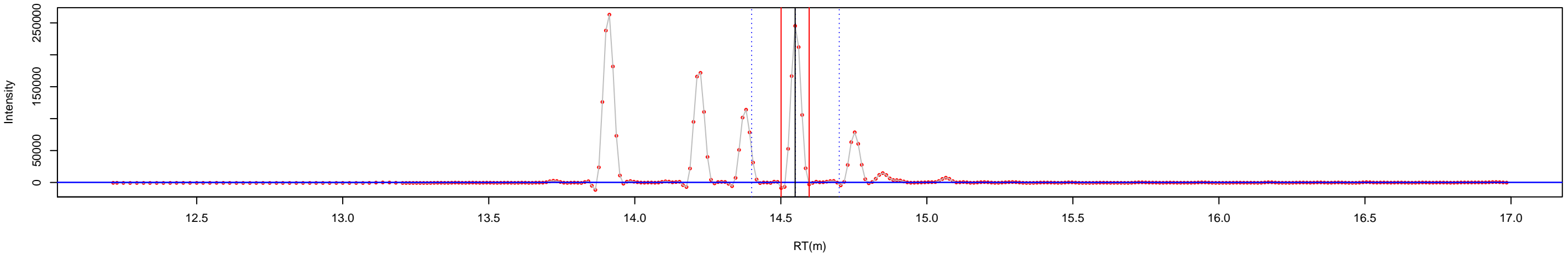




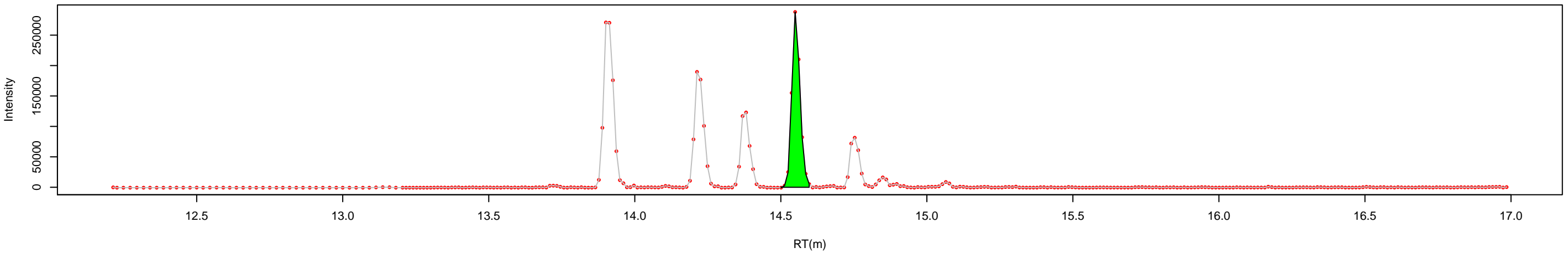
raw chromatogram | batch: 3 sample: std10-10ul-3 conc: 2 function: 1 mass: 389.35>389.35



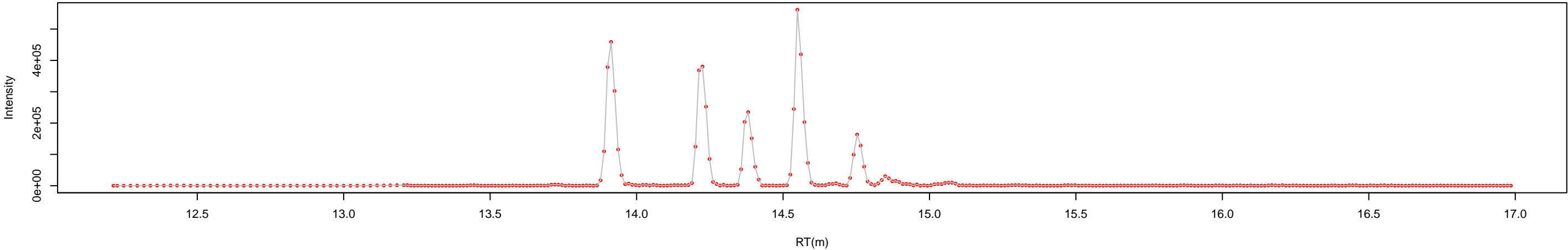
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 28.3 BLine: yes



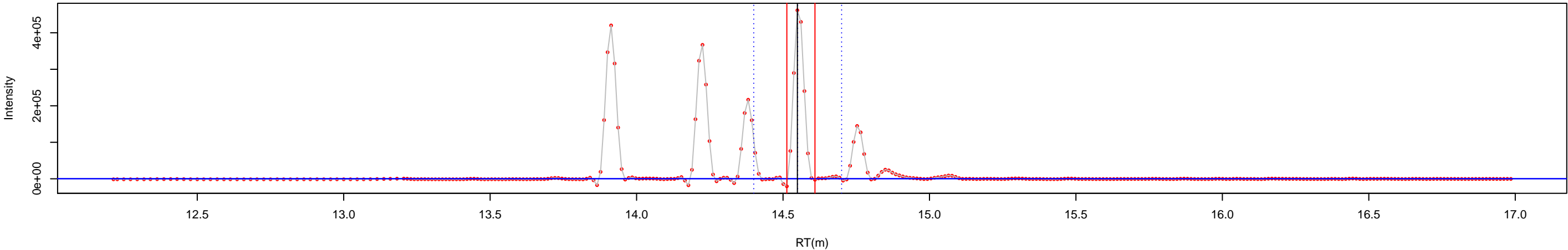
peak area | window size:3 BLine: yes



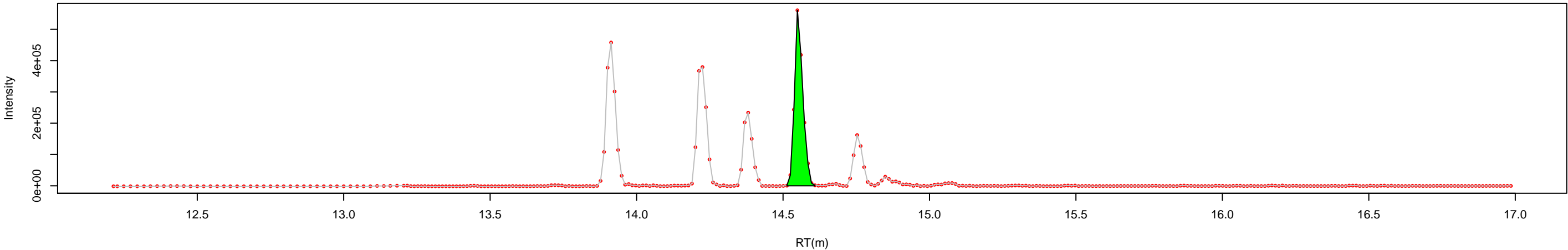
raw chromatogram | batch: 3 sample: std11-10ul-3 conc: 5 function: 1 mass: 389.35>389.35



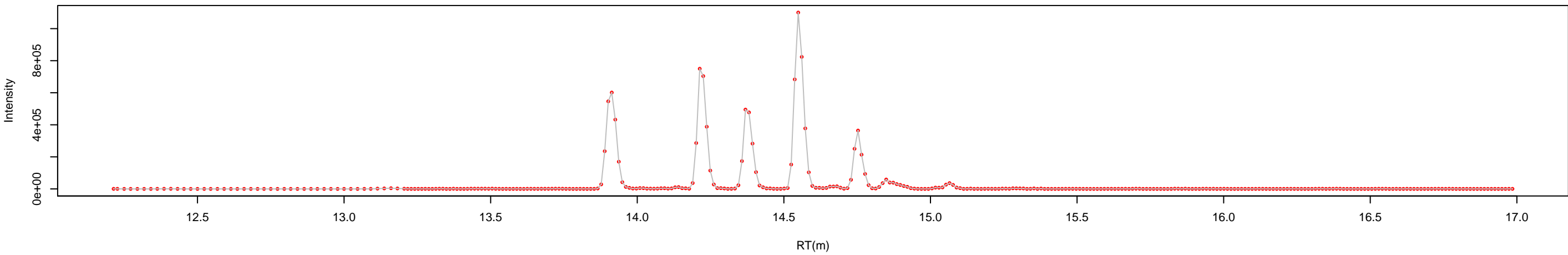
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 46.9 BLine: yes



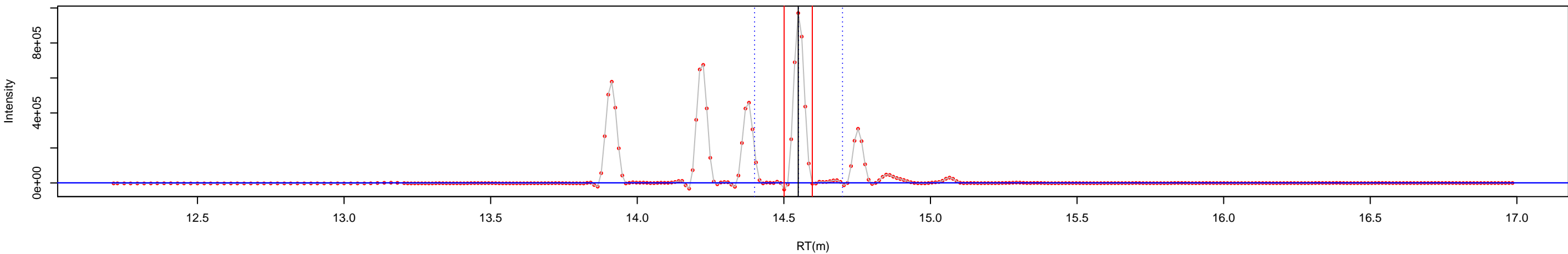
peak area | window size:3 BLine: yes



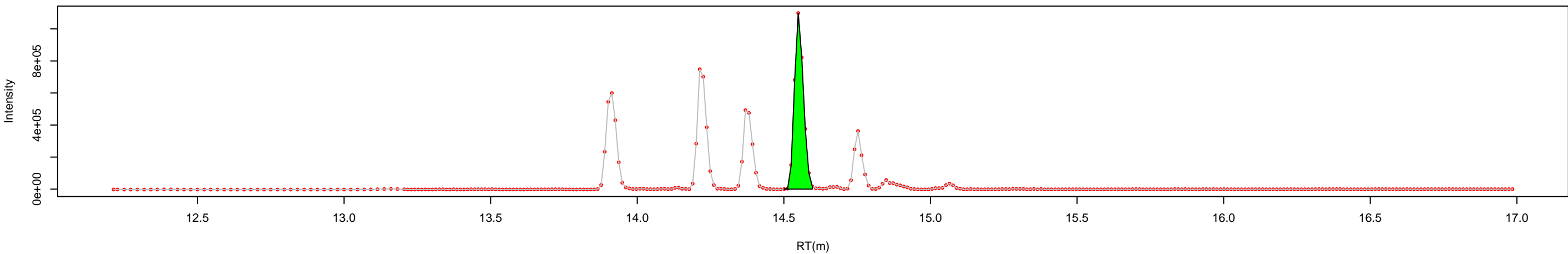
raw chromatogram | batch: 3 sample: std12-10ul-3 conc: 10 function: 1 mass: 389.35>389.35



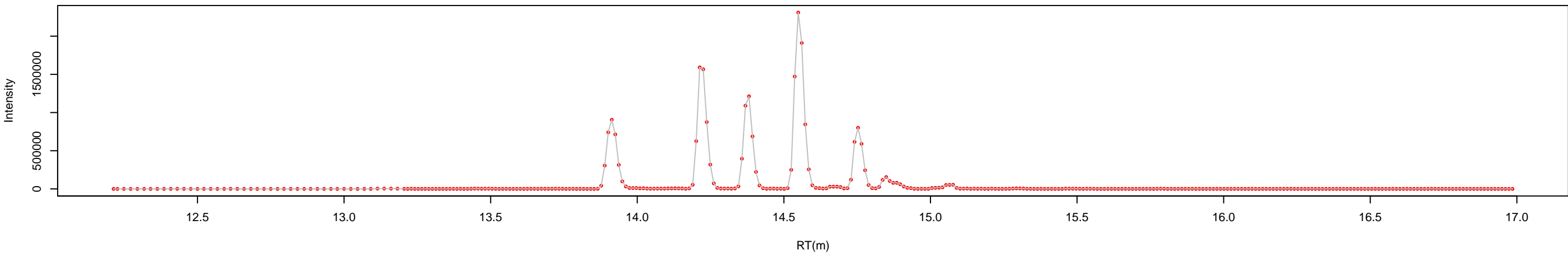
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 127 BLine: yes



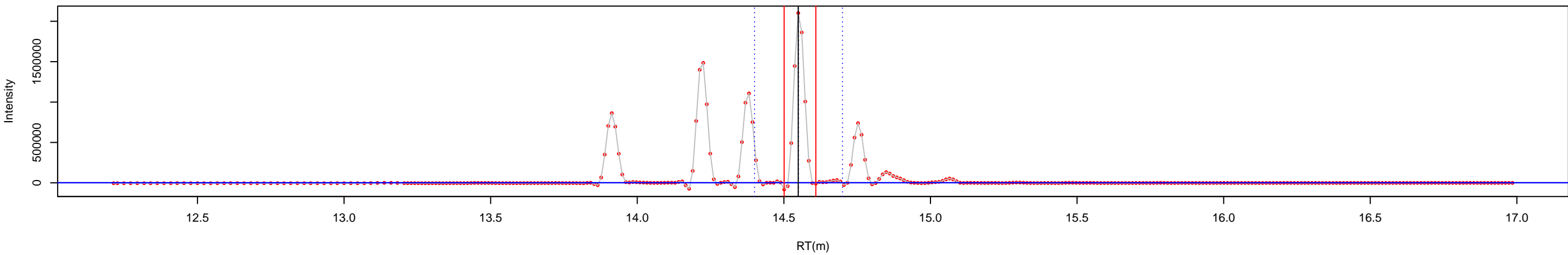
peak area | window size:3 BLine: yes



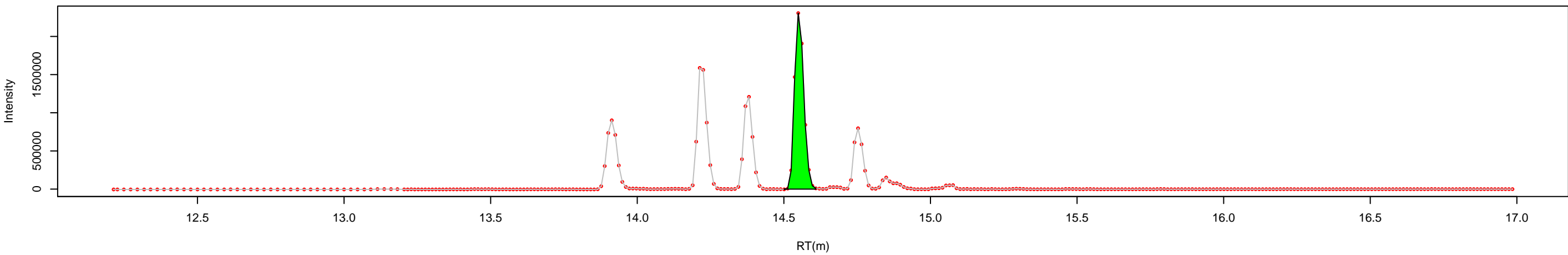
raw chromatogram | batch: 3 sample: std13-10ul-3 conc: 20 function: 1 mass: 389.35>389.35



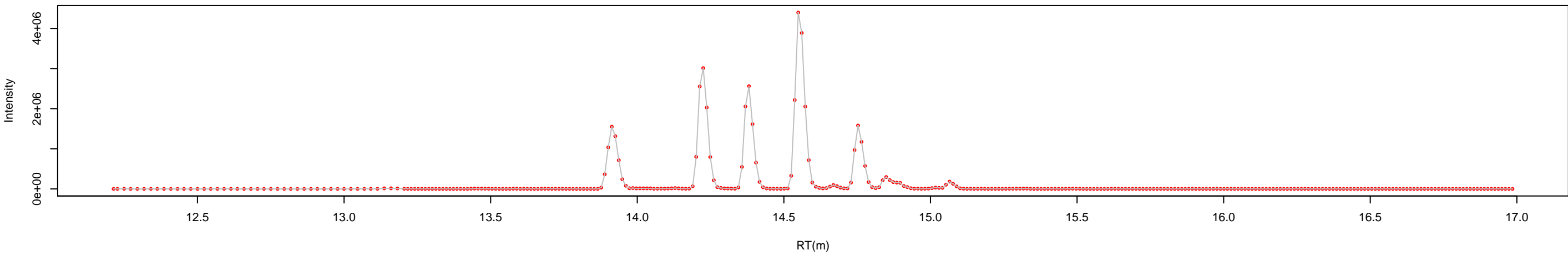
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 276 BLine: yes



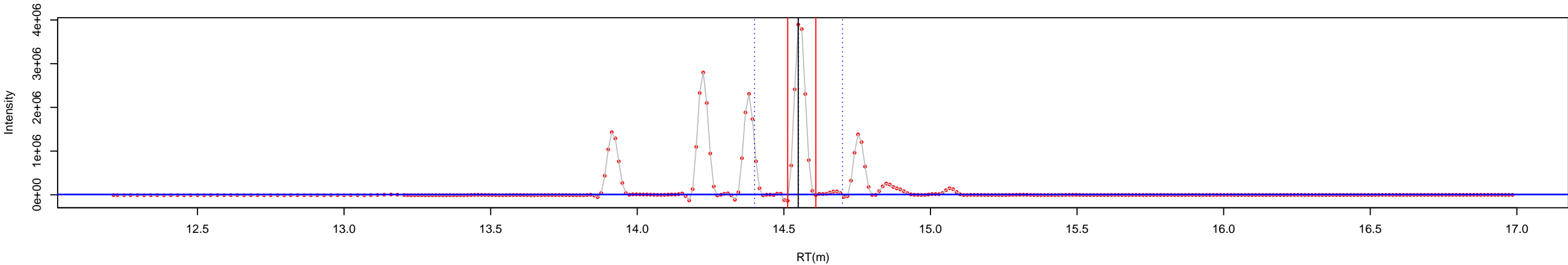
peak area | window size:3 BLine: yes



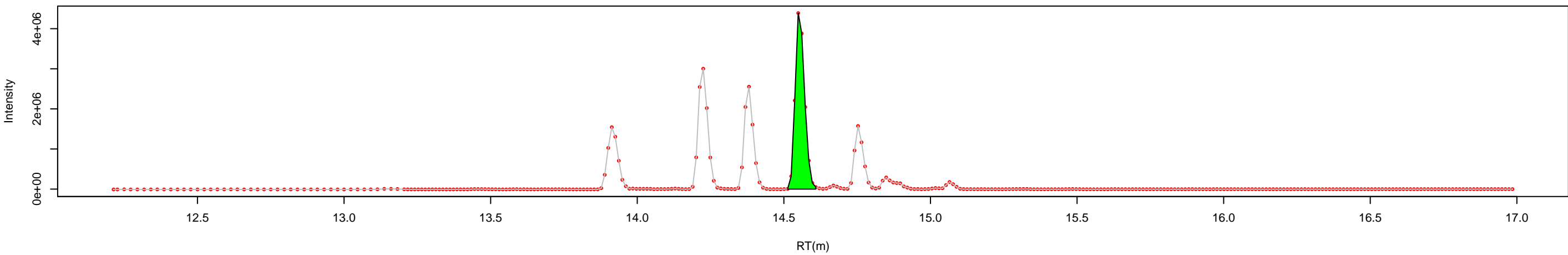
raw chromatogram | batch: 3 sample: std14-10ul-3 conc: 50 function: 1 mass: 389.35>389.35



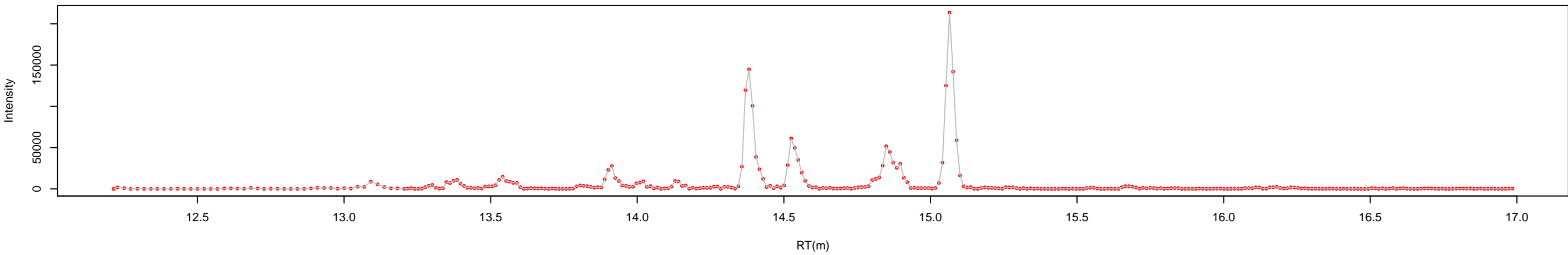
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 1310 BLine: yes



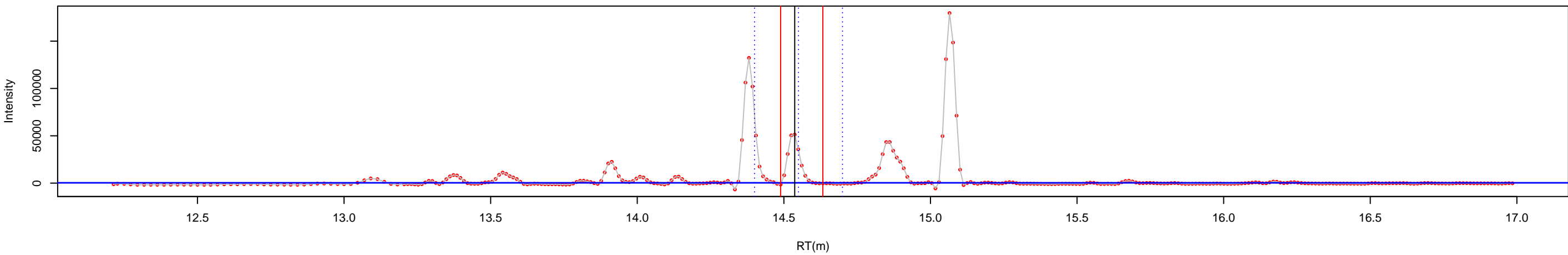
peak area | window size:3 BLine: yes



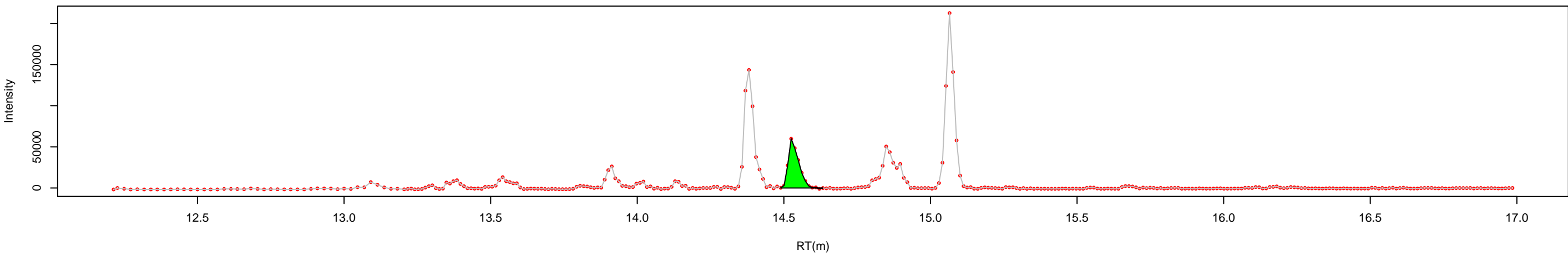
raw chromatogram | batch: 4 sample: cotor1 conc: NA function: 1 mass: 389.35>389.35



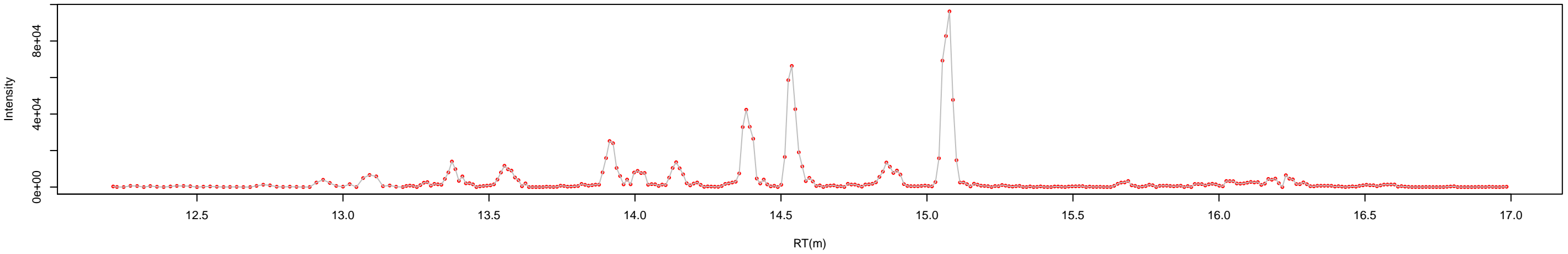
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 57.8 BLine: yes



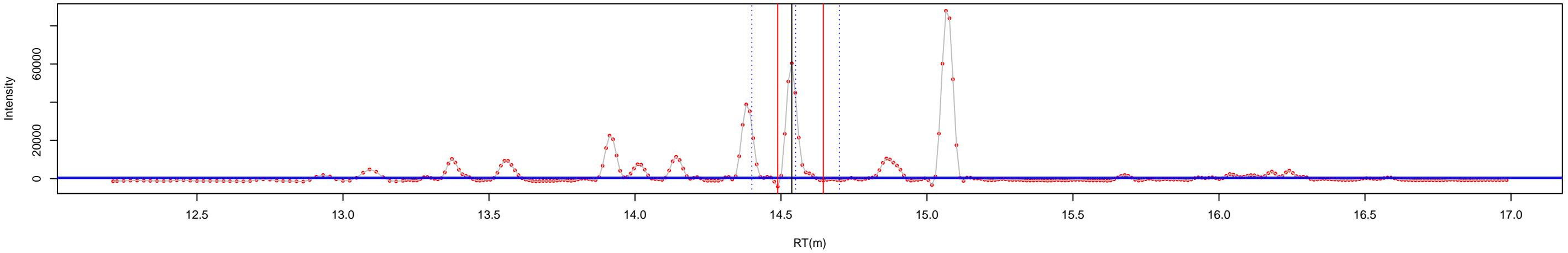
peak area | window size:3 BLine: yes



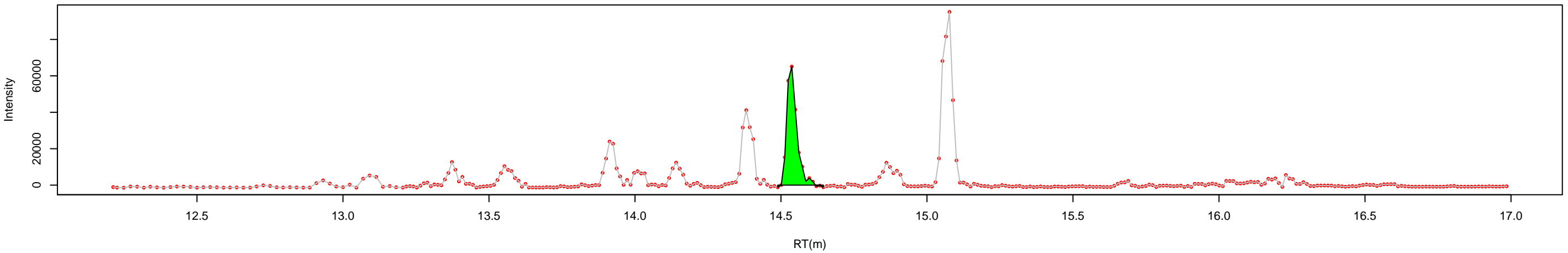
raw chromatogram | batch: 4 sample: cotor2 conc: NA function: 1 mass: 389.35>389.35



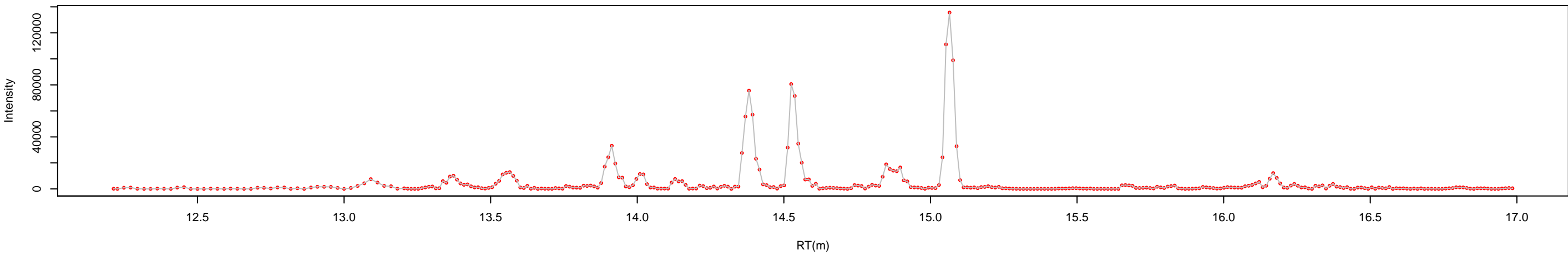
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 79.8 BLine: yes



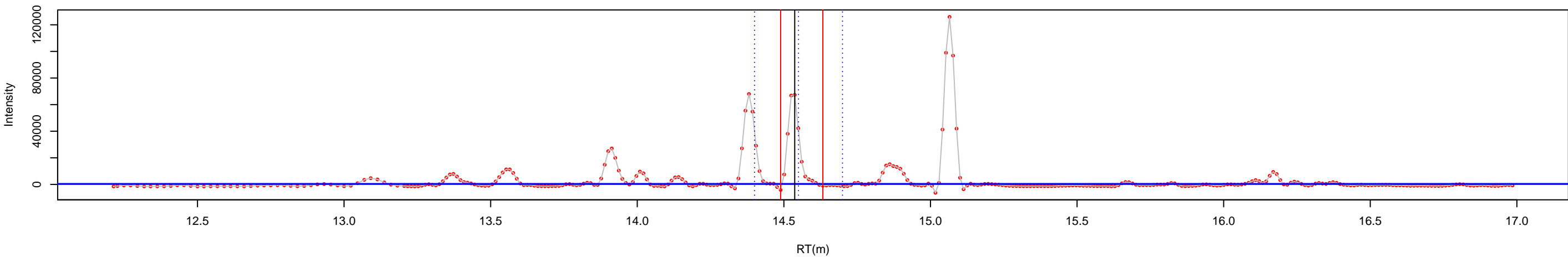
peak area | window size:3 BLine: yes



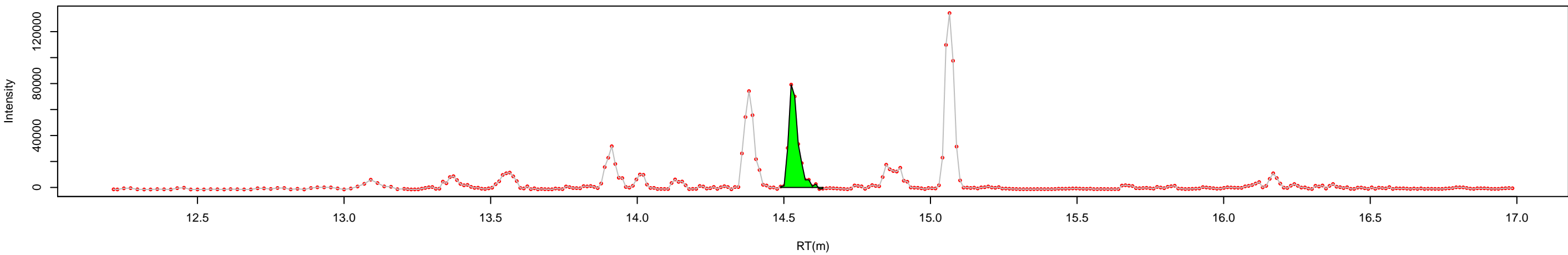
raw chromatogram | batch: 4 sample: cotor3 conc: NA function: 1 mass: 389.35>389.35



peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 60.1 BLine: yes

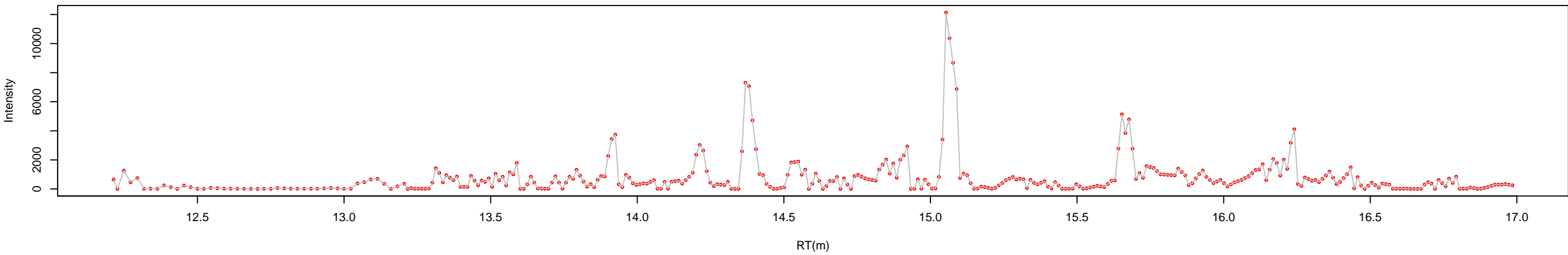


peak area | window size:3 BLine: yes

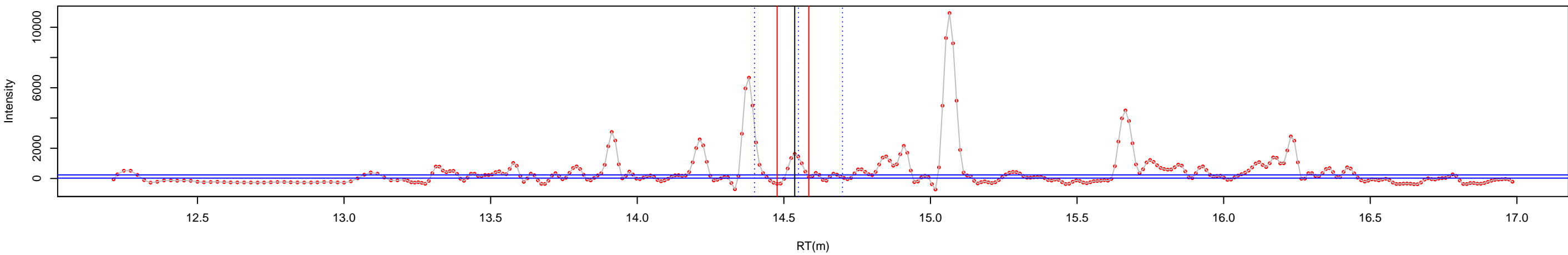




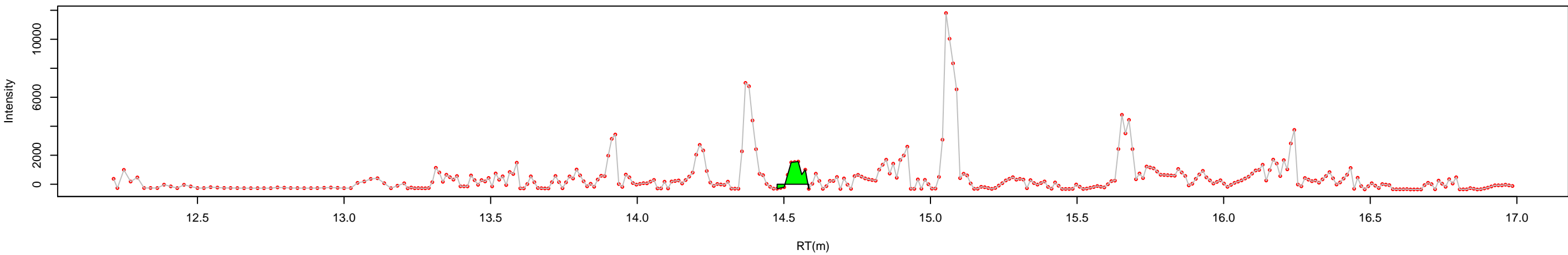
raw chromatogram | batch: 4 sample: cotor4 conc: NA function: 1 mass: 389.35>389.35



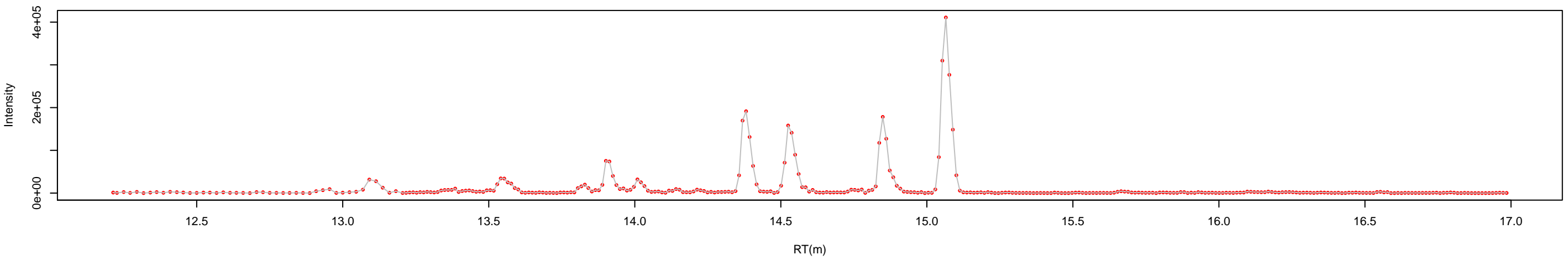
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 23.8 BLine: yes



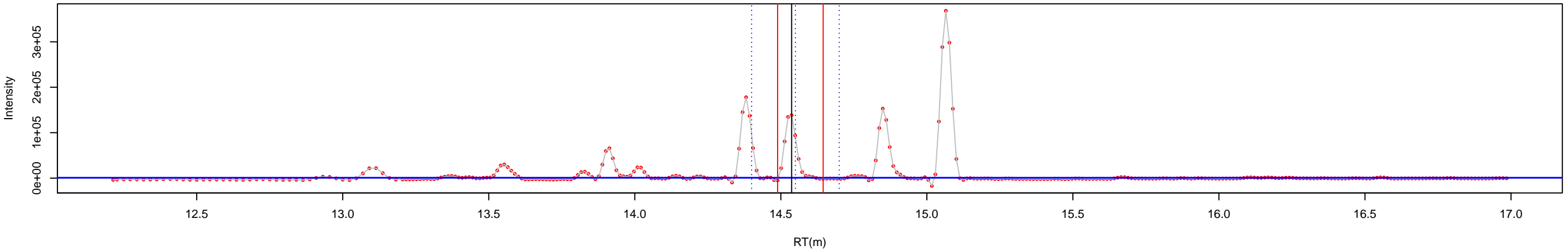
peak area | window size:3 BLine: yes



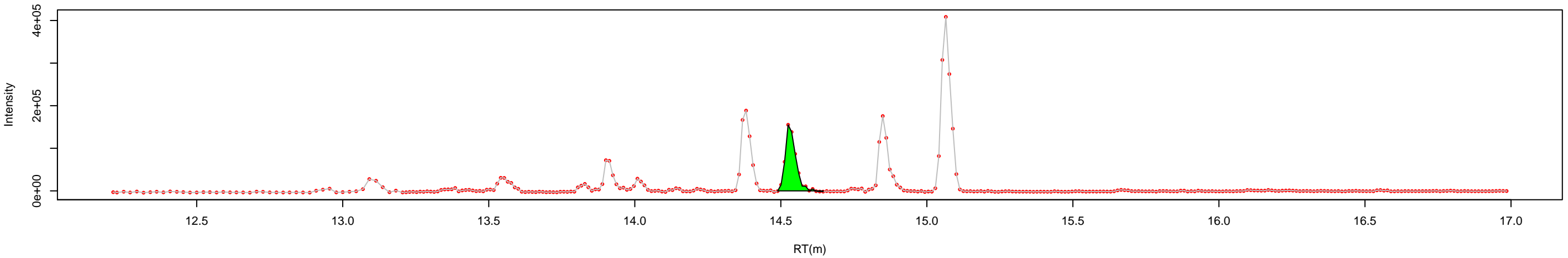
raw chromatogram | batch: 4 sample: cotor5 conc: NA function: 1 mass: 389.35>389.35



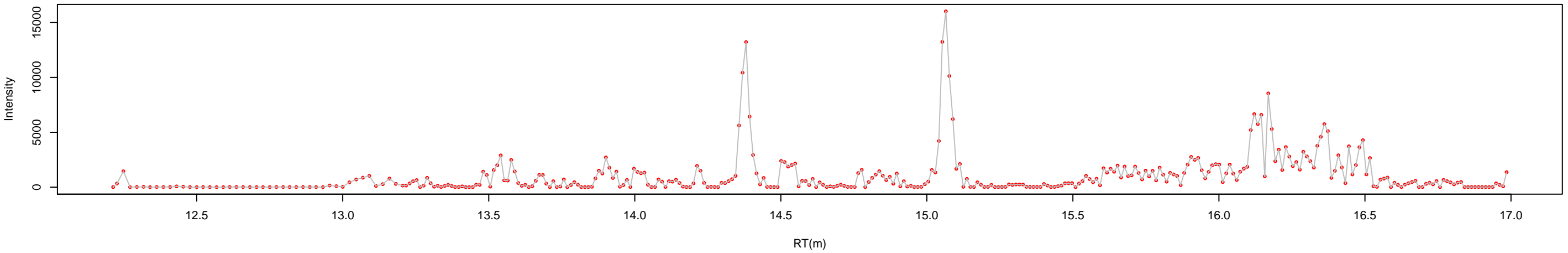
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 145 BLine: yes



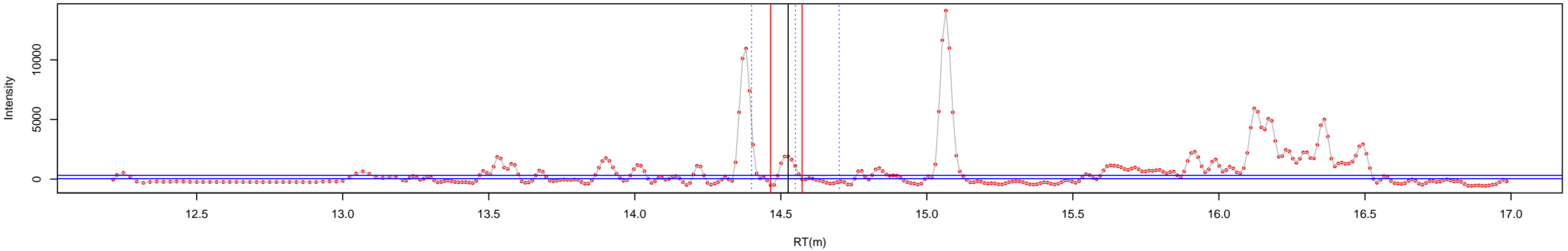
peak area | window size:3 BLine: yes



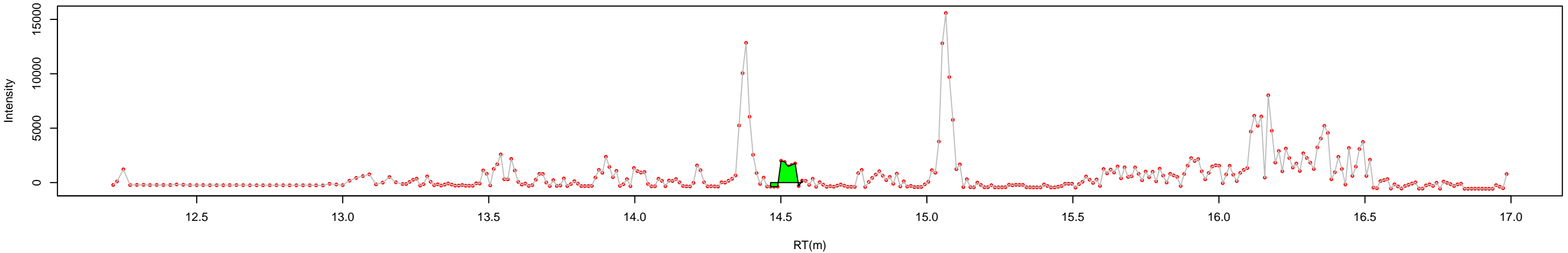
raw chromatogram | batch: 4 sample: cotor15 conc: NA function: 1 mass: 389.35>389.35



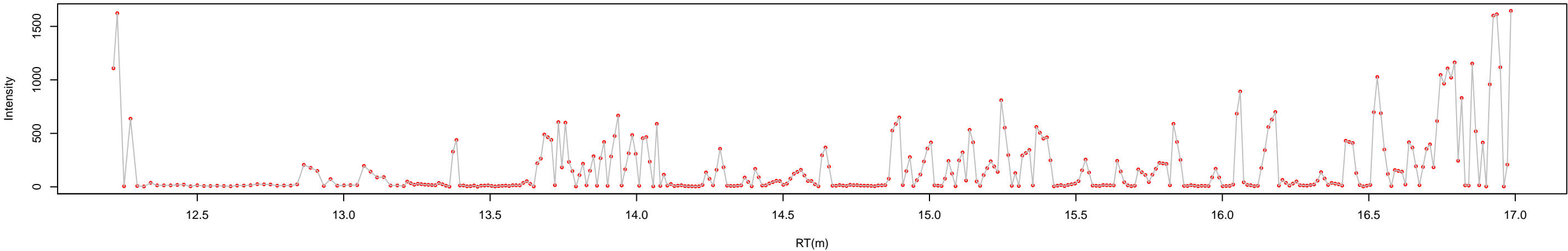
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 31.3 BLine: yes



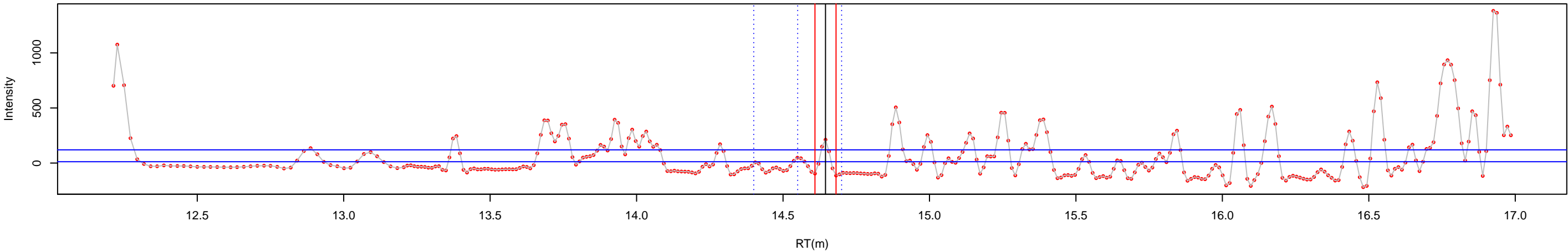
peak area | window size:3 BLine: yes



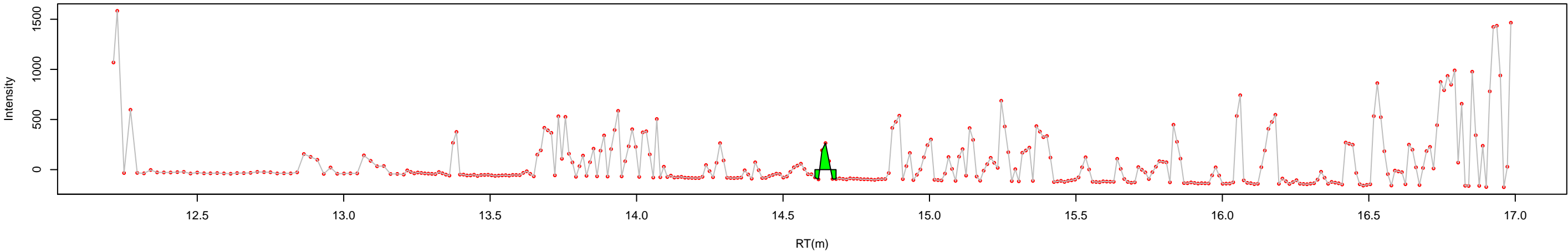
raw chromatogram | batch: 4   sample: std0-10ul-4   conc: 0.001   function: 1   mass: 389.35>389.35



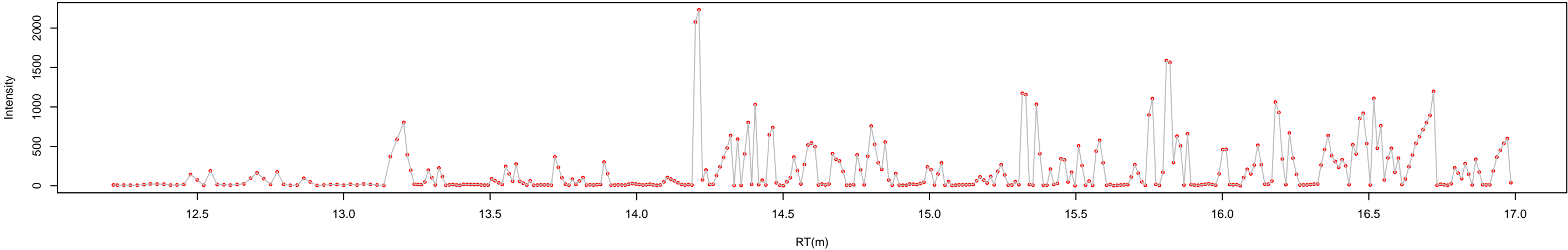
peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 12   BLine: yes



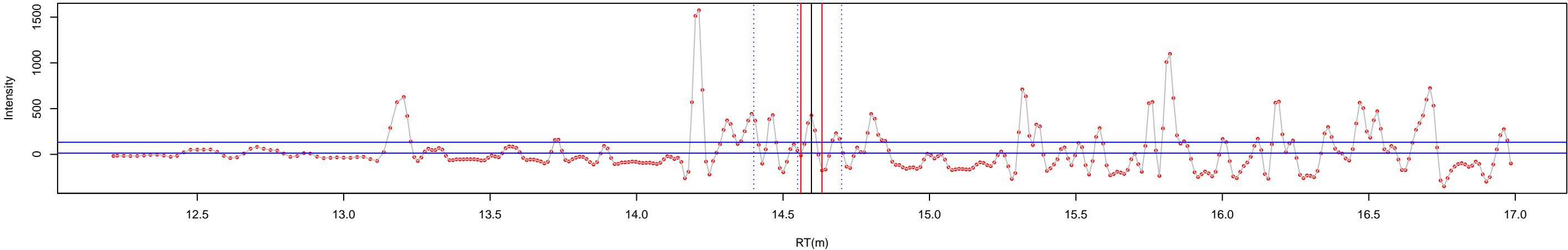
peak area | window size:3   BLine: yes



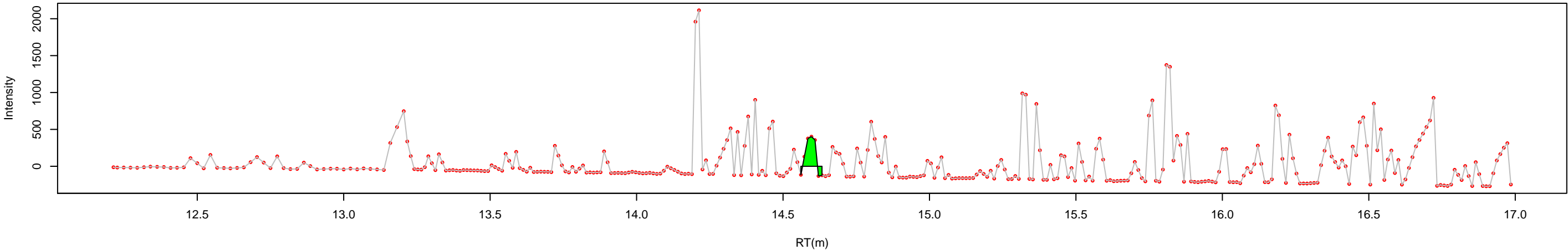
raw chromatogram | batch: 4 sample: std1-10ul-4 conc: 0.002 function: 1 mass: 389.35>389.35



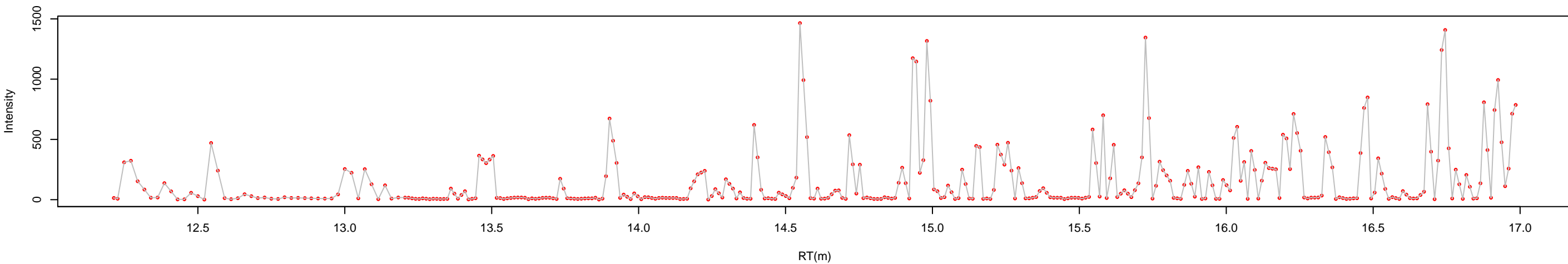
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 13.2 BLine: yes



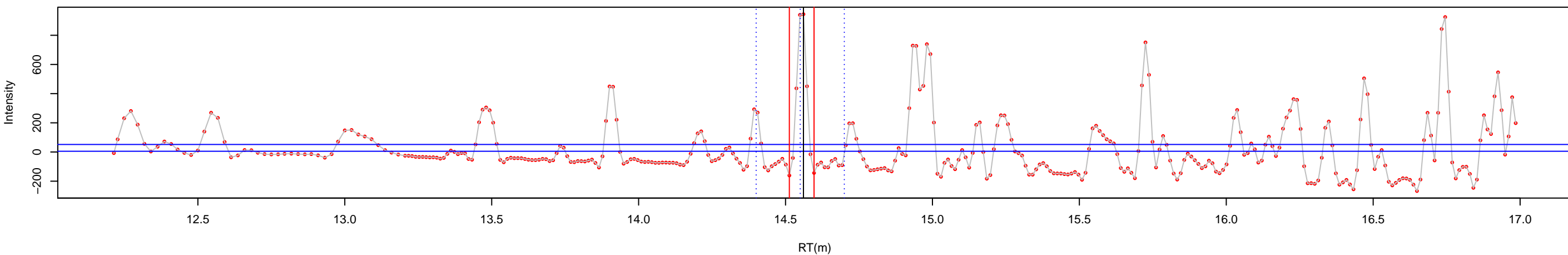
peak area | window size:3 BLine: yes



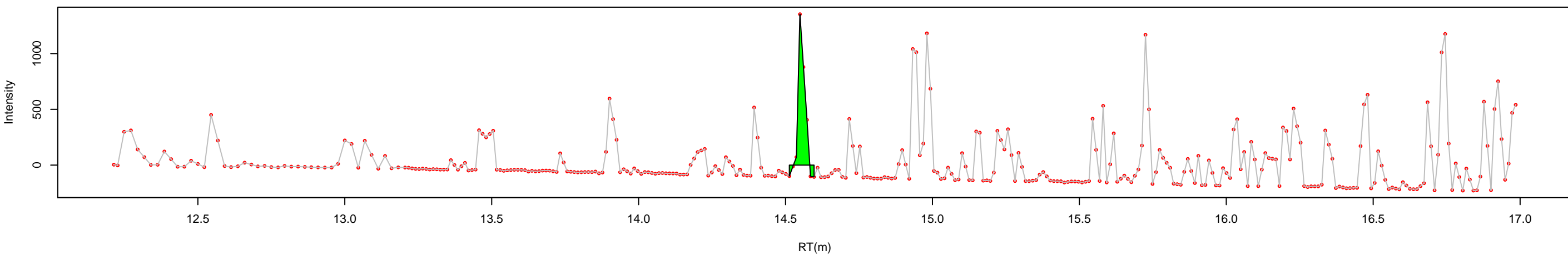
raw chromatogram | batch: 4 sample: std2-10ul-4 conc: 0.005 function: 1 mass: 389.35>389.35



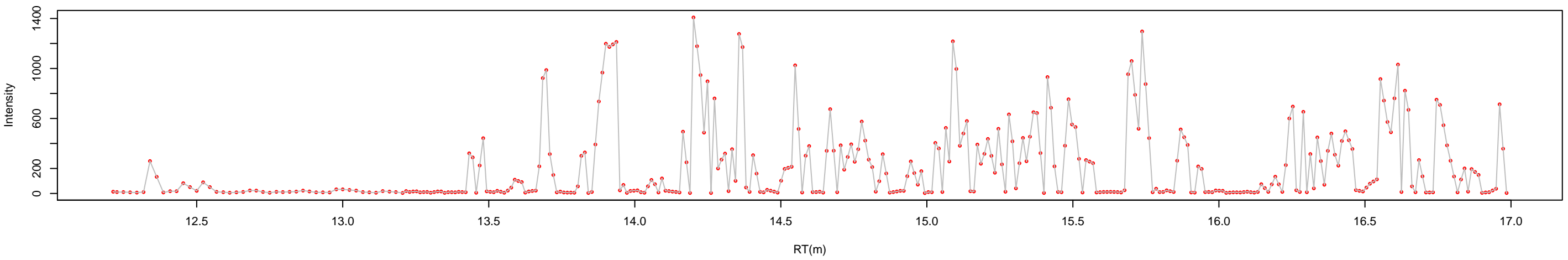
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 5.16 BLine: yes



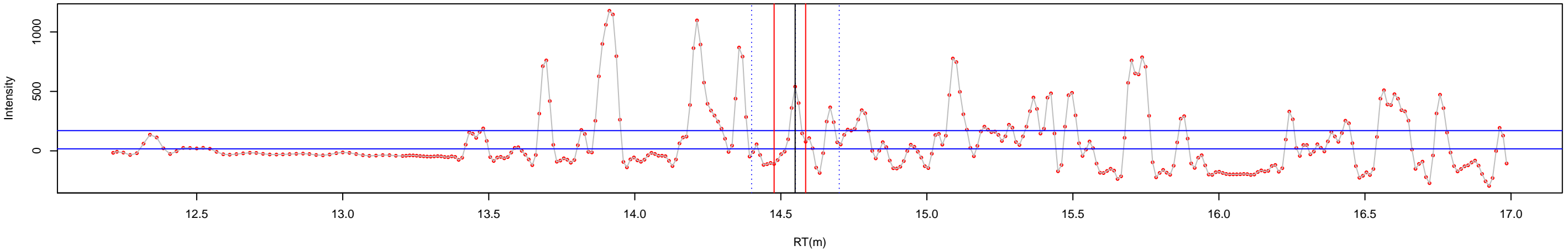
peak area | window size:3 BLine: yes



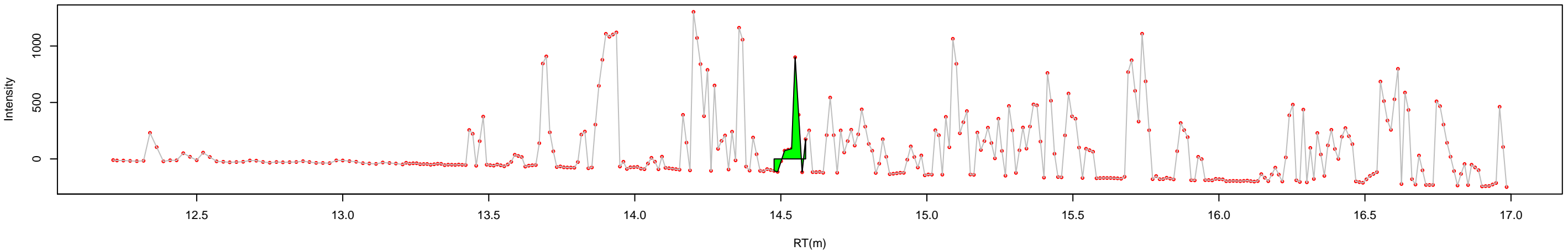
raw chromatogram | batch: 4   sample: std3-10ul-4   conc: 0.01   function: 1   mass: 389.35>389.35



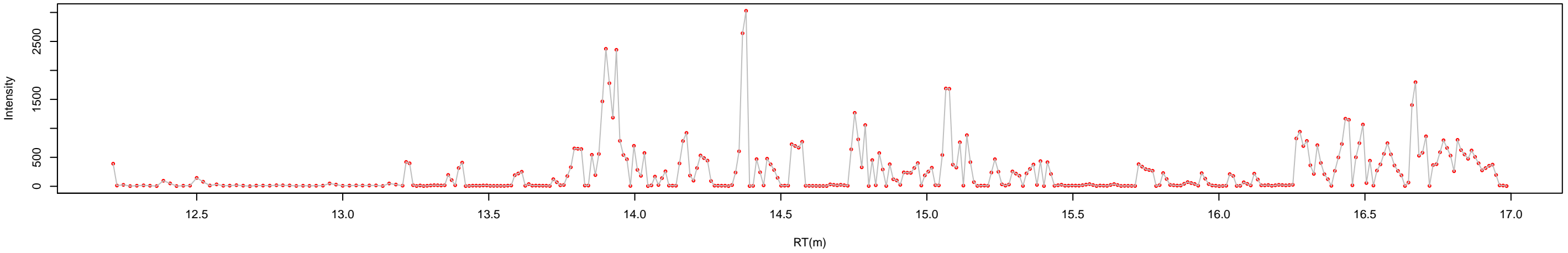
peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 17   BLine: yes



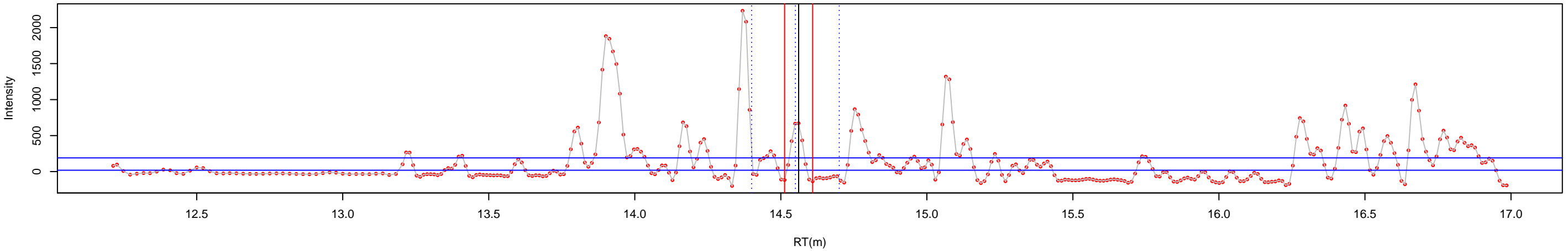
peak area | window size:3   BLine: yes



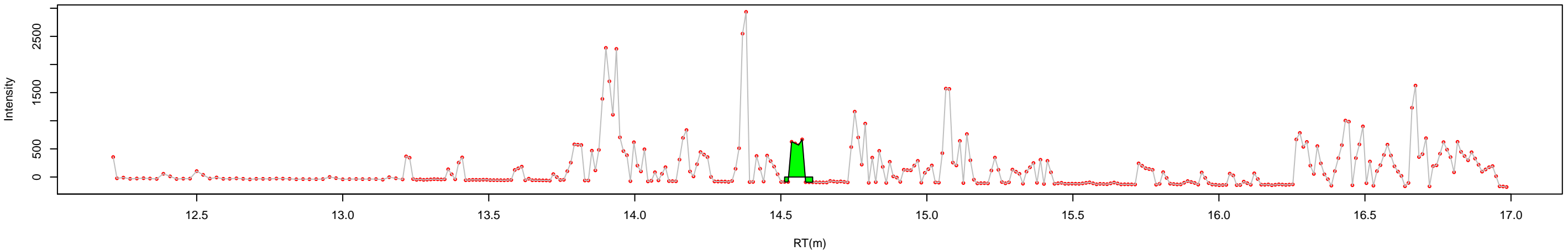
raw chromatogram | batch: 4   sample: std4-10ul-4   conc: 0.02   function: 1   mass: 389.35>389.35



peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 19   BLine: yes

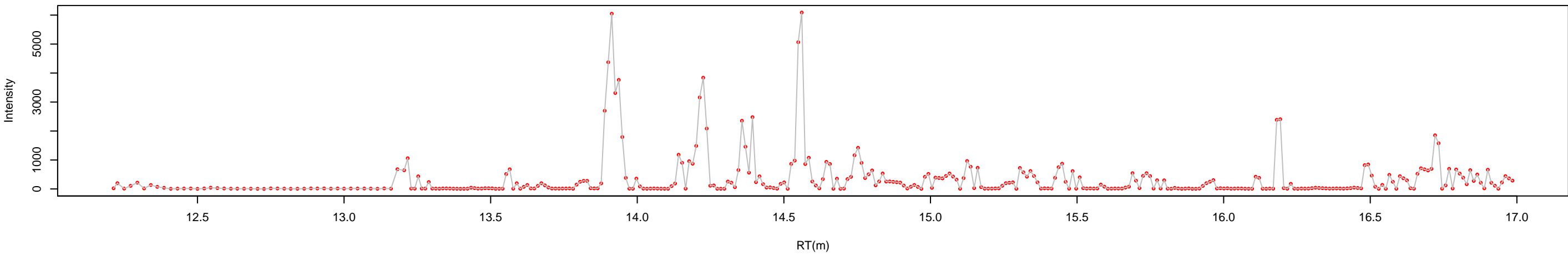


peak area | window size:3   BLine: yes

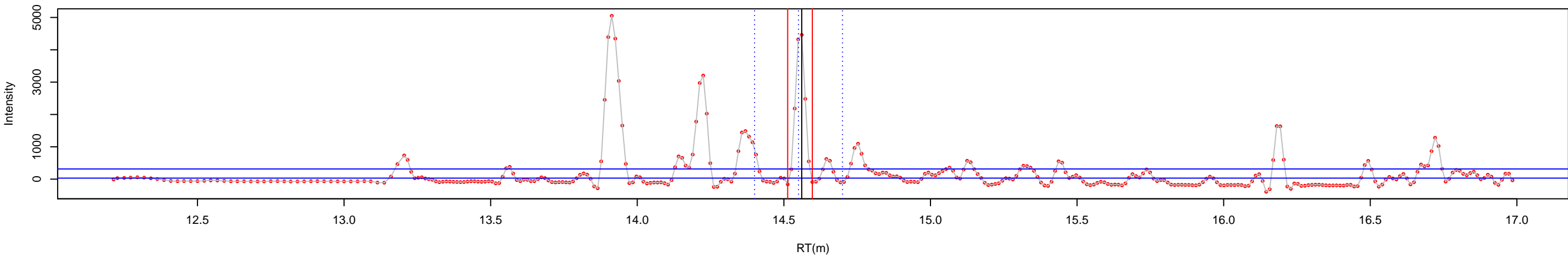




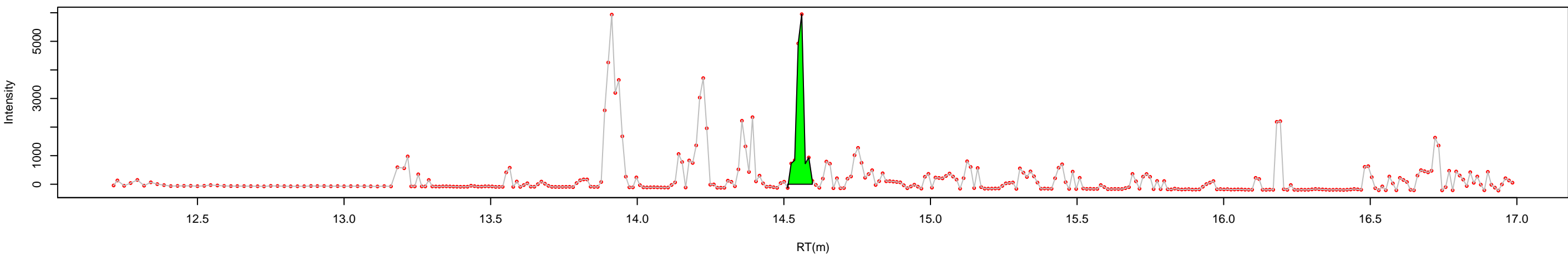
raw chromatogram | batch: 4 sample: std5-10ul-4 conc: 0.05 function: 1 mass: 389.35>389.35



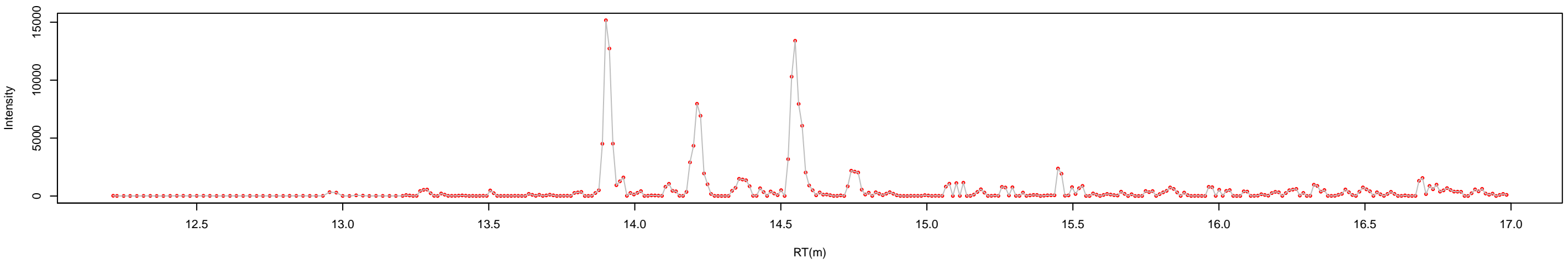
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 31.5 BLine: yes



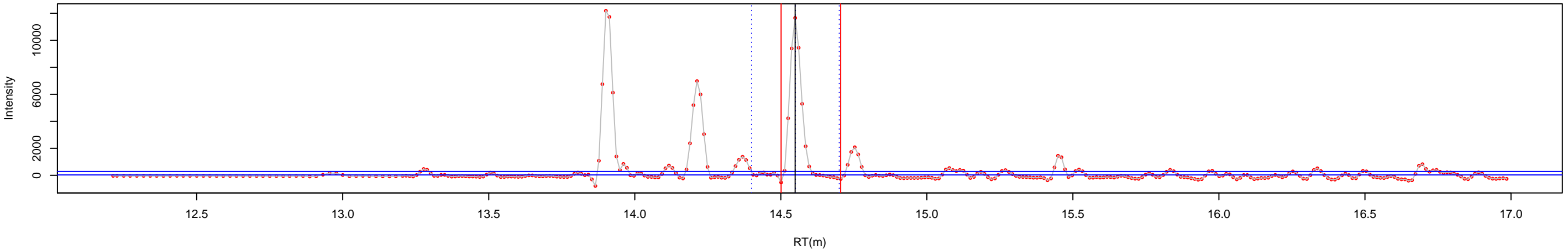
peak area | window size:3 BLine: yes



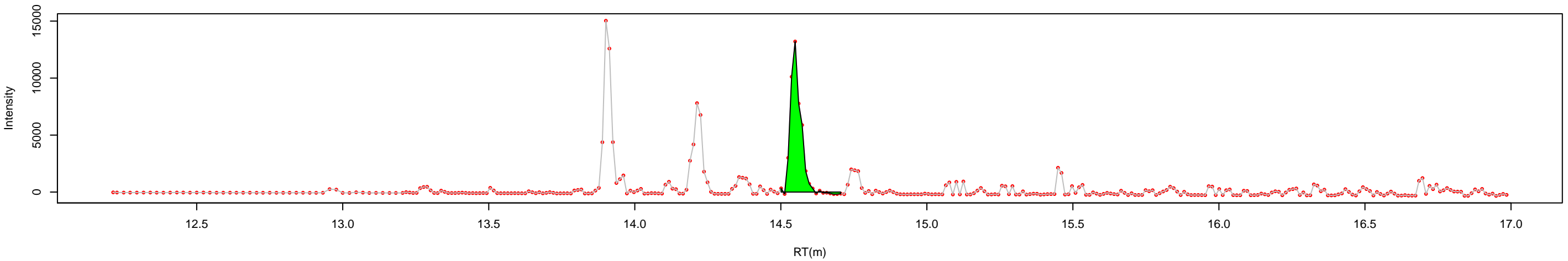
raw chromatogram | batch: 4 sample: std6-10ul-4 conc: 0.1 function: 1 mass: 389.35>389.35



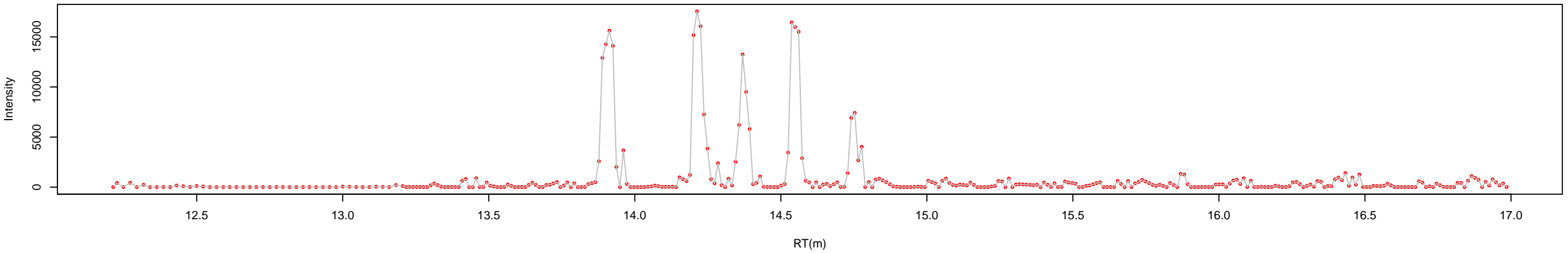
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 28.3 BLine: yes



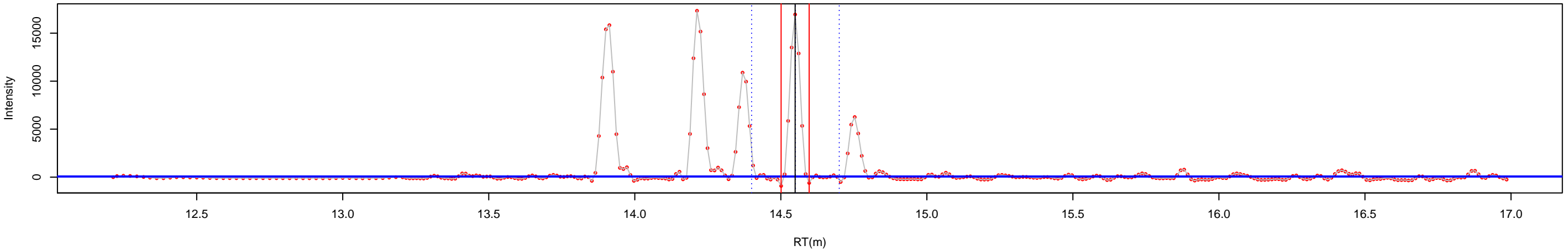
peak area | window size:3 BLine: yes



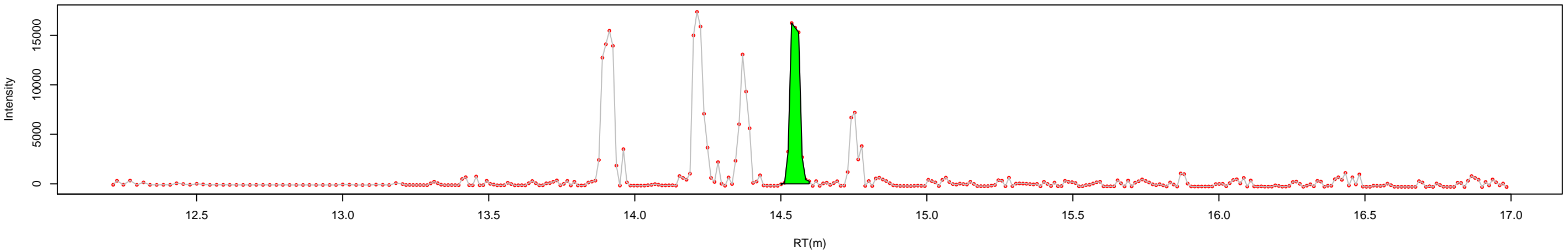
raw chromatogram | batch: 4 sample: std7-10ul-4 conc: 0.2 function: 1 mass: 389.35>389.35



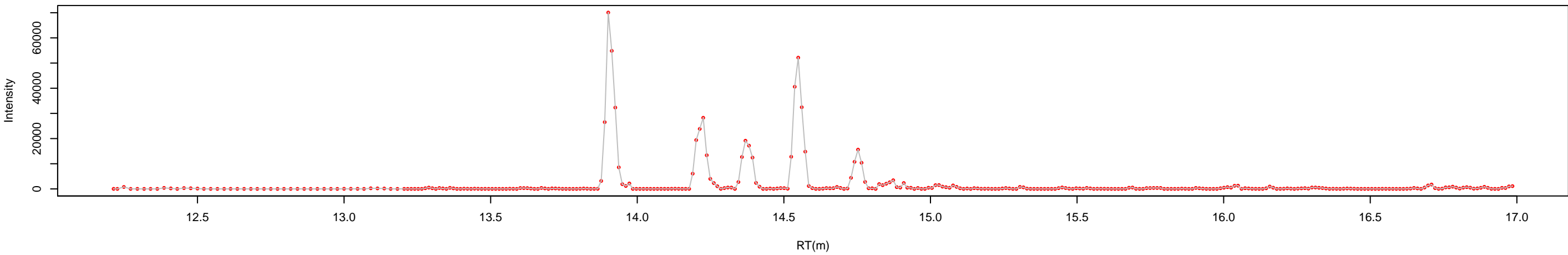
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 12.2 BLine: yes



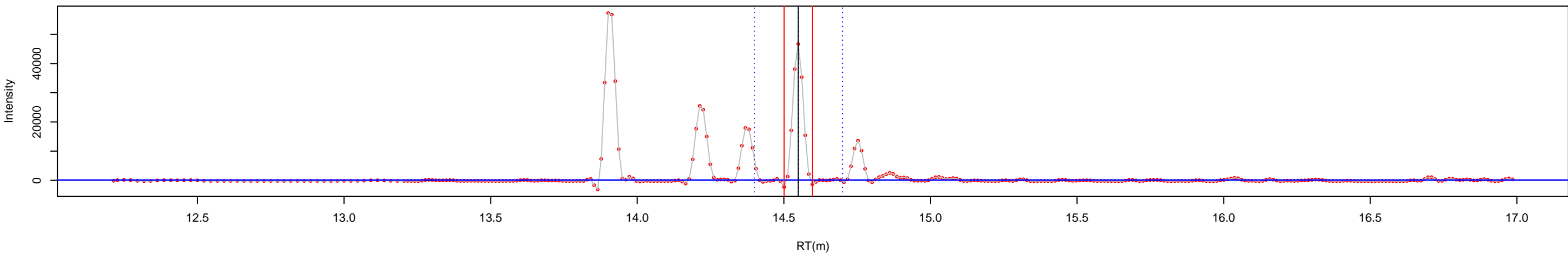
peak area | window size:3 BLine: yes



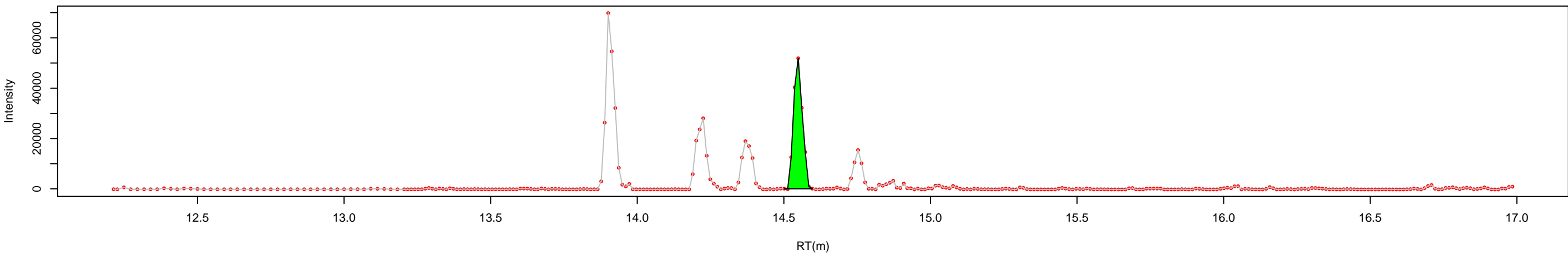
raw chromatogram | batch: 4 sample: std8-10ul-4 conc: 0.5 function: 1 mass: 389.35>389.35



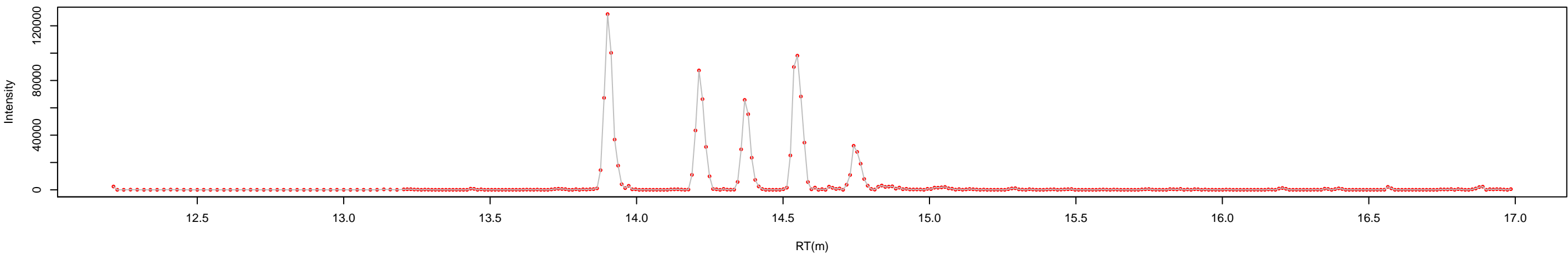
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 14 BLine: yes



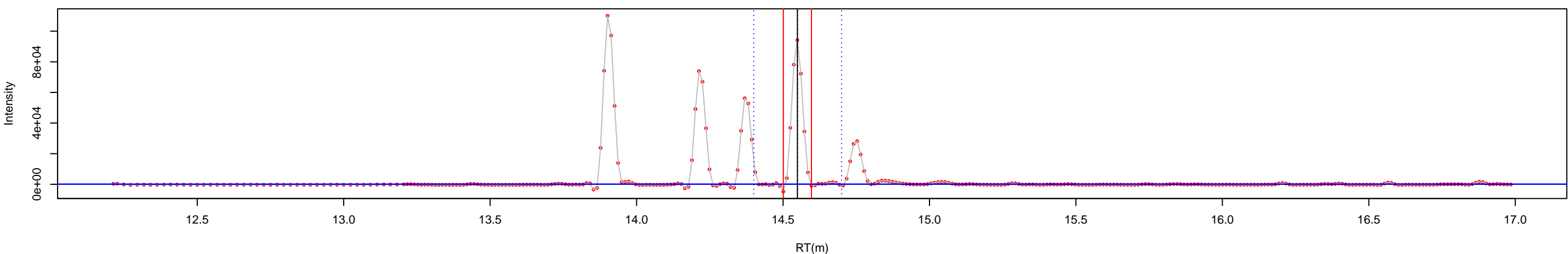
peak area | window size:3 BLine: yes



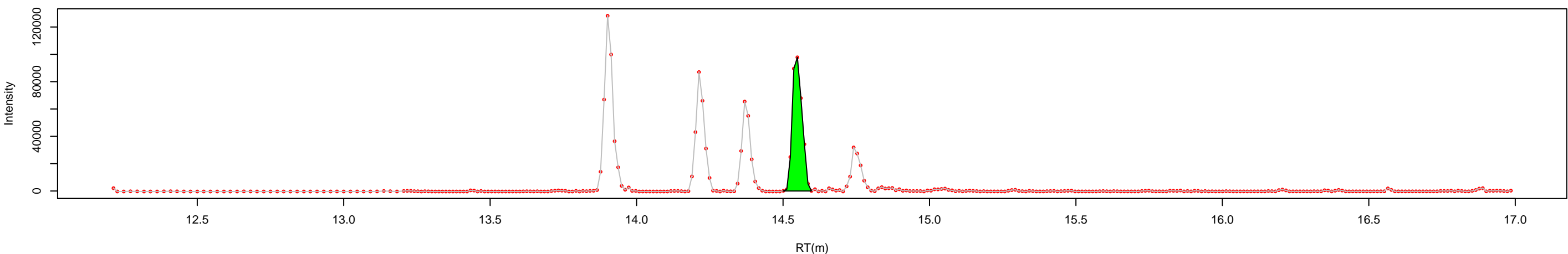
raw chromatogram | batch: 4   sample: std9-10ul-4   conc: 1   function: 1   mass: 389.35>389.35



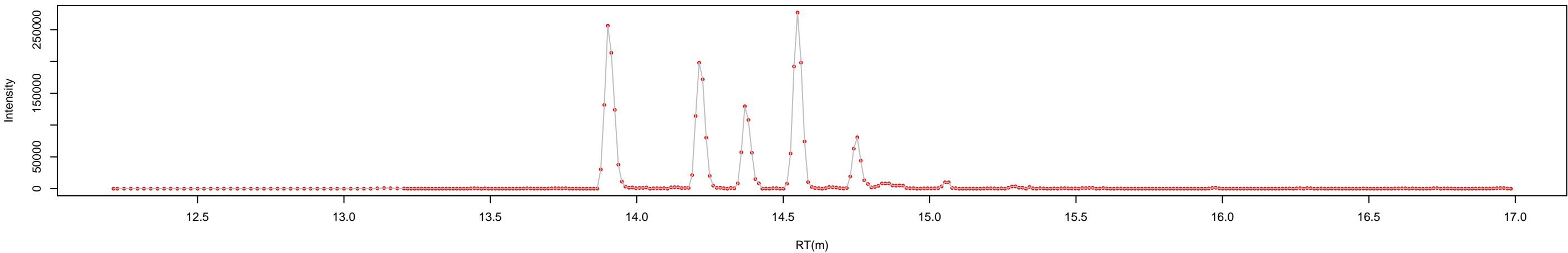
peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 17.7   BLine: yes



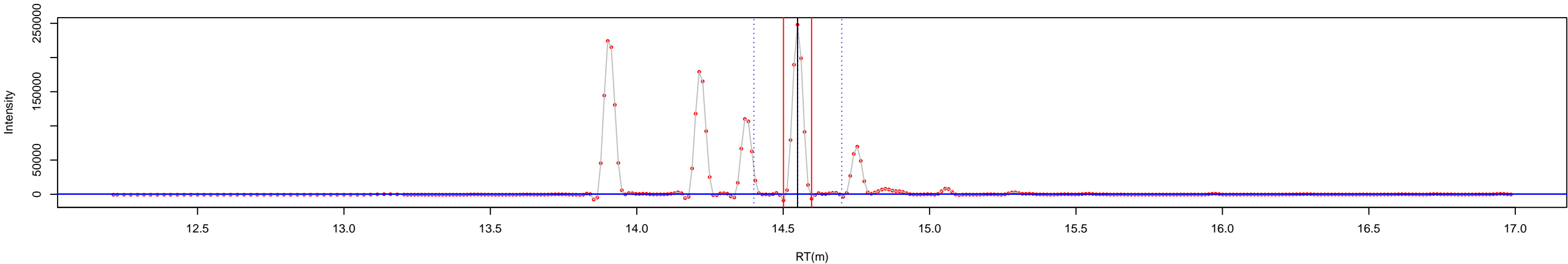
peak area | window size:3   BLine: yes



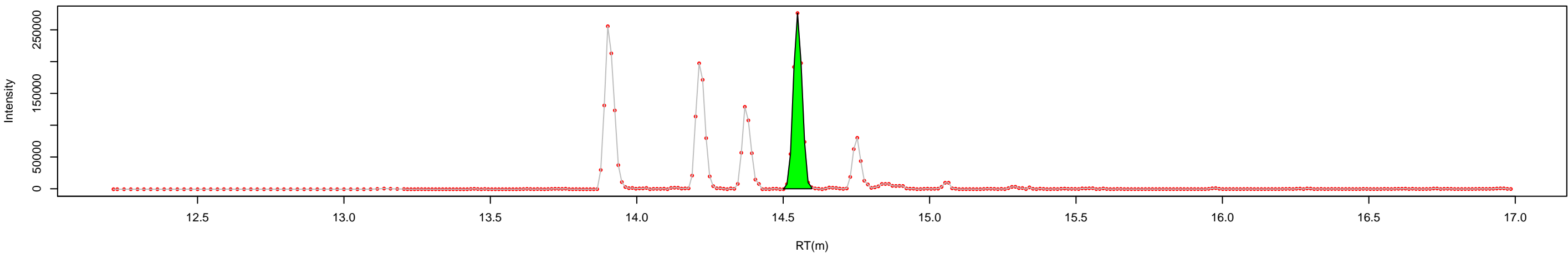
raw chromatogram | batch: 4   sample: std10-10ul-4   conc: 2   function: 1   mass: 389.35>389.35



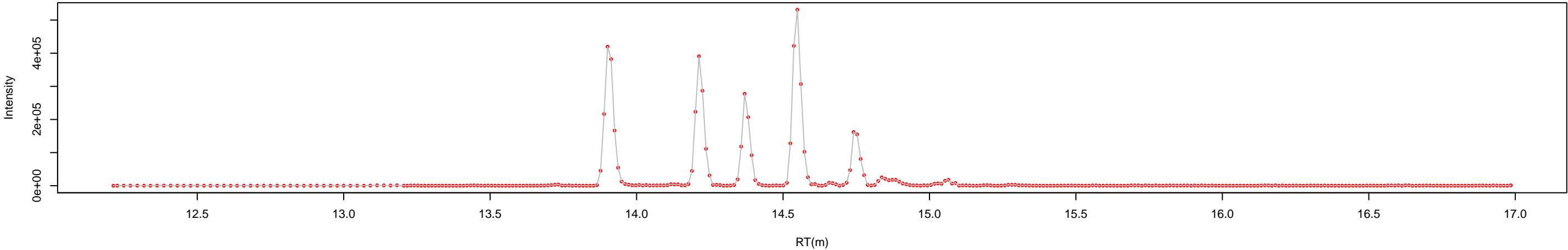
peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 51   BLine: yes



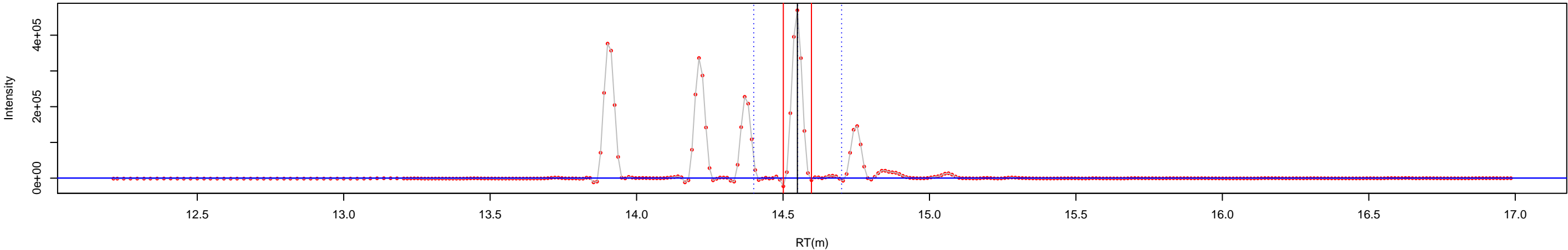
peak area | window size:3   BLine: yes



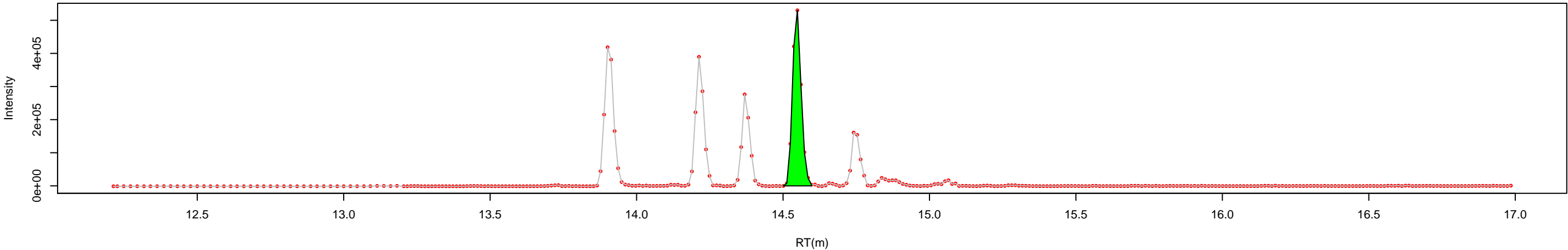
raw chromatogram | batch: 4   sample: std11-10ul-4   conc: 5   function: 1   mass: 389.35>389.35



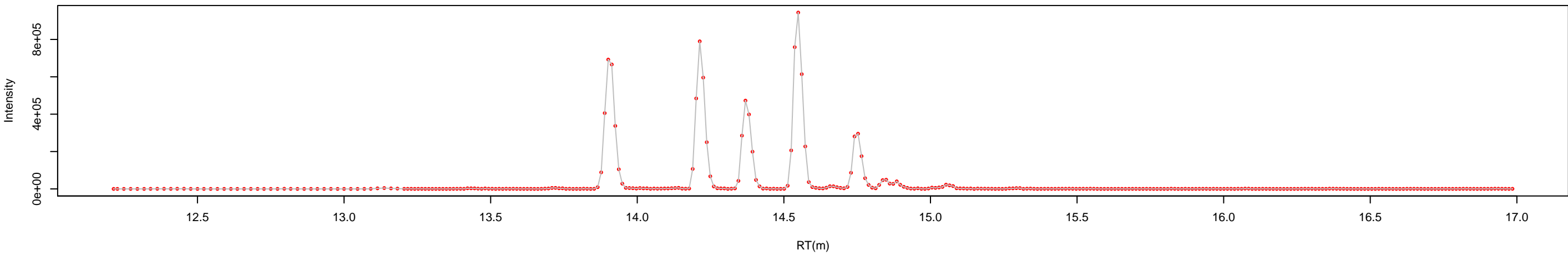
peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 52.7   BLine: yes



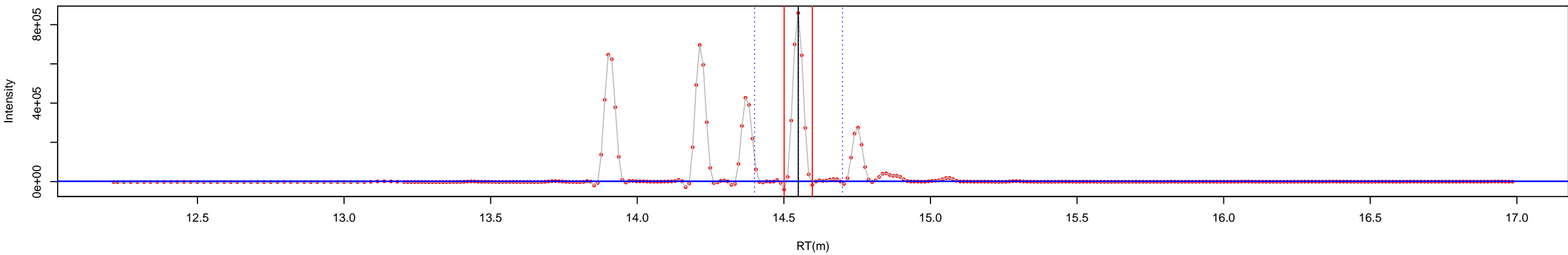
peak area | window size:3   BLine: yes



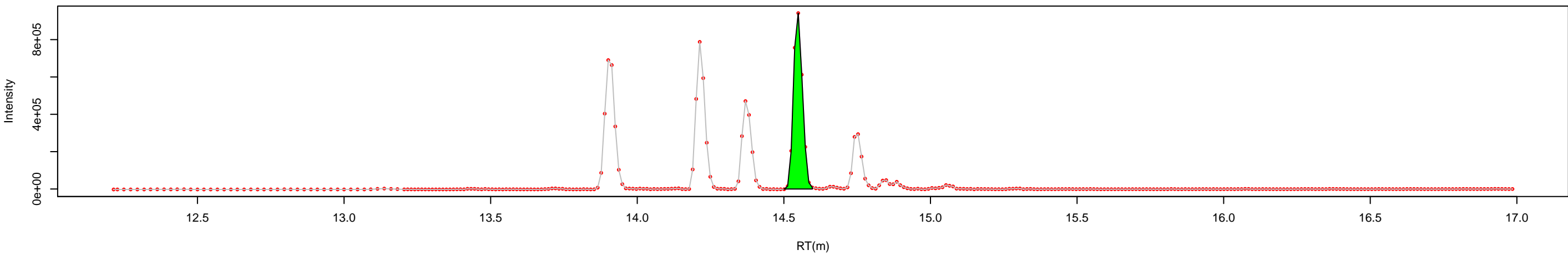
raw chromatogram | batch: 4 sample: std12-10ul-4 conc: 10 function: 1 mass: 389.35>389.35



peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 282 BLine: yes

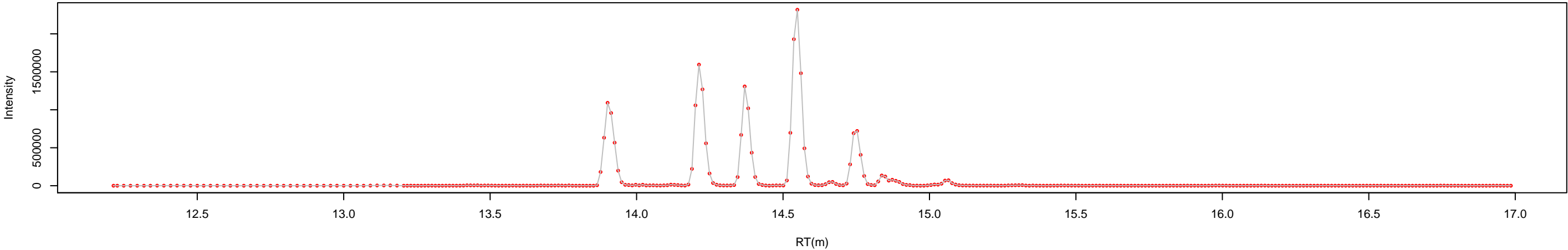


peak area | window size:3 BLine: yes

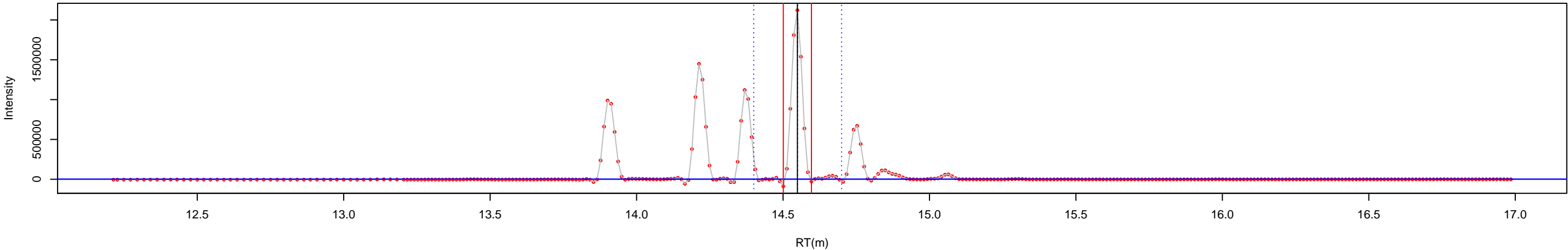




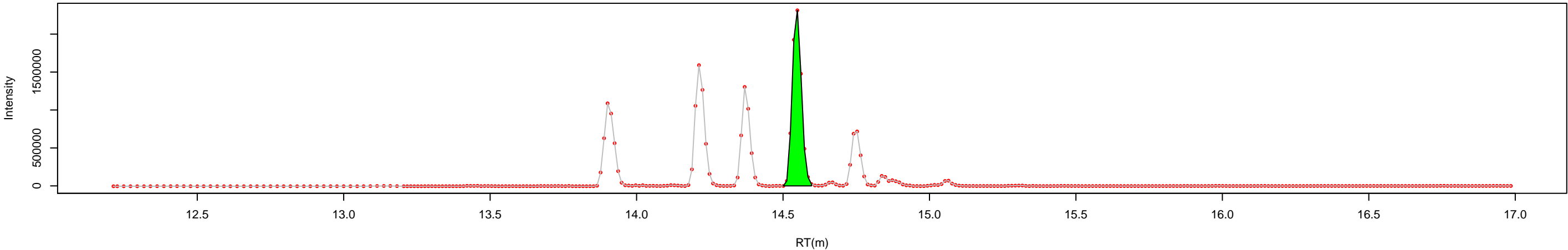
raw chromatogram | batch: 4   sample: std13-10ul-4   conc: 20   function: 1   mass: 389.35>389.35



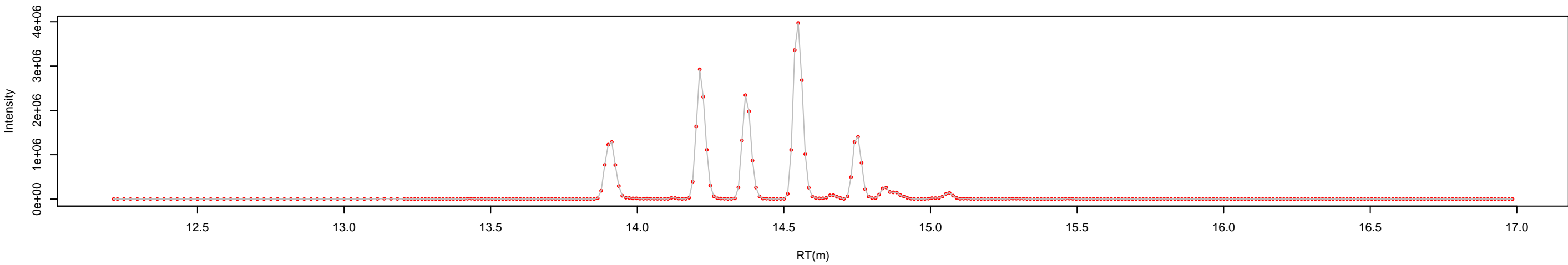
peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 309   BLine: yes



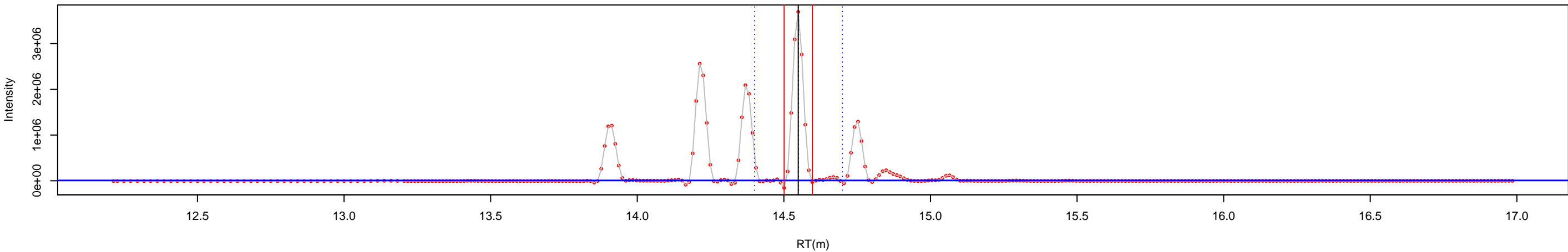
peak area | window size:3   BLine: yes



raw chromatogram | batch: 4 sample: std14-10ul-4 conc: 50 function: 1 mass: 389.35>389.35



peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 1210 BLine: yes



peak area | window size:3 BLine: yes

