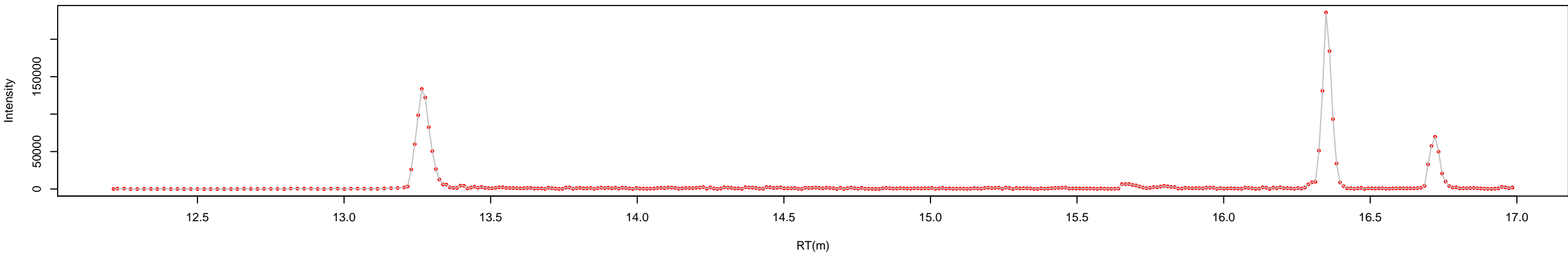
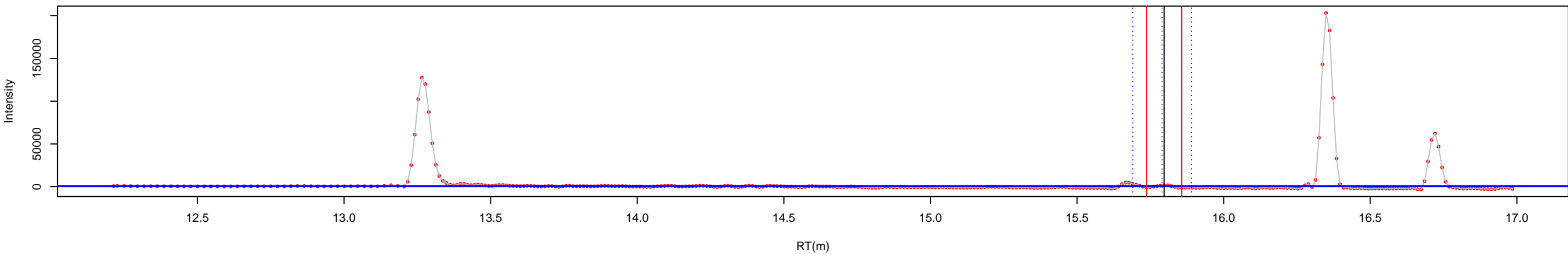


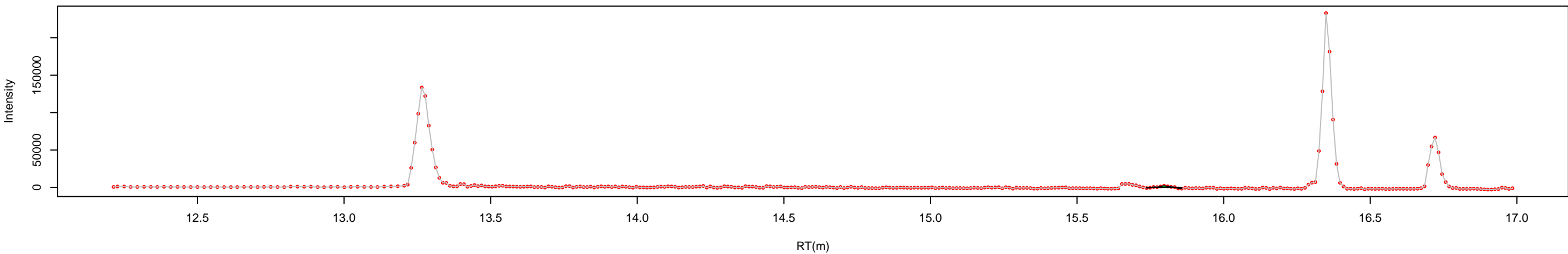
raw chromatogram | batch: 1 sample: coth10 conc: NA function: 1 mass: 375.35>375.35



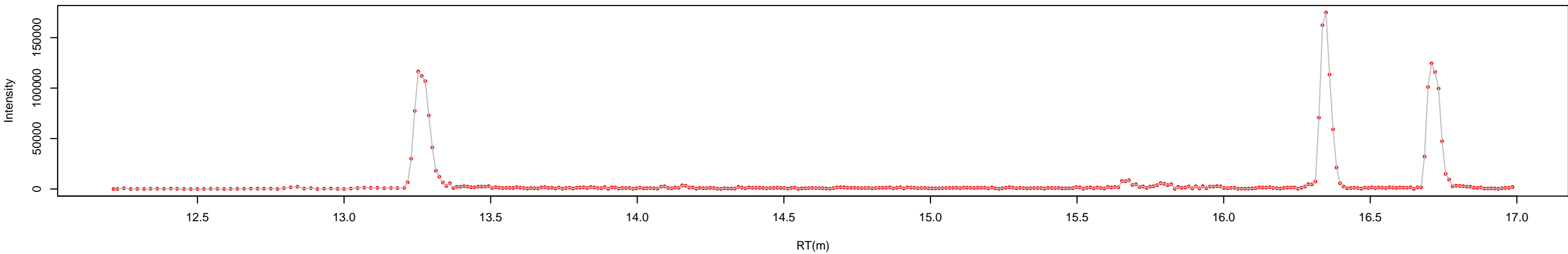
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 115 BLine: yes



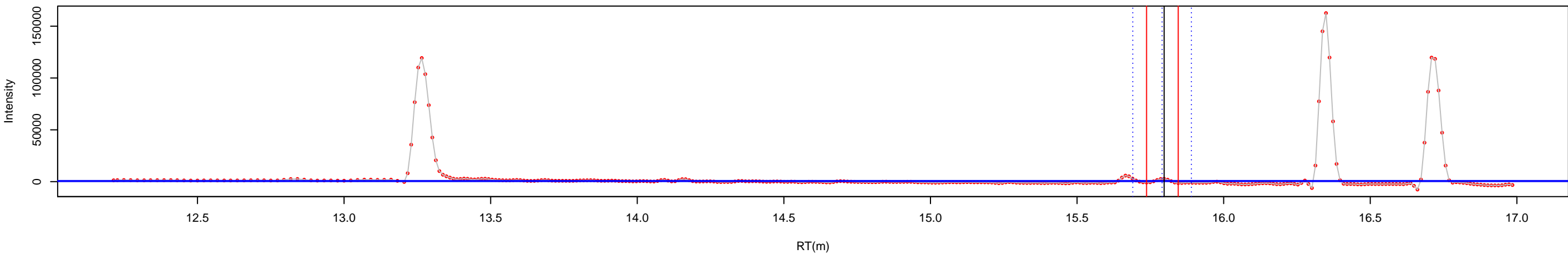
peak area | window size:3 BLine: yes



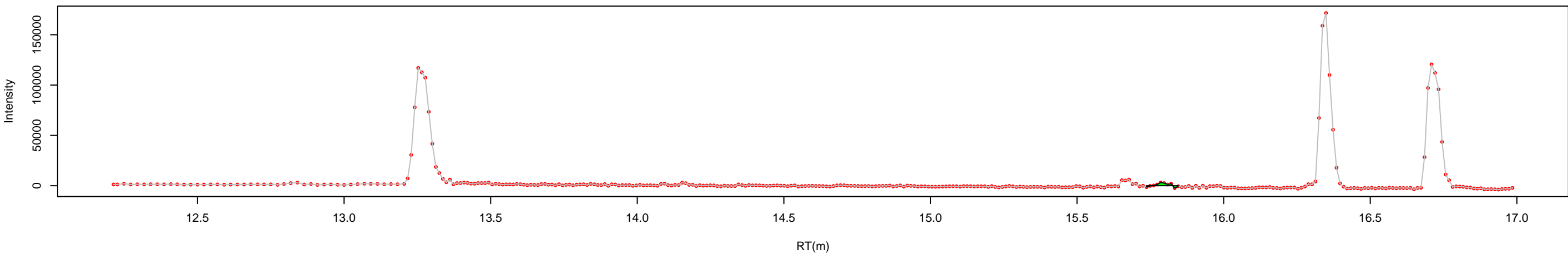
raw chromatogram | batch: 1 sample: cotn19 conc: NA function: 1 mass: 375.35>375.35



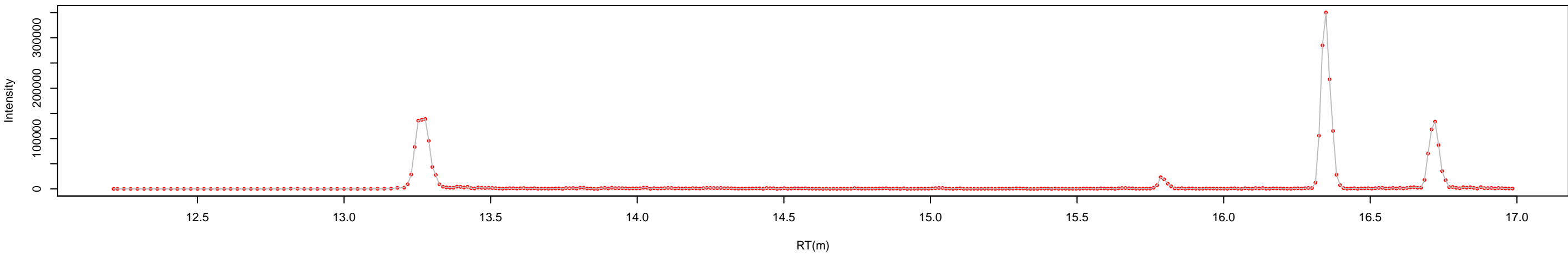
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 104 BLine: yes



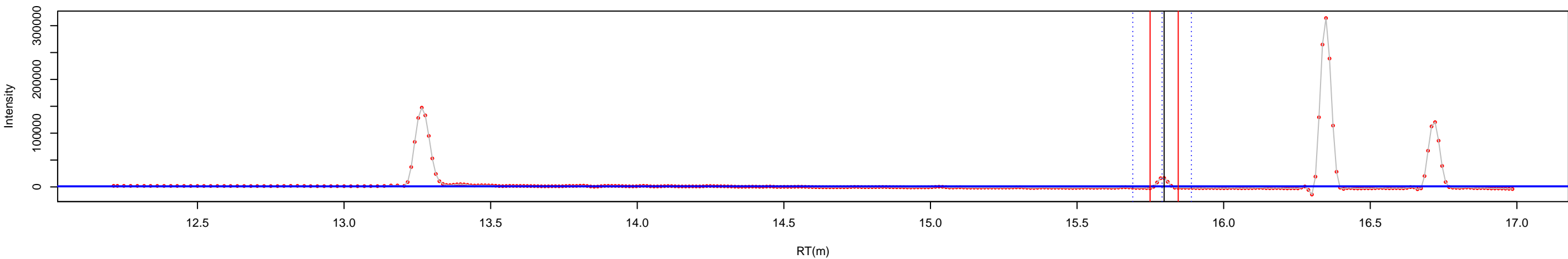
peak area | window size:3 BLine: yes



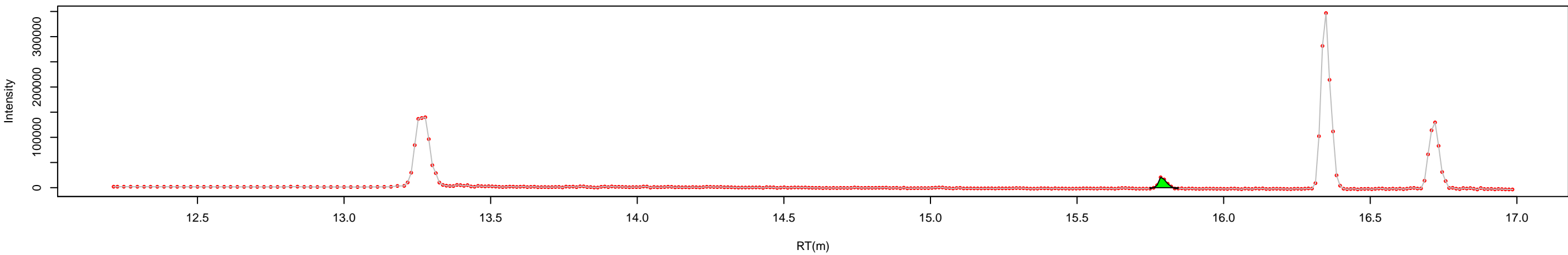
raw chromatogram | batch: 1 sample: coth11 conc: NA function: 1 mass: 375.35>375.35



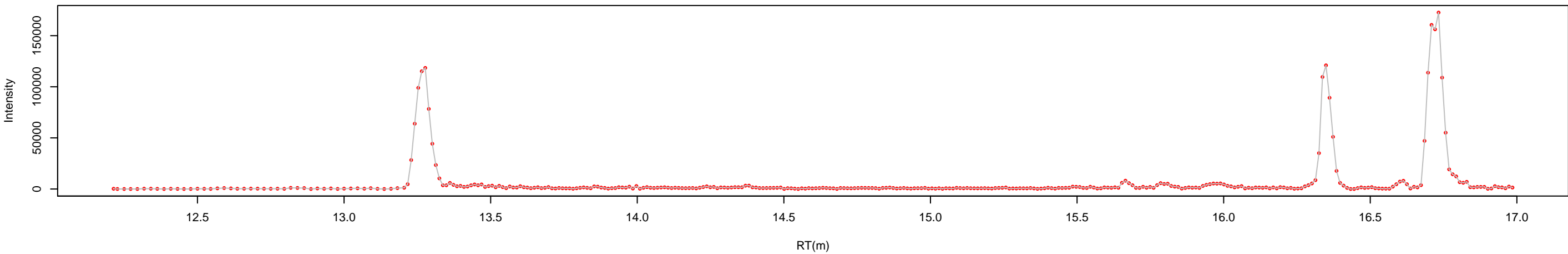
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 195 BLine: yes



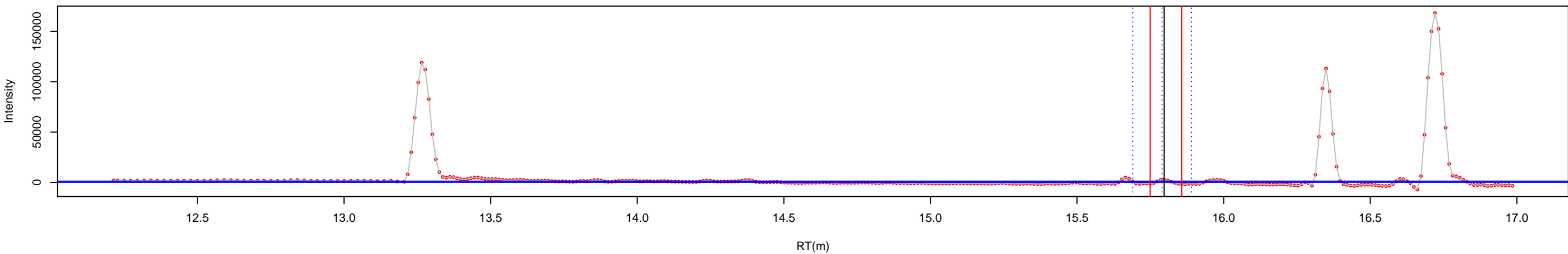
peak area | window size:3 BLine: yes



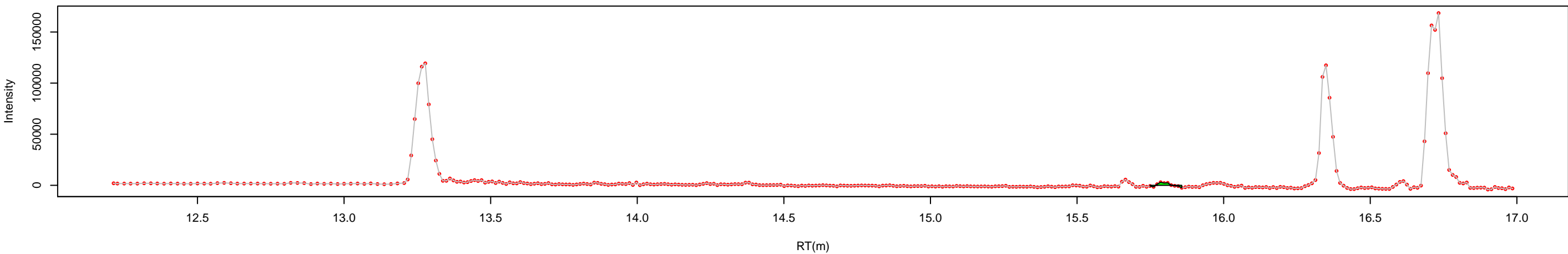
raw chromatogram | batch: 1 sample: cotn20 conc: NA function: 1 mass: 375.35>375.35



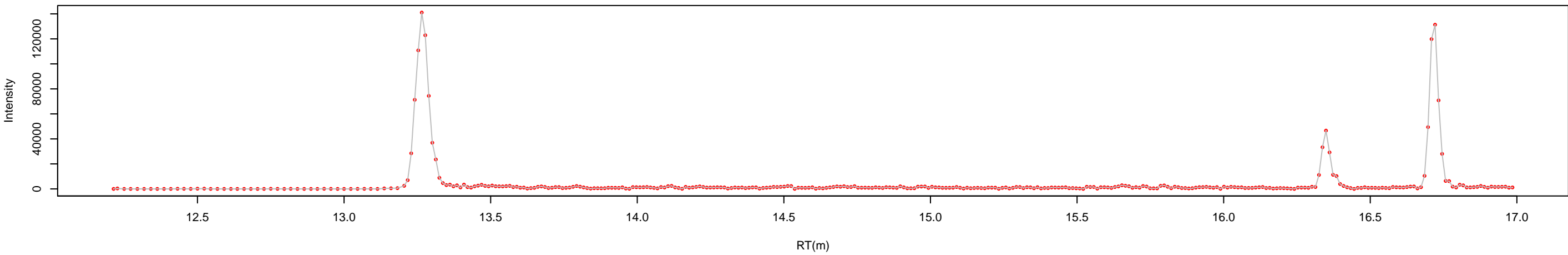
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 122 BLine: yes



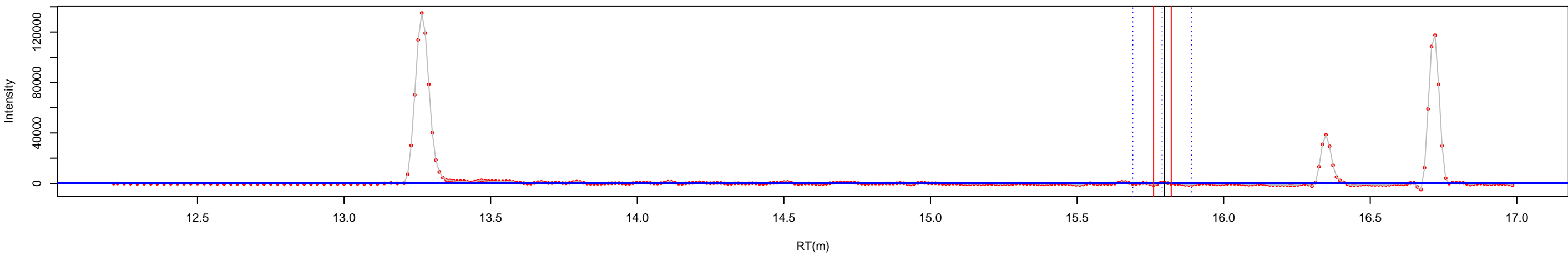
peak area | window size:3 BLine: yes



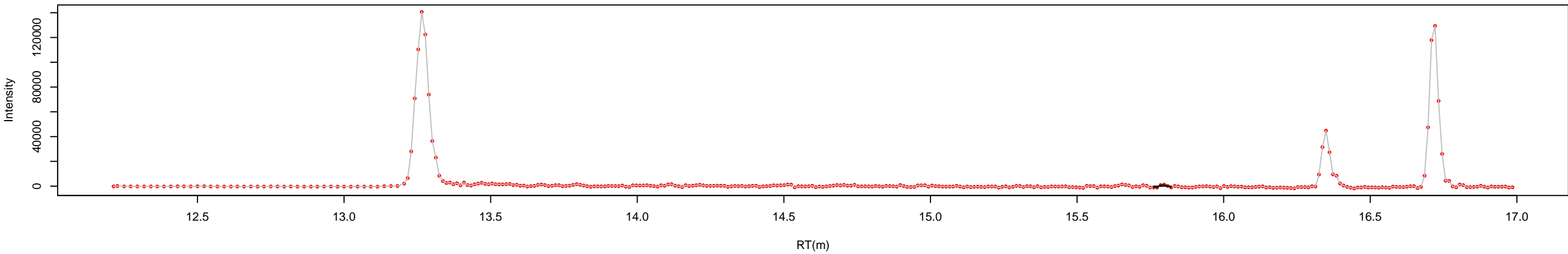
raw chromatogram | batch: 1 sample: coth12 conc: NA function: 1 mass: 375.35>375.35



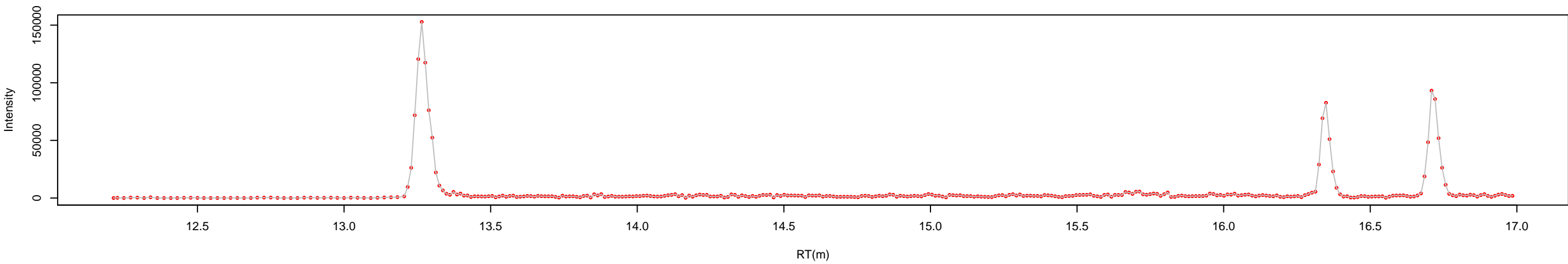
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 50.8 BLine: yes



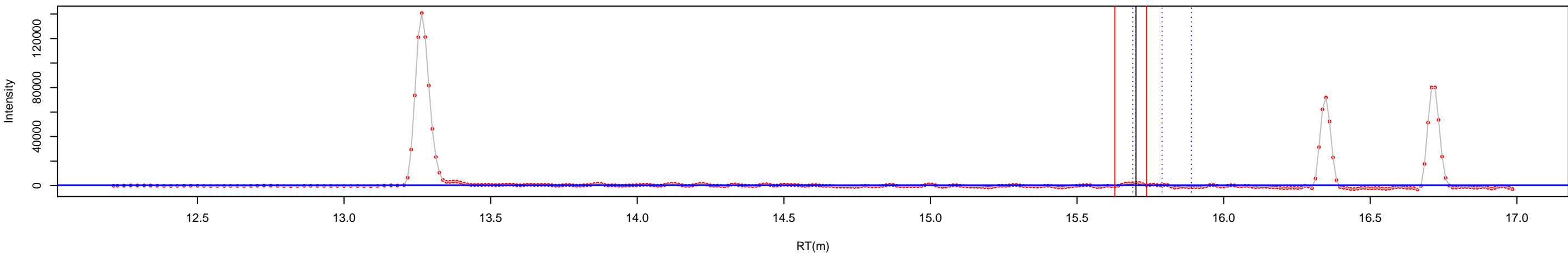
peak area | window size:3 BLine: yes



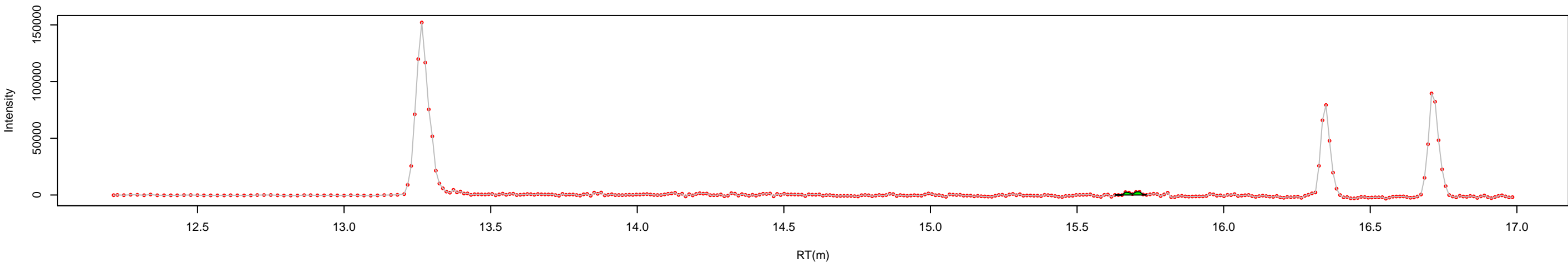
raw chromatogram | batch: 1 sample: cotn21 conc: NA function: 1 mass: 375.35>375.35

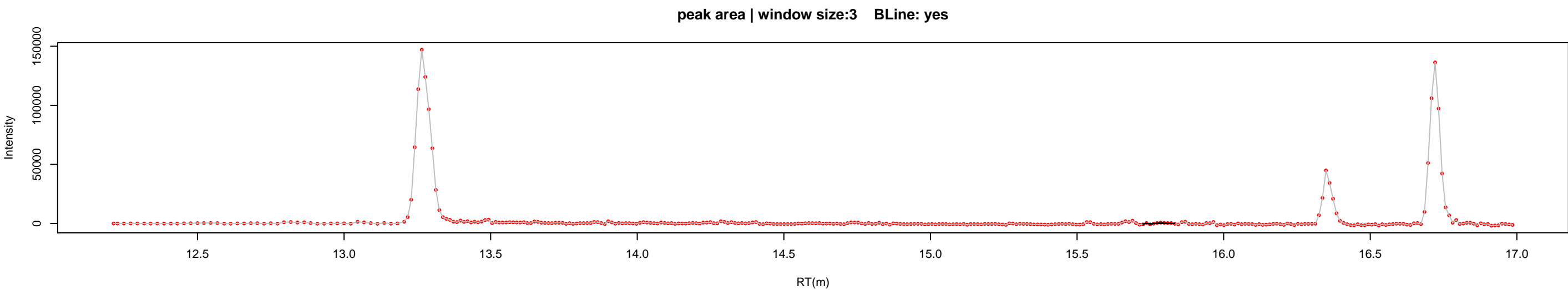
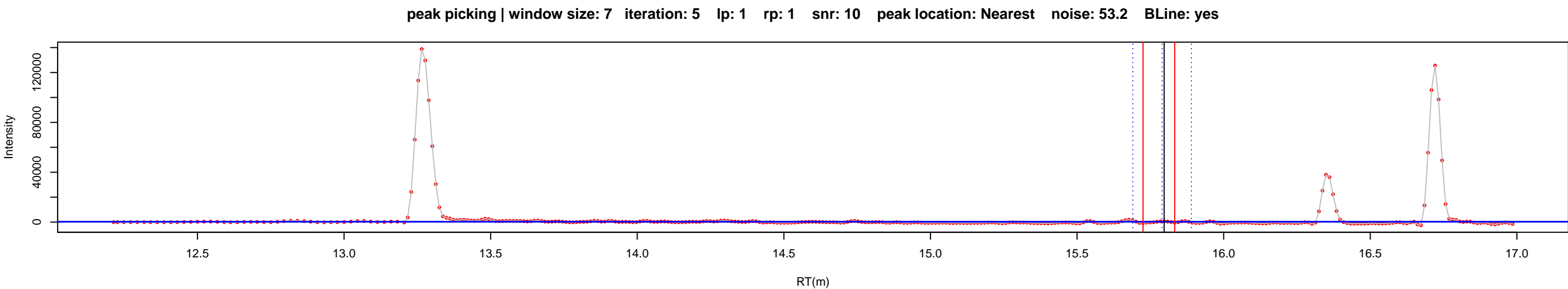
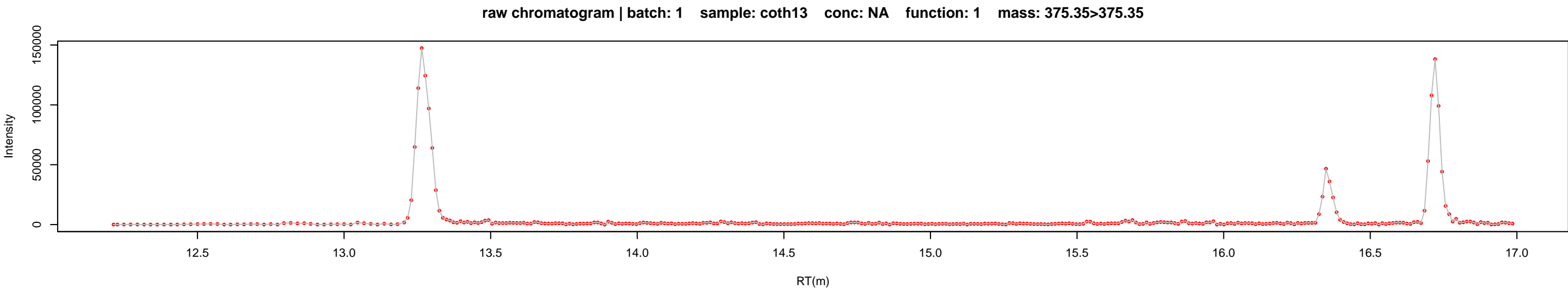


peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 53.7 BLine: yes

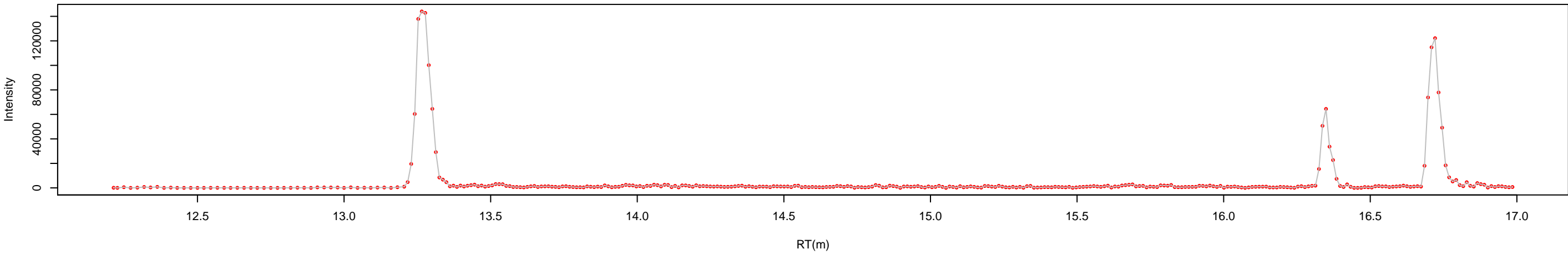


peak area | window size:3 BLine: yes

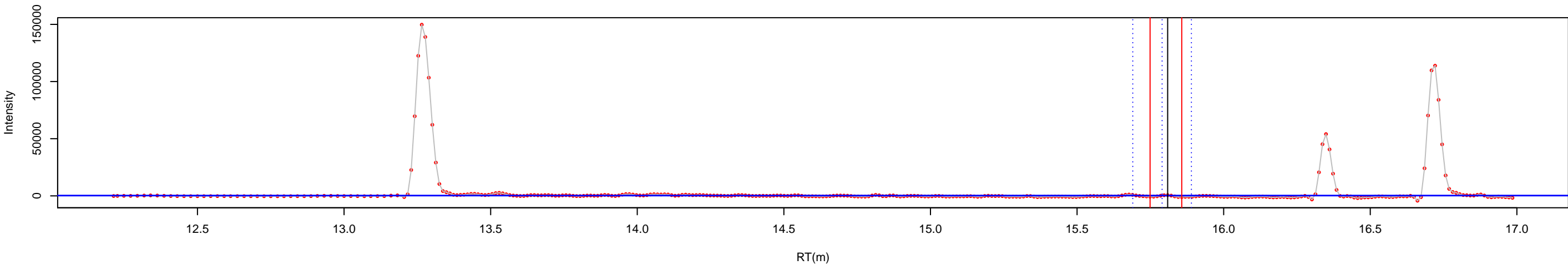




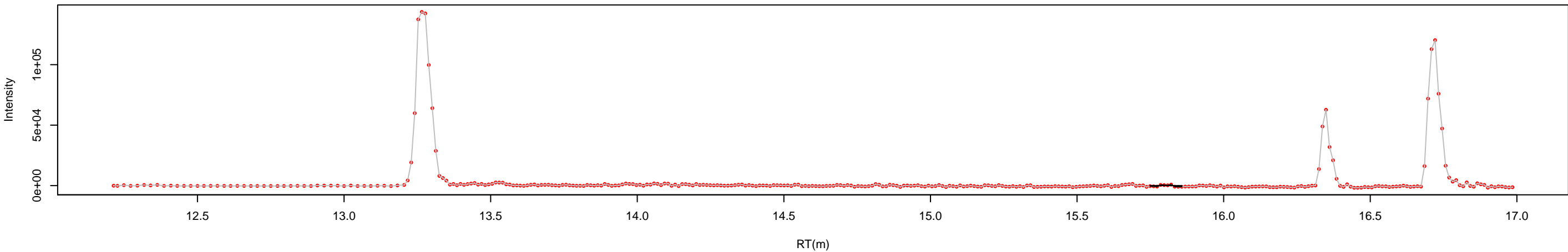
raw chromatogram | batch: 1 sample: cotn22 conc: NA function: 1 mass: 375.35>375.35



peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 47.9 BLine: yes

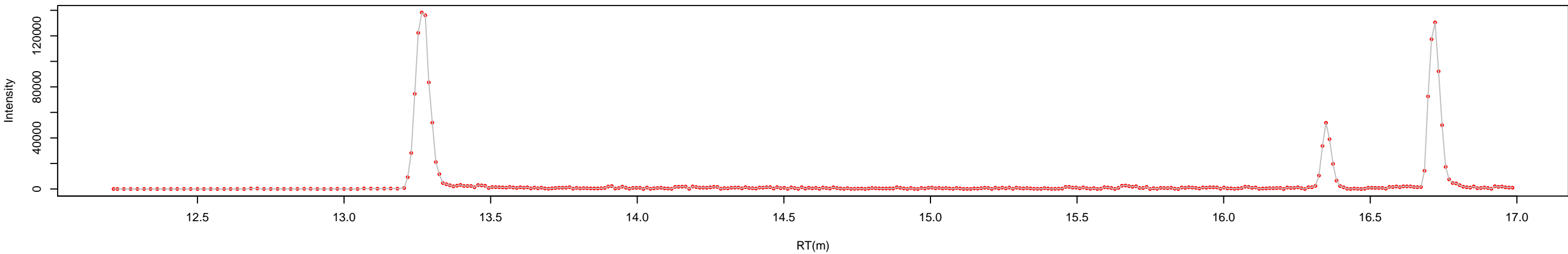


peak area | window size:3 BLine: yes

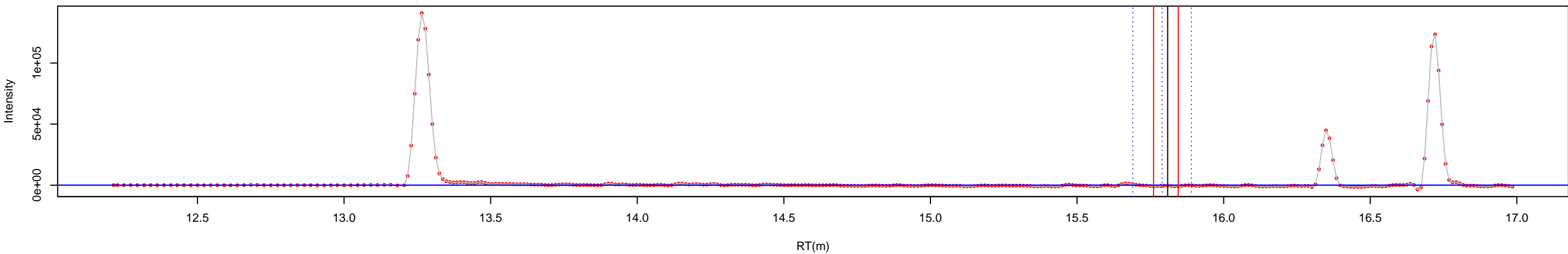




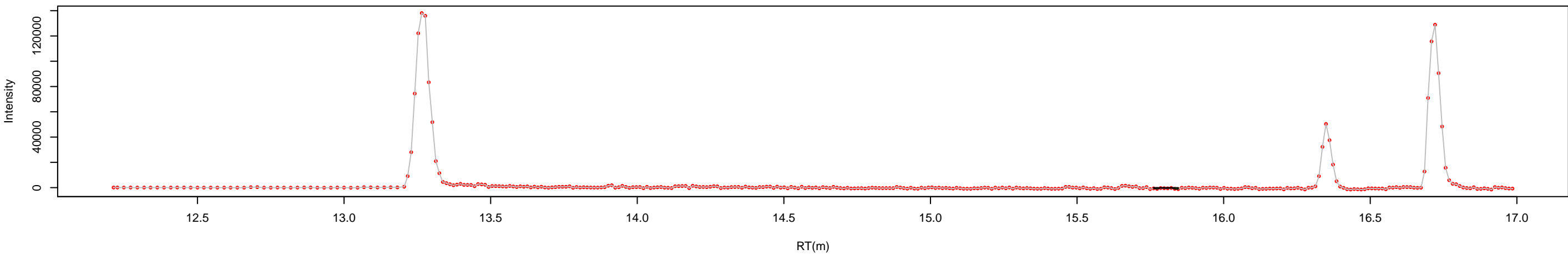
raw chromatogram | batch: 1 sample: coth14 conc: NA function: 1 mass: 375.35>375.35



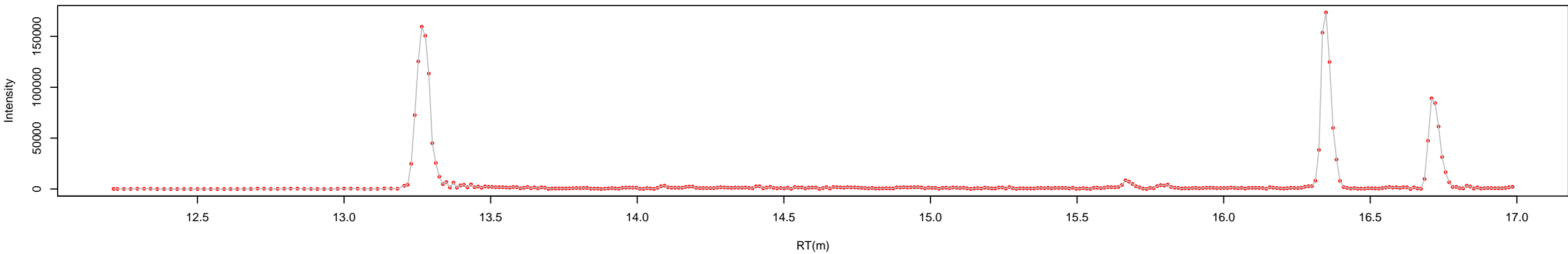
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 12.2 BLine: yes



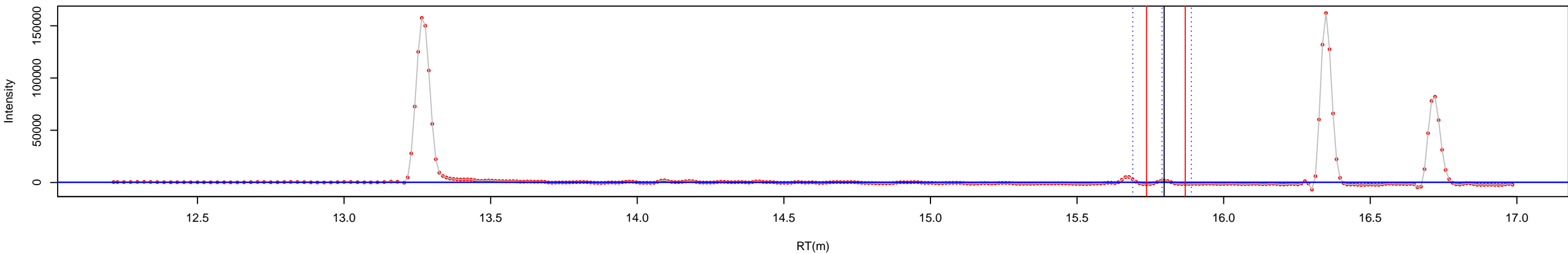
peak area | window size:3 BLine: yes



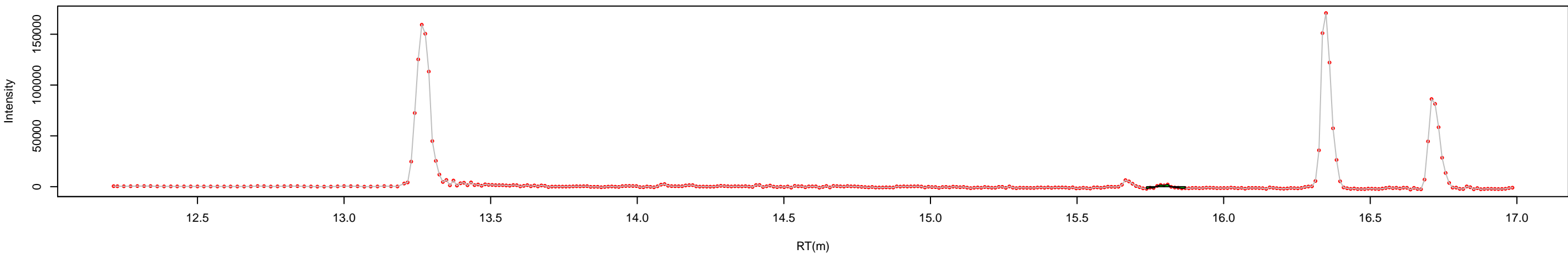
raw chromatogram | batch: 1 sample: cotn23 conc: NA function: 1 mass: 375.35>375.35



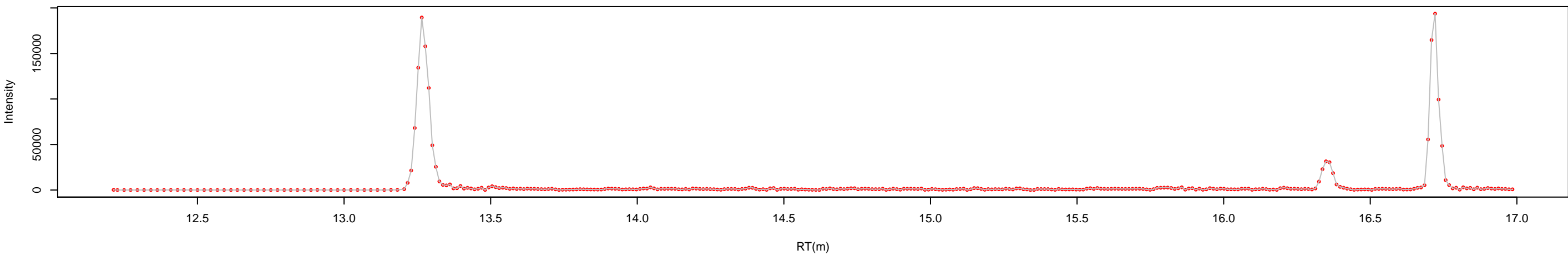
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 40.5 BLine: yes



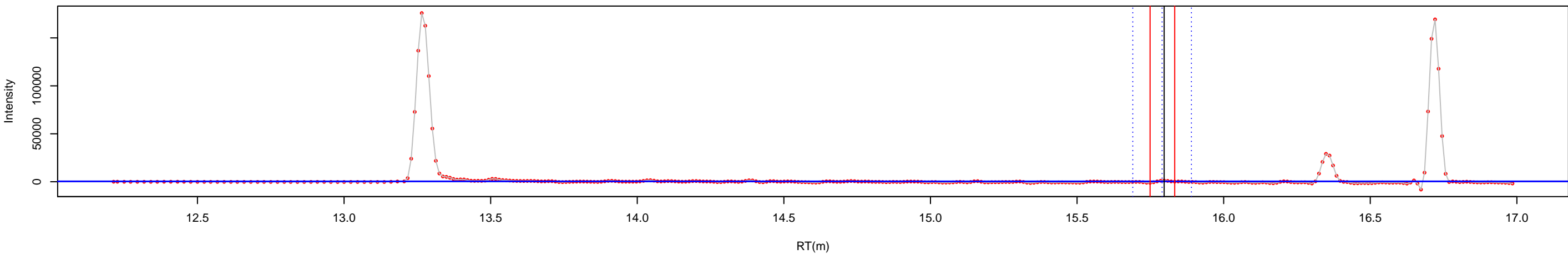
peak area | window size:3 BLine: yes



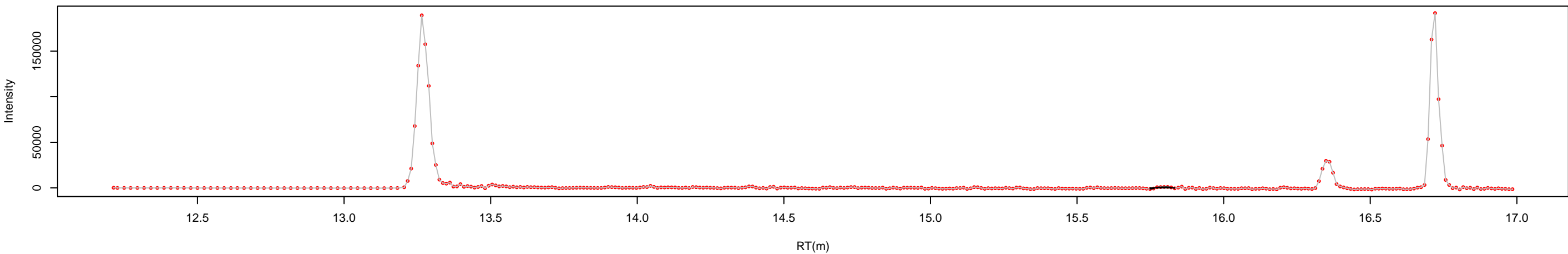
raw chromatogram | batch: 1 sample: coth15 conc: NA function: 1 mass: 375.35>375.35



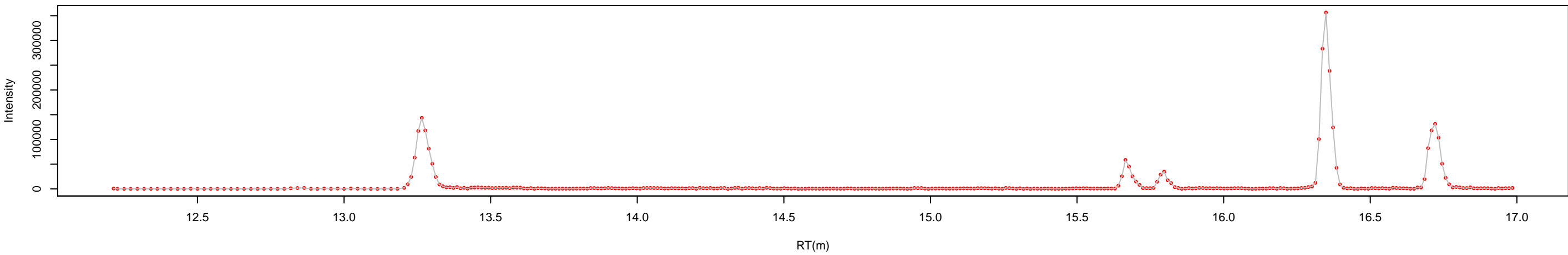
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 69 BLine: yes



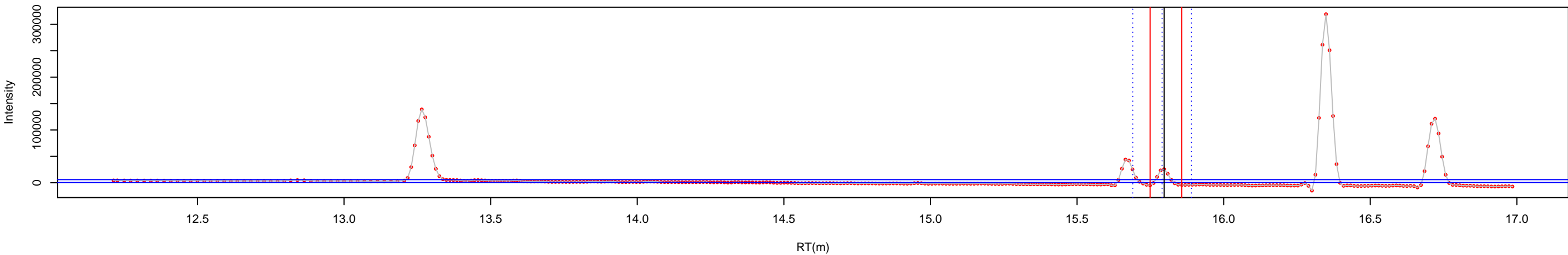
peak area | window size:3 BLine: yes



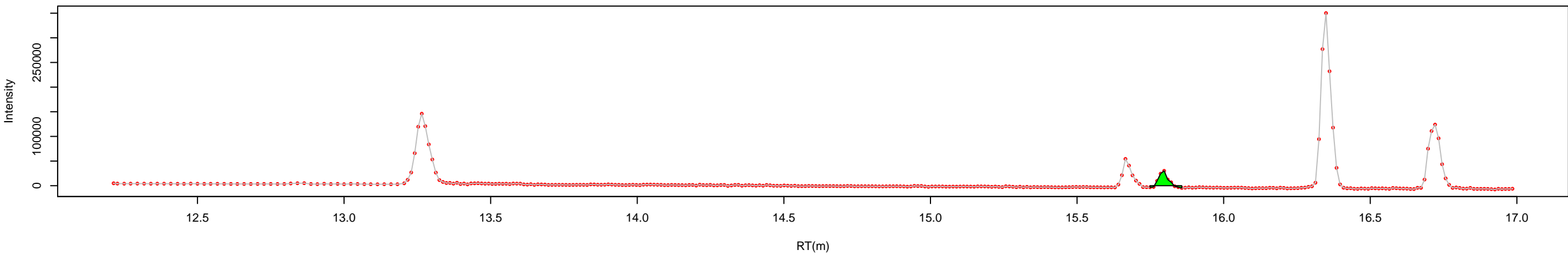
raw chromatogram | batch: 1 sample: cotn24 conc: NA function: 1 mass: 375.35>375.35



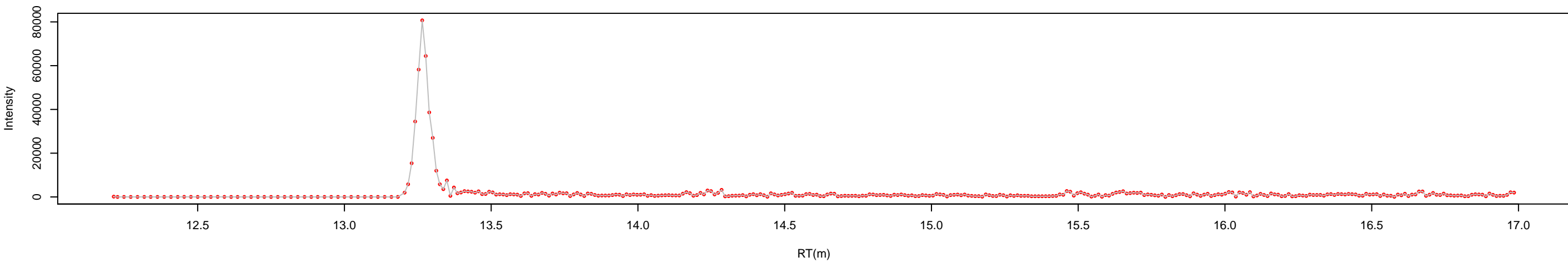
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 594 BLine: yes



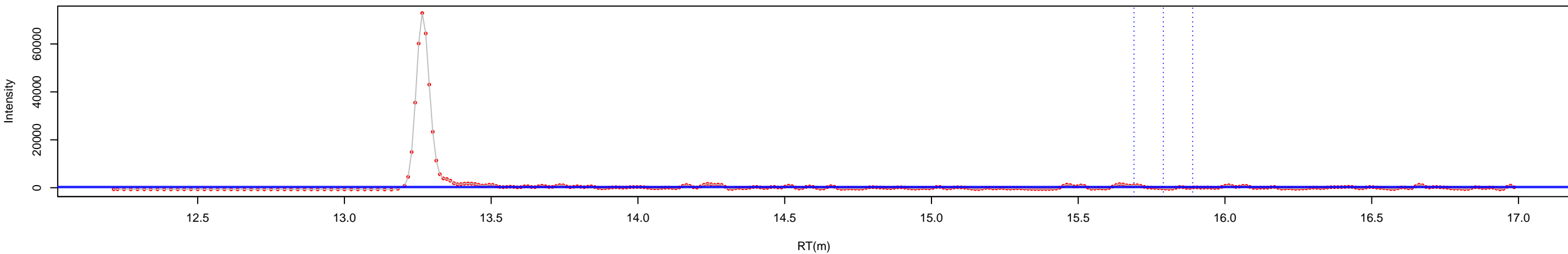
peak area | window size:3 BLine: yes



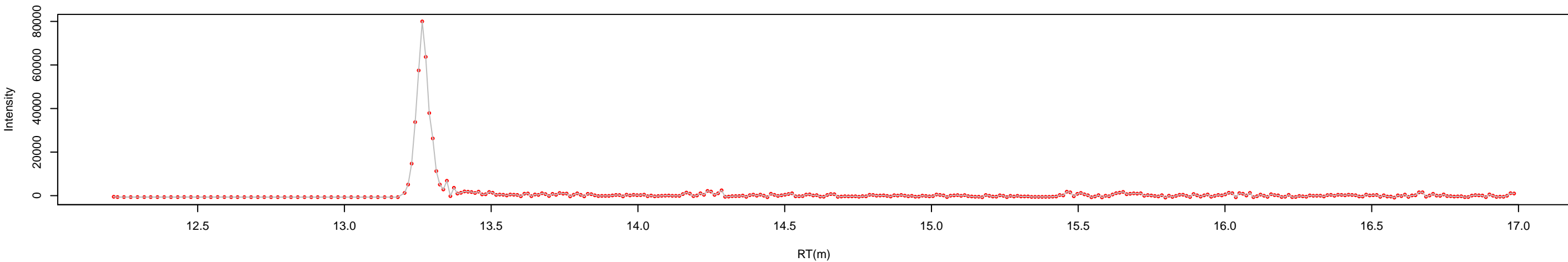
raw chromatogram | batch: 1 sample: std0-10ul-1 conc: 0.001 function: 1 mass: 375.35>375.35



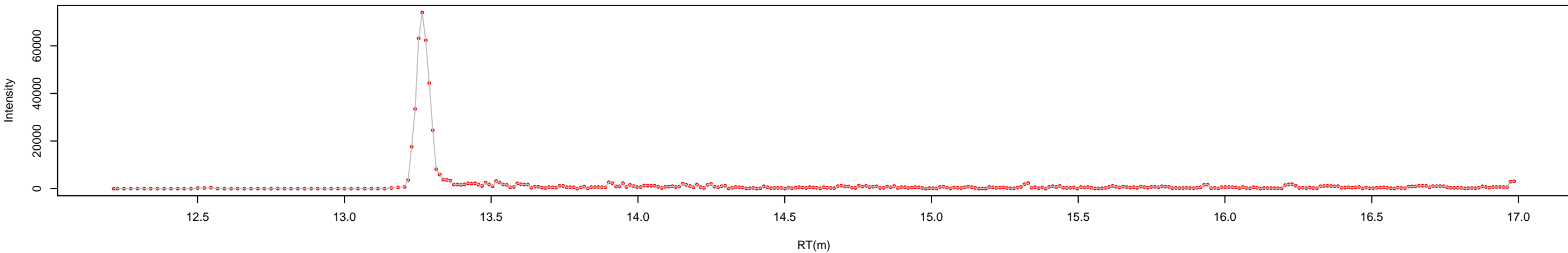
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 53.2 BLine: yes



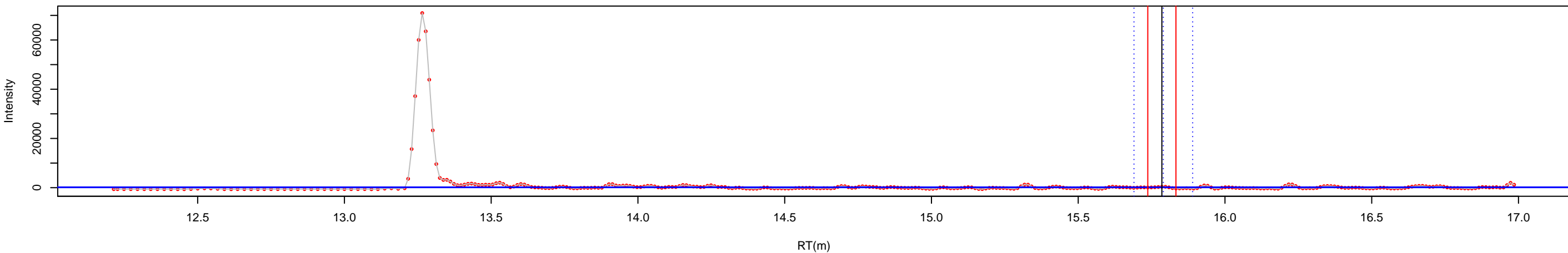
peak area | window size:3 BLine: yes



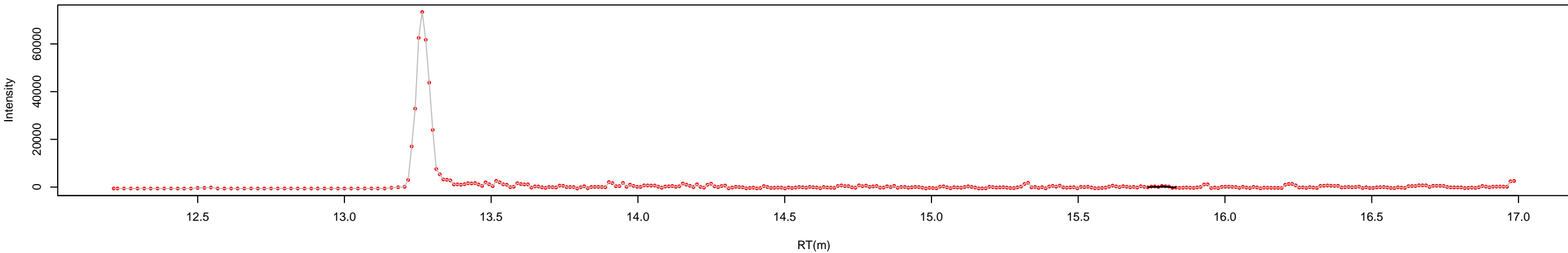
raw chromatogram | batch: 1 sample: std1-10ul-1 conc: 0.002 function: 1 mass: 375.35>375.35



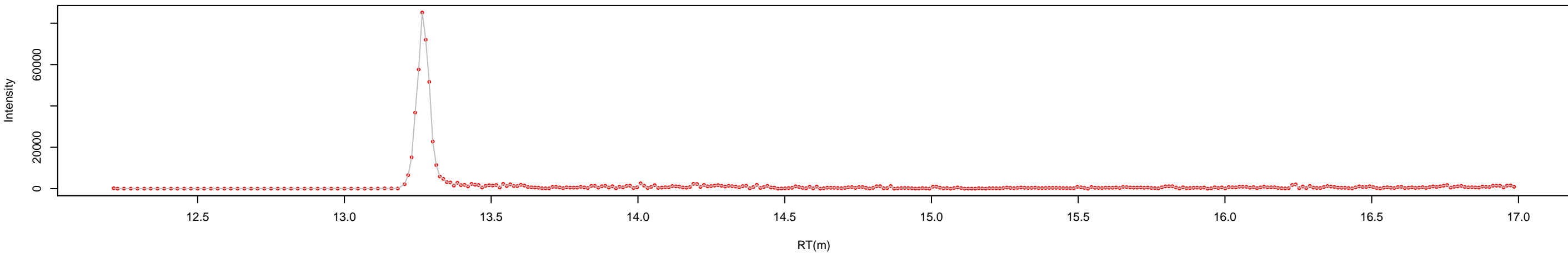
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 27.3 BLine: yes



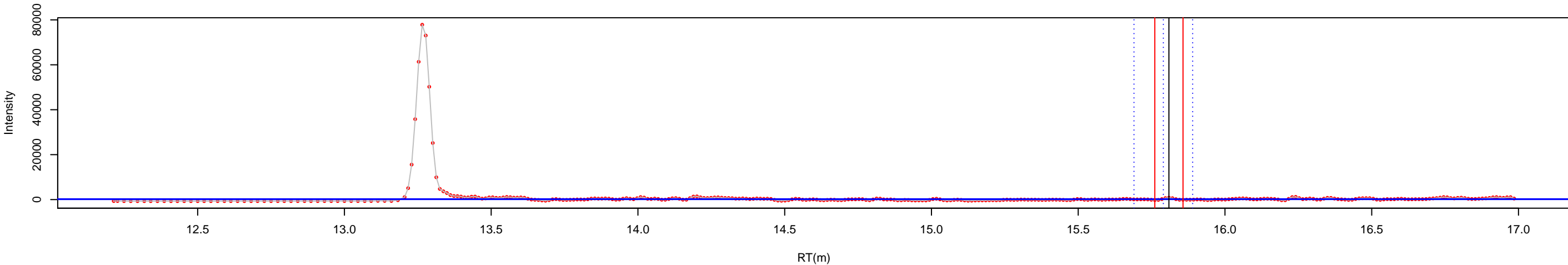
peak area | window size:3 BLine: yes



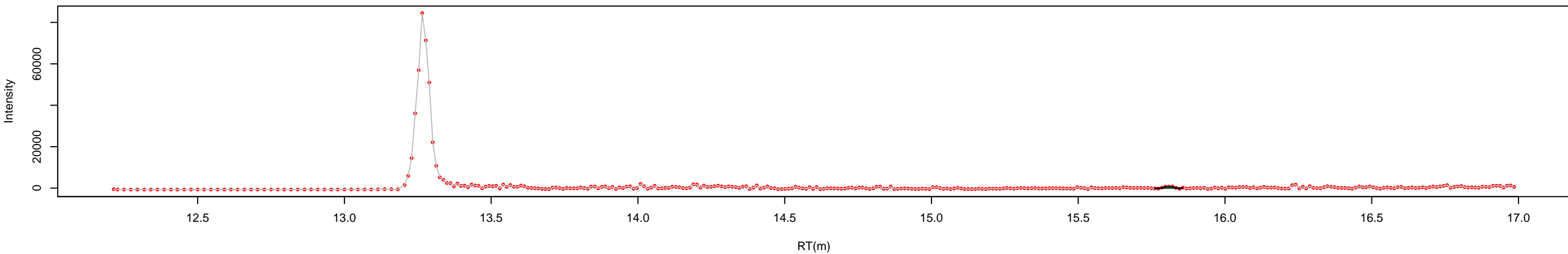
raw chromatogram | batch: 1 sample: std2-10ul-1 conc: 0.005 function: 1 mass: 375.35>375.35



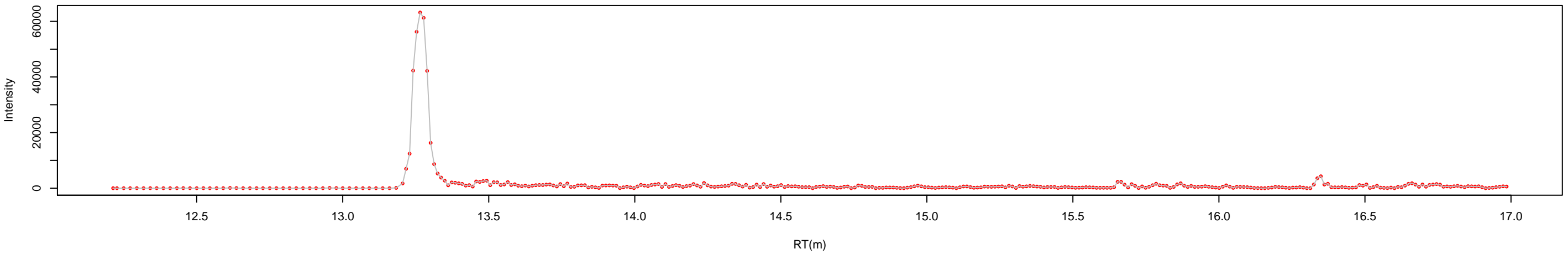
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 33.5 BLine: yes



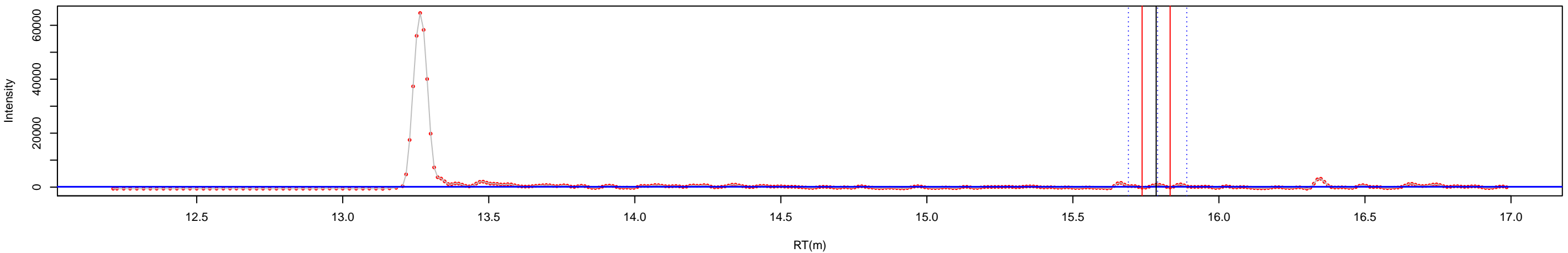
peak area | window size:3 BLine: yes



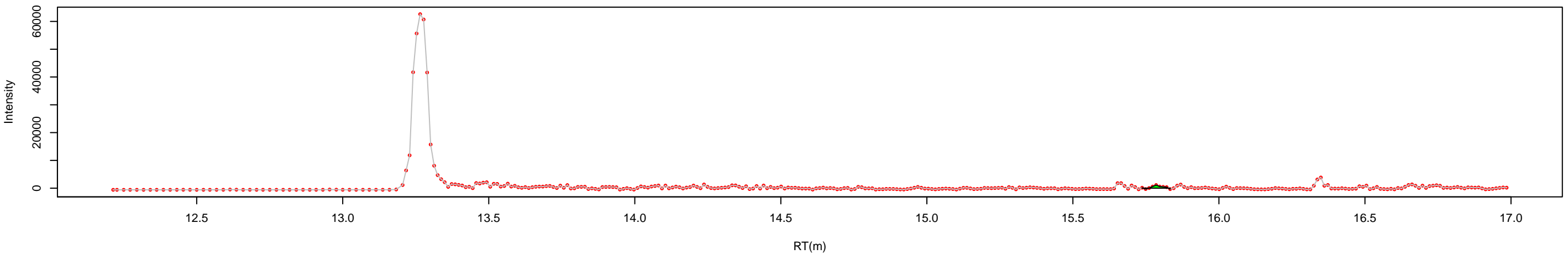
raw chromatogram | batch: 1 sample: std3-10ul-1 conc: 0.01 function: 1 mass: 375.35>375.35



peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 23.2 BLine: yes

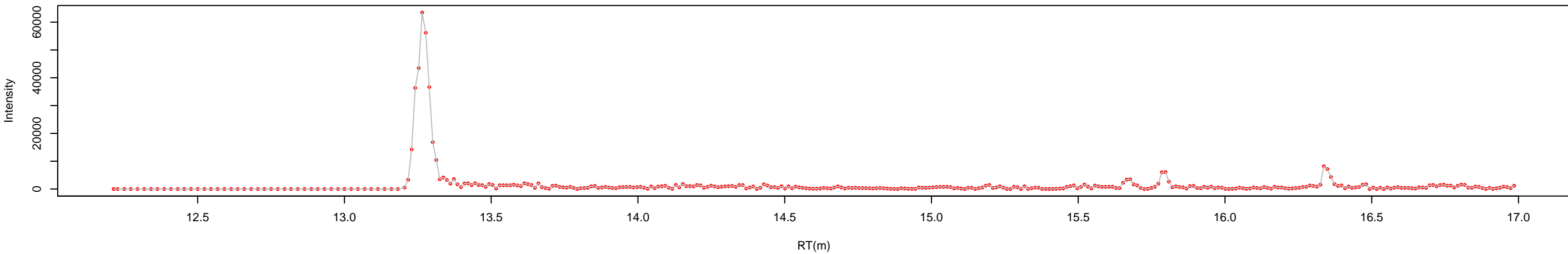


peak area | window size:3 BLine: yes

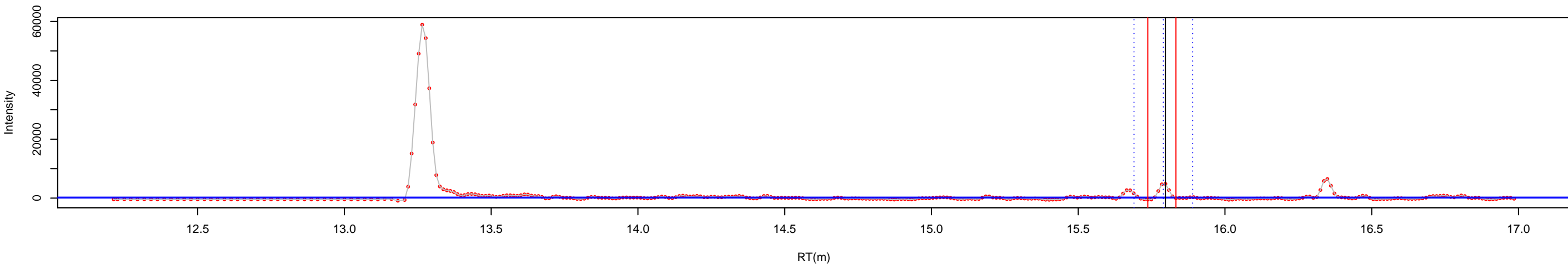




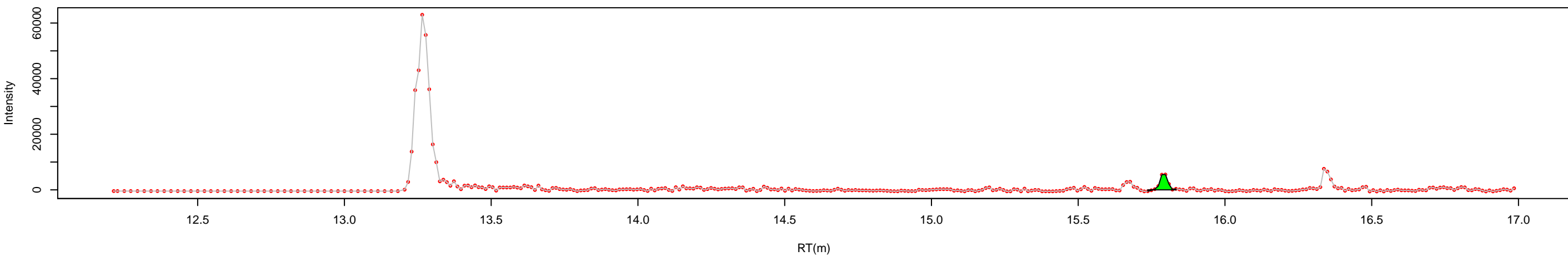
raw chromatogram | batch: 1 sample: std4-10ul-1 conc: 0.02 function: 1 mass: 375.35>375.35



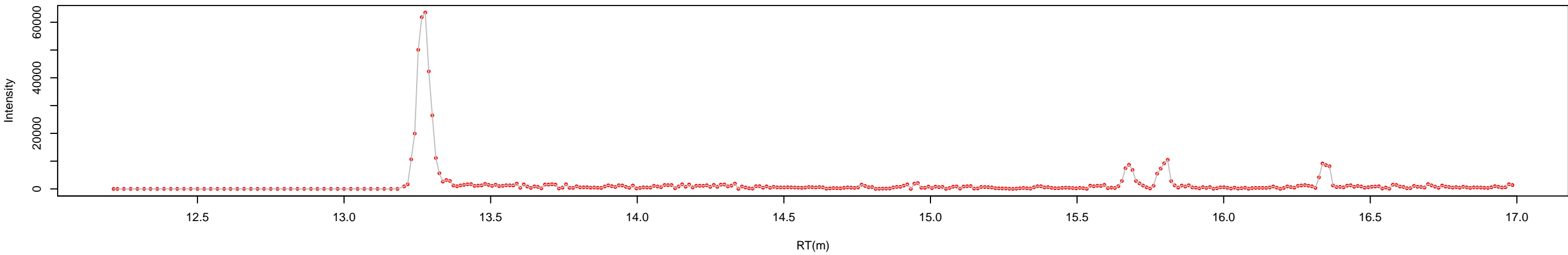
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 32 BLine: yes



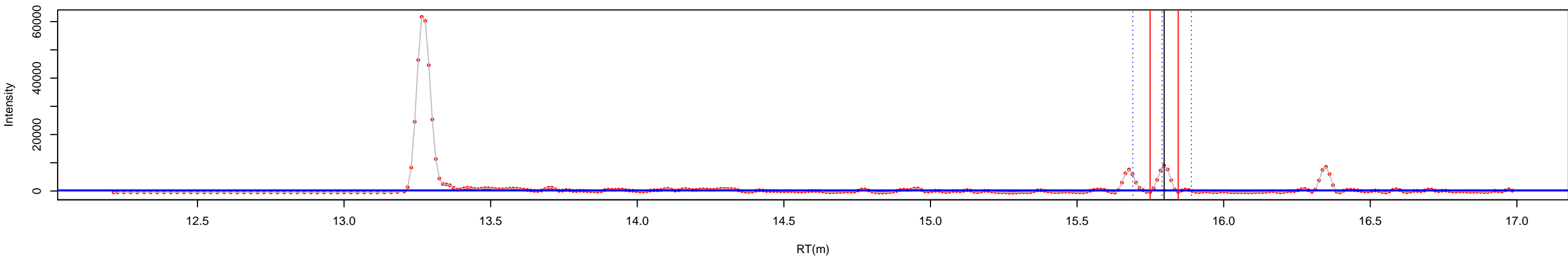
peak area | window size:3 BLine: yes



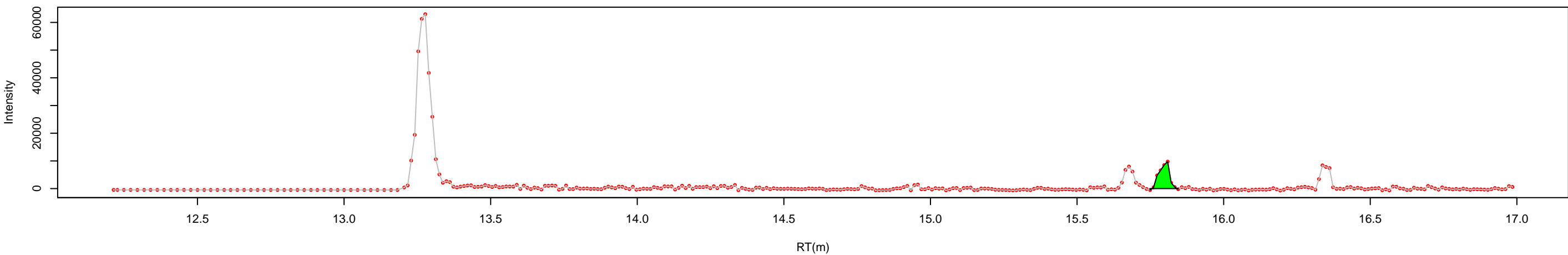
raw chromatogram | batch: 1 sample: std5-10ul-1 conc: 0.05 function: 1 mass: 375.35>375.35



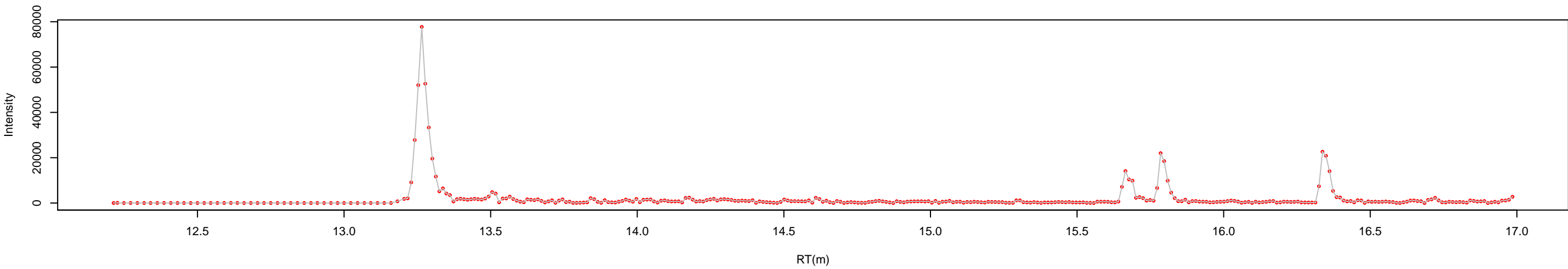
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 37.6 BLine: yes



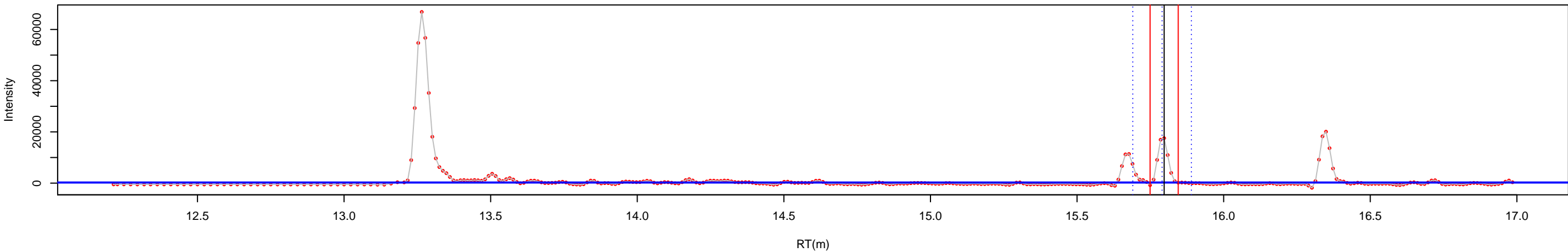
peak area | window size:3 BLine: yes



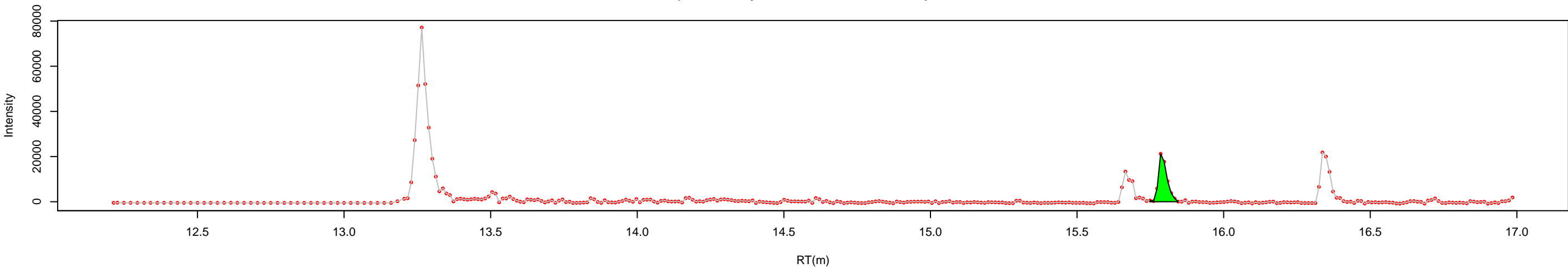
raw chromatogram | batch: 1 sample: std6-10ul-1 conc: 0.1 function: 1 mass: 375.35>375.35



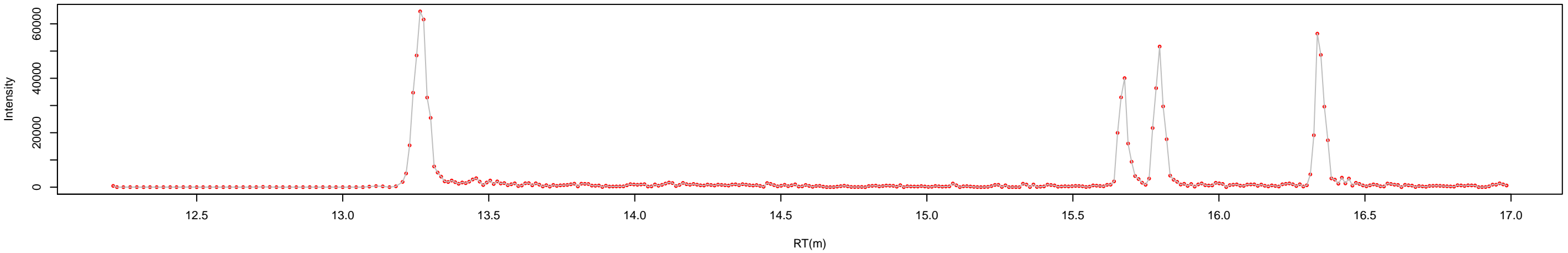
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 43.1 BLine: yes



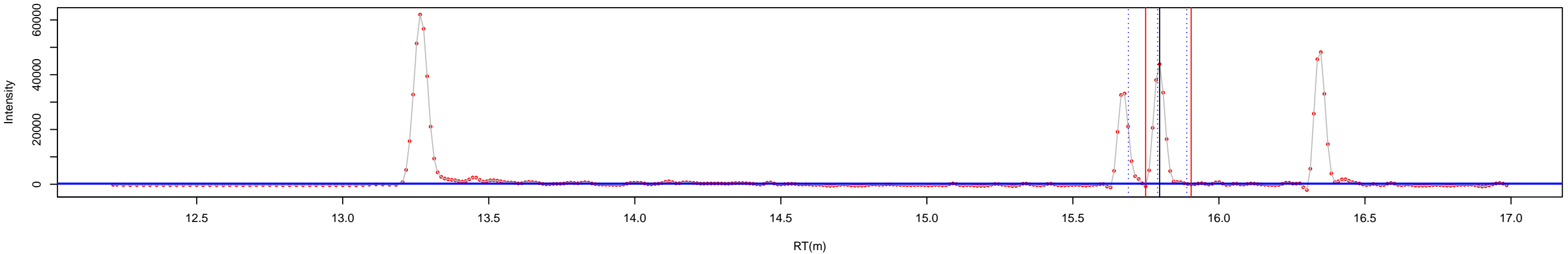
peak area | window size:3 BLine: yes



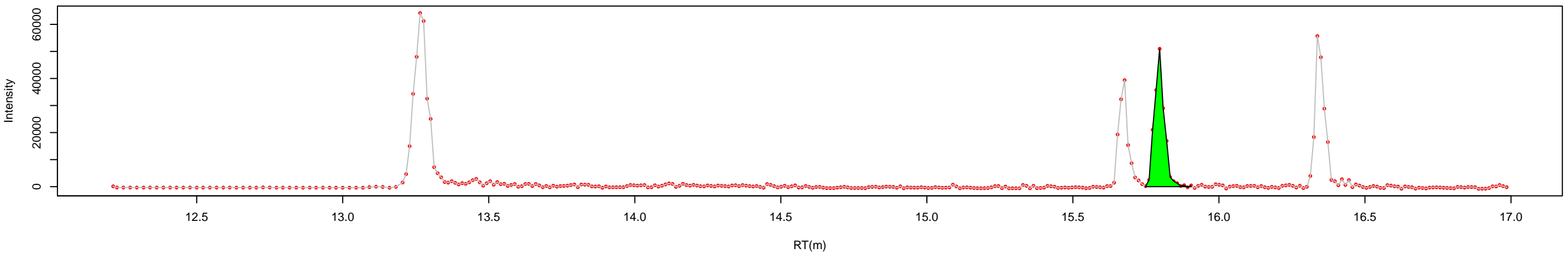
raw chromatogram | batch: 1 sample: std7-10ul-1 conc: 0.2 function: 1 mass: 375.35>375.35



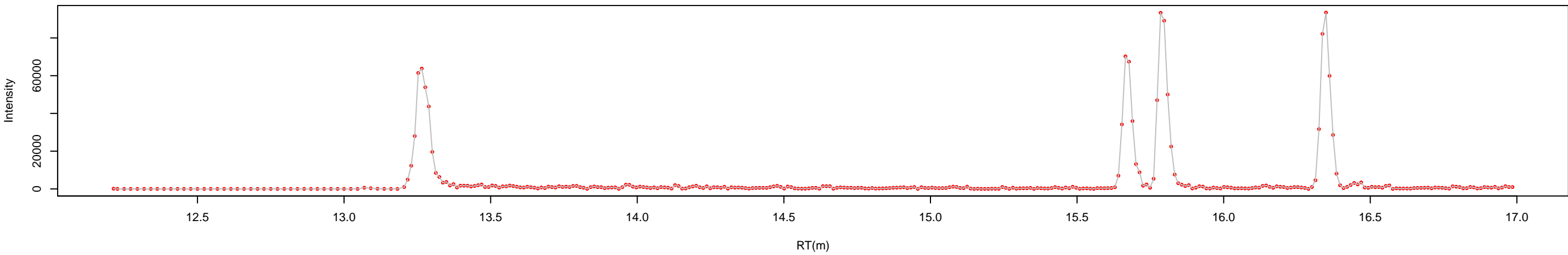
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 40.5 BLine: yes



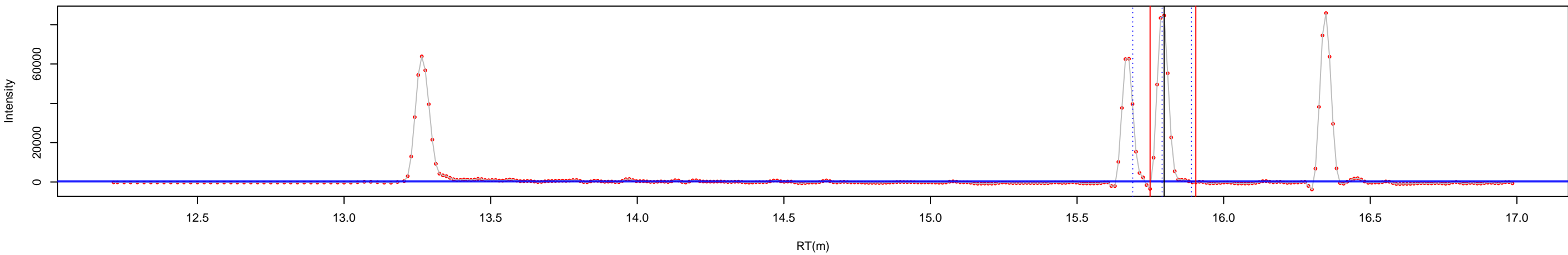
peak area | window size:3 BLine: yes



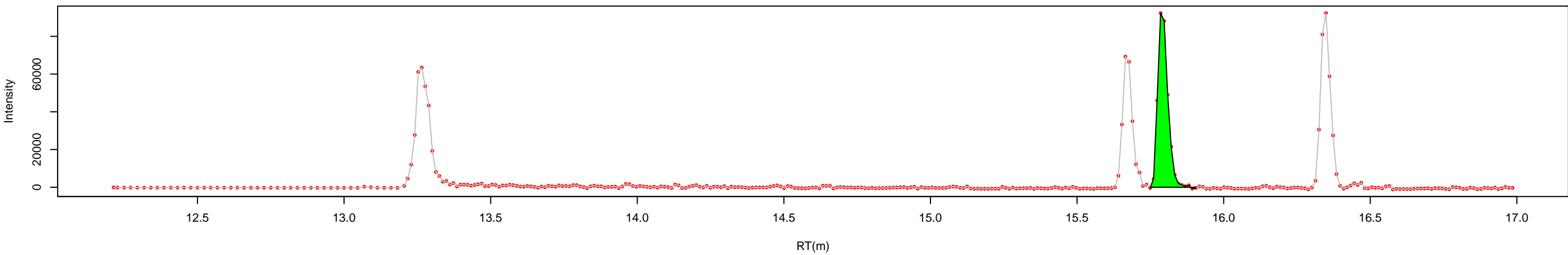
raw chromatogram | batch: 1 sample: std8-10ul-1 conc: 0.5 function: 1 mass: 375.35>375.35



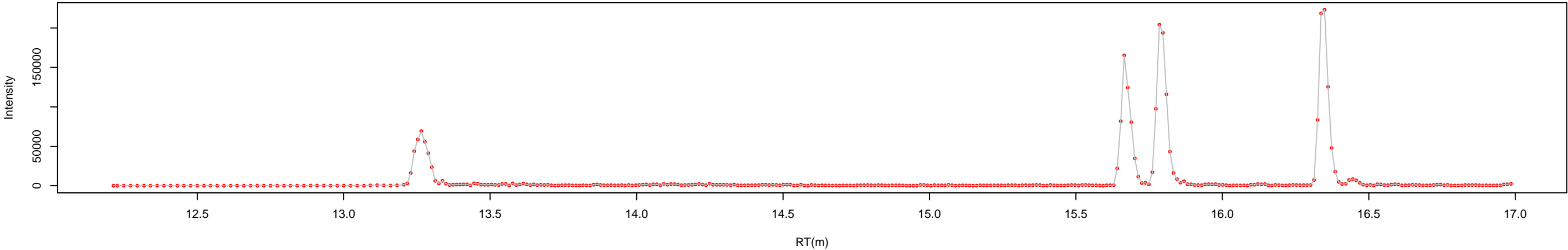
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 54.1 BLine: yes



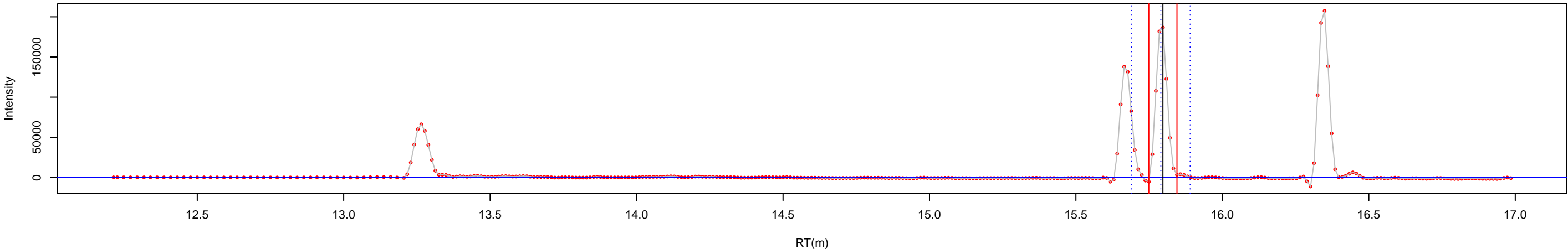
peak area | window size:3 BLine: yes



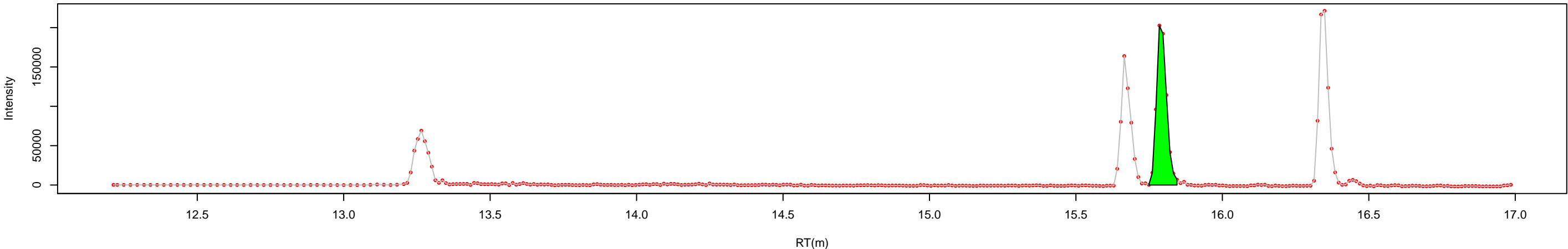
raw chromatogram | batch: 1   sample: std9-10ul-1   conc: 1   function: 1   mass: 375.35>375.35



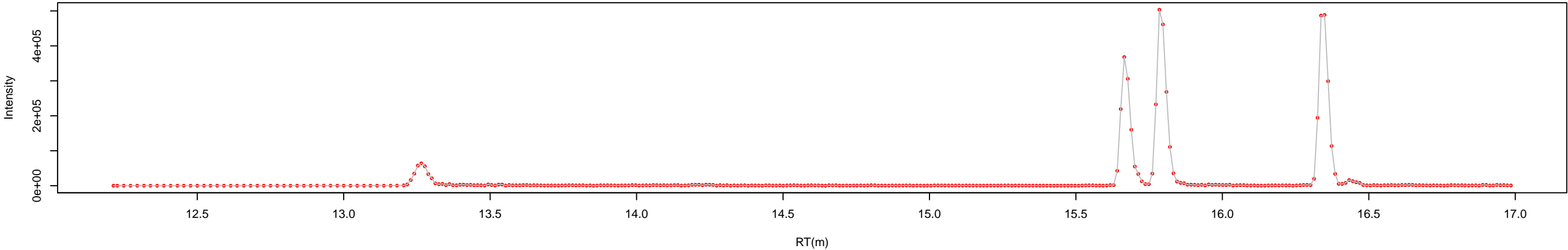
peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 30.7   BLine: yes



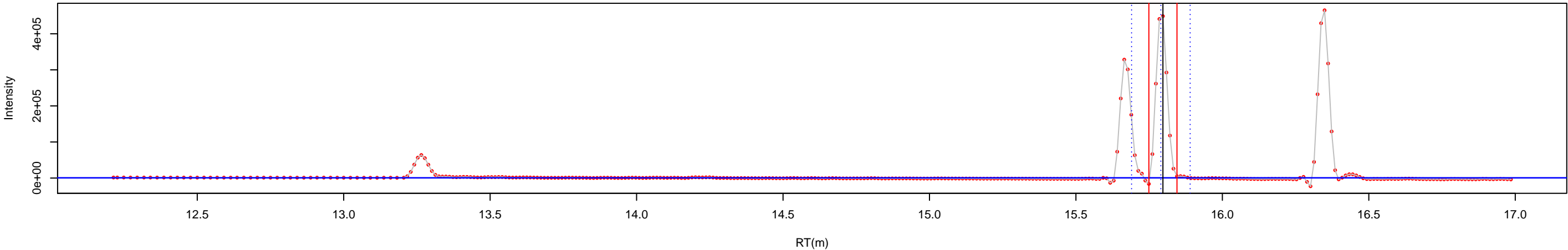
peak area | window size:3   BLine: yes



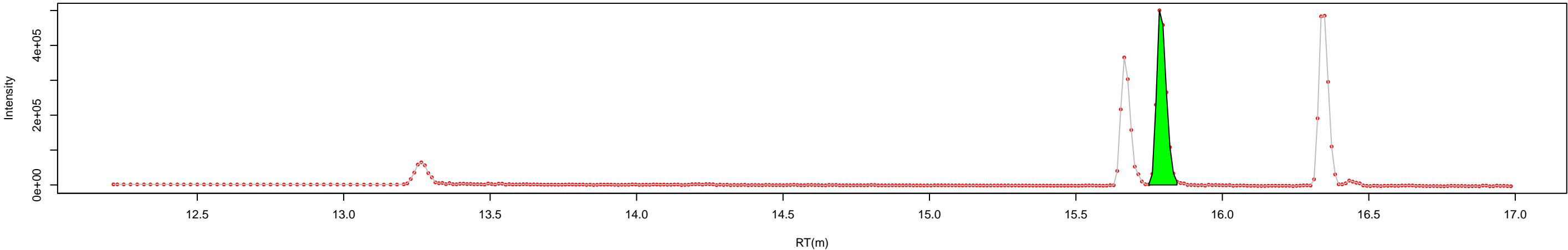
raw chromatogram | batch: 1   sample: std10-10ul-1   conc: 2   function: 1   mass: 375.35>375.35



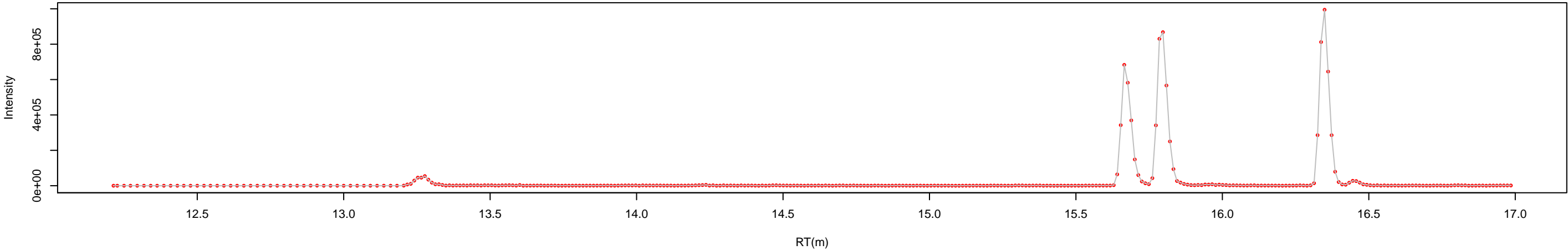
peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 113   BLine: yes



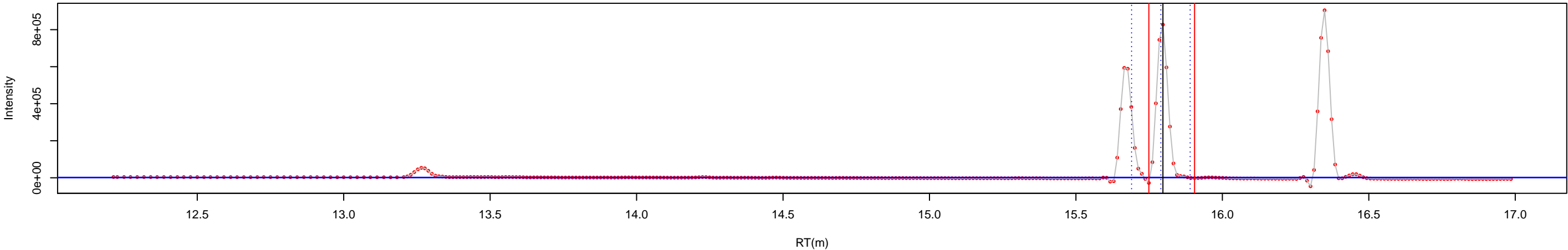
peak area | window size:3   BLine: yes



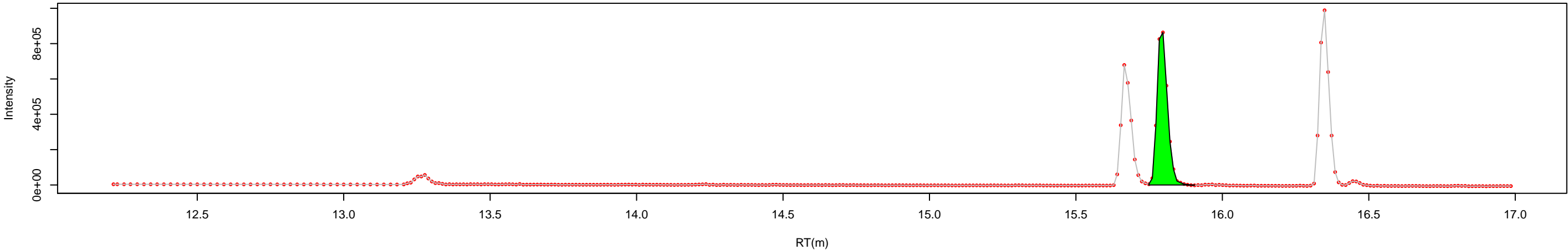
raw chromatogram | batch: 1   sample: std11-10ul-1   conc: 5   function: 1   mass: 375.35>375.35



peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 251   BLine: yes

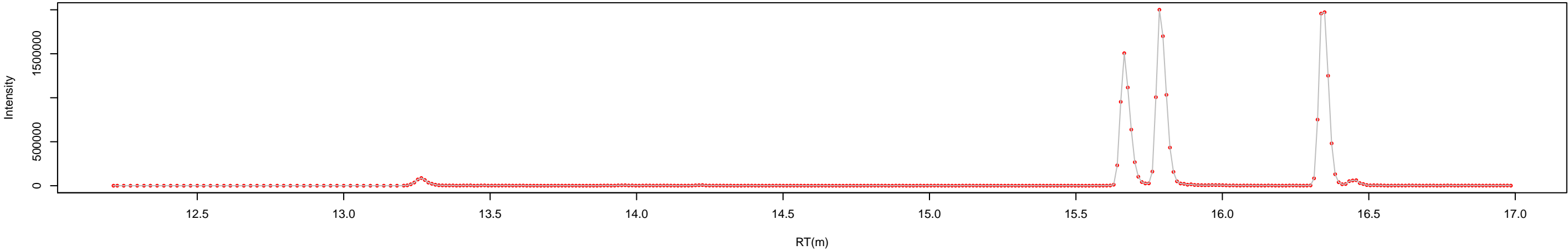


peak area | window size:3   BLine: yes

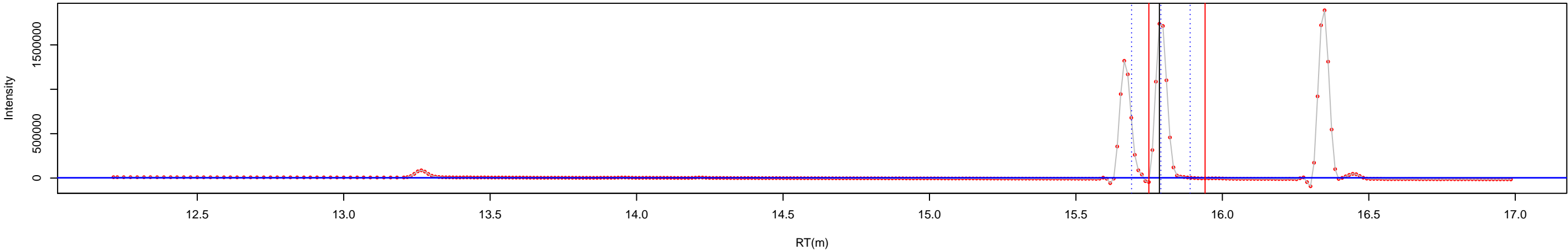




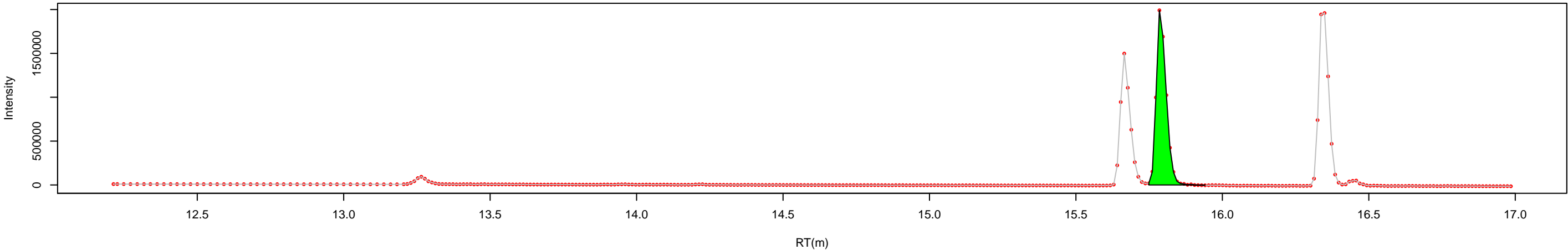
raw chromatogram | batch: 1   sample: std12-10ul-1   conc: 10   function: 1   mass: 375.35>375.35



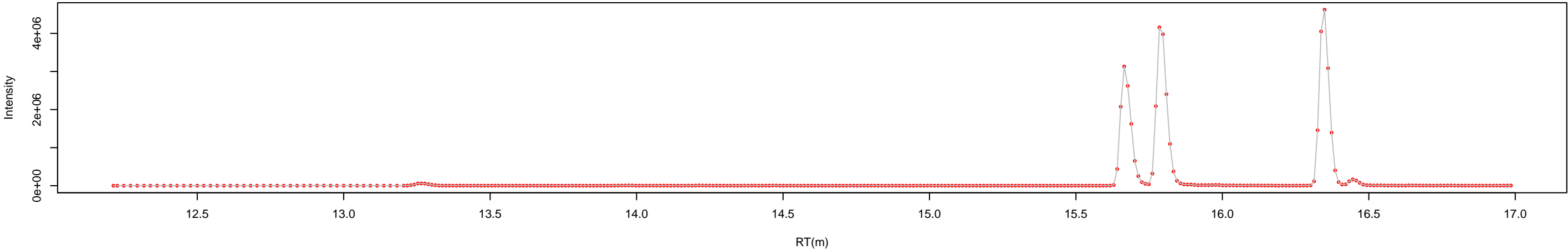
peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 576   BLine: yes



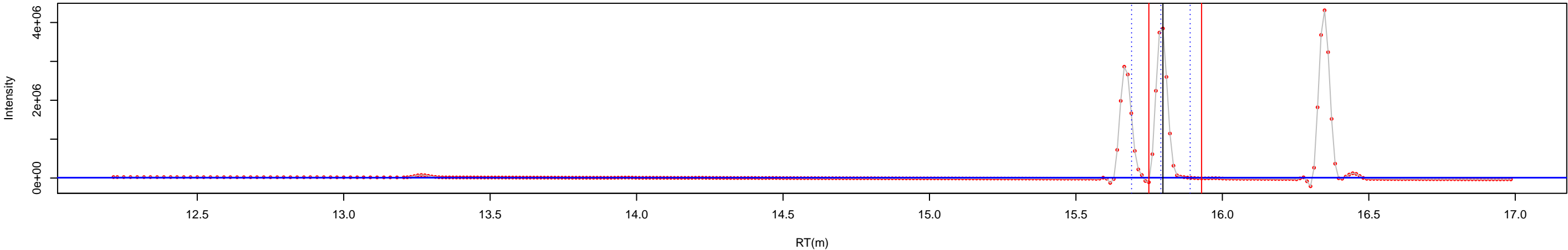
peak area | window size:3   BLine: yes



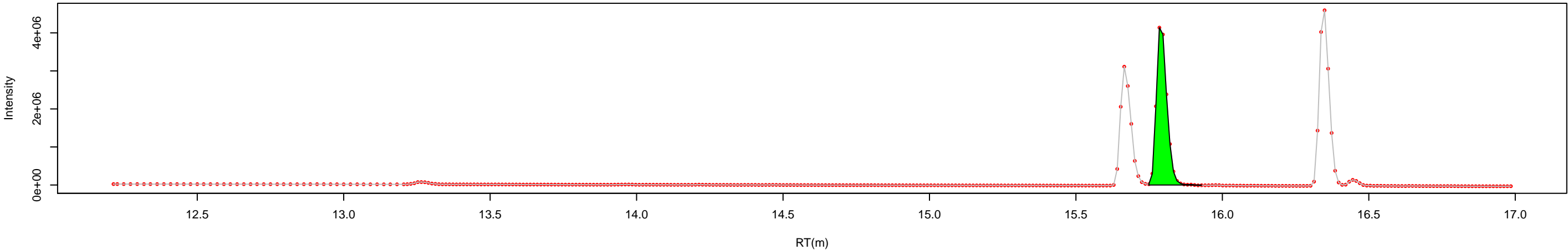
raw chromatogram | batch: 1   sample: std13-10ul-1   conc: 20   function: 1   mass: 375.35>375.35



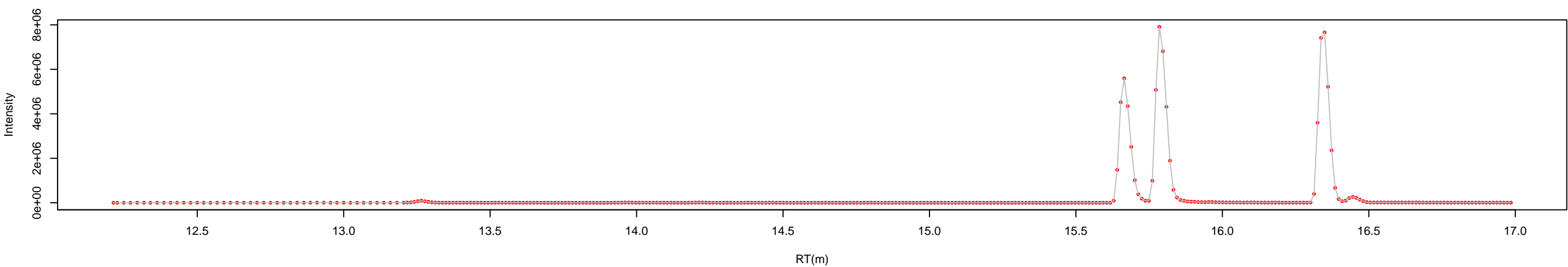
peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 1660   BLine: yes



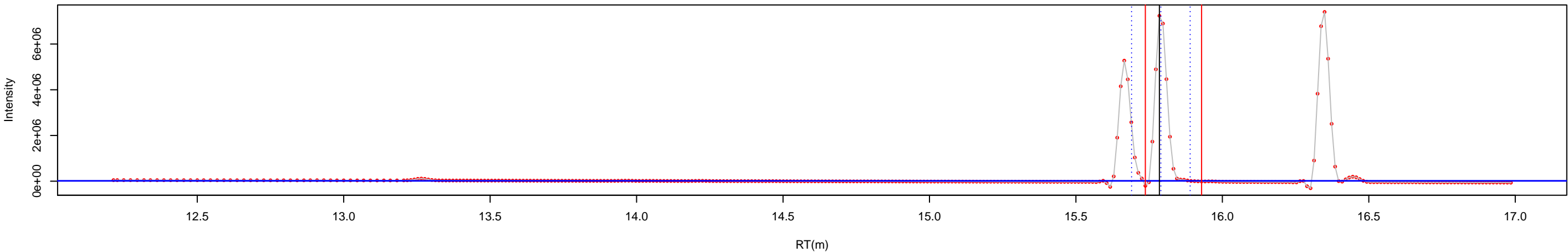
peak area | window size:3   BLine: yes



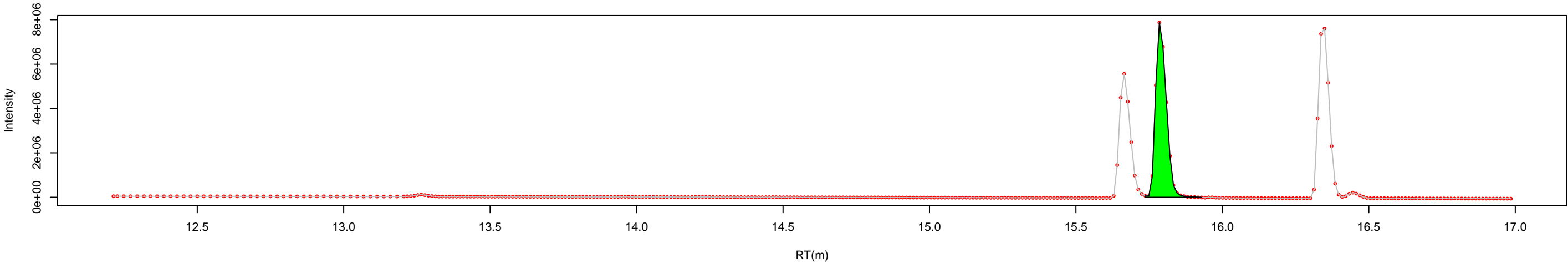
raw chromatogram | batch: 1   sample: std14-10ul-1   conc: 50   function: 1   mass: 375.35>375.35



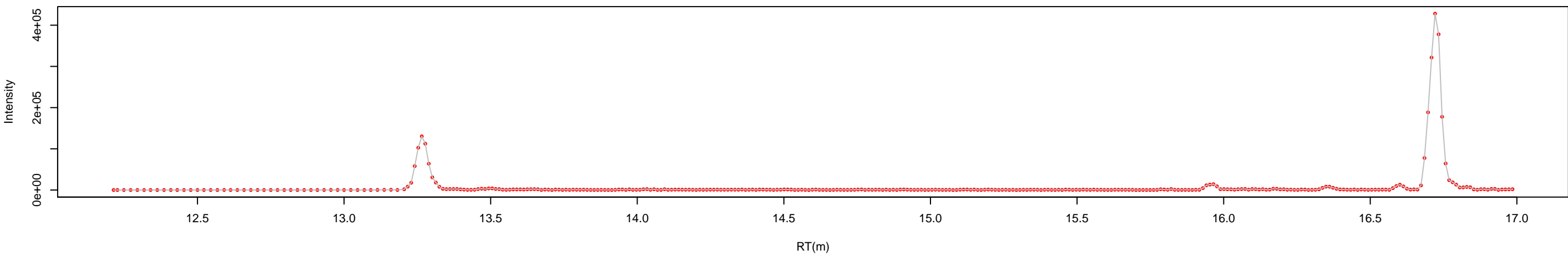
peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 2640   BLine: yes



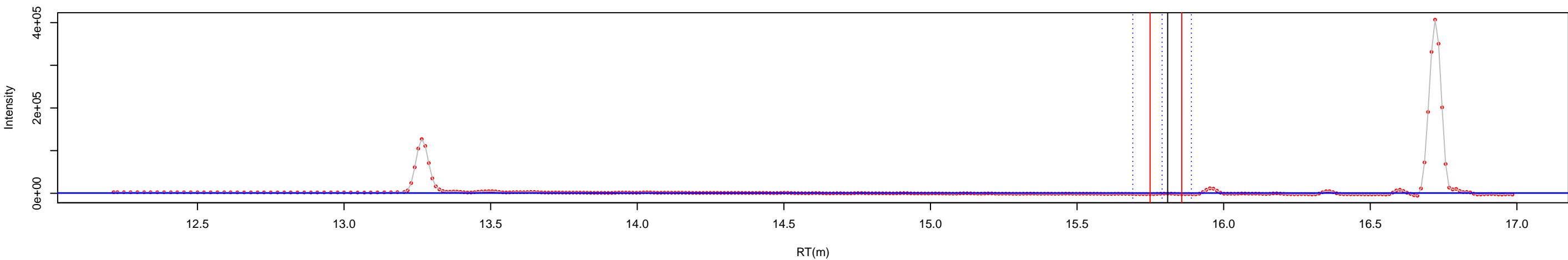
peak area | window size:3   BLine: yes



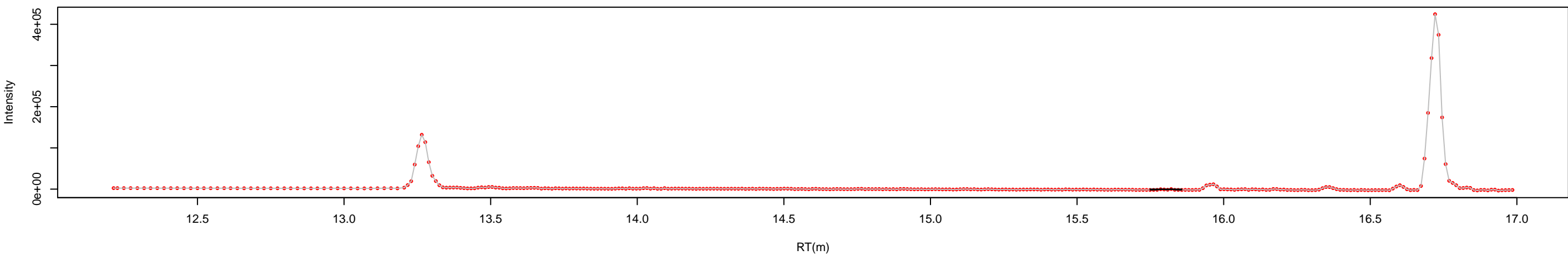
raw chromatogram | batch: 2 sample: coth45 conc: NA function: 1 mass: 375.35>375.35



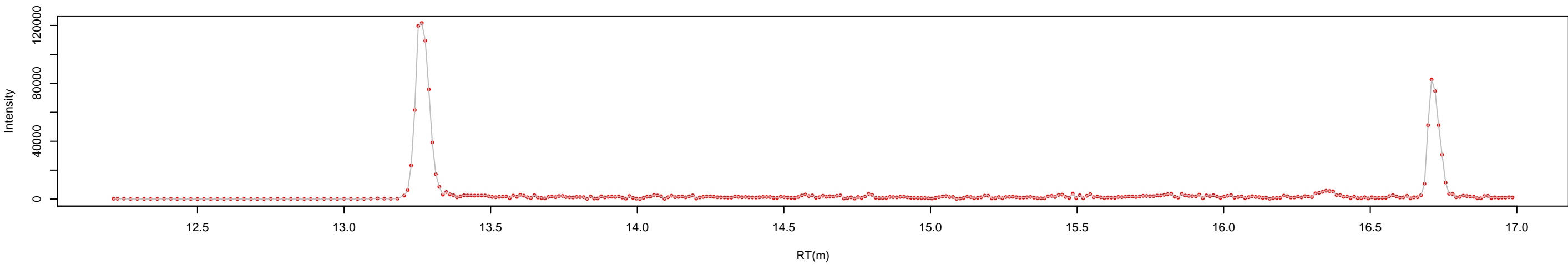
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 107 BLine: yes



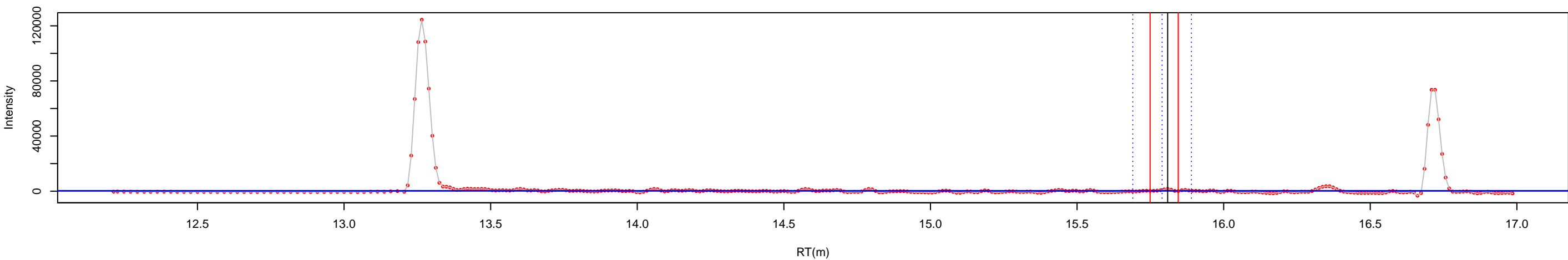
peak area | window size:3 BLine: yes



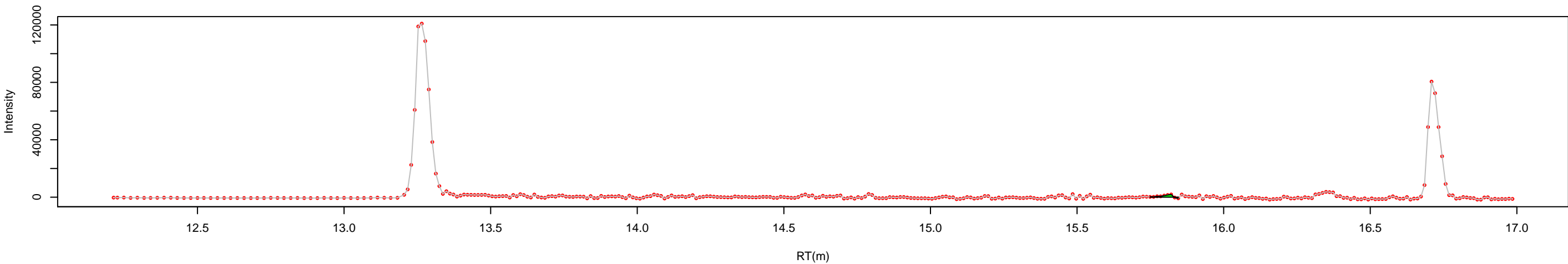
raw chromatogram | batch: 2 sample: coth46 conc: NA function: 1 mass: 375.35>375.35



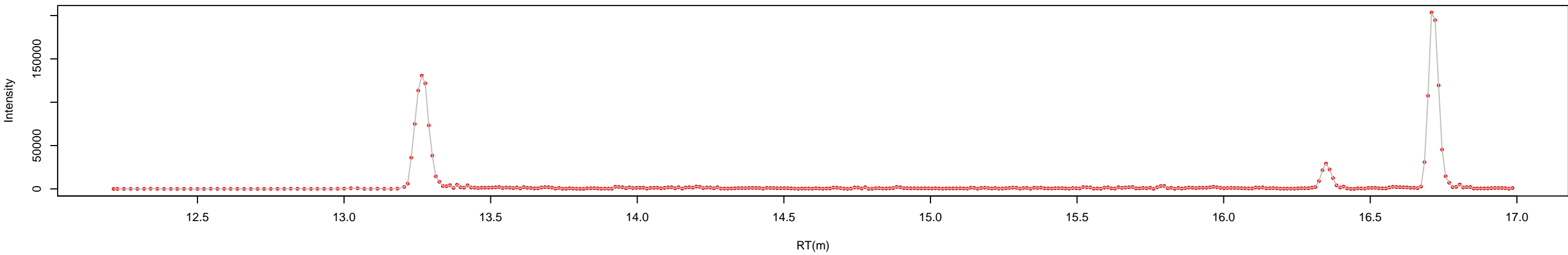
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 43.4 BLine: yes



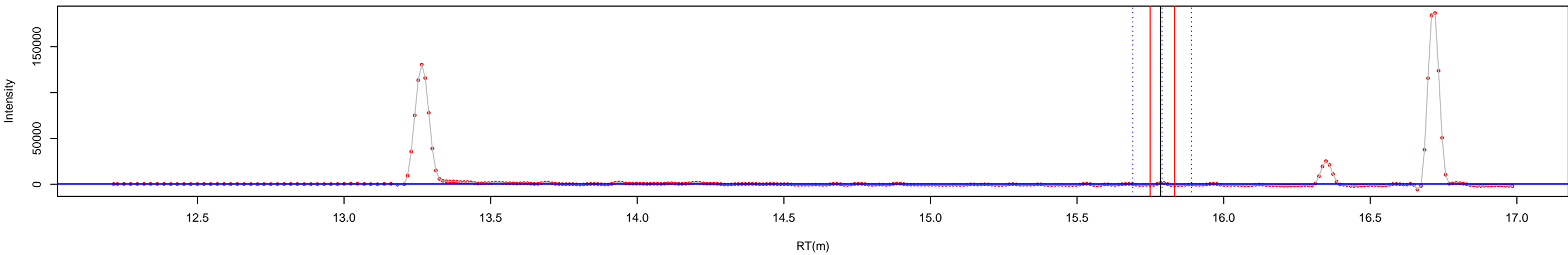
peak area | window size:3 BLine: yes



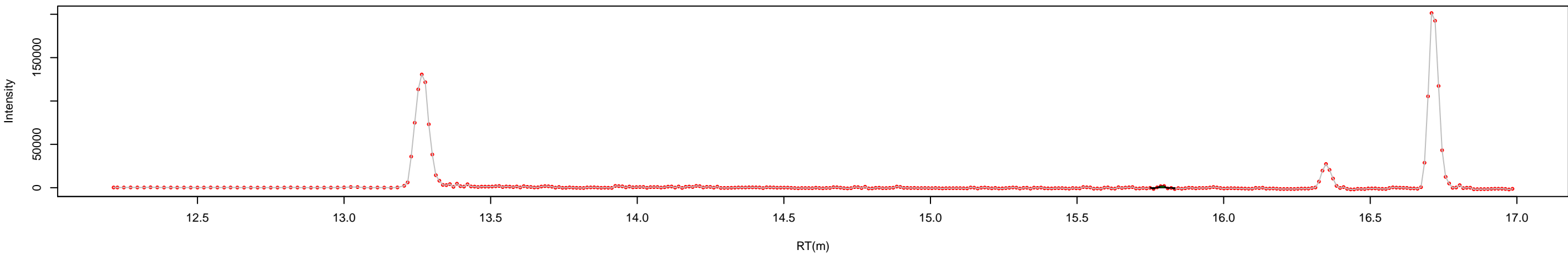
raw chromatogram | batch: 2 sample: coth47 conc: NA function: 1 mass: 375.35>375.35



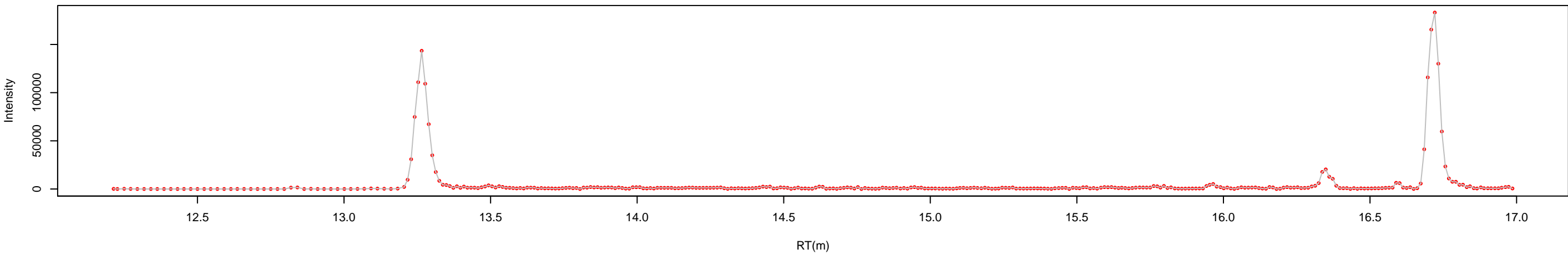
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 42.5 BLine: yes



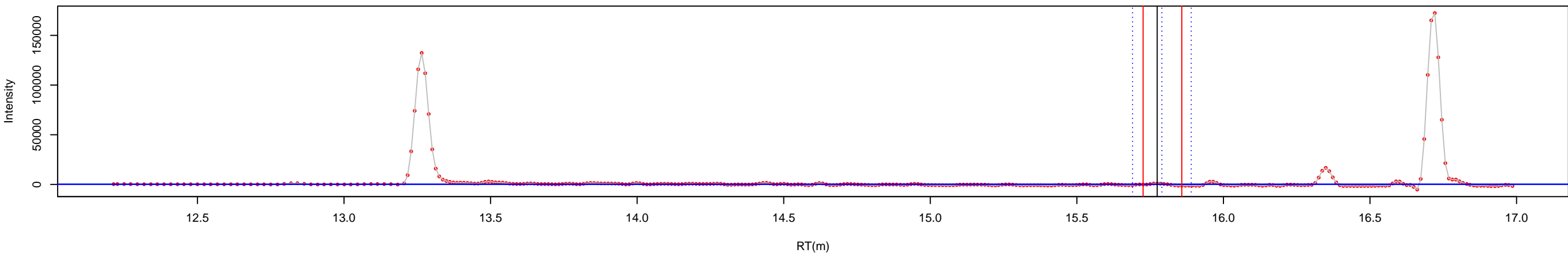
peak area | window size:3 BLine: yes



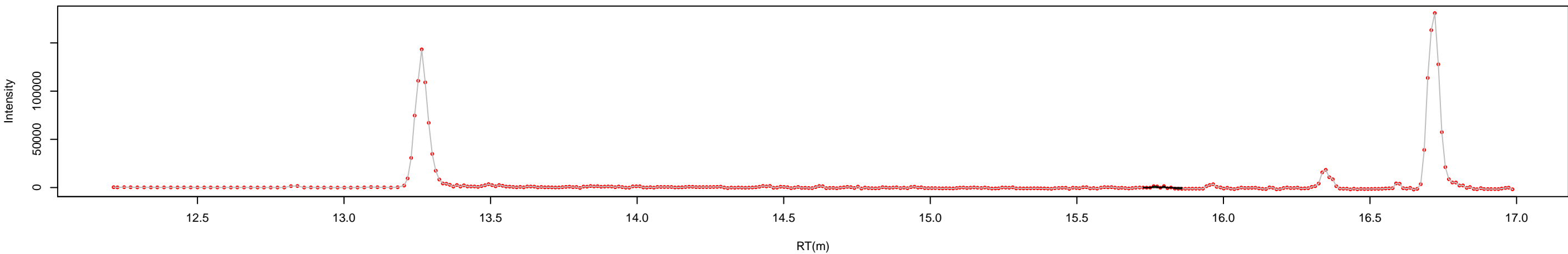
raw chromatogram | batch: 2 sample: coth48 conc: NA function: 1 mass: 375.35>375.35



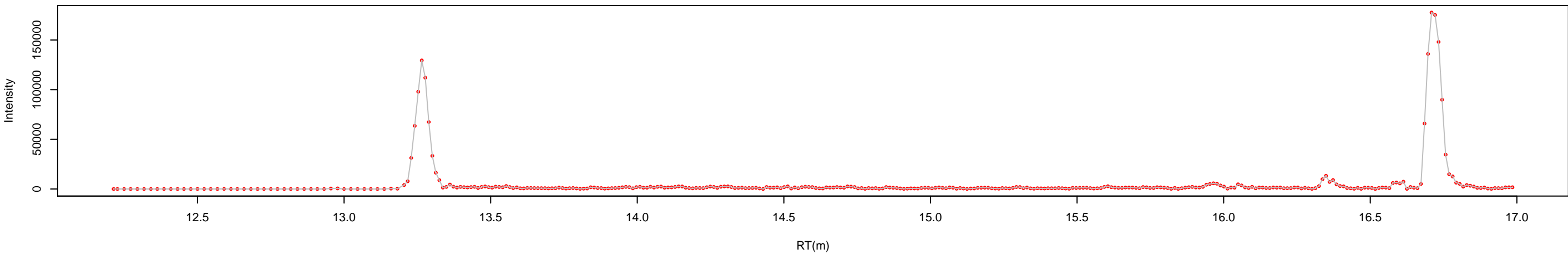
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 29.3 BLine: yes



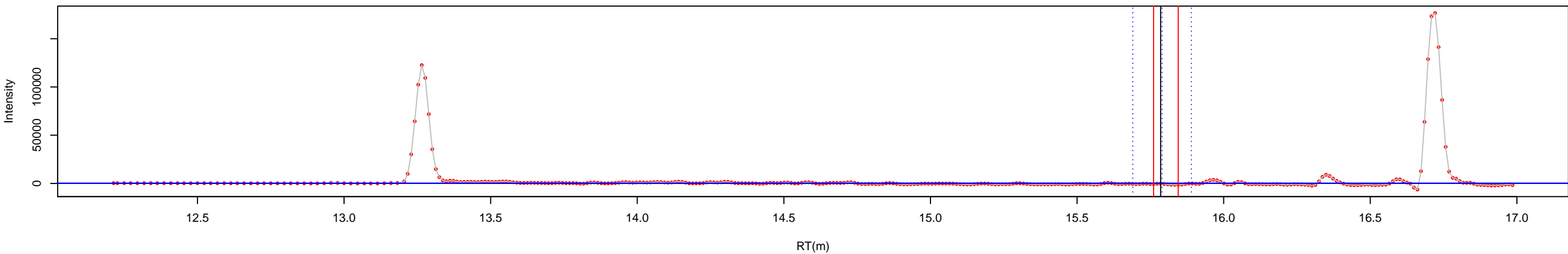
peak area | window size:3 BLine: yes



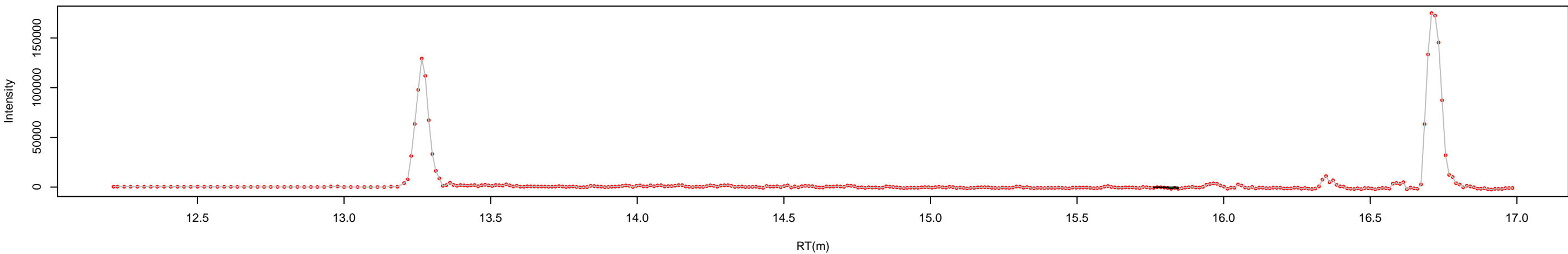
raw chromatogram | batch: 2 sample: coth49 conc: NA function: 1 mass: 375.35>375.35



peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 33 BLine: yes

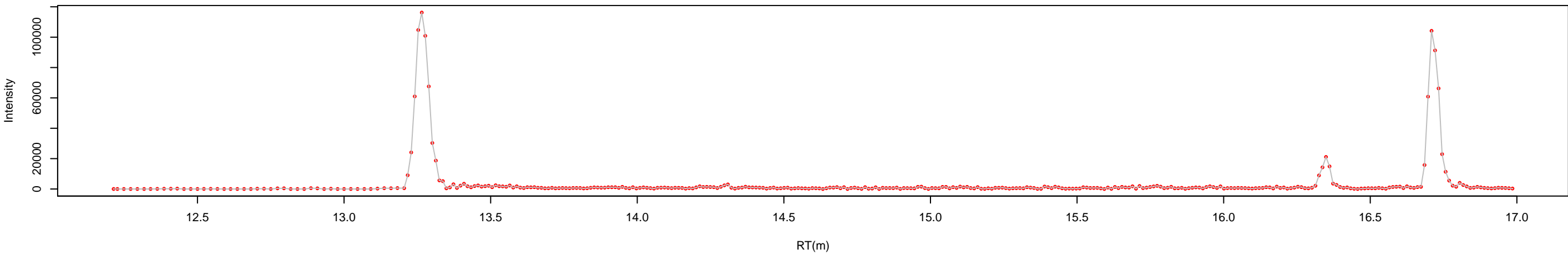


peak area | window size:3 BLine: yes

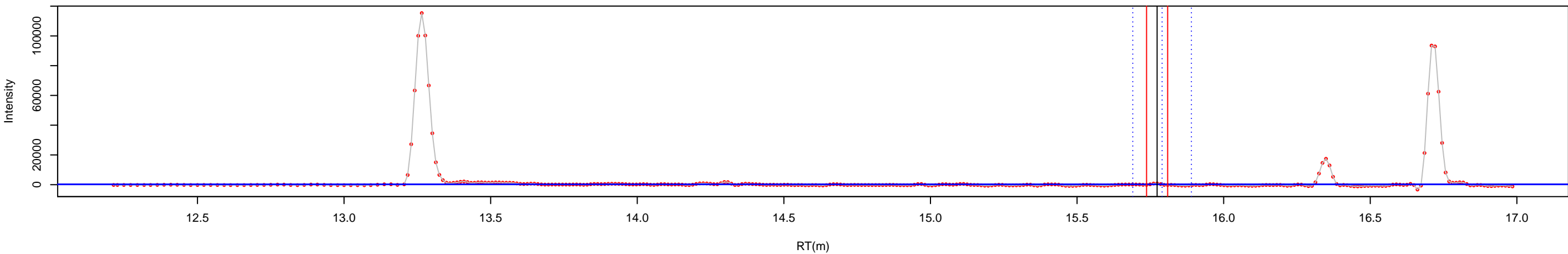




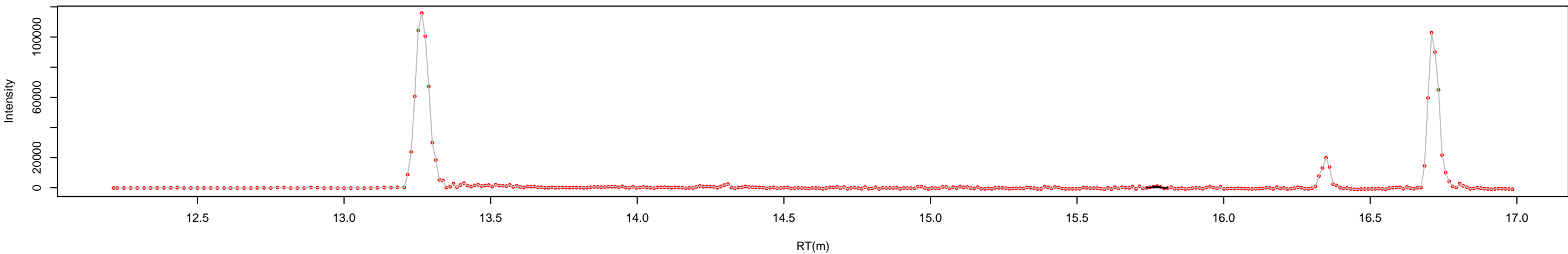
raw chromatogram | batch: 2 sample: coth50 conc: NA function: 1 mass: 375.35>375.35



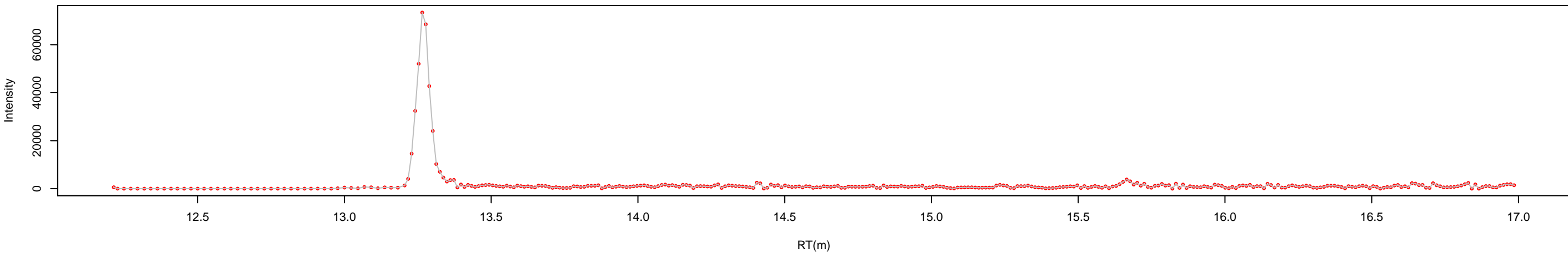
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 41.4 BLine: yes



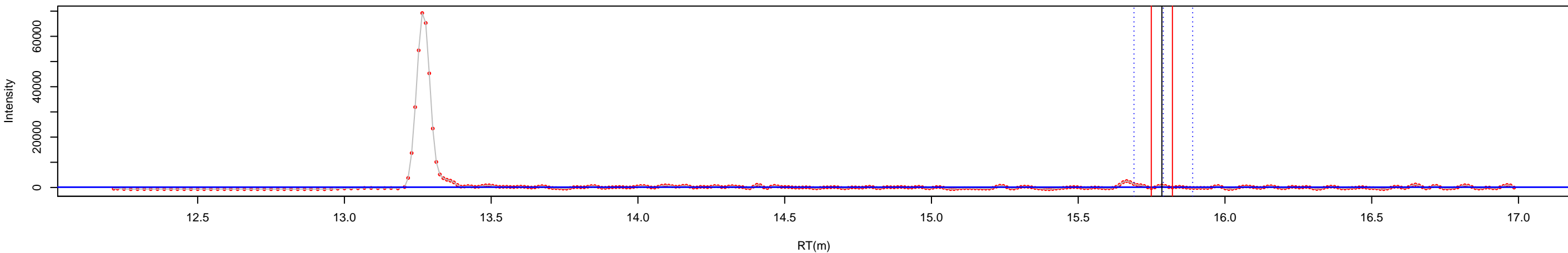
peak area | window size:3 BLine: yes



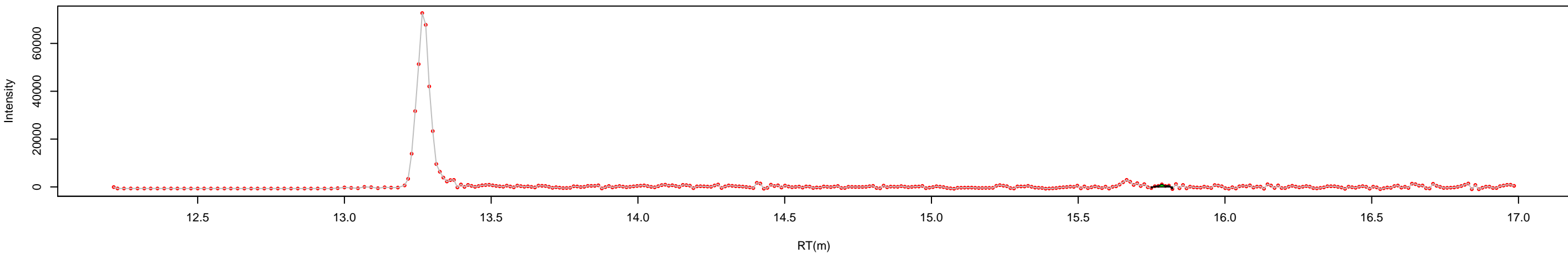
raw chromatogram | batch: 2 sample: std0-10ul-2 conc: 0.001 function: 1 mass: 375.35>375.35



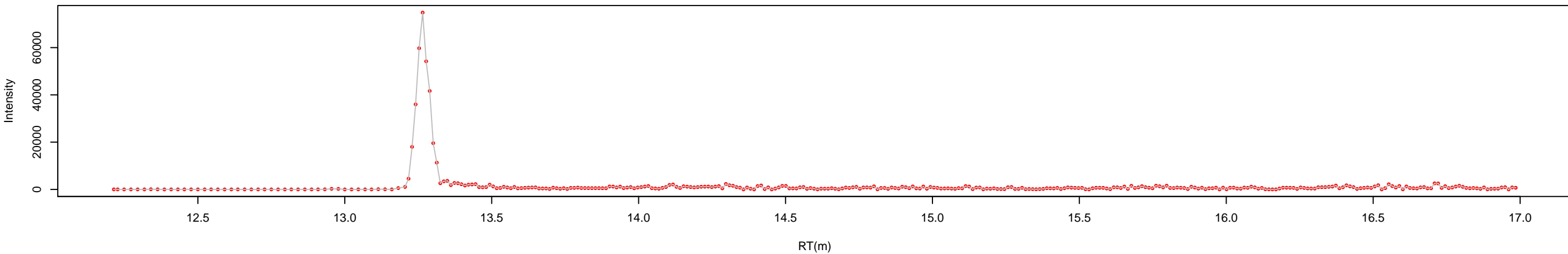
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 21 BLine: yes



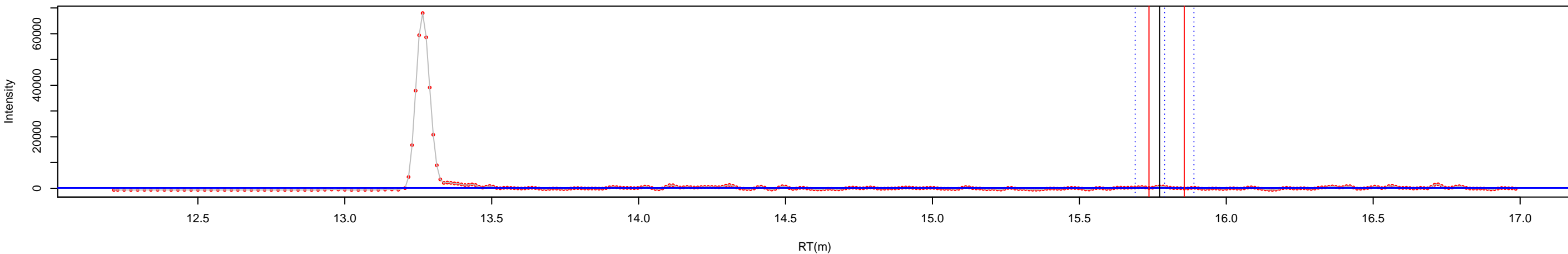
peak area | window size:3 BLine: yes



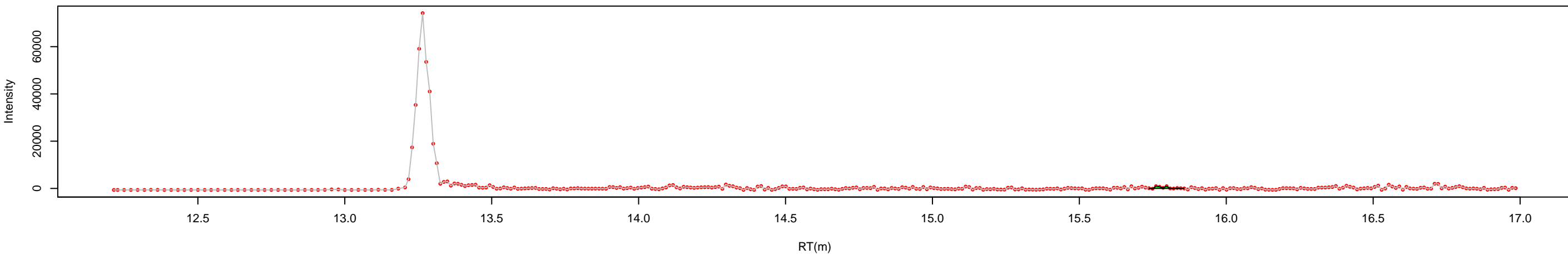
raw chromatogram | batch: 2 sample: std1-10ul-2 conc: 0.002 function: 1 mass: 375.35>375.35



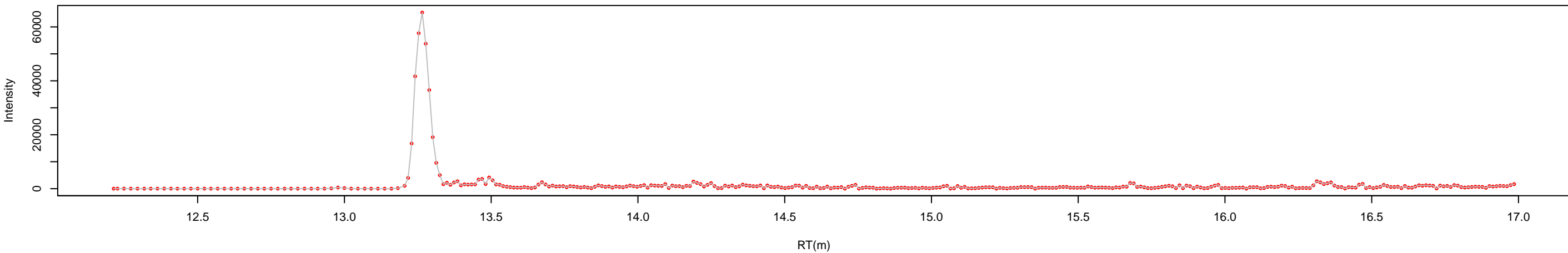
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 22.9 BLine: yes



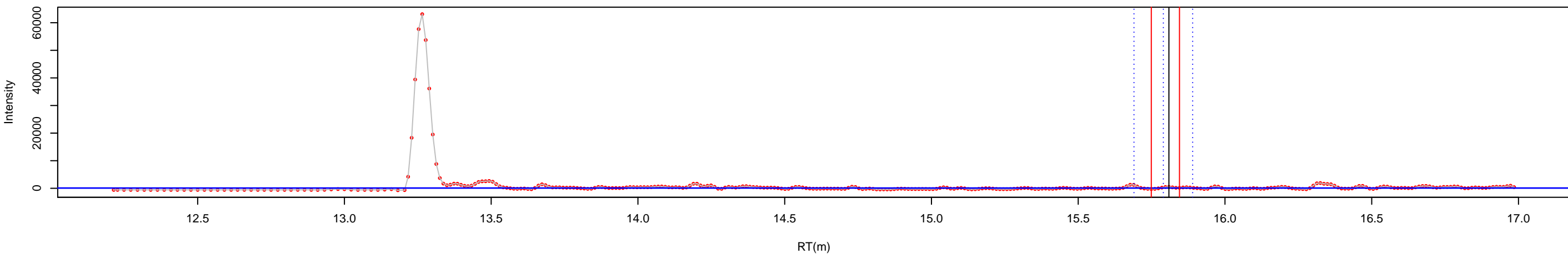
peak area | window size:3 BLine: yes



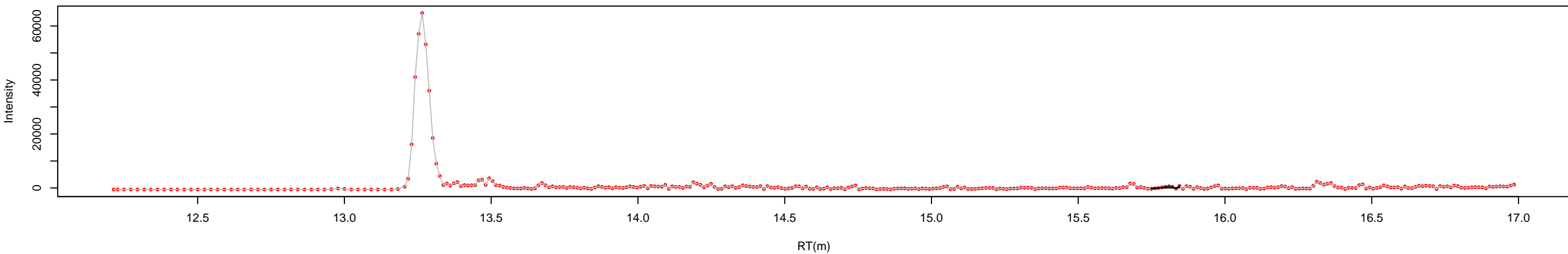
raw chromatogram | batch: 2 sample: std2-10ul-2 conc: 0.005 function: 1 mass: 375.35>375.35



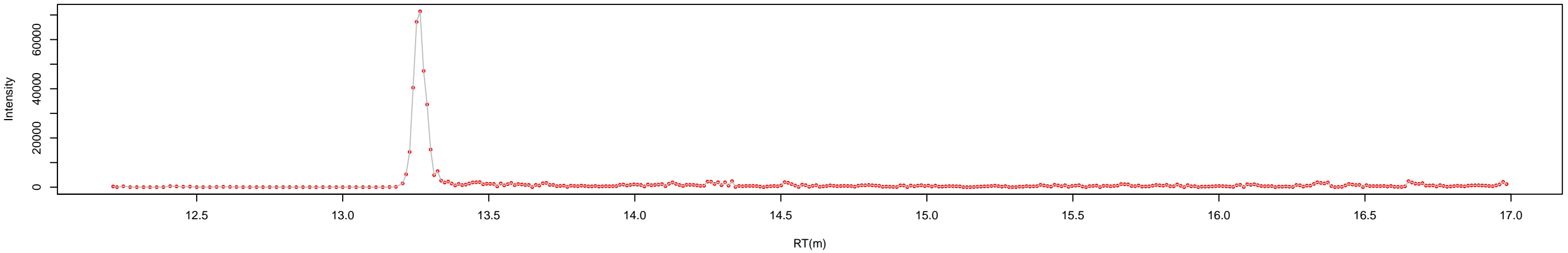
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 16.4 BLine: yes



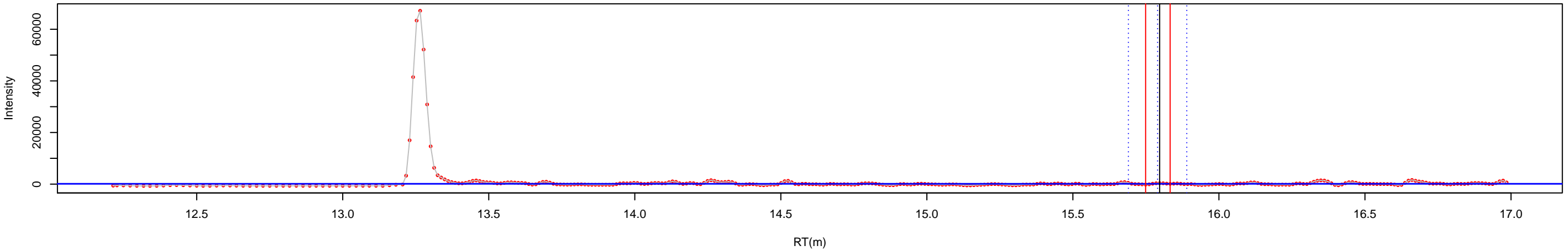
peak area | window size:3 BLine: yes



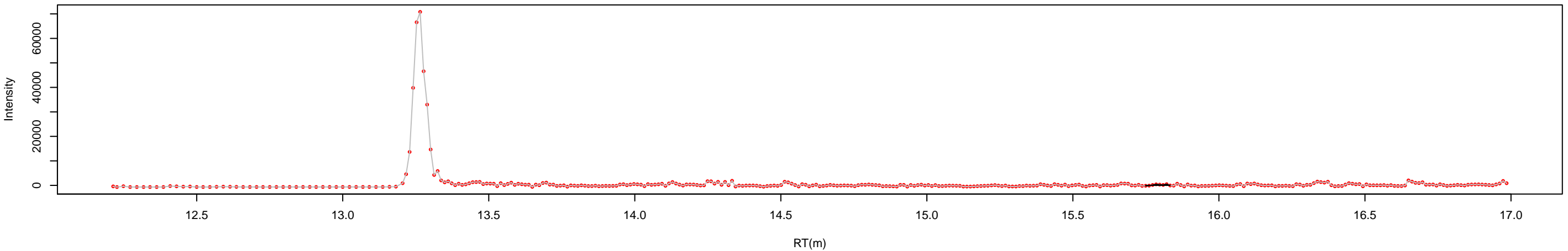
raw chromatogram | batch: 2   sample: std3-10ul-2   conc: 0.01   function: 1   mass: 375.35>375.35



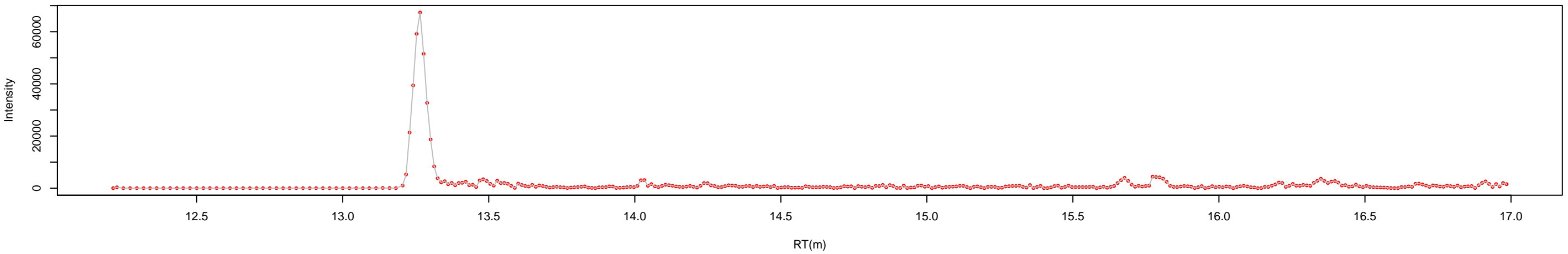
peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 21.9   BLine: yes



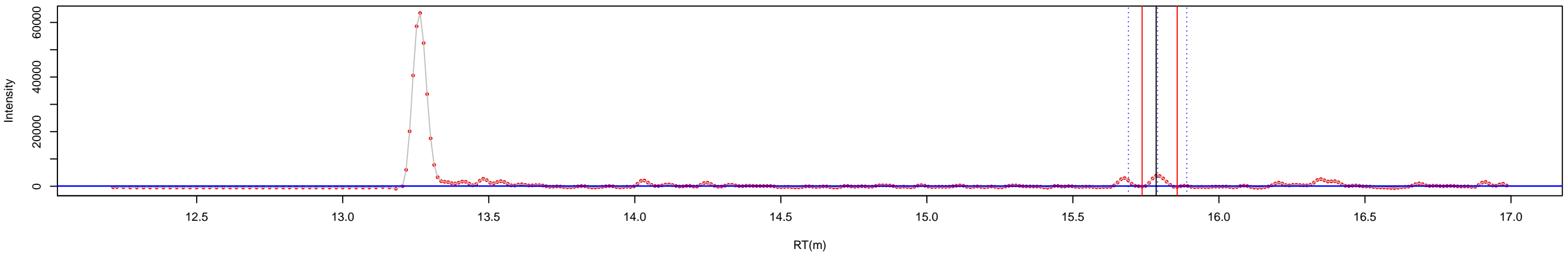
peak area | window size:3   BLine: yes



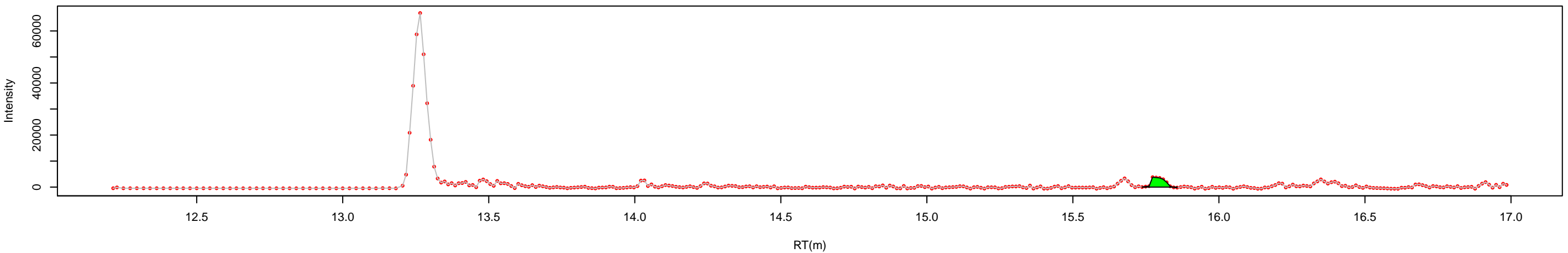
raw chromatogram | batch: 2 sample: std4-10ul-2 conc: 0.02 function: 1 mass: 375.35>375.35



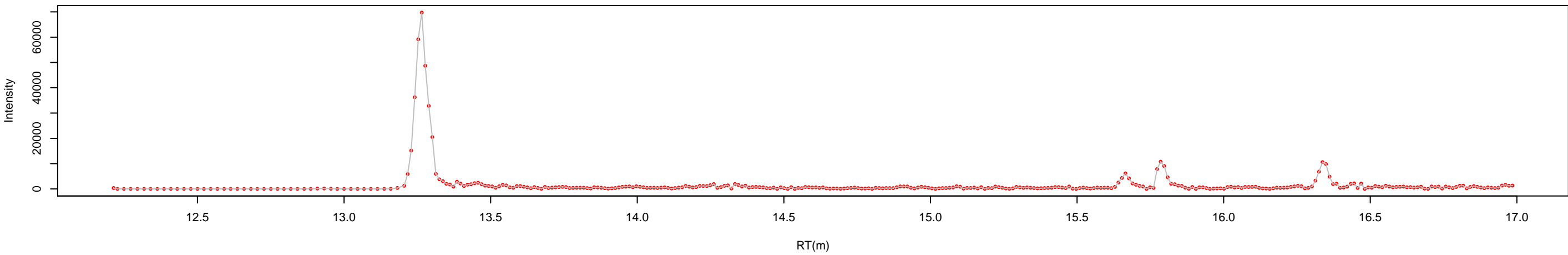
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 14.9 BLine: yes



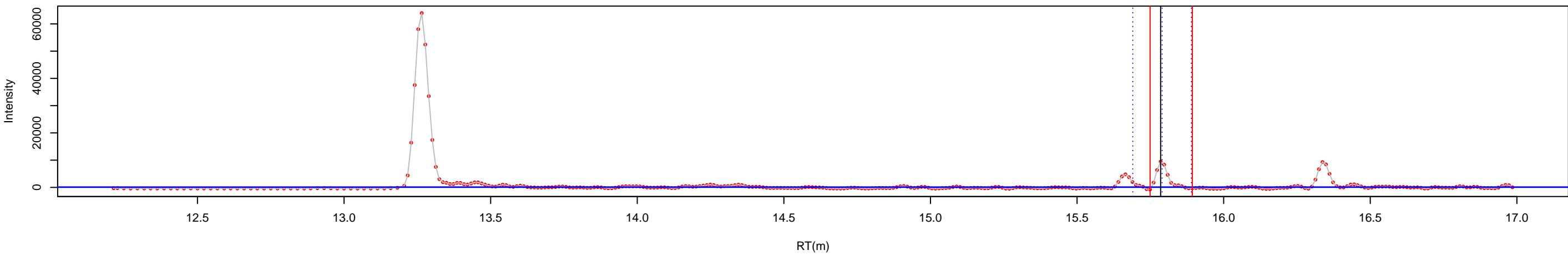
peak area | window size:3 BLine: yes



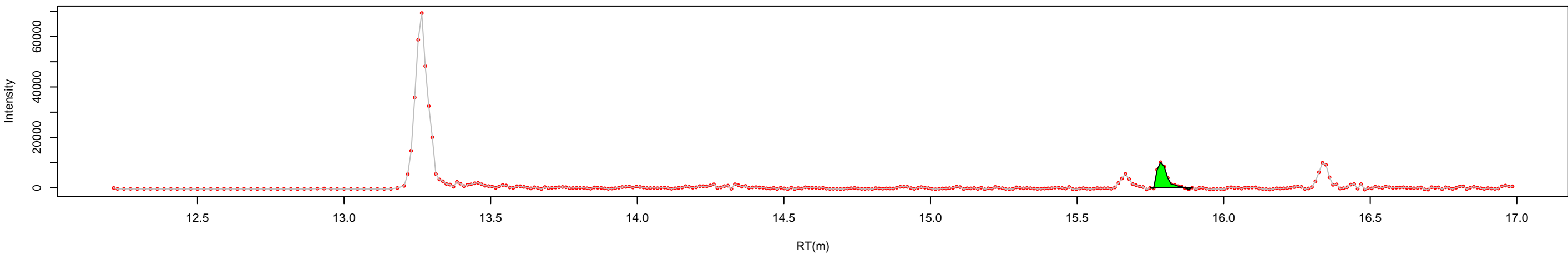
raw chromatogram | batch: 2 sample: std5-10ul-2 conc: 0.05 function: 1 mass: 375.35>375.35



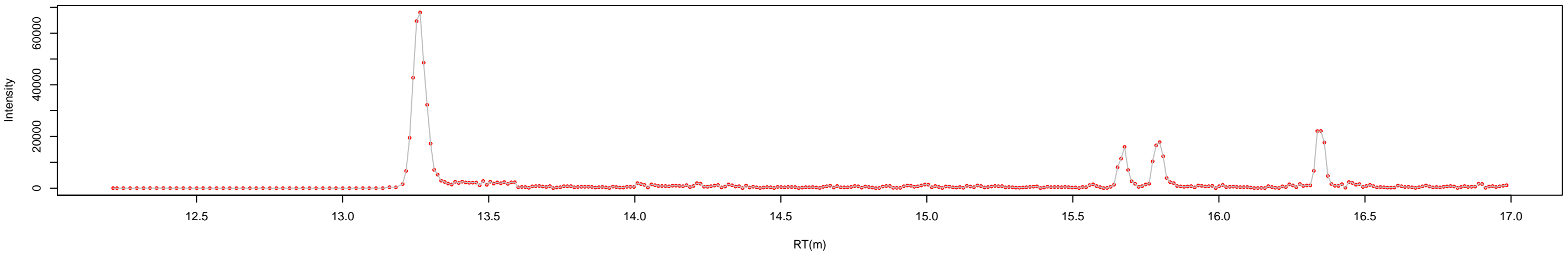
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 18.3 BLine: yes



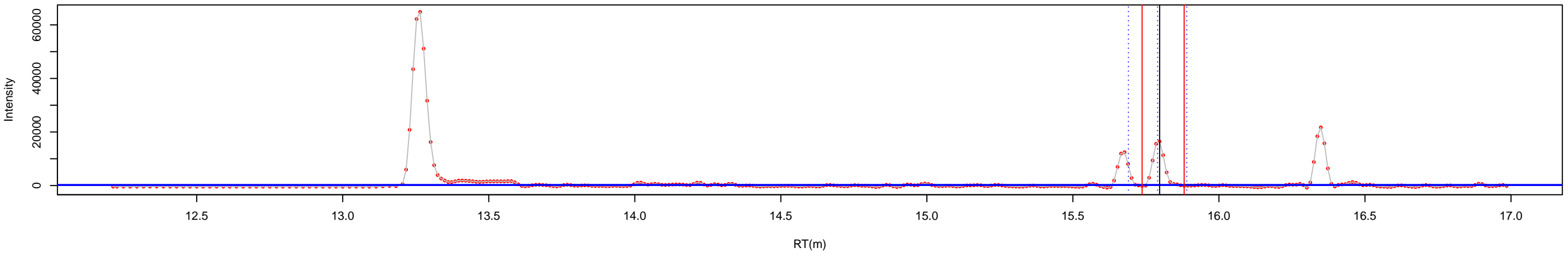
peak area | window size:3 BLine: yes



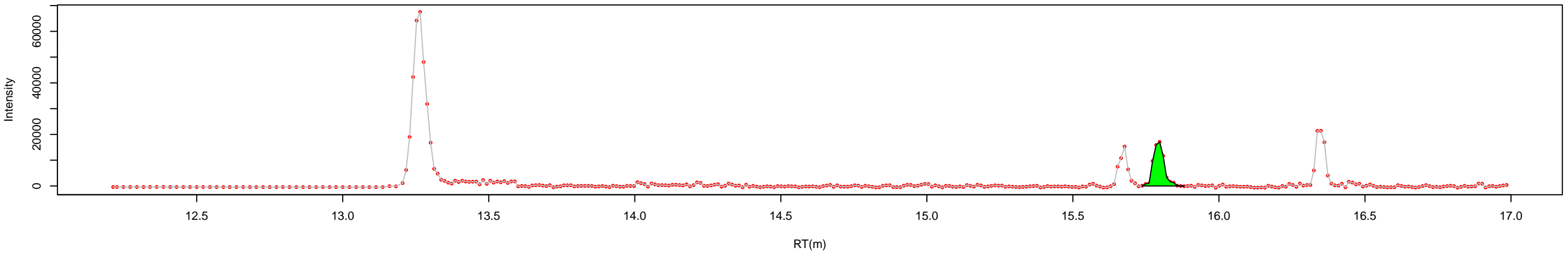
raw chromatogram | batch: 2 sample: std6-10ul-2 conc: 0.1 function: 1 mass: 375.35>375.35



peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 36.7 BLine: yes

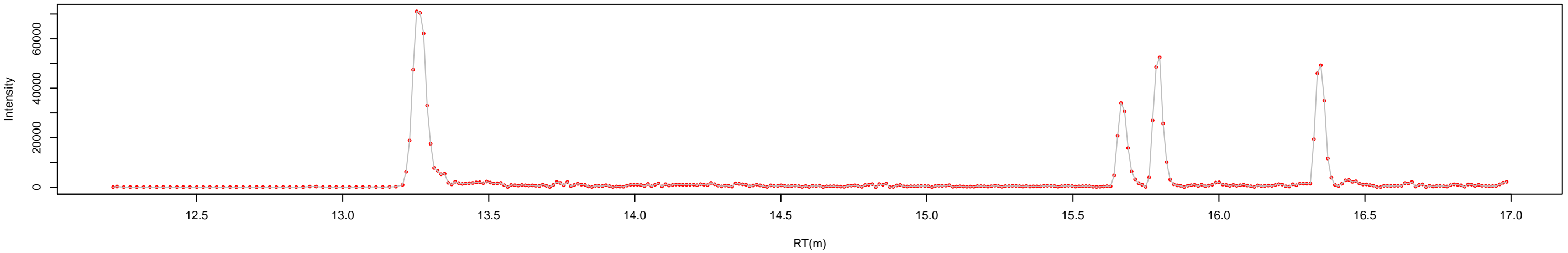


peak area | window size:3 BLine: yes

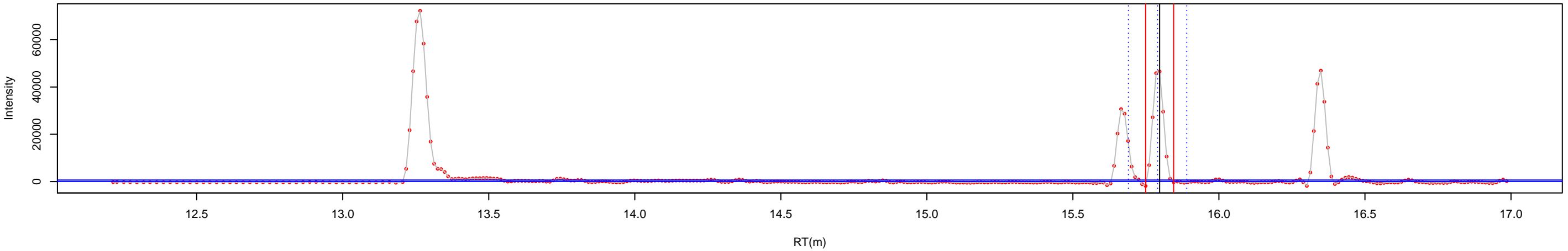




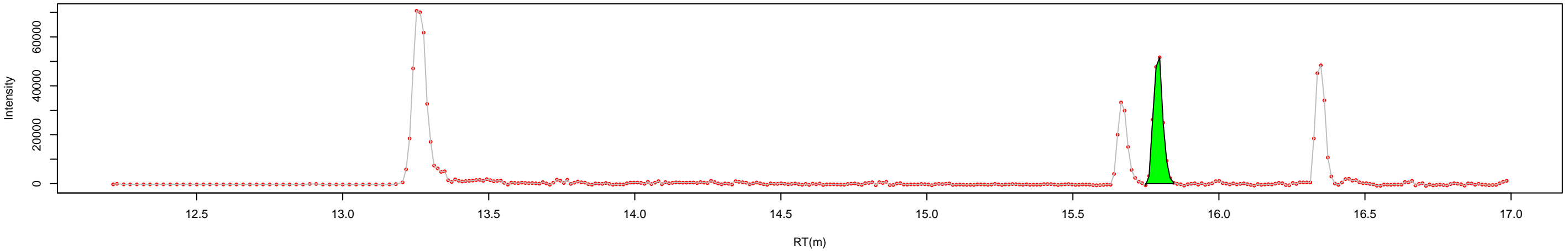
raw chromatogram | batch: 2 sample: std7-10ul-2 conc: 0.2 function: 1 mass: 375.35>375.35



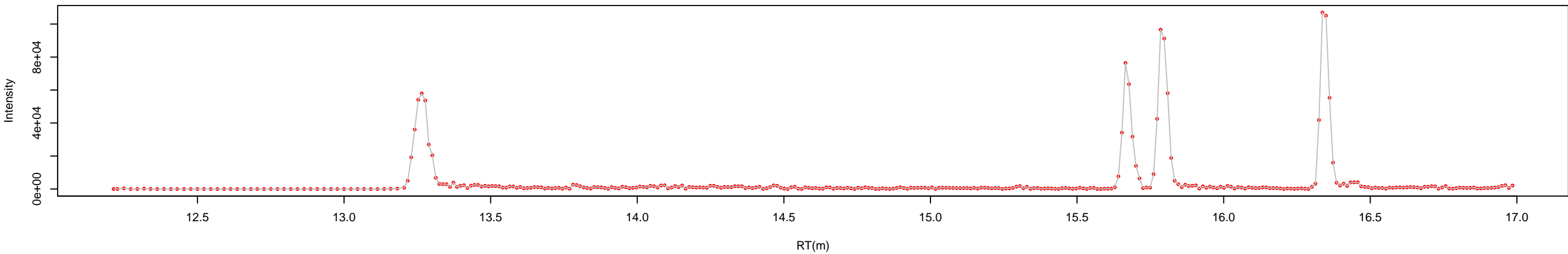
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 65 BLine: yes



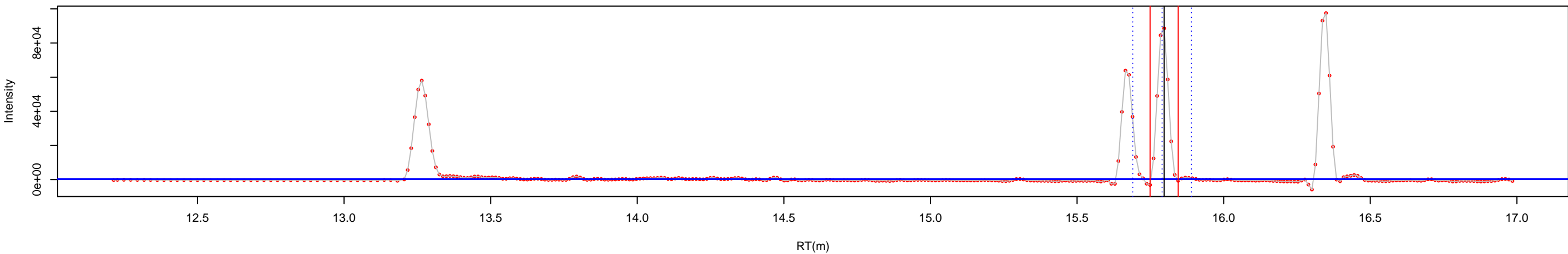
peak area | window size:3 BLine: yes



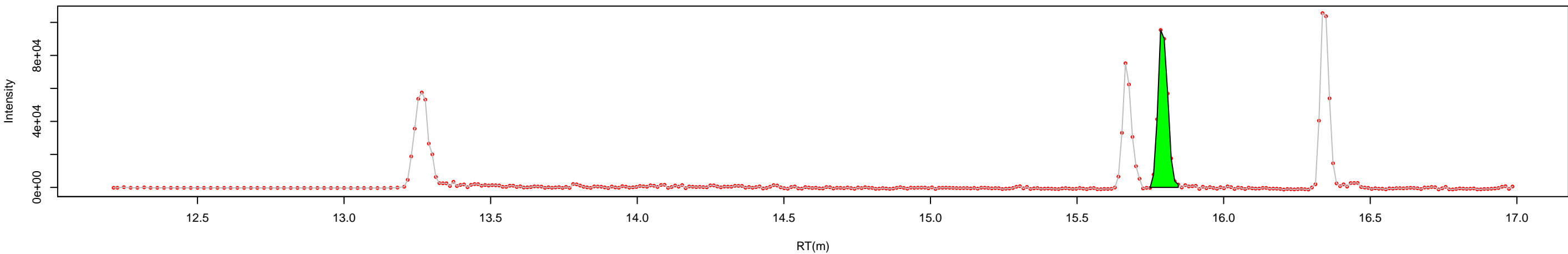
raw chromatogram | batch: 2 sample: std8-10ul-2 conc: 0.5 function: 1 mass: 375.35>375.35



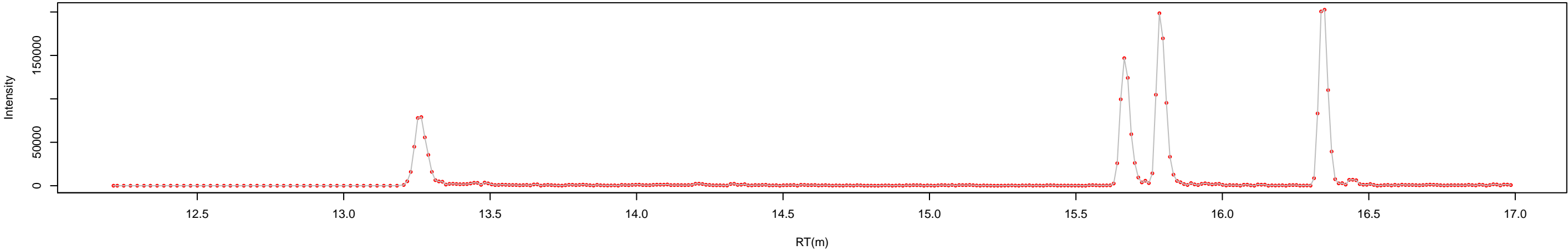
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 57.3 BLine: yes



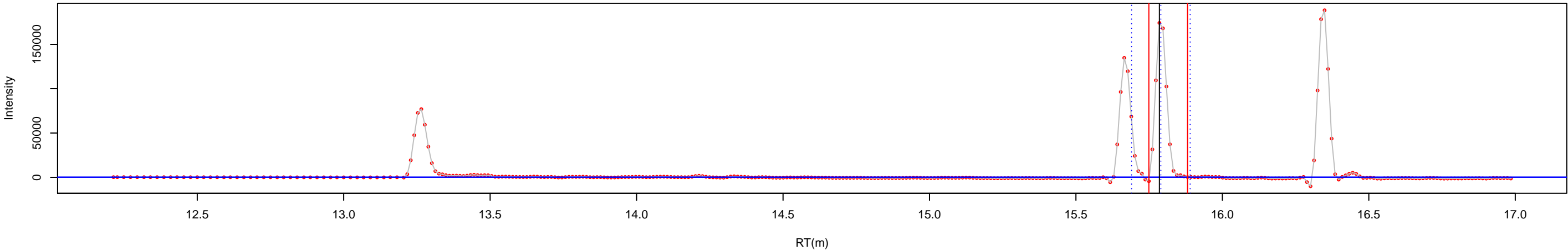
peak area | window size:3 BLine: yes



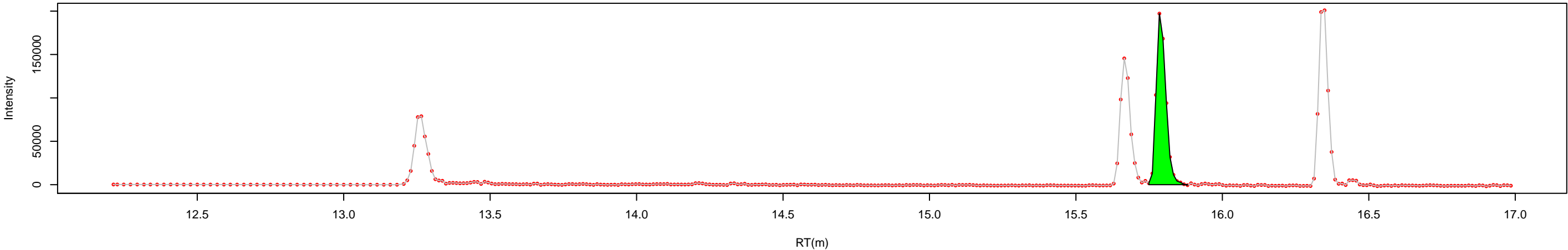
raw chromatogram | batch: 2   sample: std9-10ul-2   conc: 1   function: 1   mass: 375.35>375.35



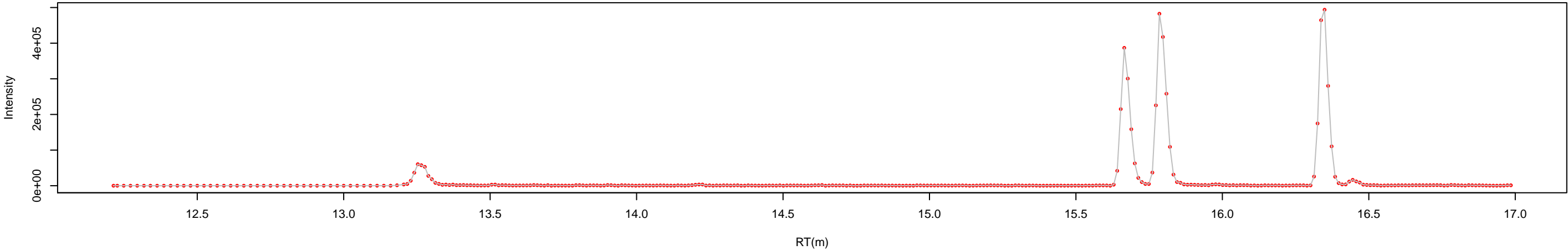
peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 33.7   BLine: yes



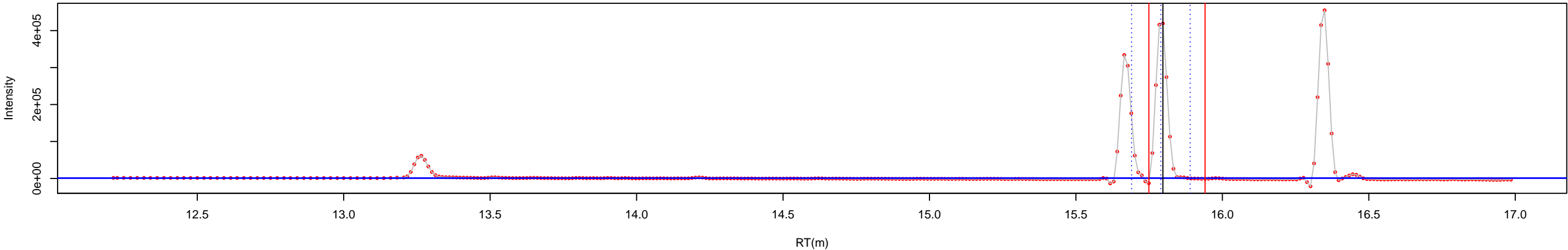
peak area | window size:3   BLine: yes



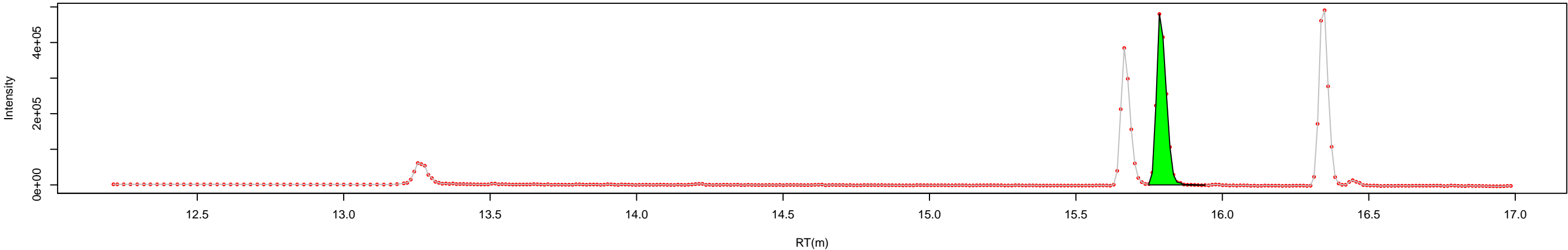
raw chromatogram | batch: 2   sample: std10-10ul-2   conc: 2   function: 1   mass: 375.35>375.35



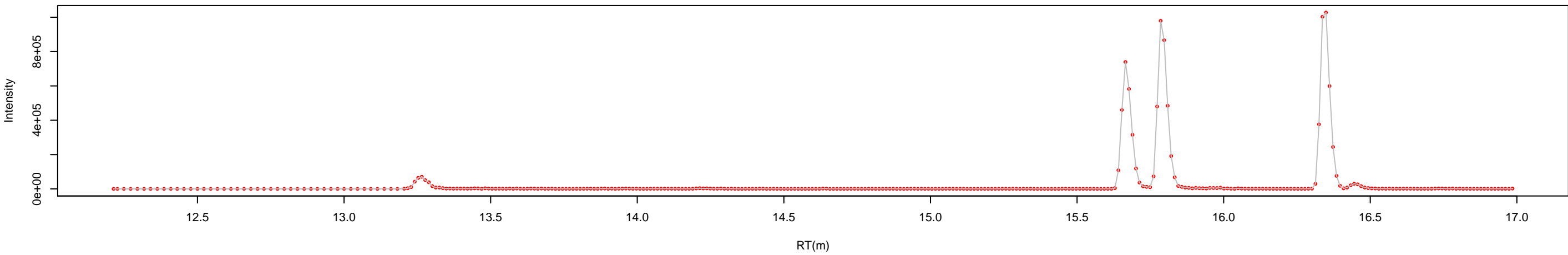
peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 168   BLine: yes



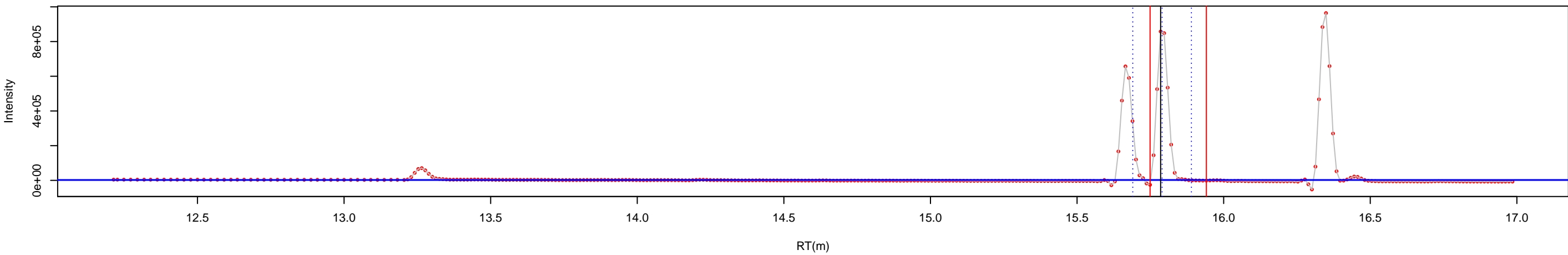
peak area | window size:3   BLine: yes



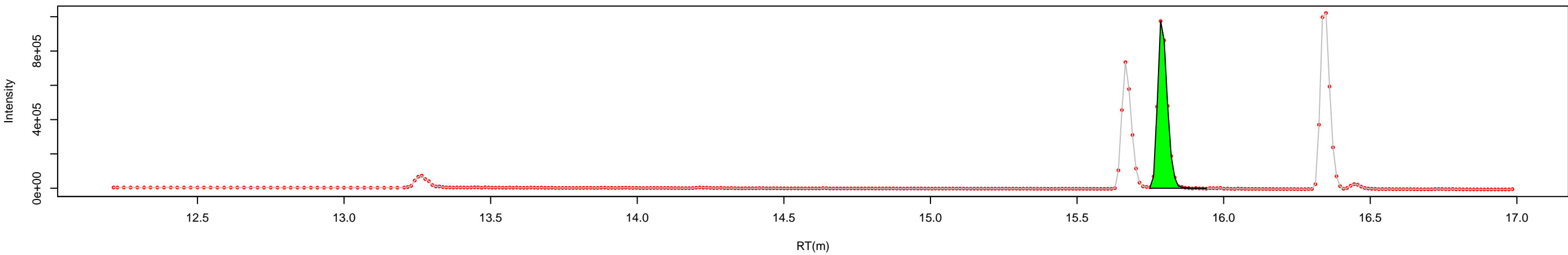
raw chromatogram | batch: 2 sample: std11-10ul-2-1 conc: 5 function: 1 mass: 375.35>375.35



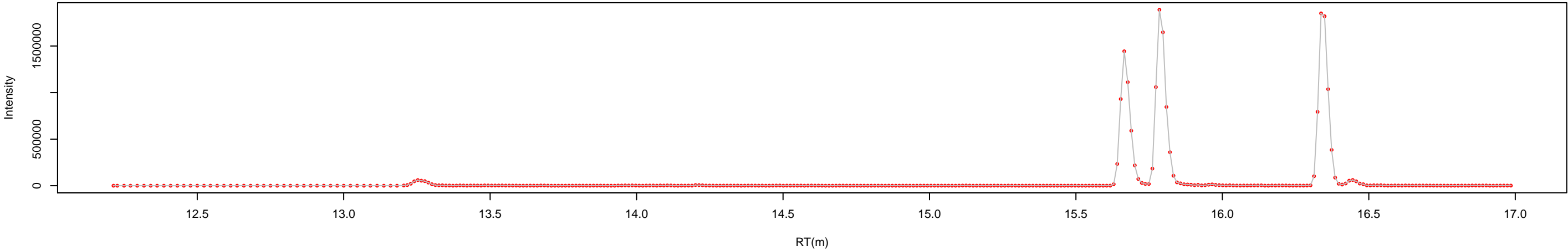
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 390 BLine: yes



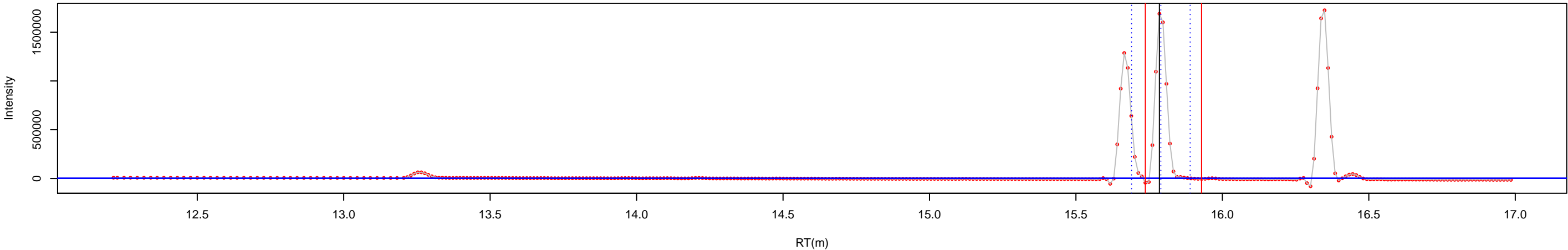
peak area | window size:3 BLine: yes



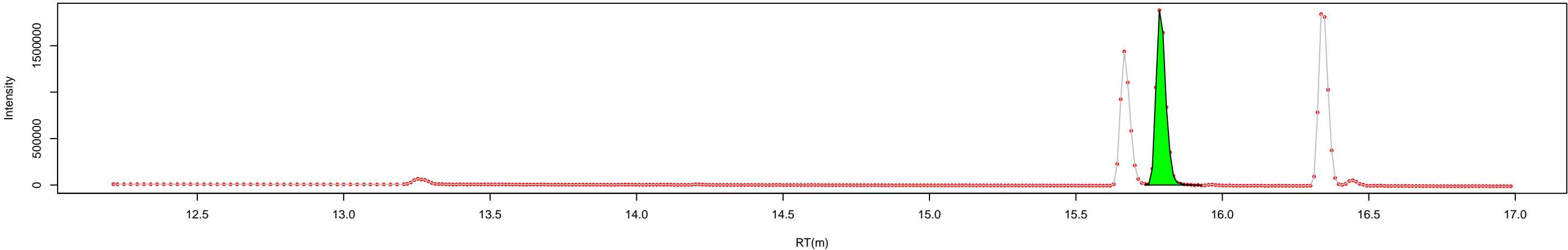
raw chromatogram | batch: 2   sample: std12-10ul-2-1   conc: 10   function: 1   mass: 375.35>375.35



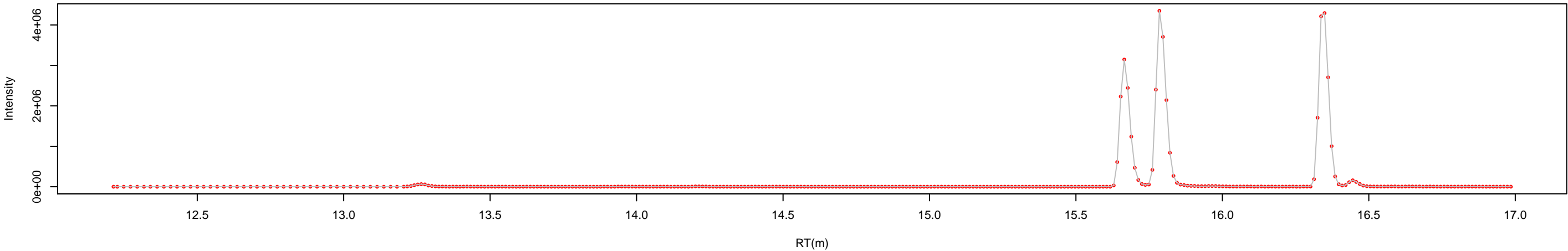
peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 533   BLine: yes



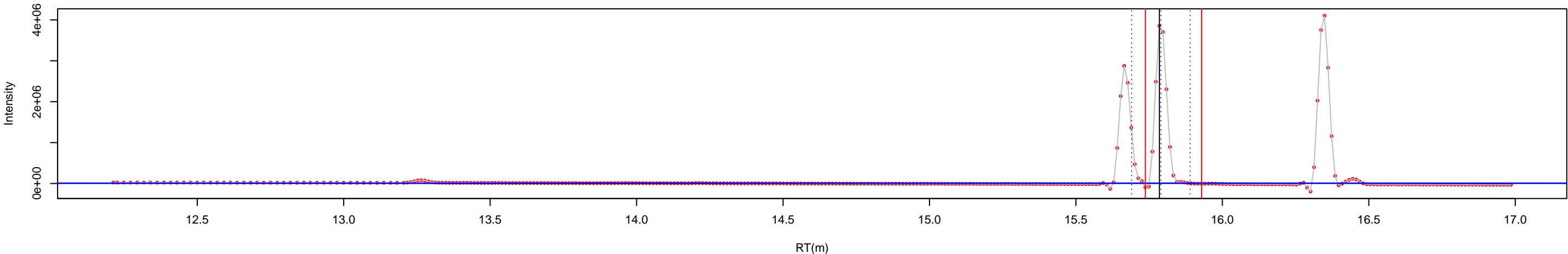
peak area | window size:3   BLine: yes



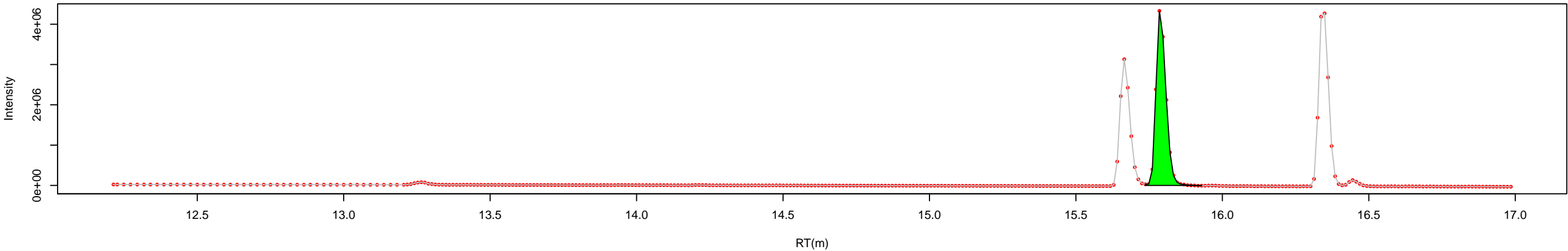
raw chromatogram | batch: 2   sample: std13-10ul-2-1   conc: 20   function: 1   mass: 375.35>375.35



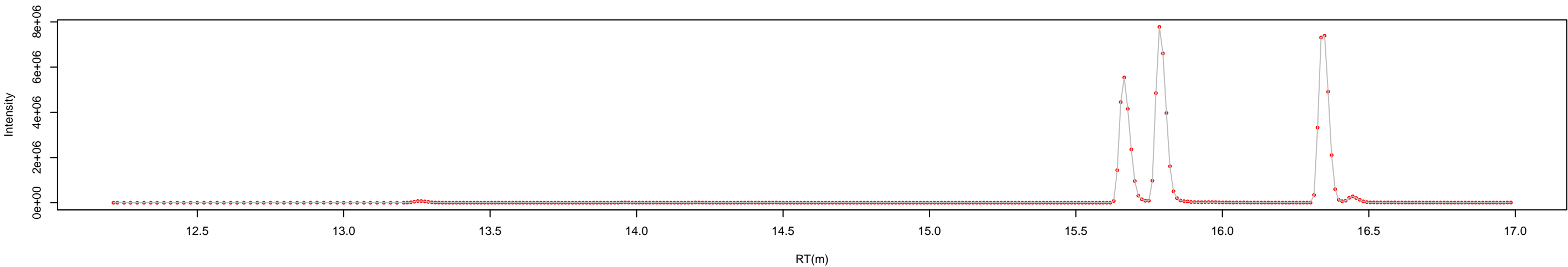
peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 1050   BLine: yes



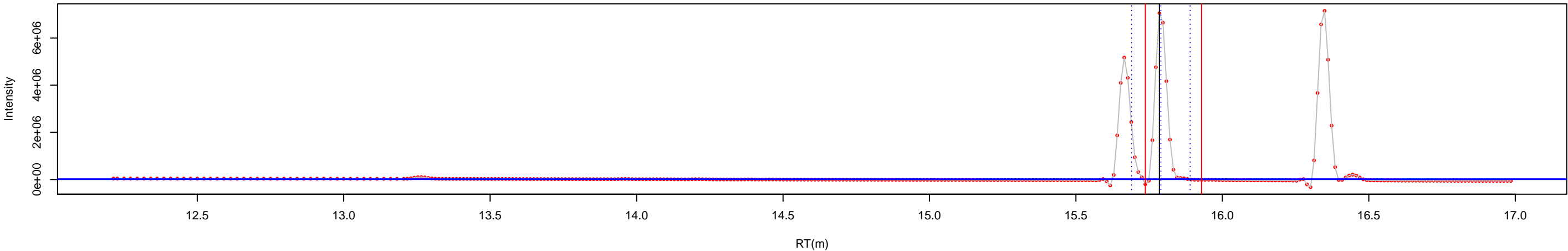
peak area | window size:3   BLine: yes



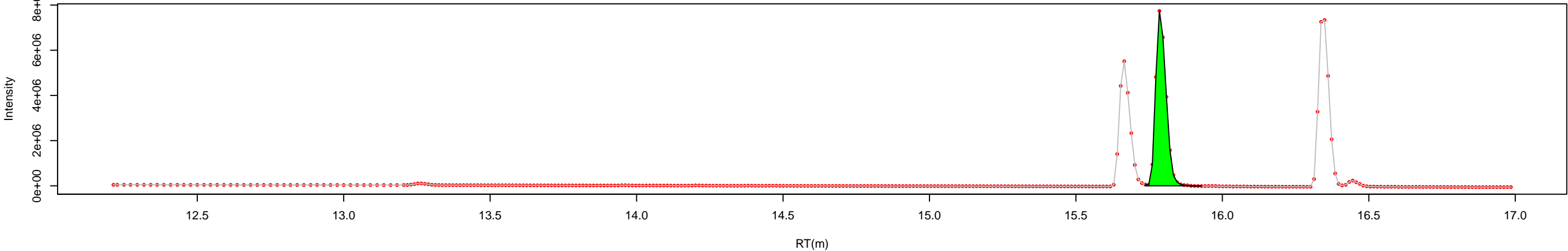
raw chromatogram | batch: 2   sample: std14-10ul-2-1   conc: 50   function: 1   mass: 375.35>375.35



peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 2760   BLine: yes

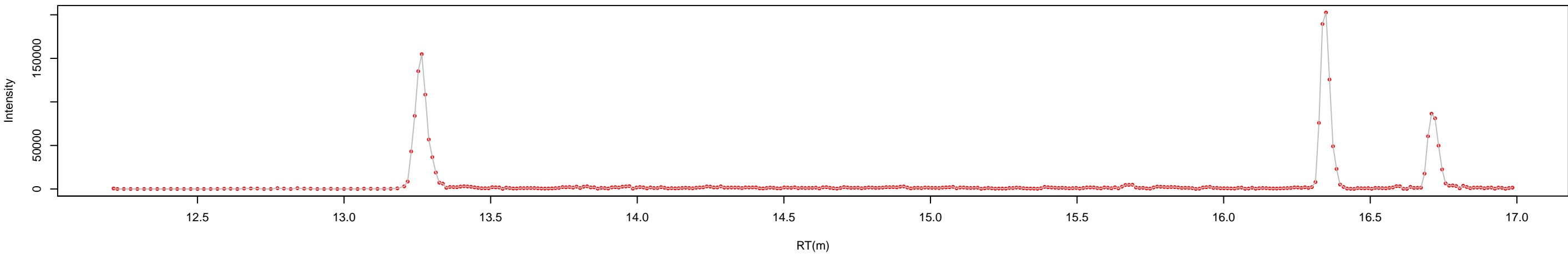


peak area | window size:3   BLine: yes

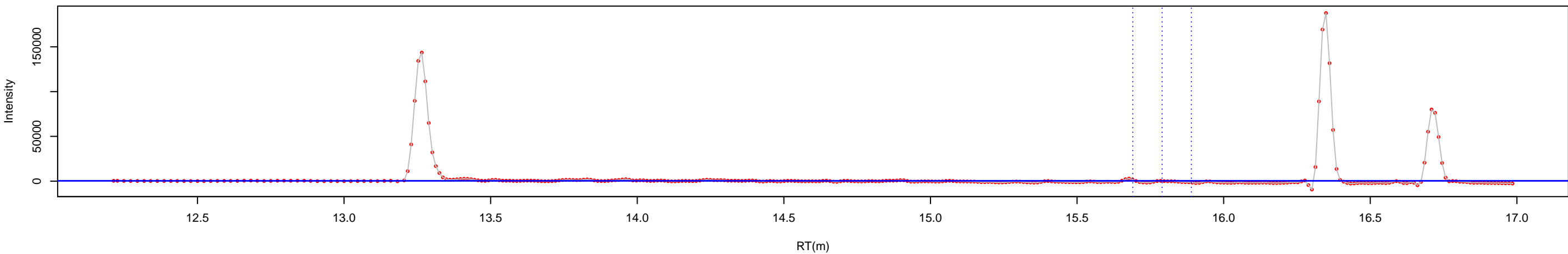




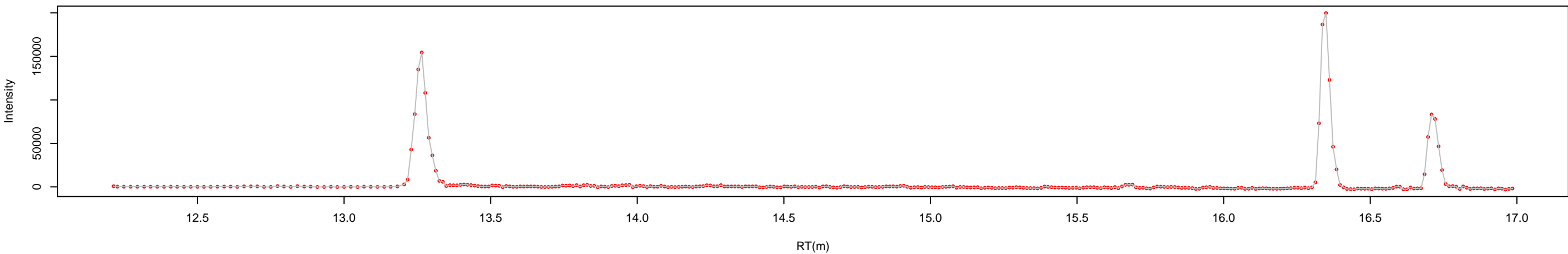
raw chromatogram | batch: 3 sample: cotn65 conc: NA function: 1 mass: 375.35>375.35



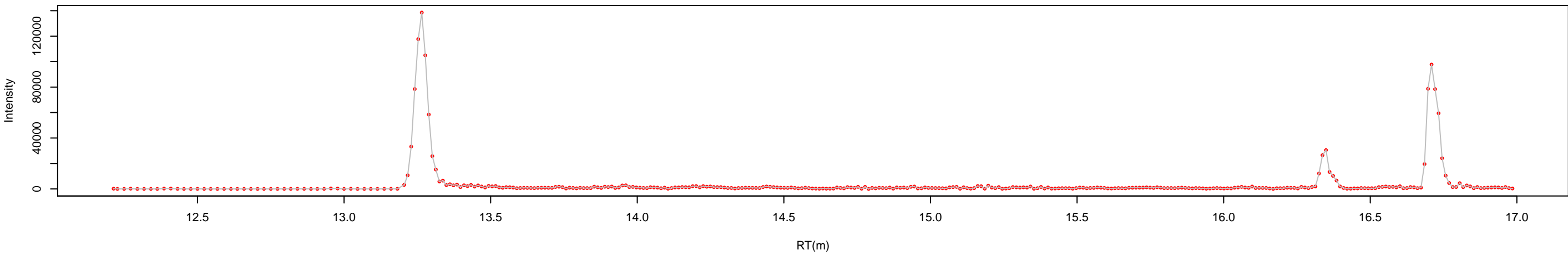
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 64.1 BLine: yes



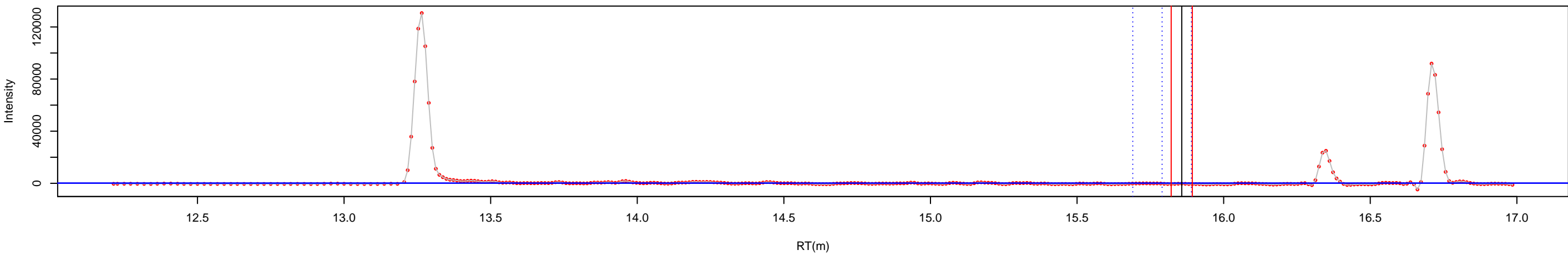
peak area | window size:3 BLine: yes



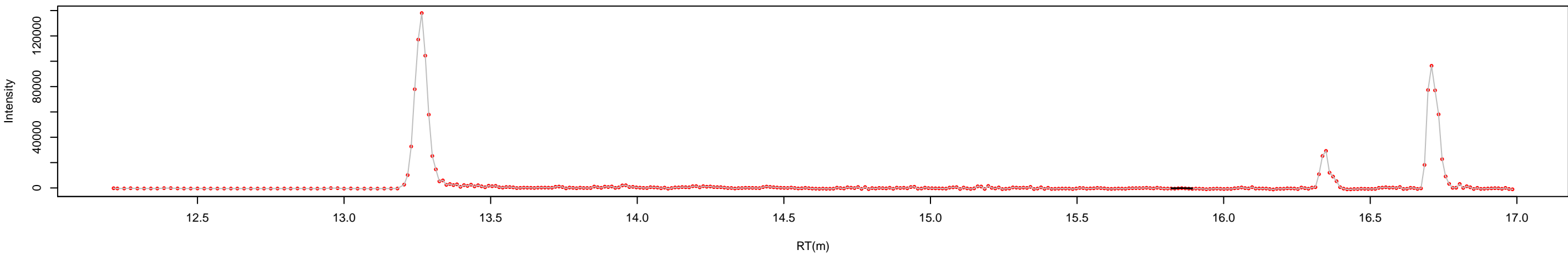
raw chromatogram | batch: 3 sample: cotn66 conc: NA function: 1 mass: 375.35>375.35



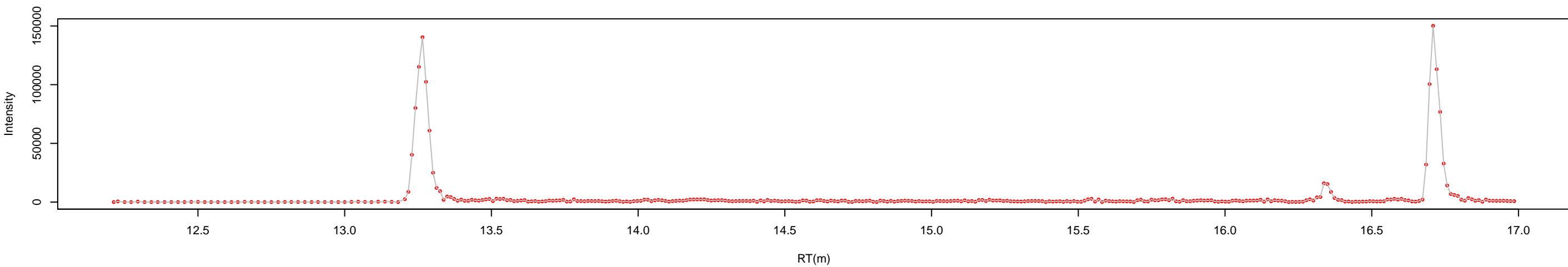
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 29.6 BLine: yes



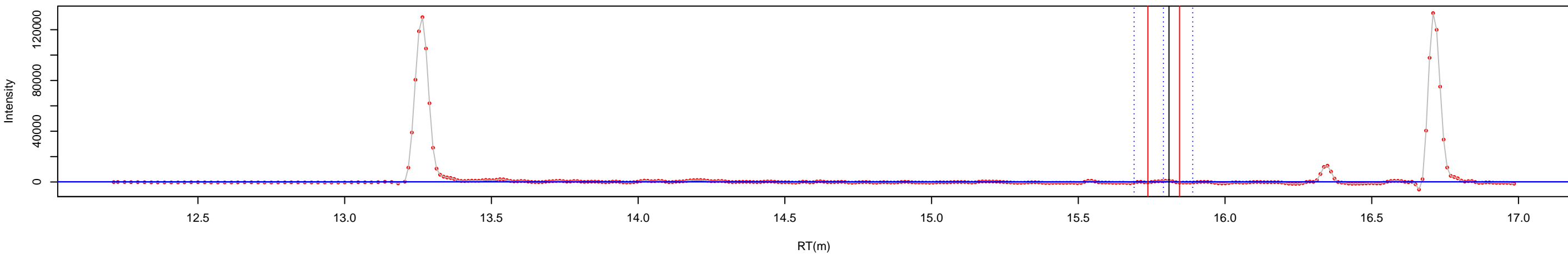
peak area | window size:3 BLine: yes



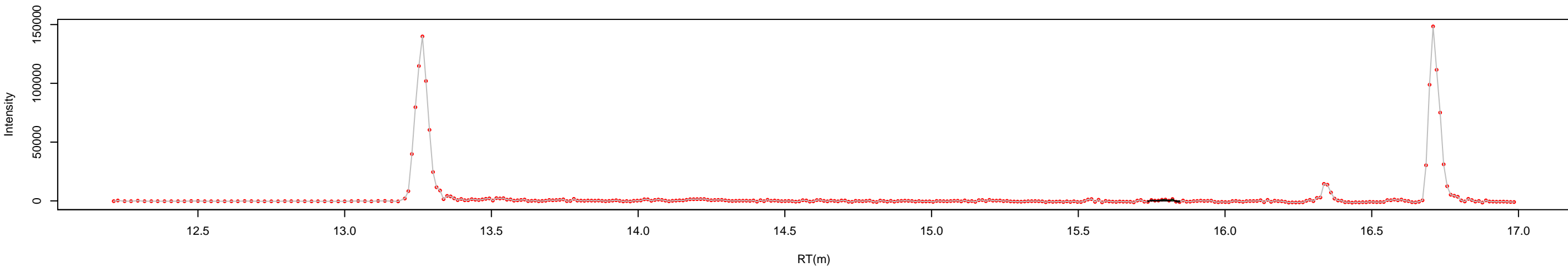
raw chromatogram | batch: 3 sample: cotn67 conc: NA function: 1 mass: 375.35>375.35



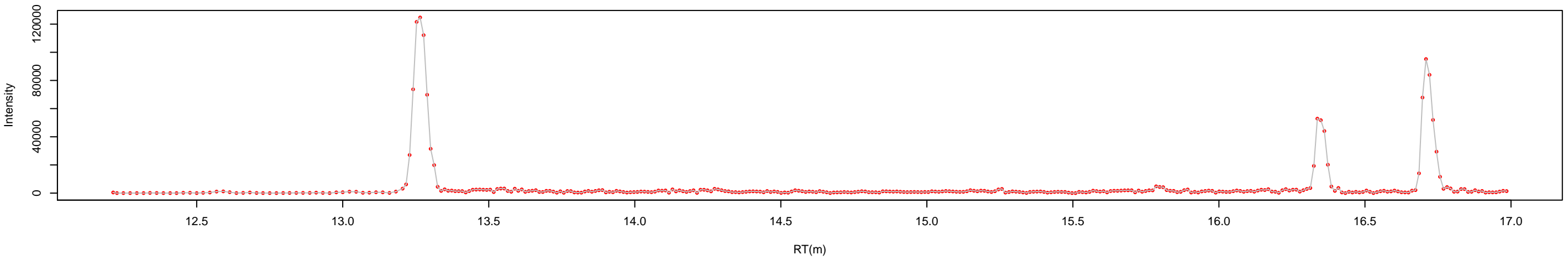
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 23.6 BLine: yes



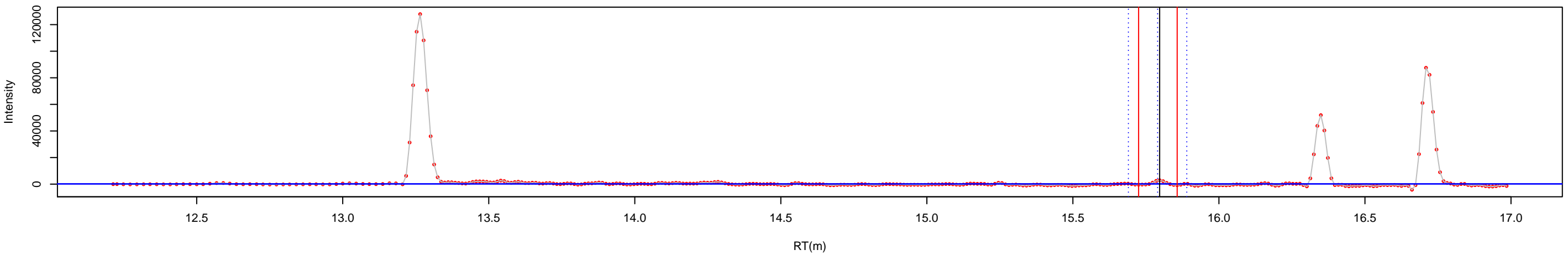
peak area | window size:3 BLine: yes



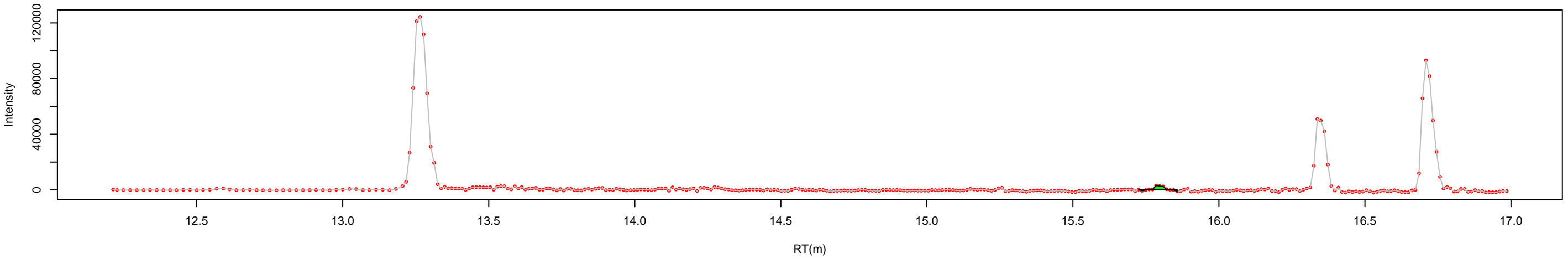
raw chromatogram | batch: 3 sample: cotn195 conc: NA function: 1 mass: 375.35>375.35



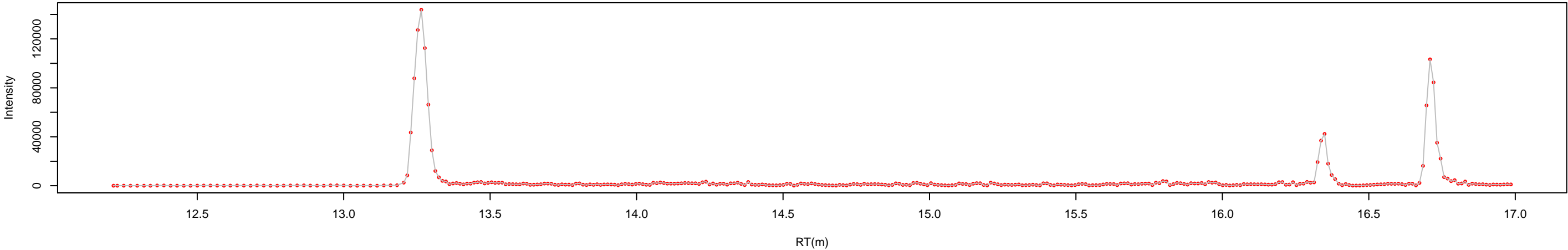
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 30.4 BLine: yes



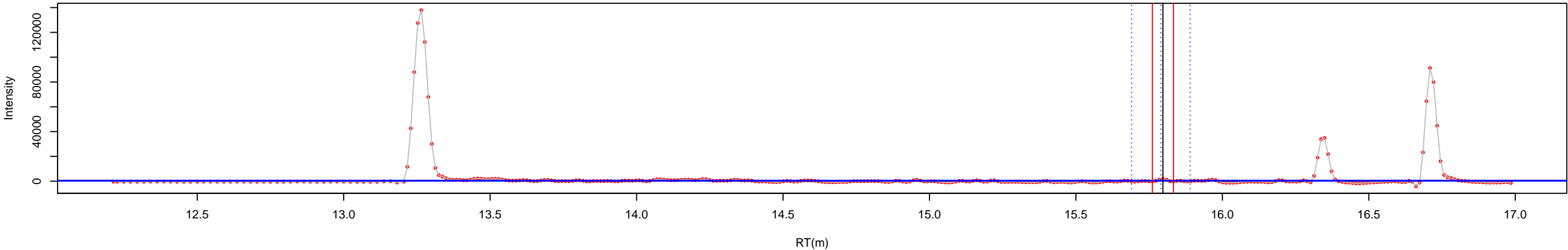
peak area | window size:3 BLine: yes



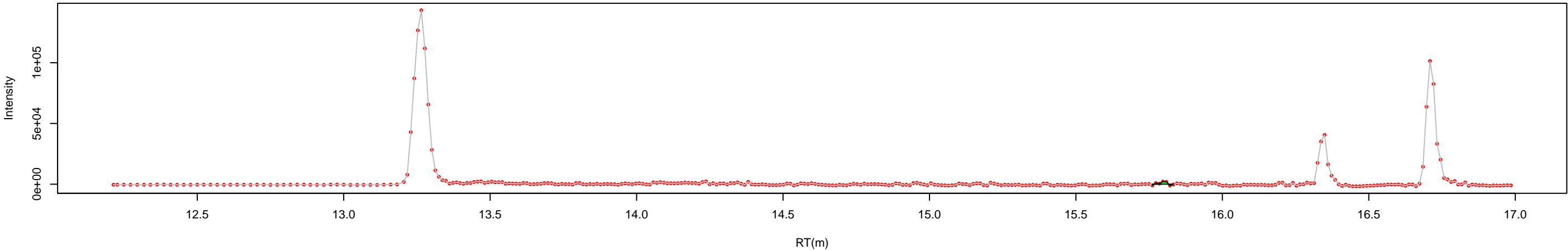
raw chromatogram | batch: 3   sample: cotn196   conc: NA   function: 1   mass: 375.35>375.35



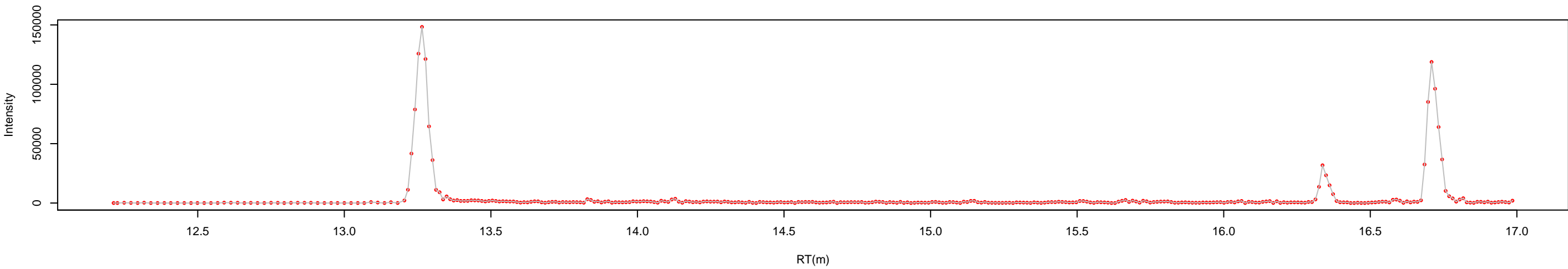
peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 64.9   BLine: yes



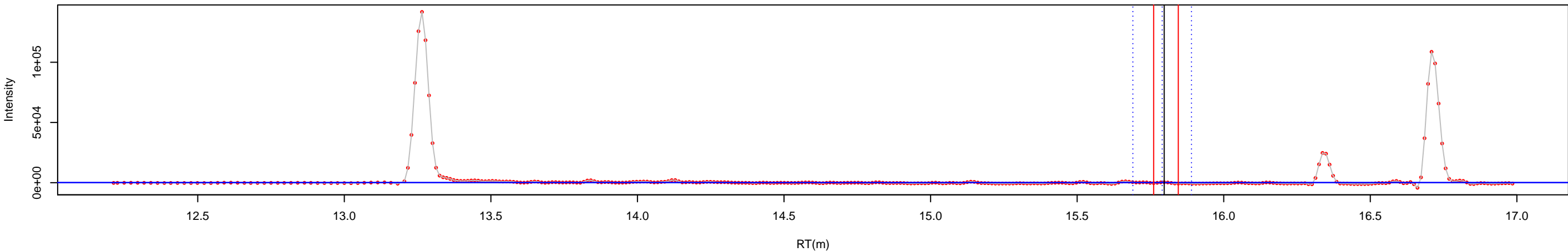
peak area | window size:3   BLine: yes



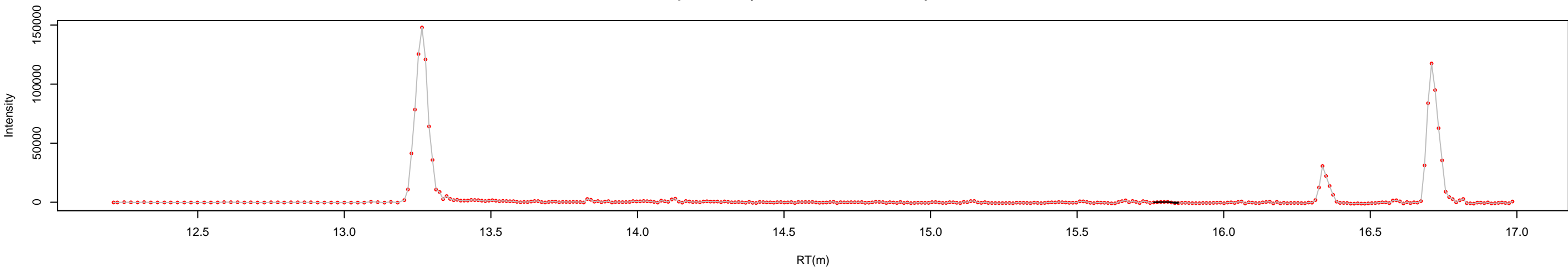
raw chromatogram | batch: 3 sample: cotn197 conc: NA function: 1 mass: 375.35>375.35



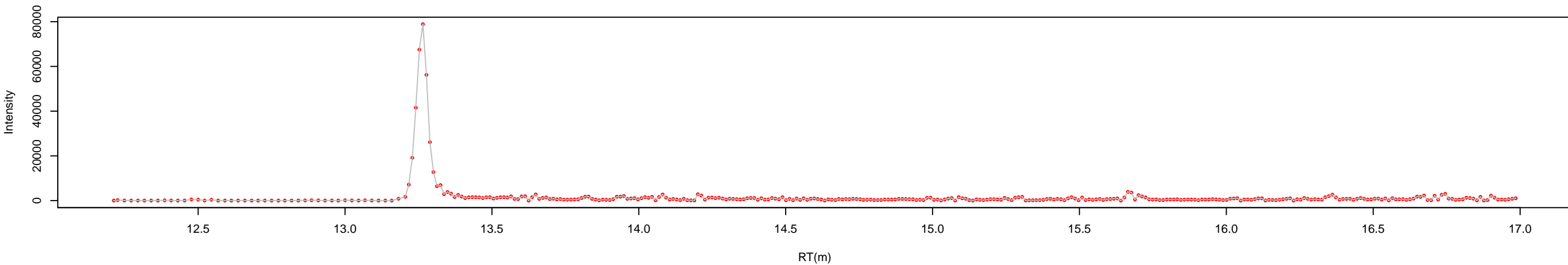
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 19.5 BLine: yes



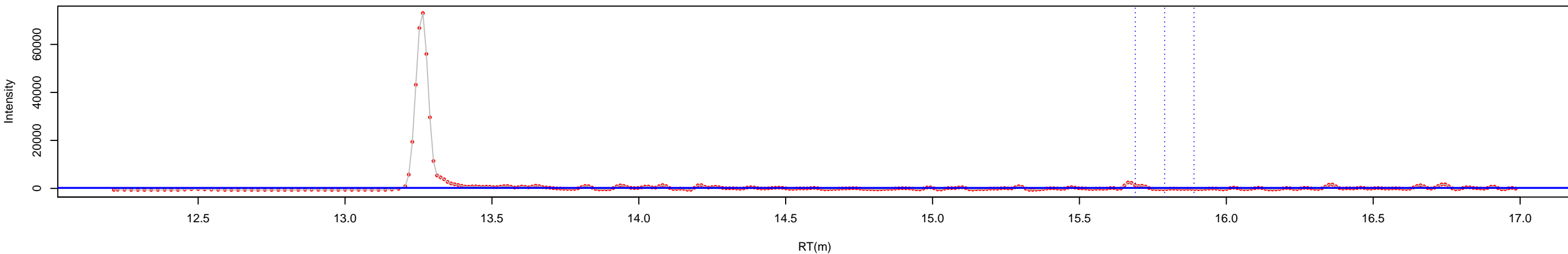
peak area | window size:3 BLine: yes



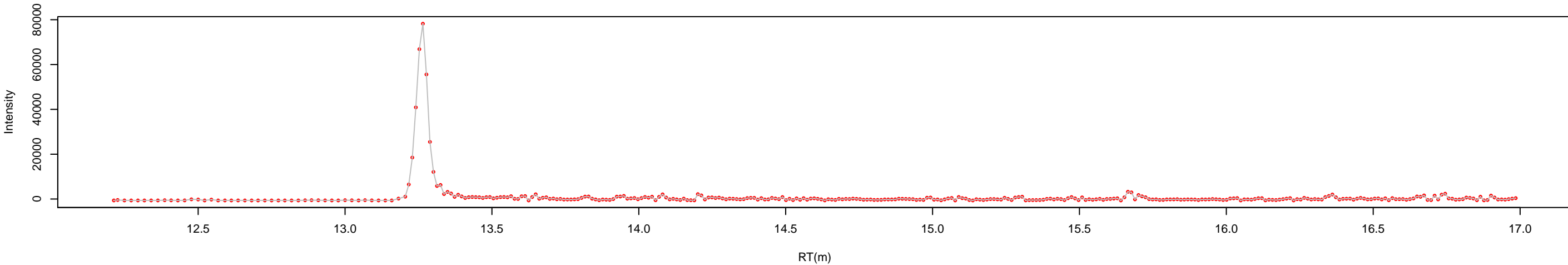
raw chromatogram | batch: 3 sample: std0-10ul-3 conc: 0.001 function: 1 mass: 375.35>375.35



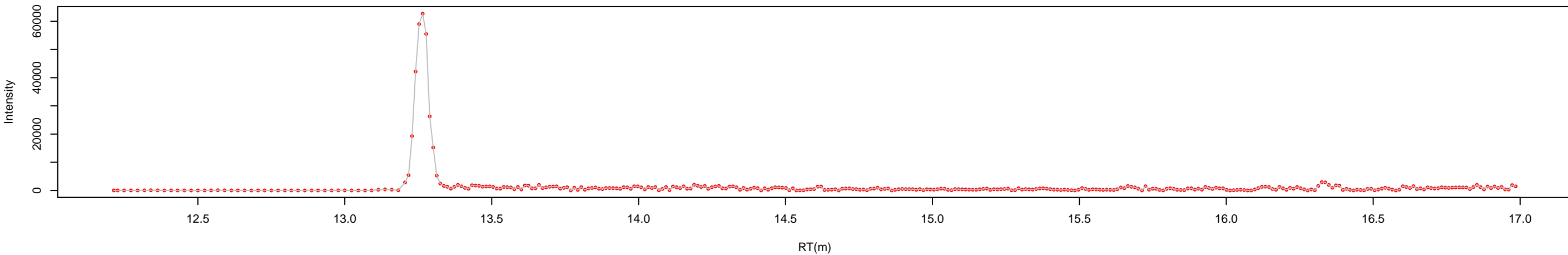
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 37.6 BLine: yes



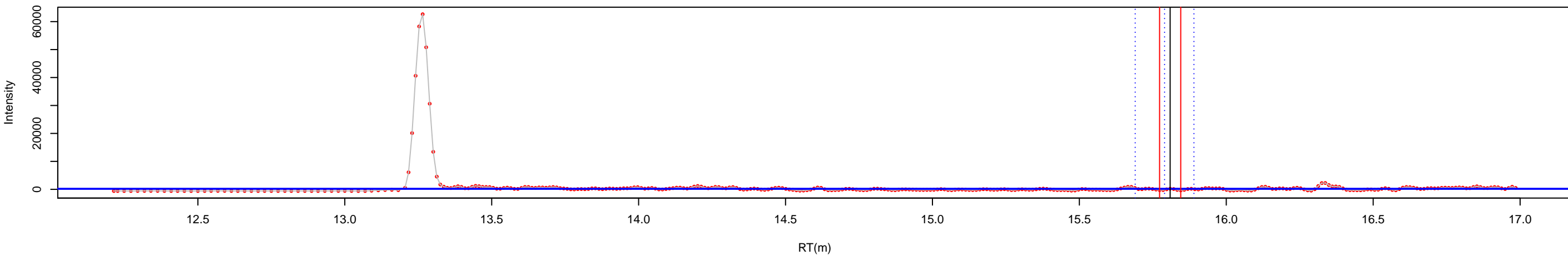
peak area | window size:3 BLine: yes



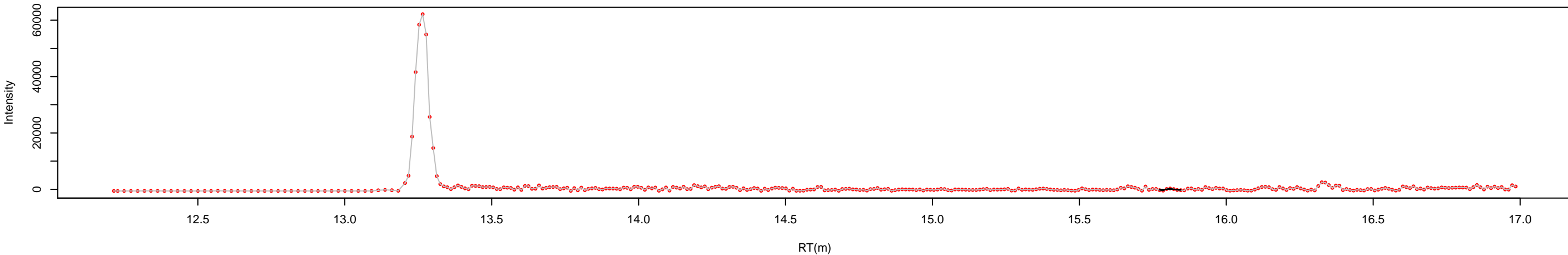
raw chromatogram | batch: 3 sample: std1-10ul-3 conc: 0.002 function: 1 mass: 375.35>375.35



peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 34.8 BLine: yes

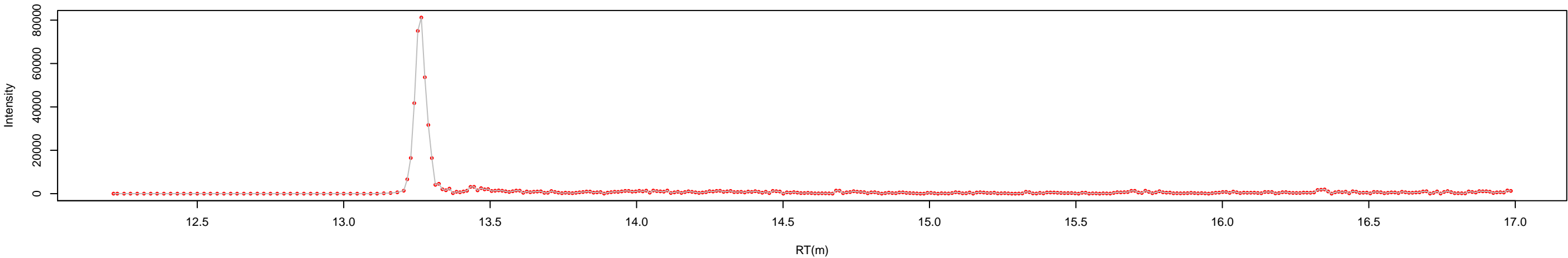


peak area | window size:3 BLine: yes

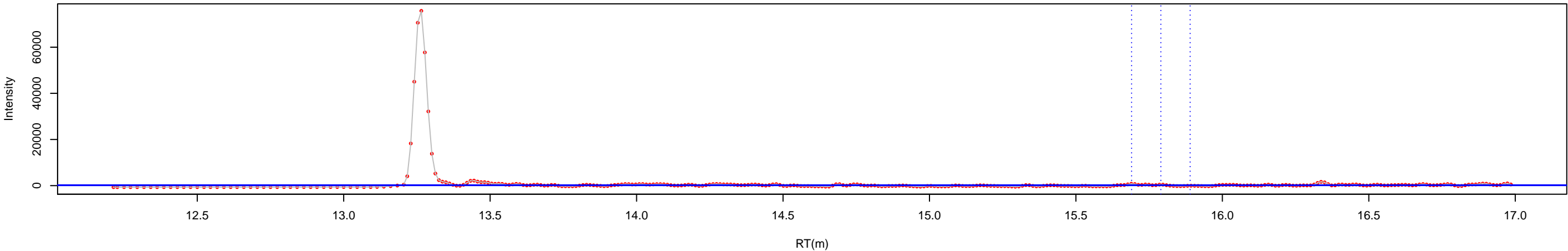




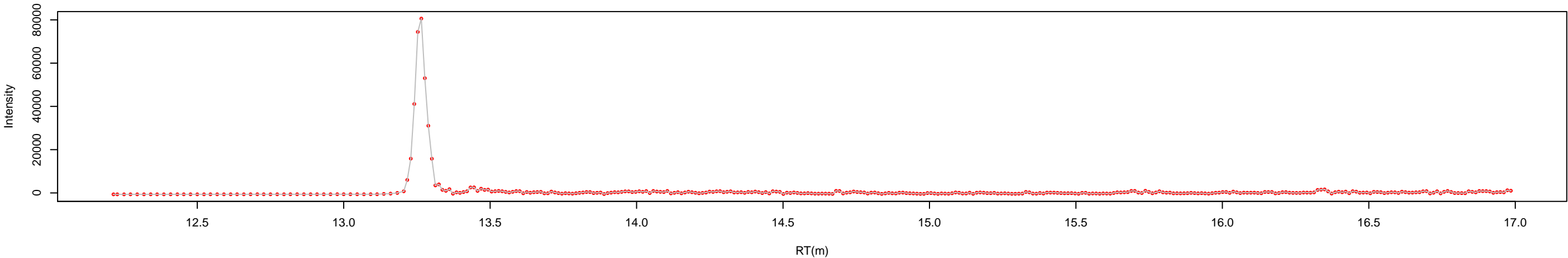
raw chromatogram | batch: 3 sample: std2-10ul-3 conc: 0.005 function: 1 mass: 375.35>375.35



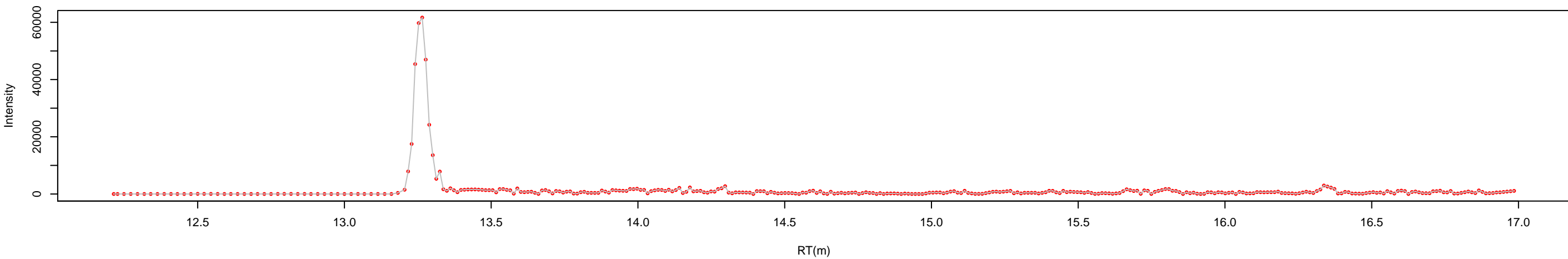
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 31.8 BLine: yes



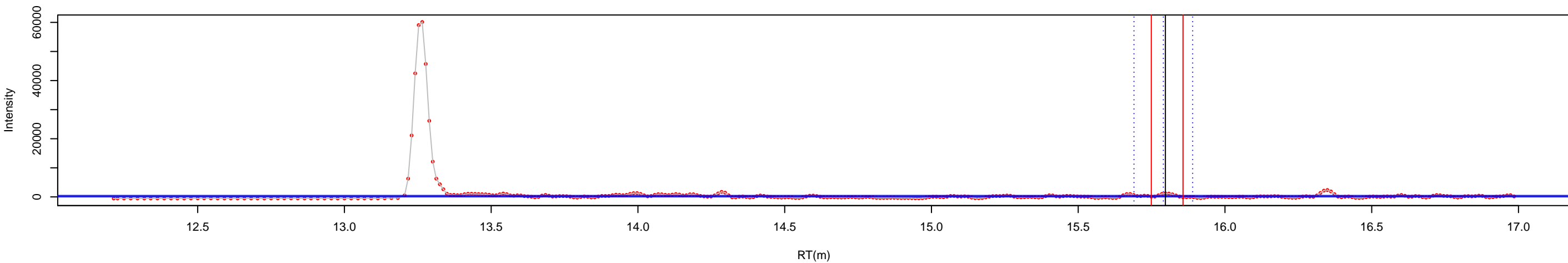
peak area | window size:3 BLine: yes



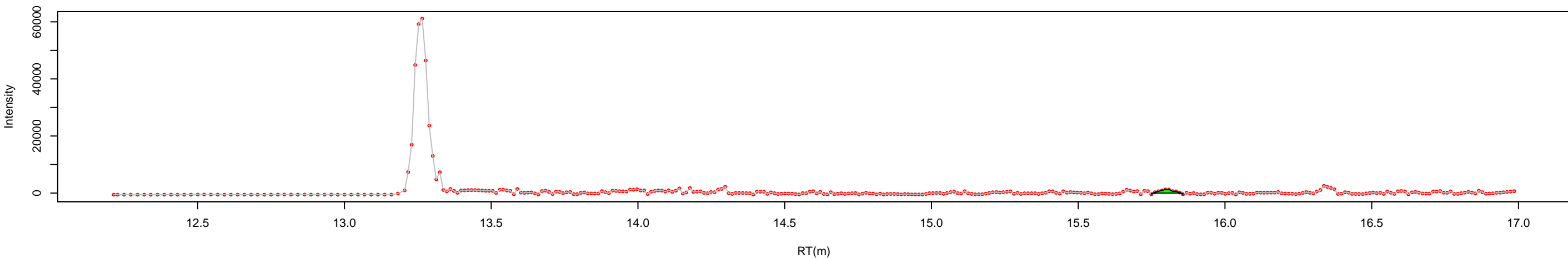
raw chromatogram | batch: 3 sample: std3-10ul-3 conc: 0.01 function: 1 mass: 375.35>375.35



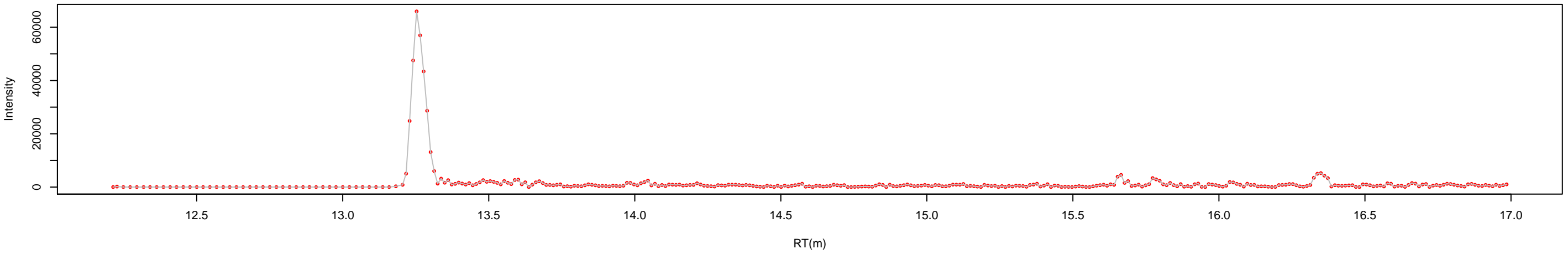
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 48 BLine: yes



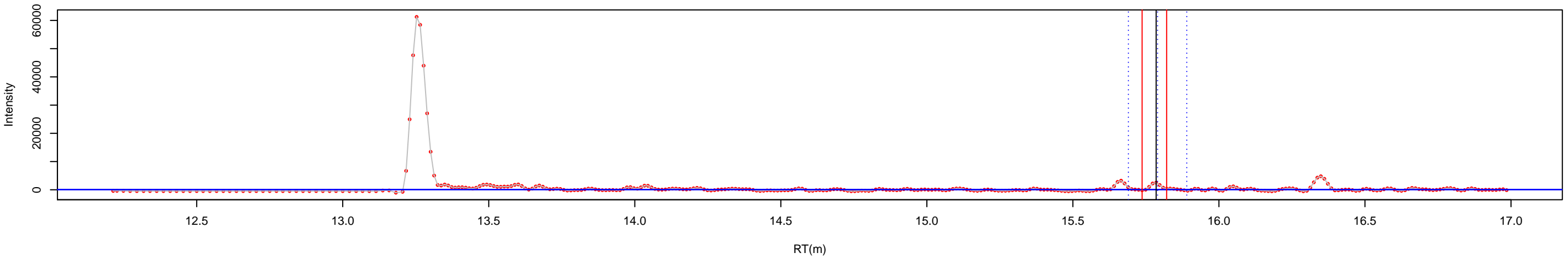
peak area | window size:3 BLine: yes



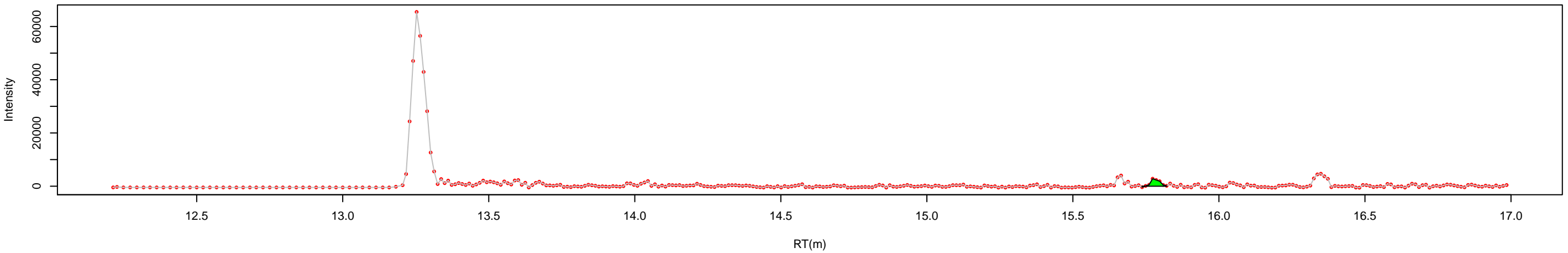
raw chromatogram | batch: 3 sample: std4-10ul-3 conc: 0.02 function: 1 mass: 375.35>375.35



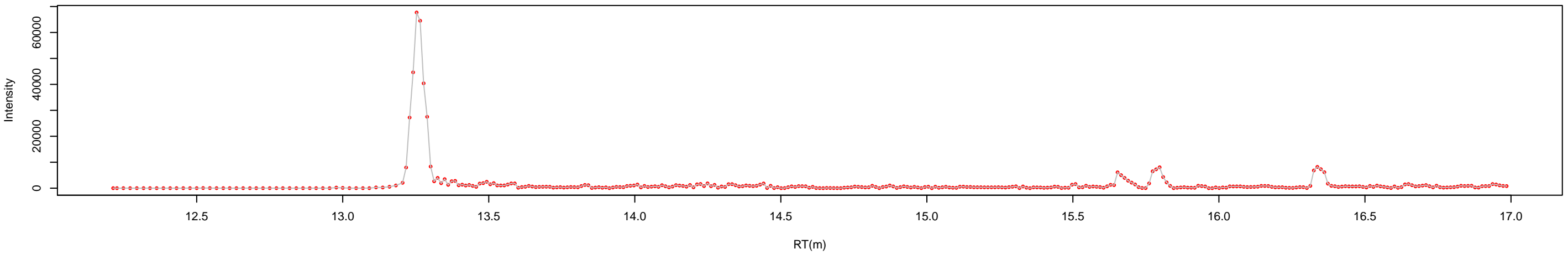
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 11.9 BLine: yes



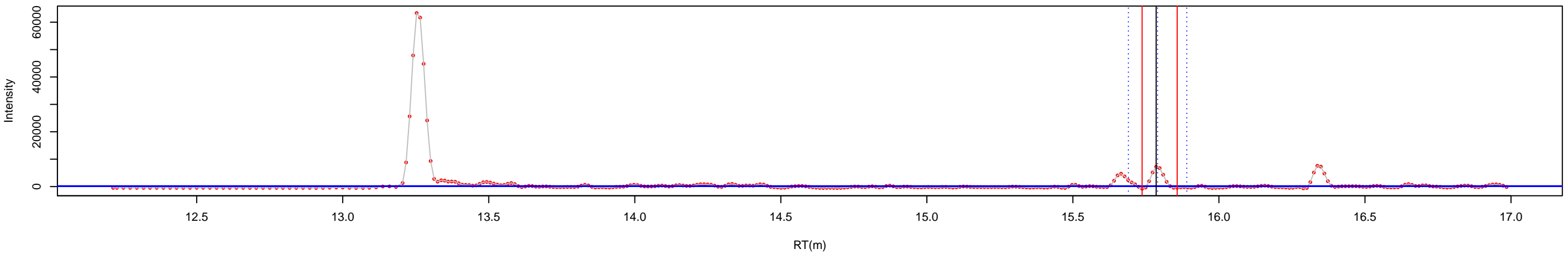
peak area | window size:3 BLine: yes



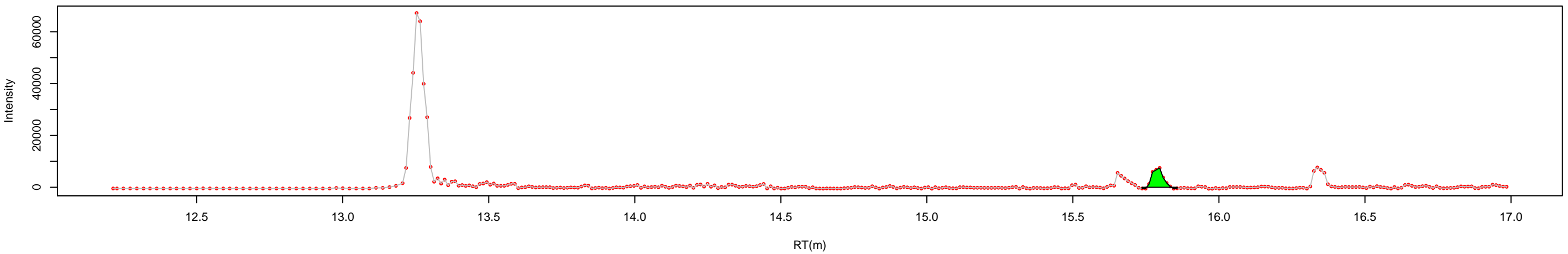
raw chromatogram | batch: 3 sample: std5-10ul-3 conc: 0.05 function: 1 mass: 375.35>375.35



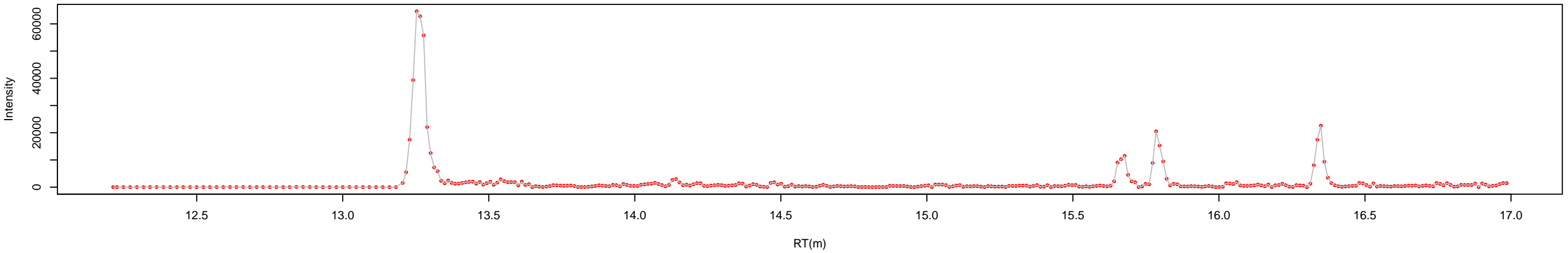
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 28.4 BLine: yes



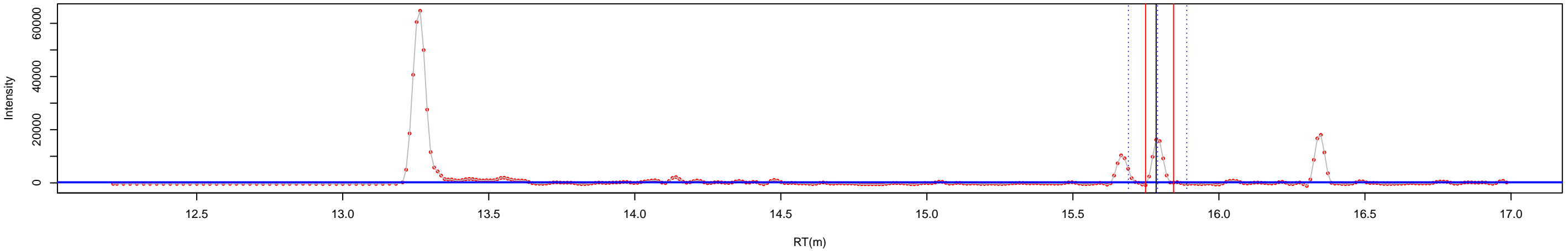
peak area | window size:3 BLine: yes



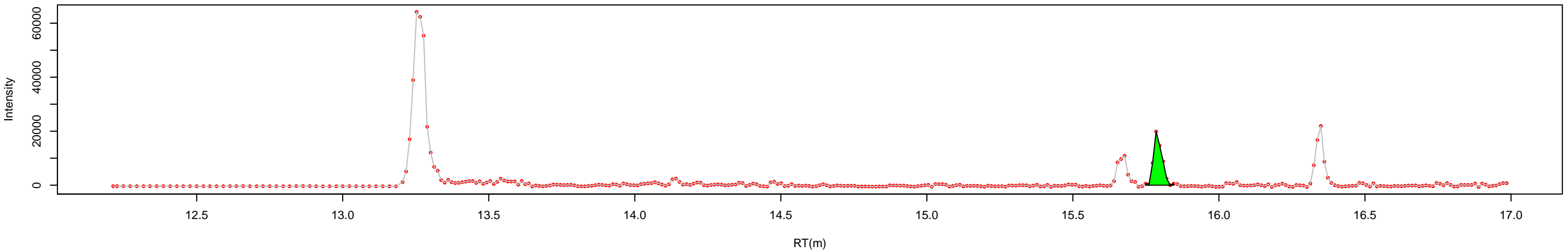
raw chromatogram | batch: 3 sample: std6-10ul-3 conc: 0.1 function: 1 mass: 375.35>375.35



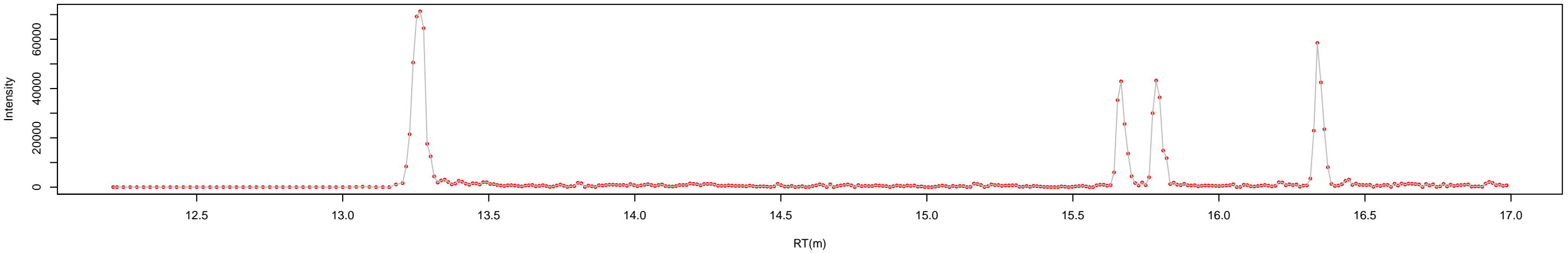
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 40.4 BLine: yes



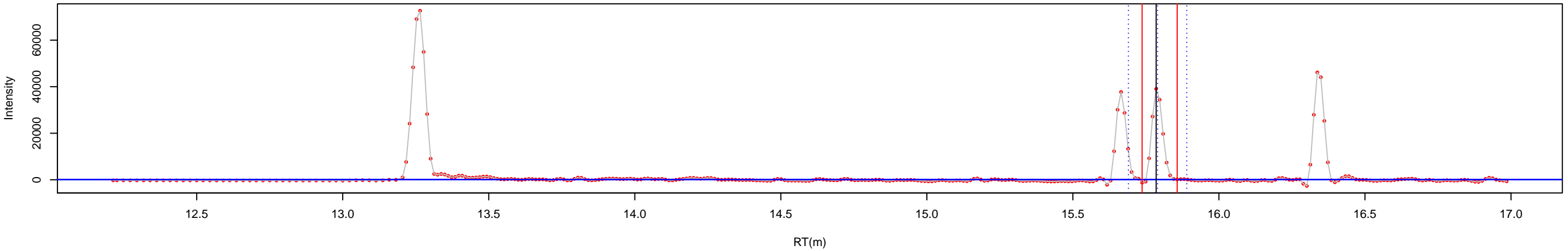
peak area | window size:3 BLine: yes



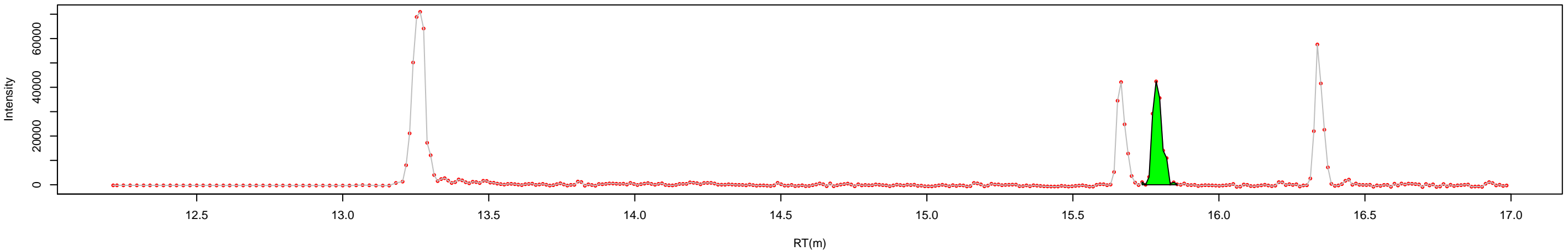
raw chromatogram | batch: 3   sample: std7-10ul-3   conc: 0.2   function: 1   mass: 375.35>375.35



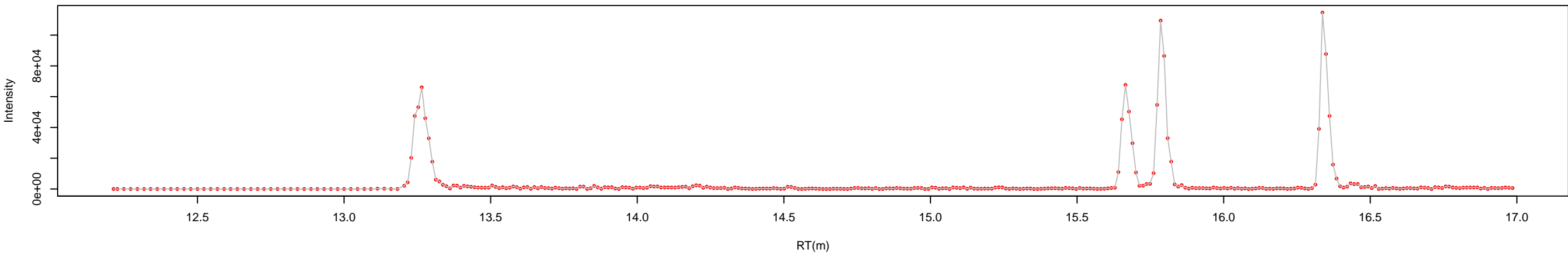
peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 17.4   BLine: yes



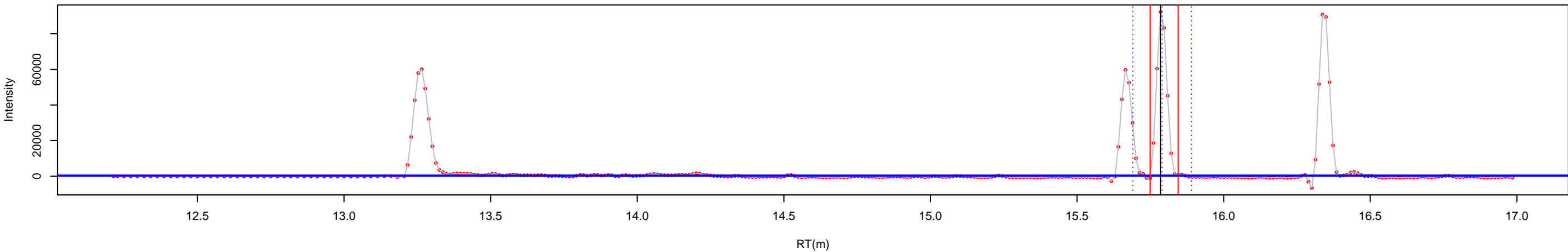
peak area | window size:3   BLine: yes



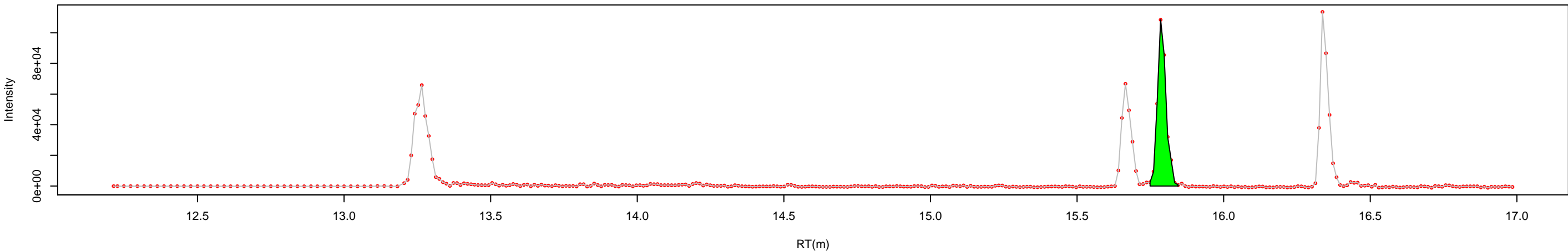
raw chromatogram | batch: 3 sample: std8-10ul-3 conc: 0.5 function: 1 mass: 375.35>375.35



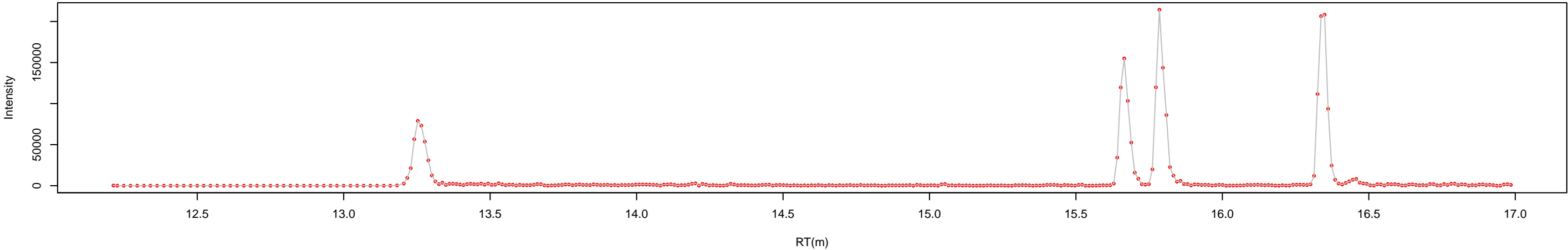
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 64.6 BLine: yes



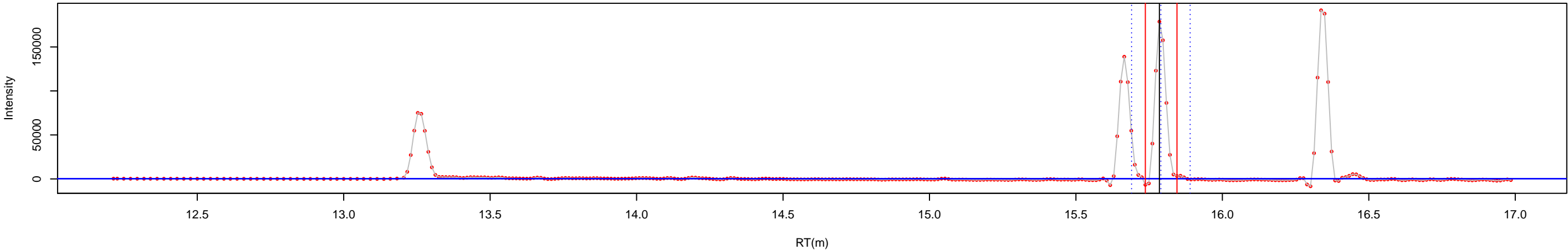
peak area | window size:3 BLine: yes



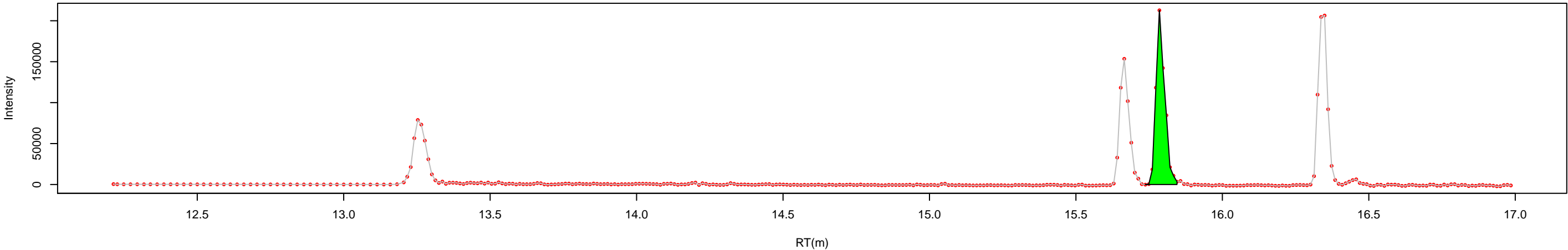
raw chromatogram | batch: 3   sample: std9-10ul-3   conc: 1   function: 1   mass: 375.35>375.35



peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 46.3   BLine: yes

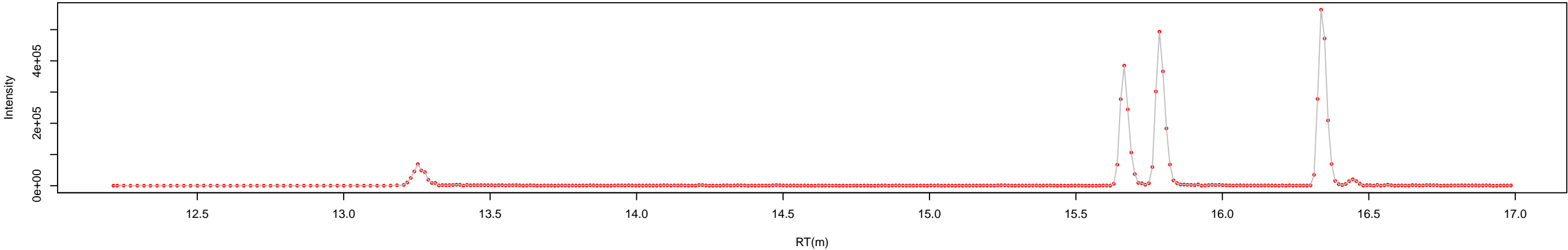


peak area | window size:3   BLine: yes

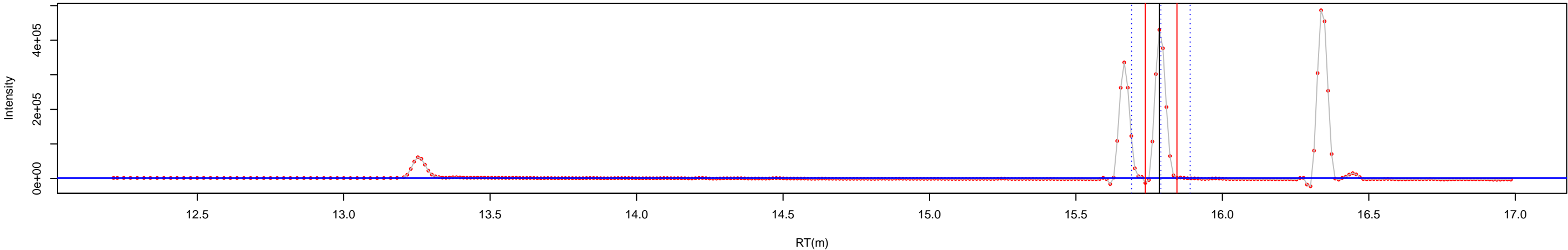




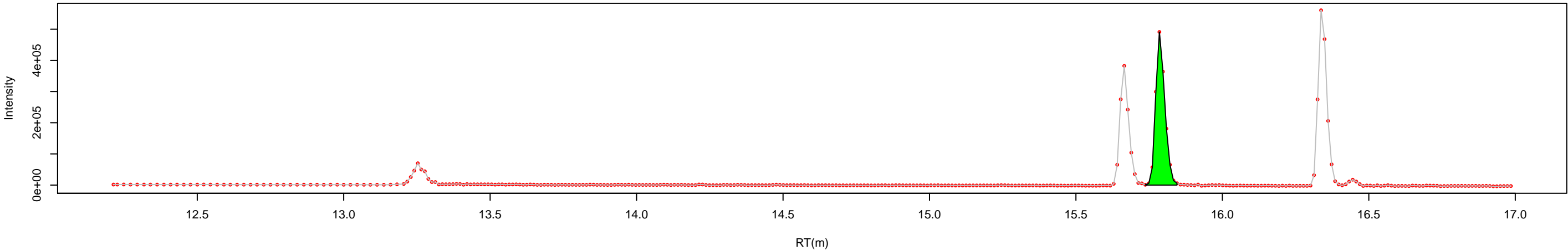
raw chromatogram | batch: 3   sample: std10-10ul-3   conc: 2   function: 1   mass: 375.35>375.35



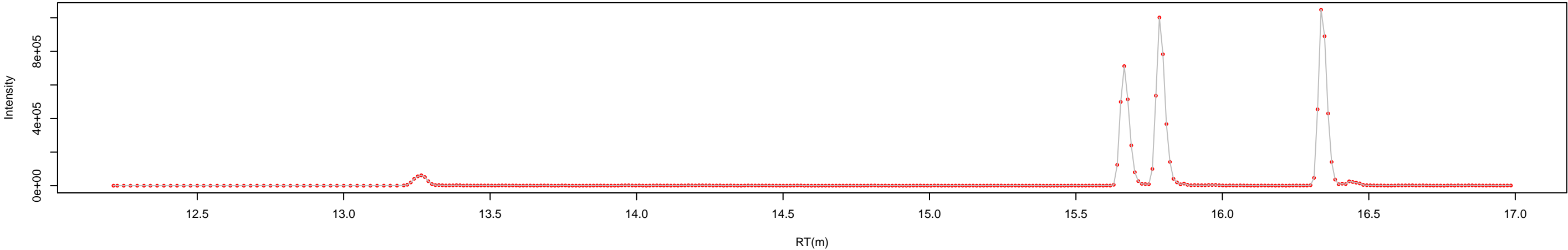
peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 217   BLine: yes



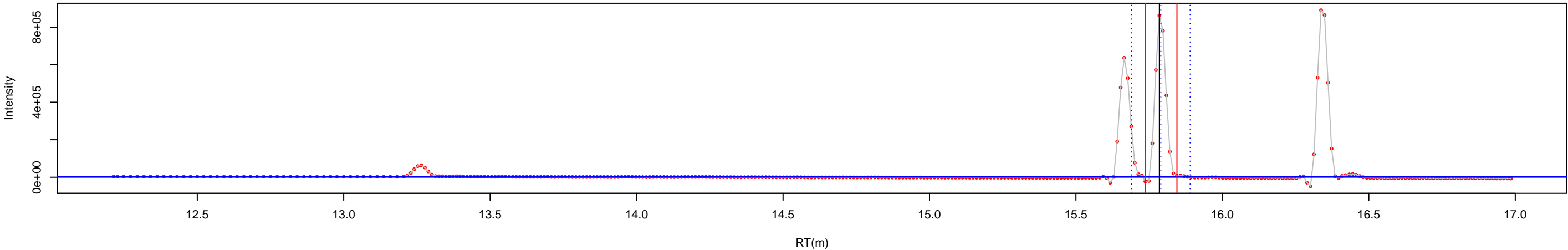
peak area | window size:3   BLine: yes



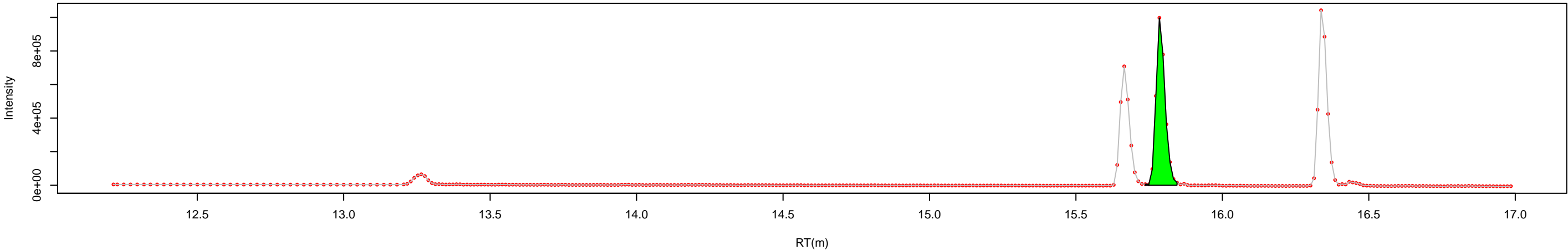
raw chromatogram | batch: 3   sample: std11-10ul-3   conc: 5   function: 1   mass: 375.35>375.35



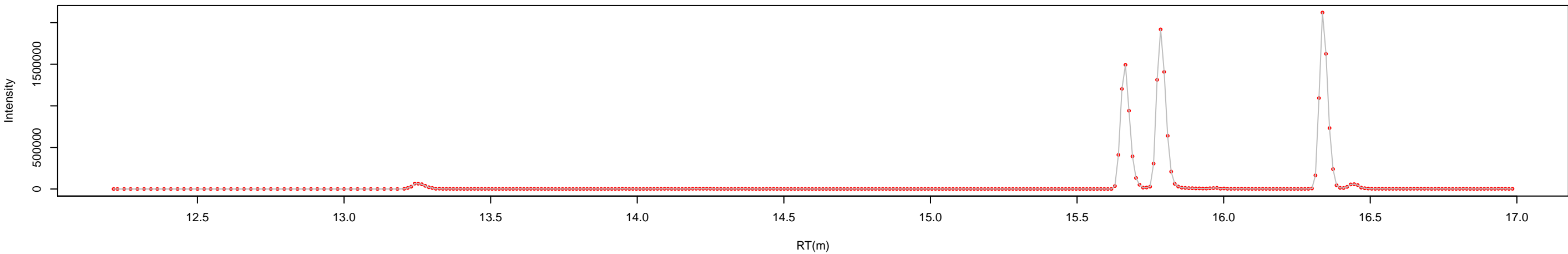
peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 362   BLine: yes



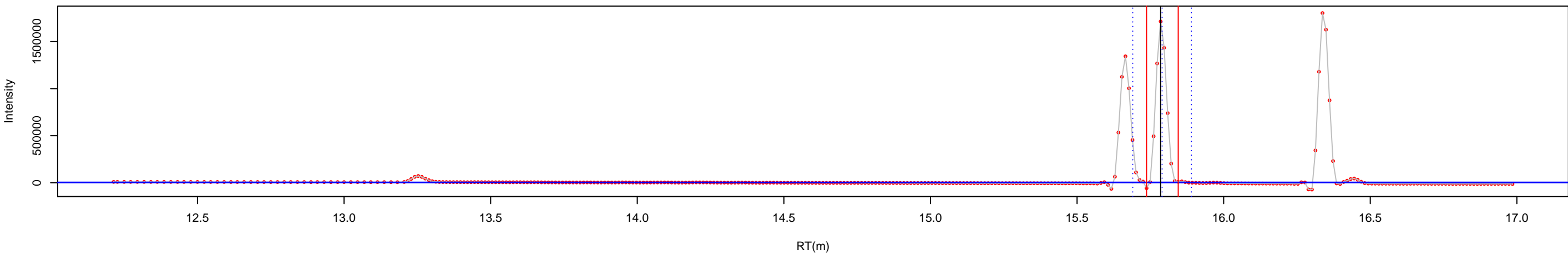
peak area | window size:3   BLine: yes



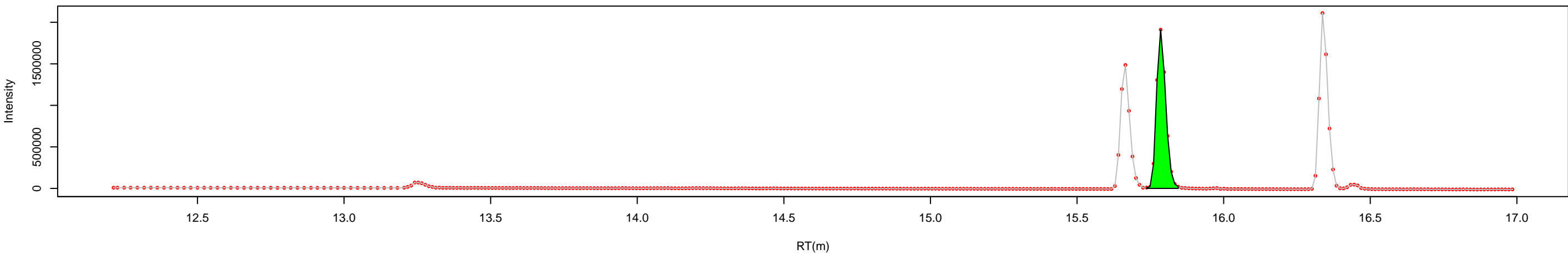
raw chromatogram | batch: 3 sample: std12-10ul-3 conc: 10 function: 1 mass: 375.35>375.35



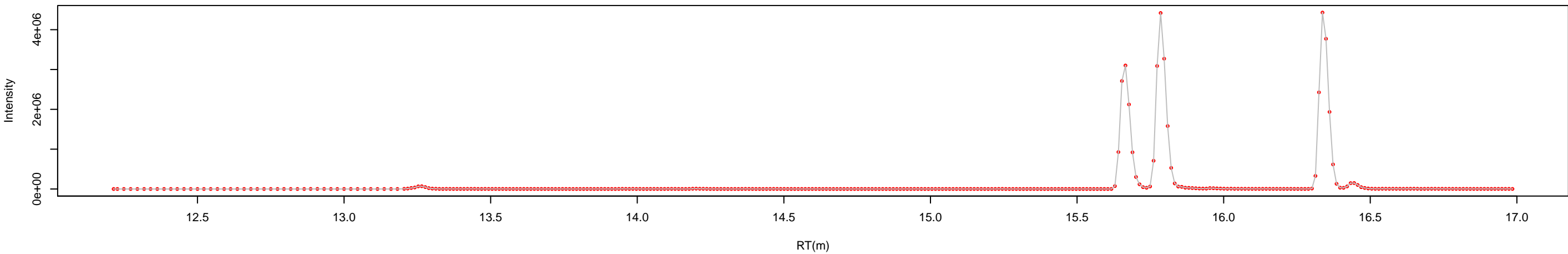
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 600 BLine: yes



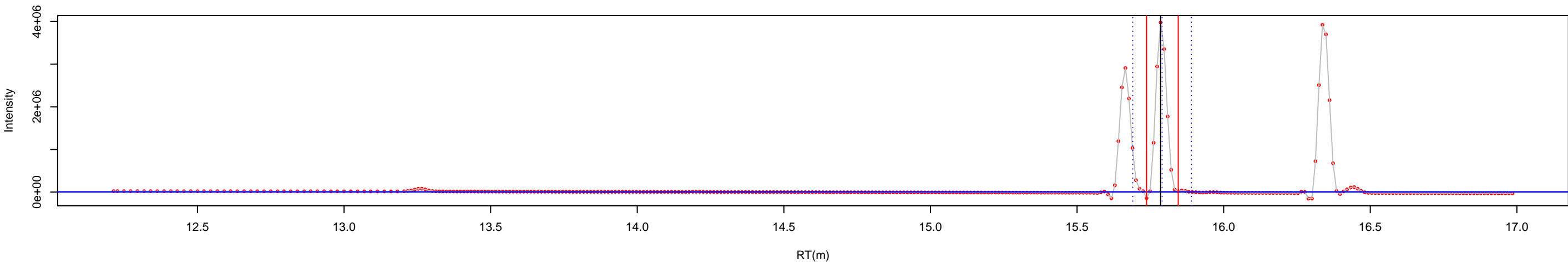
peak area | window size:3 BLine: yes



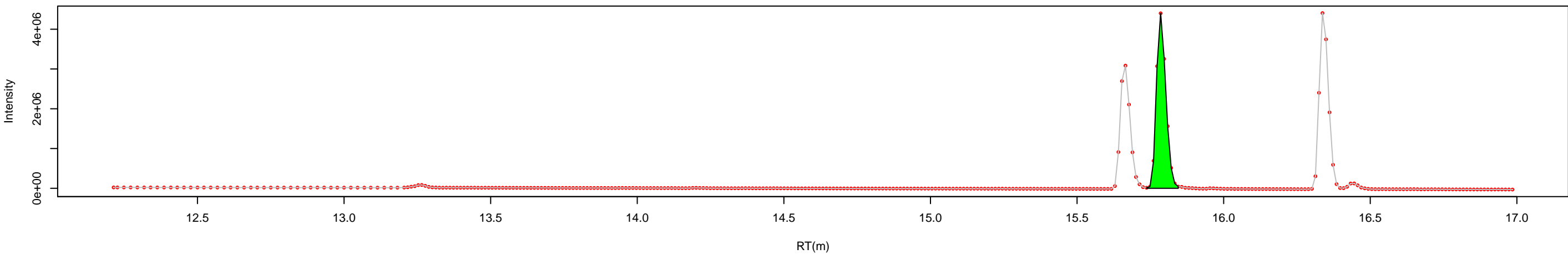
raw chromatogram | batch: 3 sample: std13-10ul-3 conc: 20 function: 1 mass: 375.35>375.35



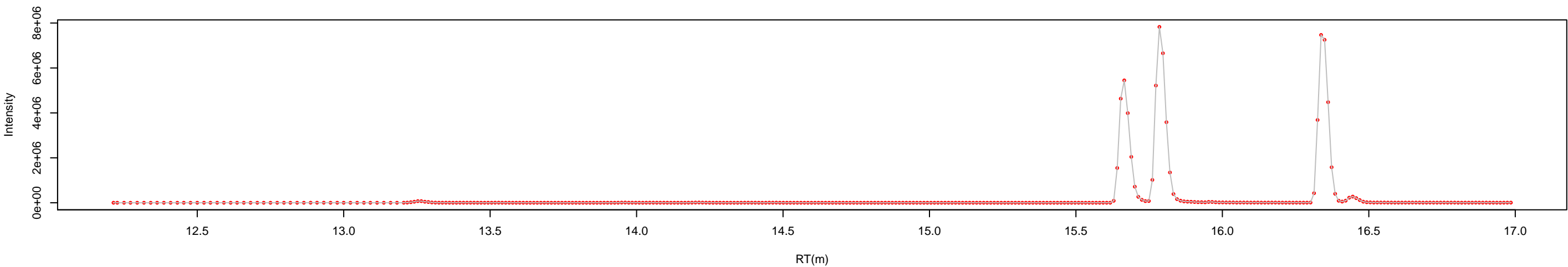
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 841 BLine: yes



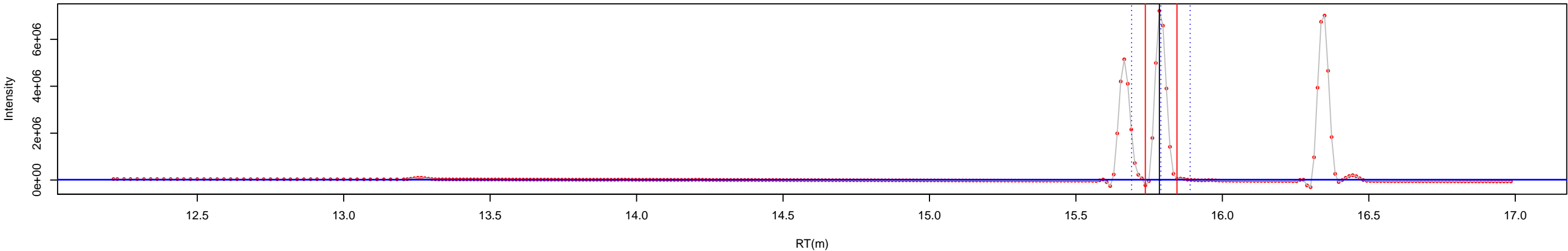
peak area | window size:3 BLine: yes



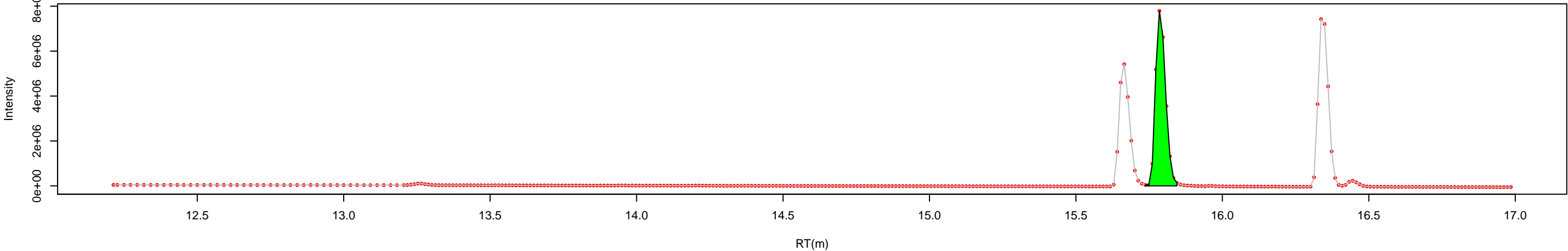
raw chromatogram | batch: 3   sample: std14-10ul-3   conc: 50   function: 1   mass: 375.35>375.35



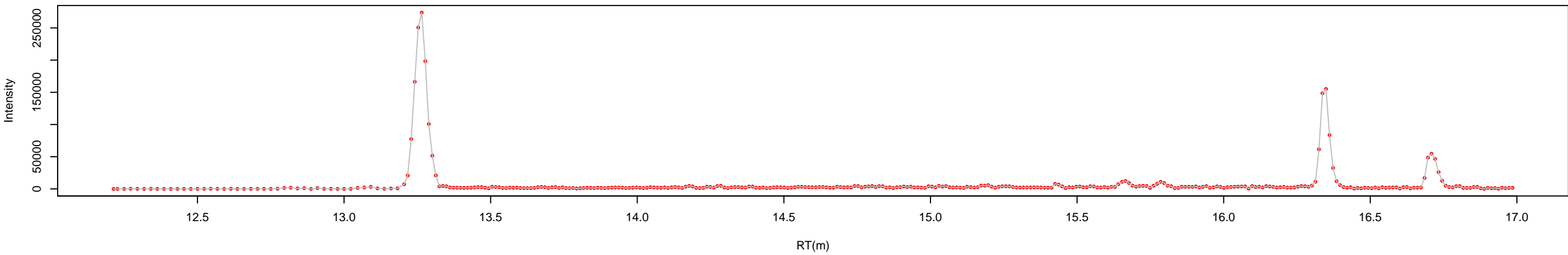
peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 2760   BLine: yes



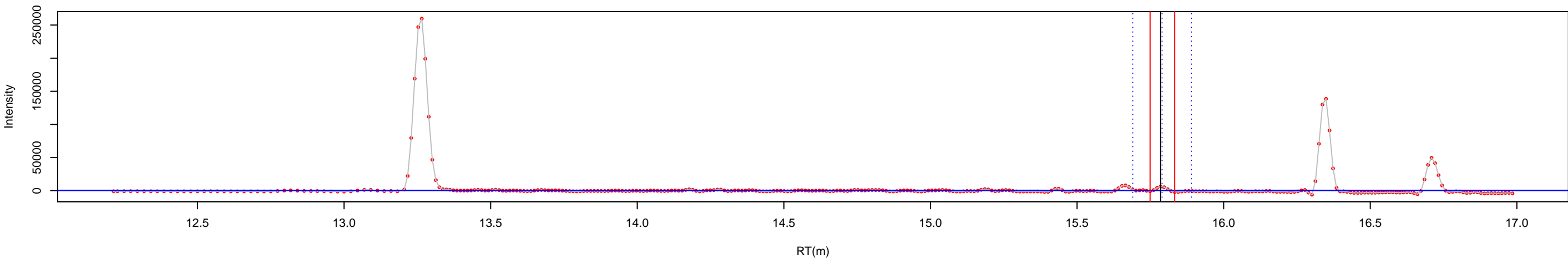
peak area | window size:3   BLine: yes



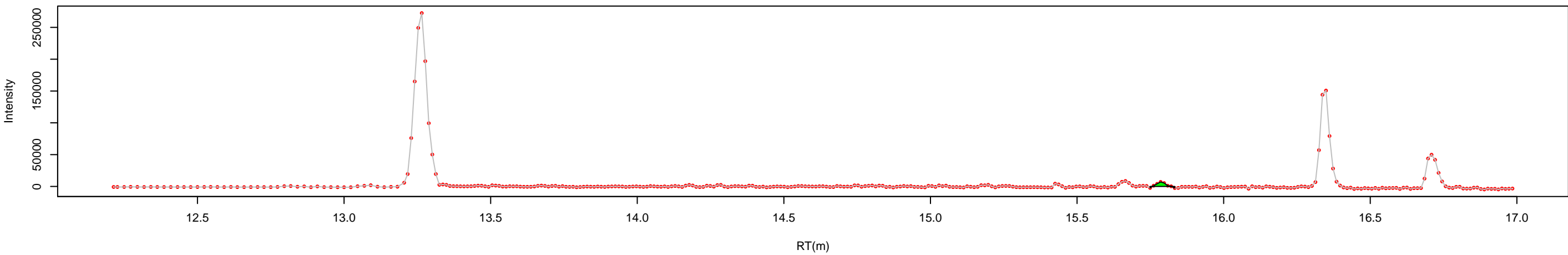
raw chromatogram | batch: 4 sample: cotor1 conc: NA function: 1 mass: 375.35>375.35



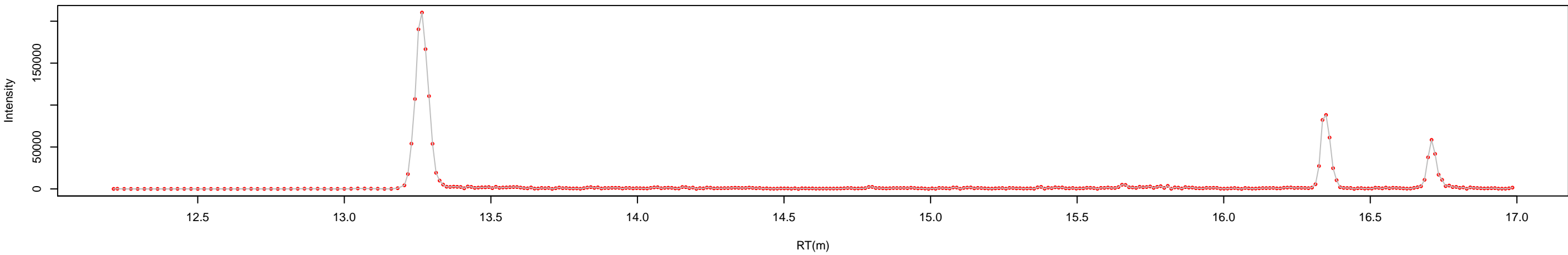
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 52.9 BLine: yes



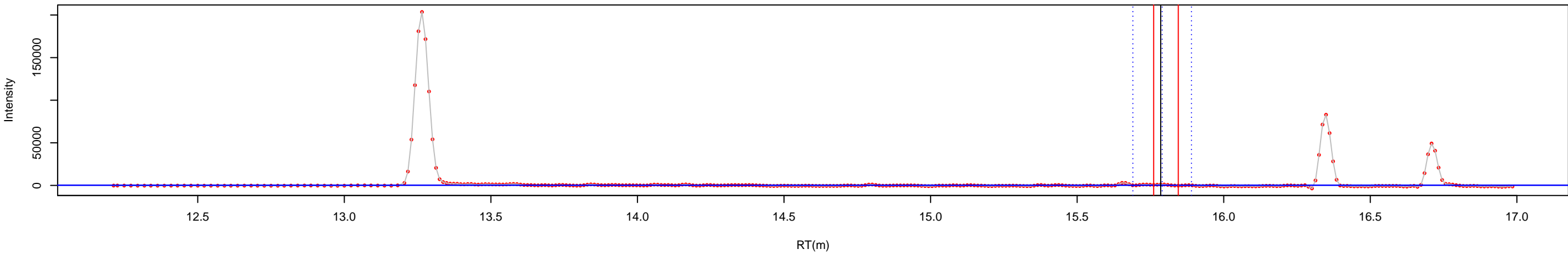
peak area | window size:3 BLine: yes



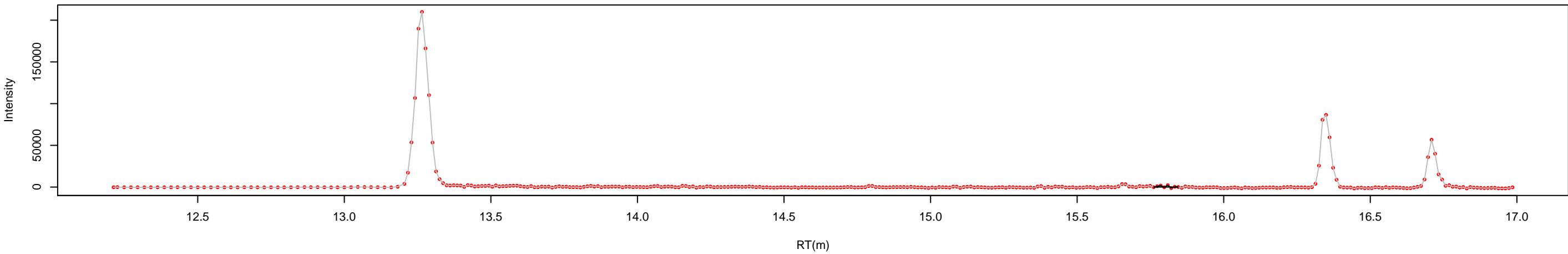
raw chromatogram | batch: 4 sample: cotor2 conc: NA function: 1 mass: 375.35>375.35



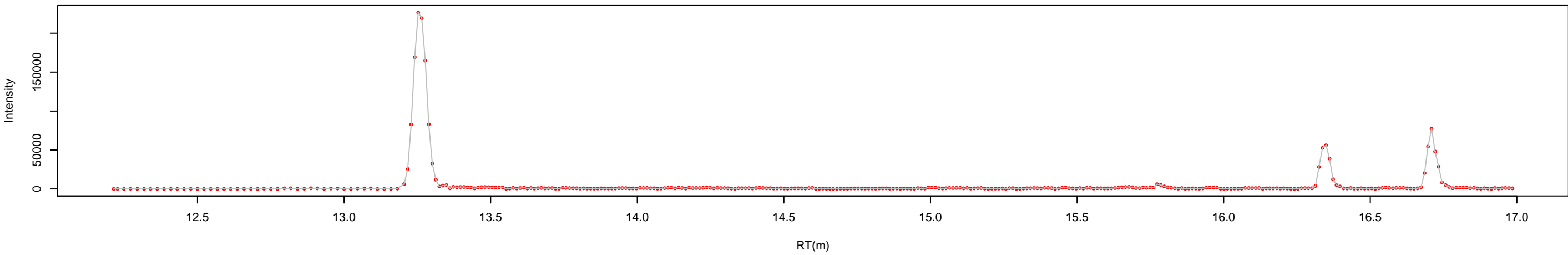
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 37 BLine: yes



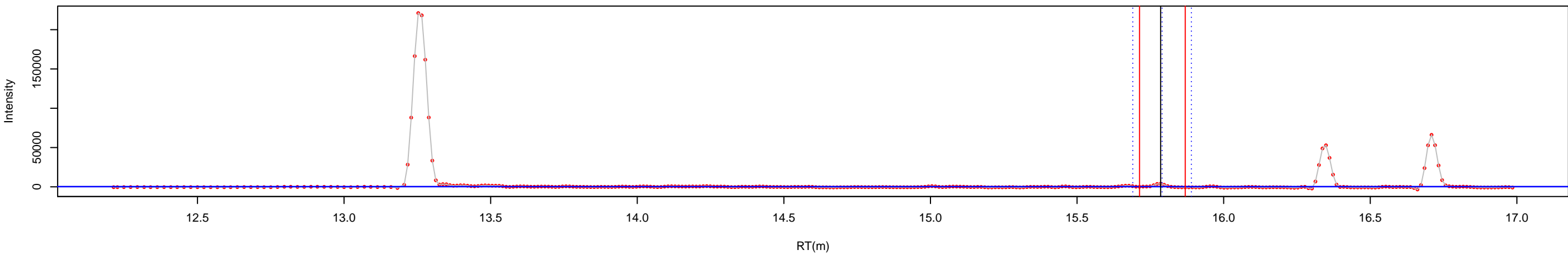
peak area | window size:3 BLine: yes



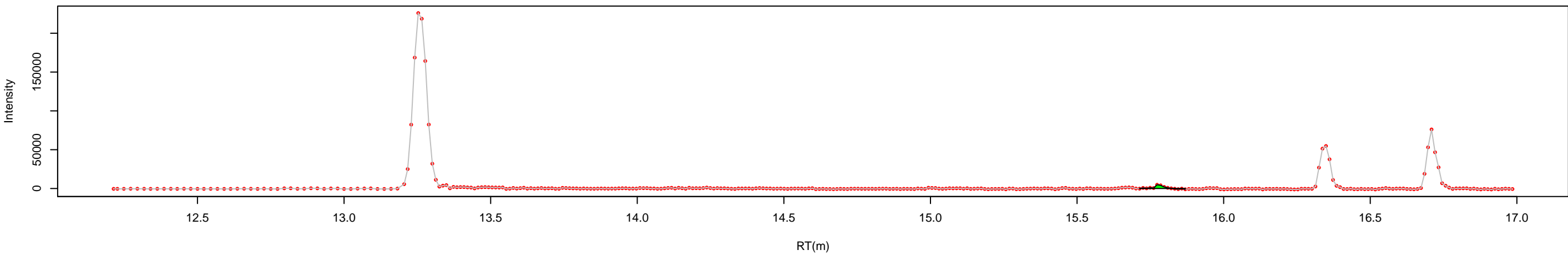
raw chromatogram | batch: 4 sample: cotor3 conc: NA function: 1 mass: 375.35>375.35



peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 47.4 BLine: yes

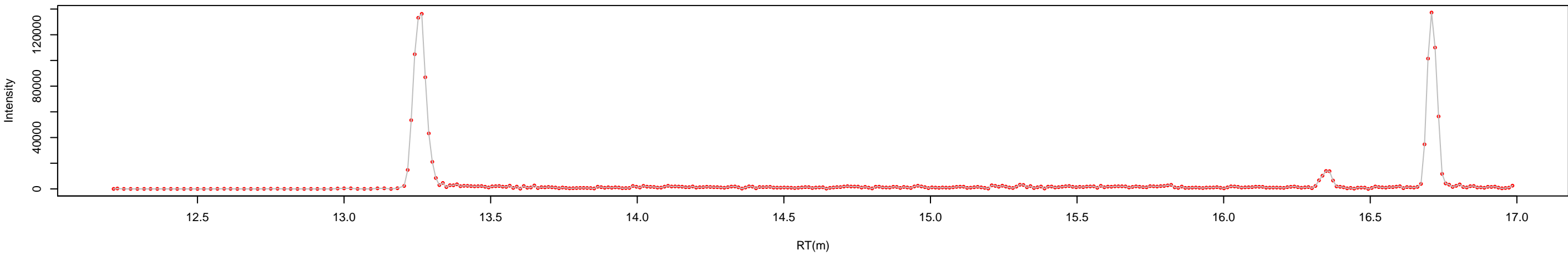


peak area | window size:3 BLine: yes

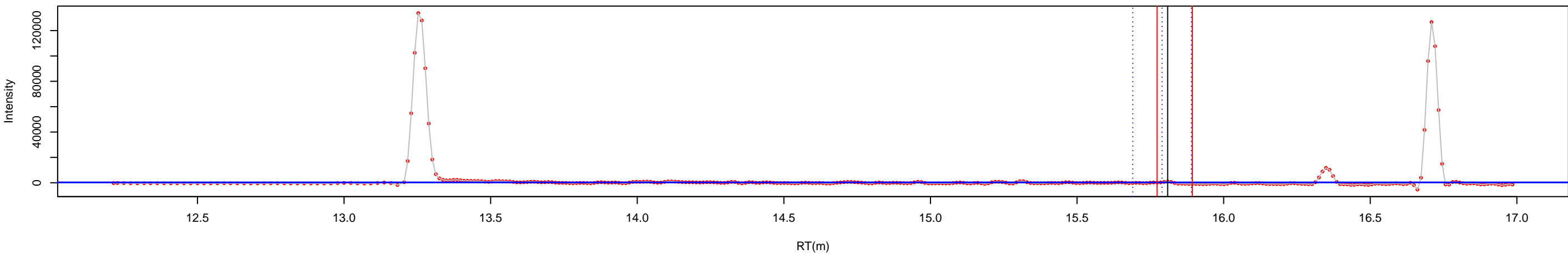




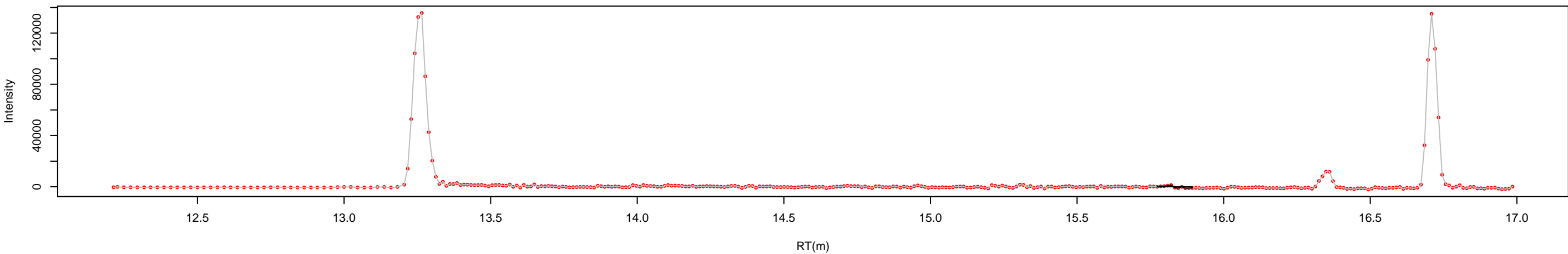
raw chromatogram | batch: 4 sample: cotor4 conc: NA function: 1 mass: 375.35>375.35



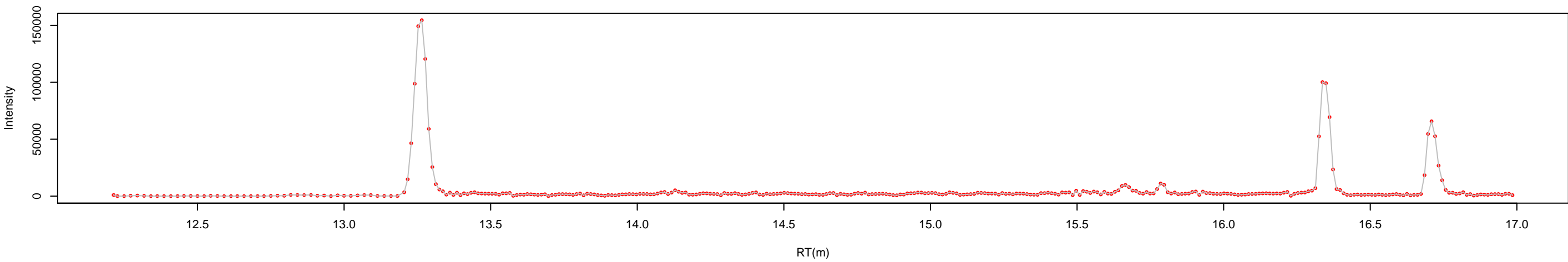
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 50.5 BLine: yes



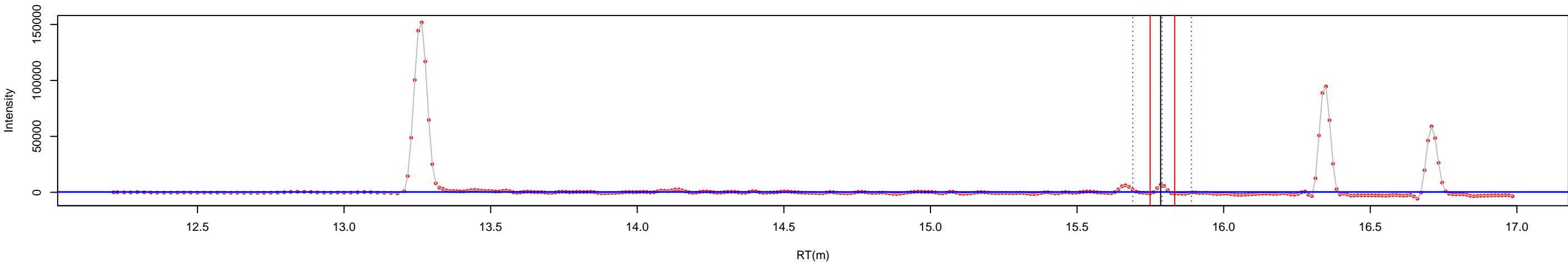
peak area | window size:3 BLine: yes



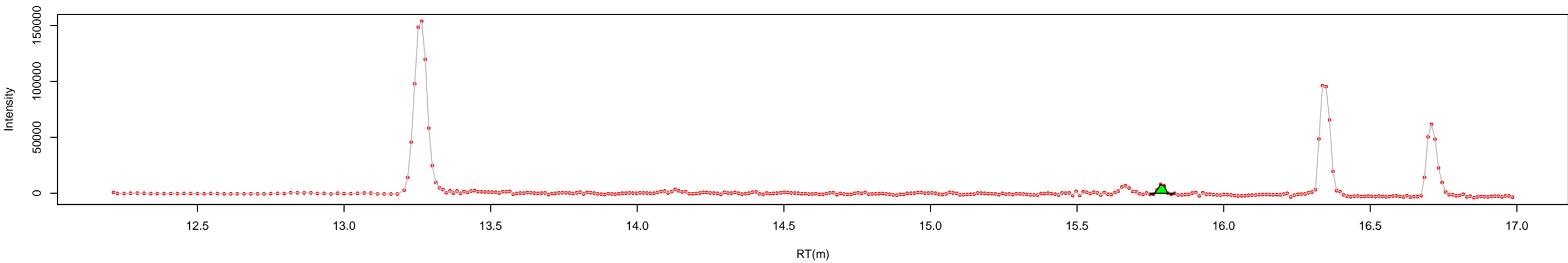
raw chromatogram | batch: 4 sample: cotor5 conc: NA function: 1 mass: 375.35>375.35



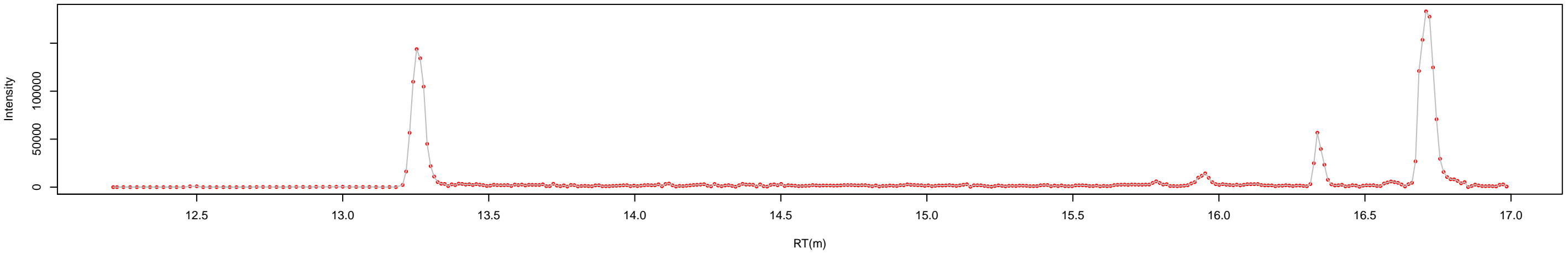
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 52.7 BLine: yes



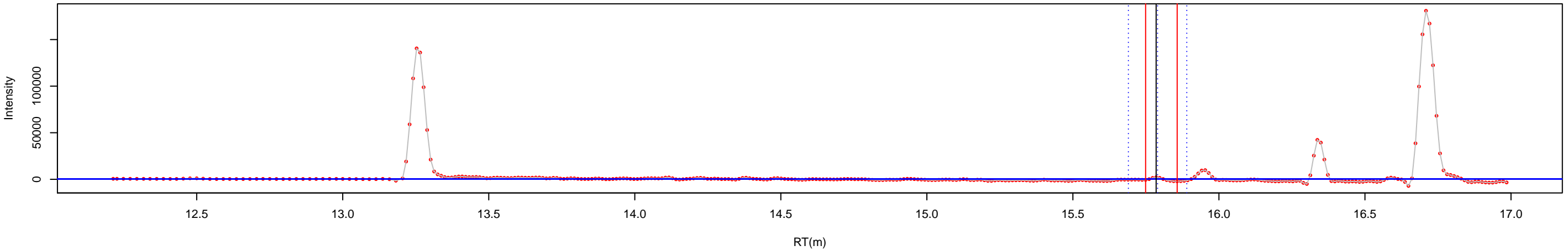
peak area | window size:3 BLine: yes



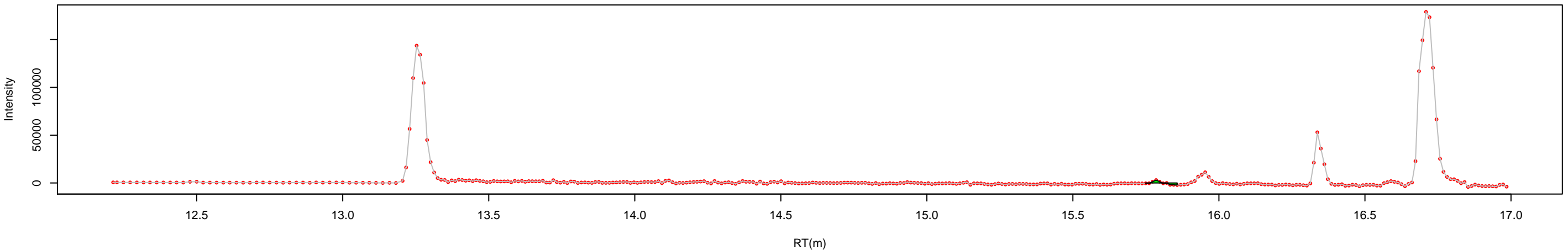
raw chromatogram | batch: 4 sample: cotor15 conc: NA function: 1 mass: 375.35>375.35



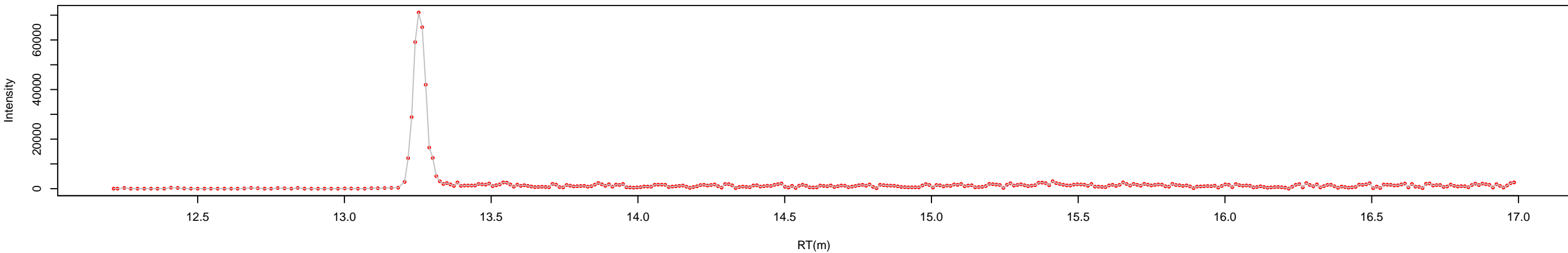
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 62.8 BLine: yes



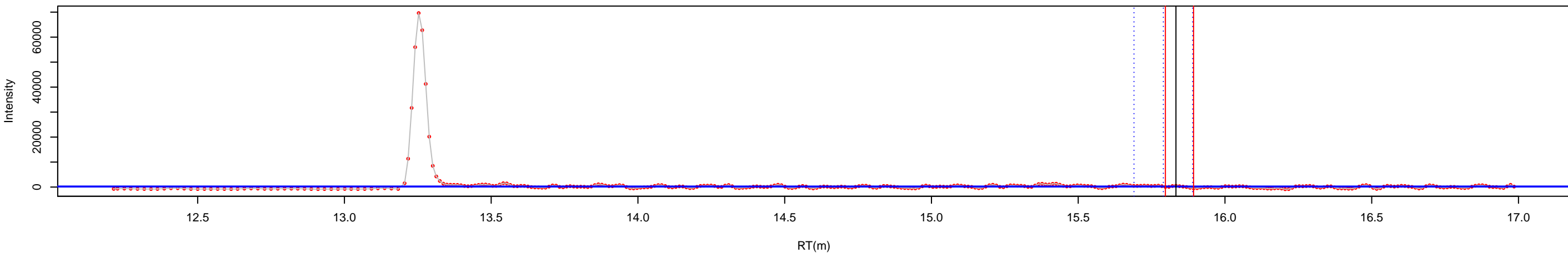
peak area | window size:3 BLine: yes



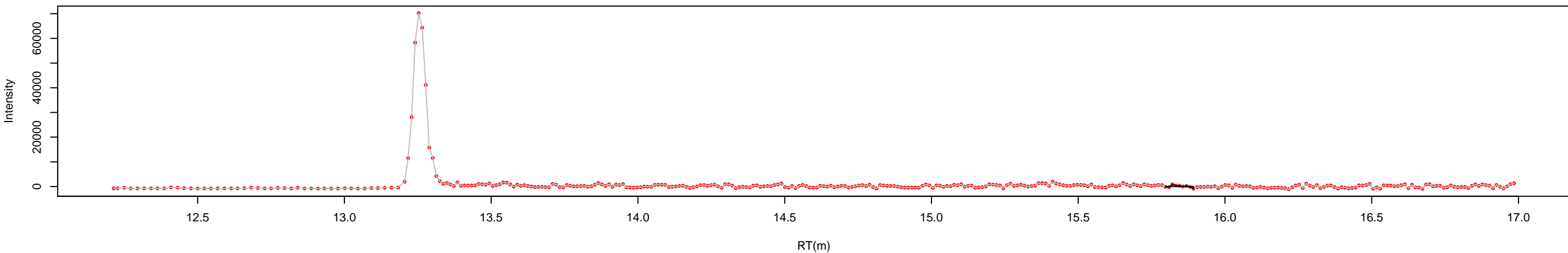
raw chromatogram | batch: 4 sample: std0-10ul-4 conc: 0.001 function: 1 mass: 375.35>375.35



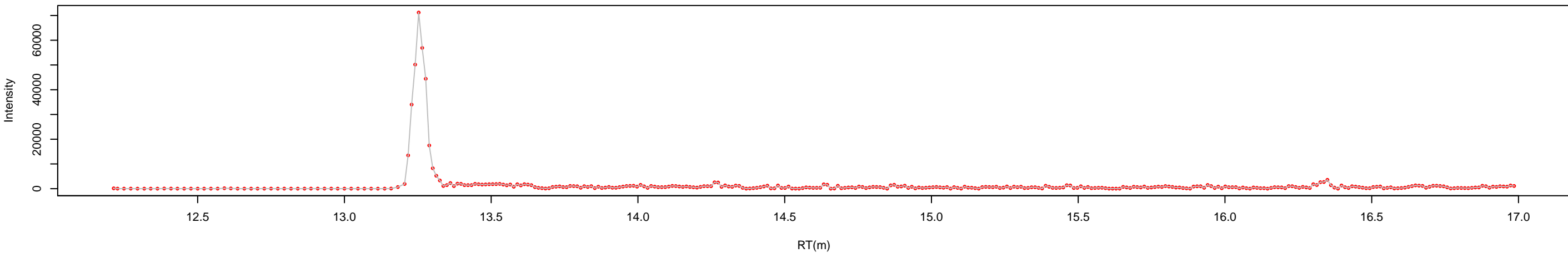
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 39.3 BLine: yes



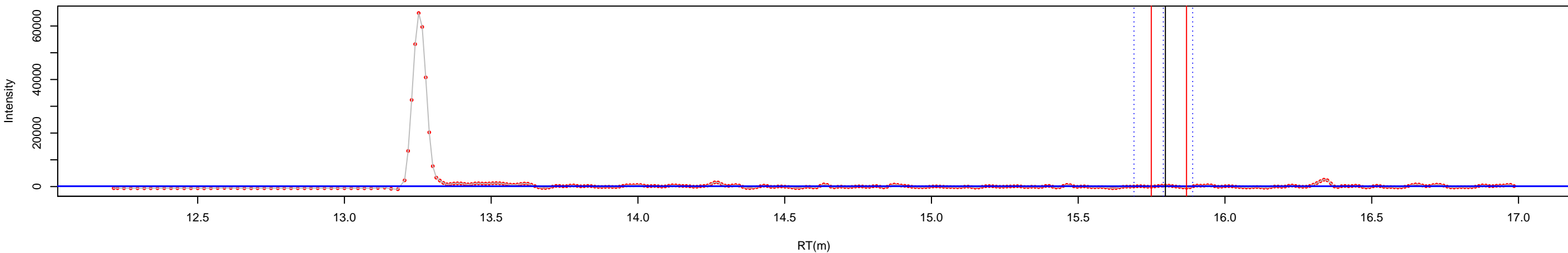
peak area | window size:3 BLine: yes



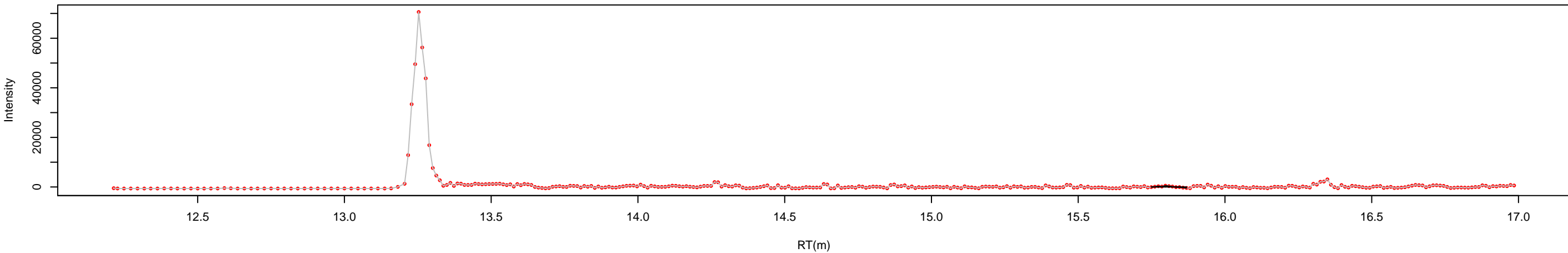
raw chromatogram | batch: 4 sample: std1-10ul-4 conc: 0.002 function: 1 mass: 375.35>375.35



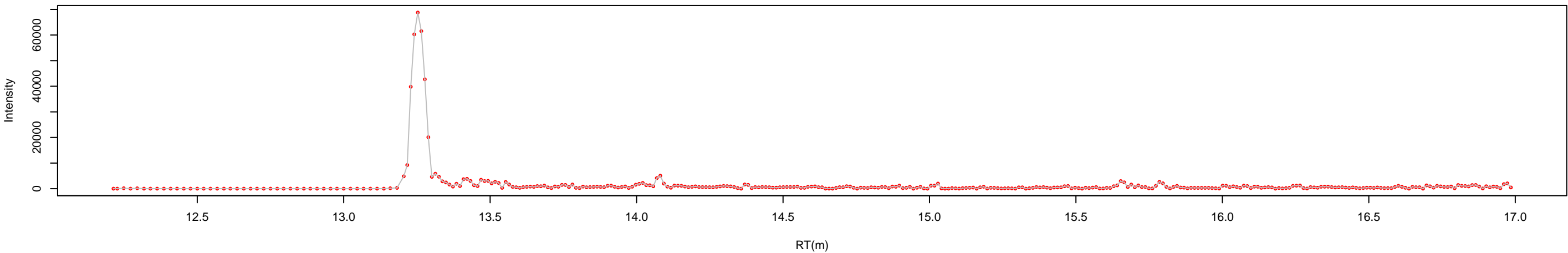
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 24.1 BLine: yes



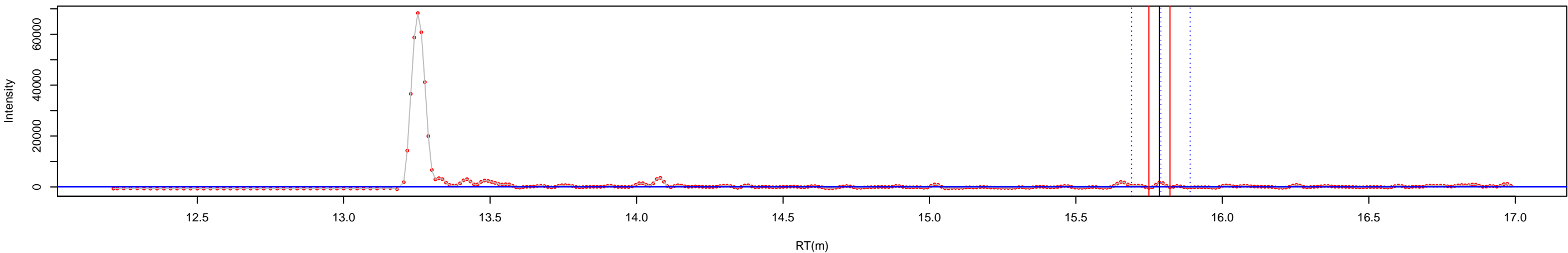
peak area | window size:3 BLine: yes



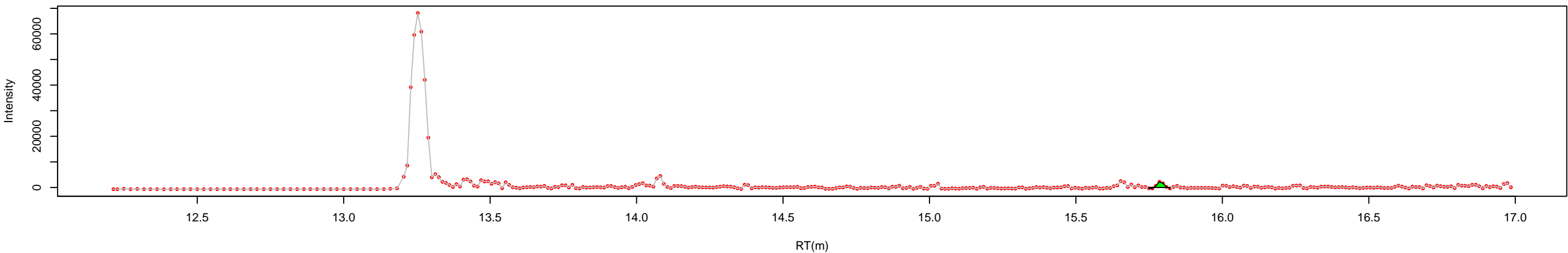
raw chromatogram | batch: 4   sample: std2-10ul-4   conc: 0.005   function: 1   mass: 375.35>375.35



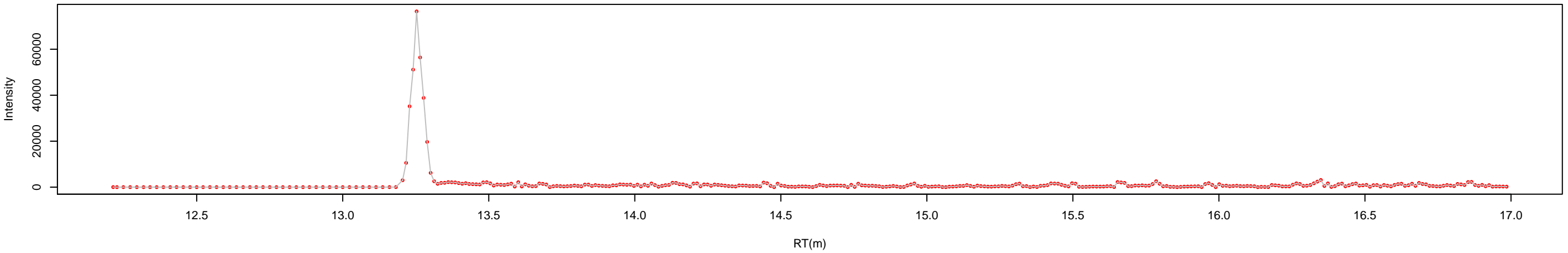
peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 18.3   BLine: yes



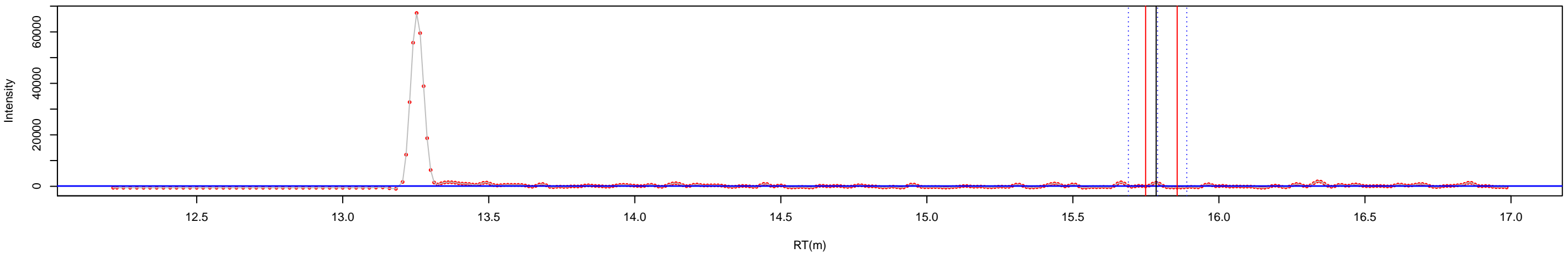
peak area | window size:3   BLine: yes



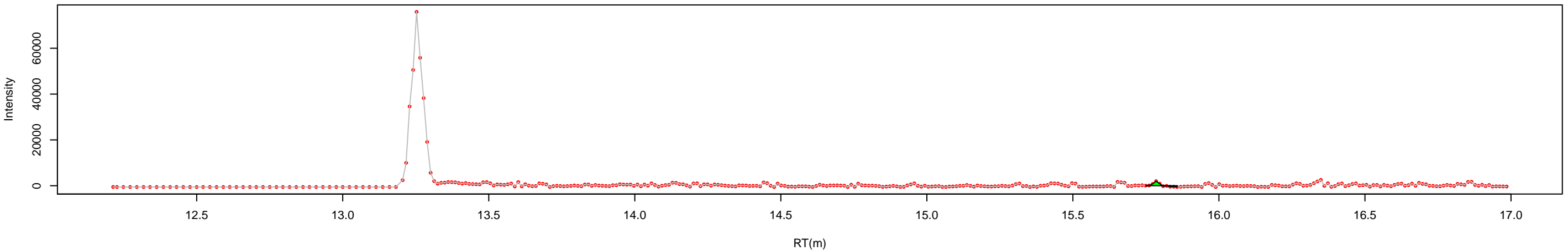
raw chromatogram | batch: 4   sample: std3-10ul-4   conc: 0.01   function: 1   mass: 375.35>375.35



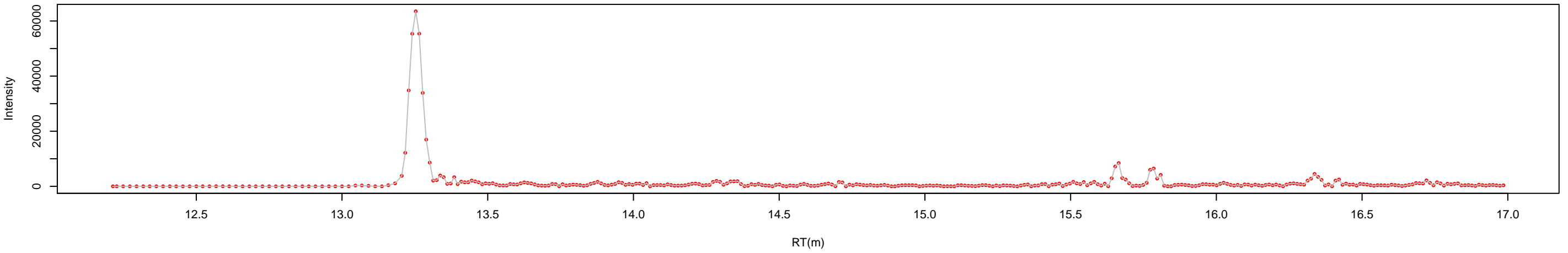
peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 19.4   BLine: yes



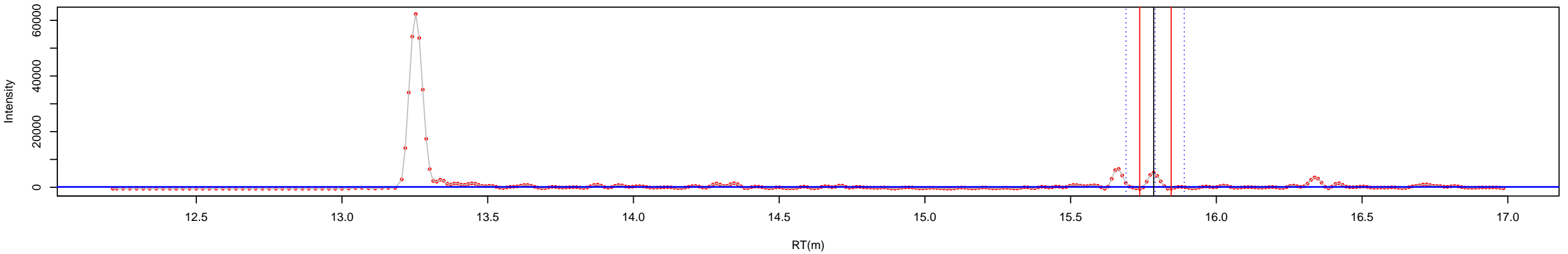
peak area | window size:3   BLine: yes



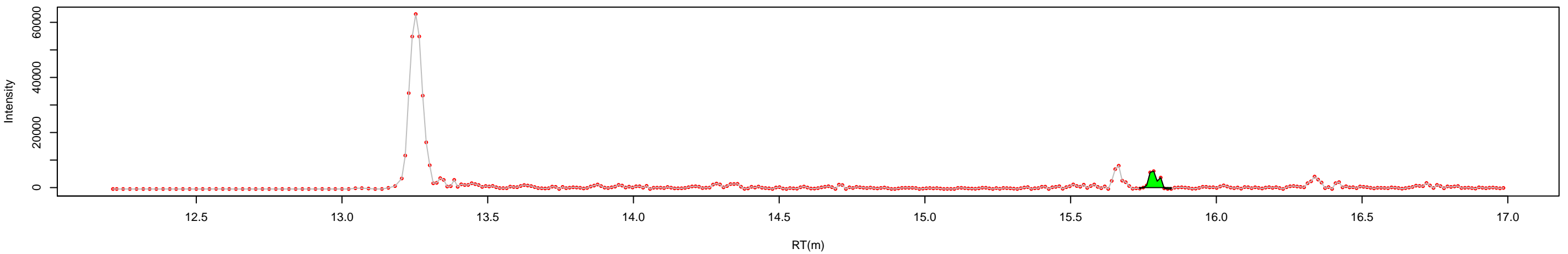
raw chromatogram | batch: 4   sample: std4-10ul-4   conc: 0.02   function: 1   mass: 375.35>375.35



peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 22.9   BLine: yes

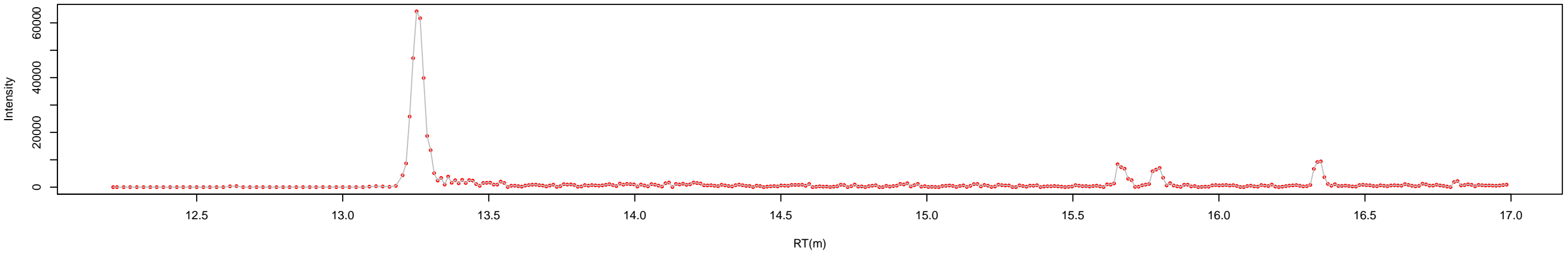


peak area | window size:3   BLine: yes

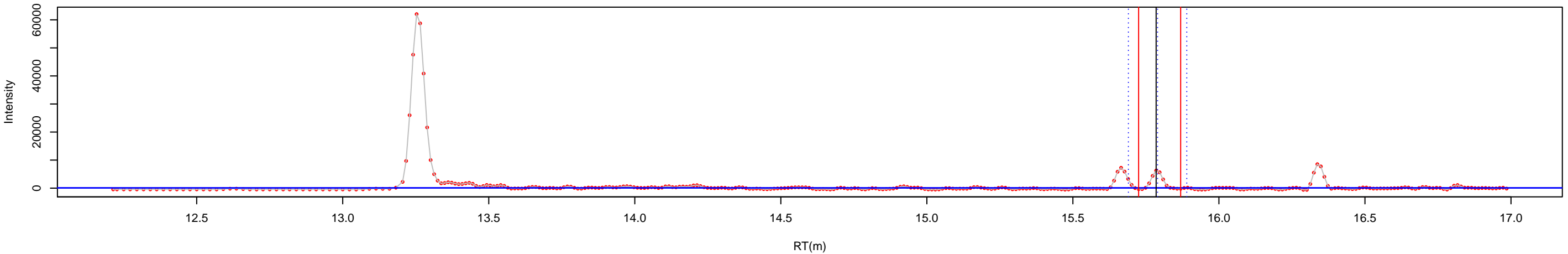




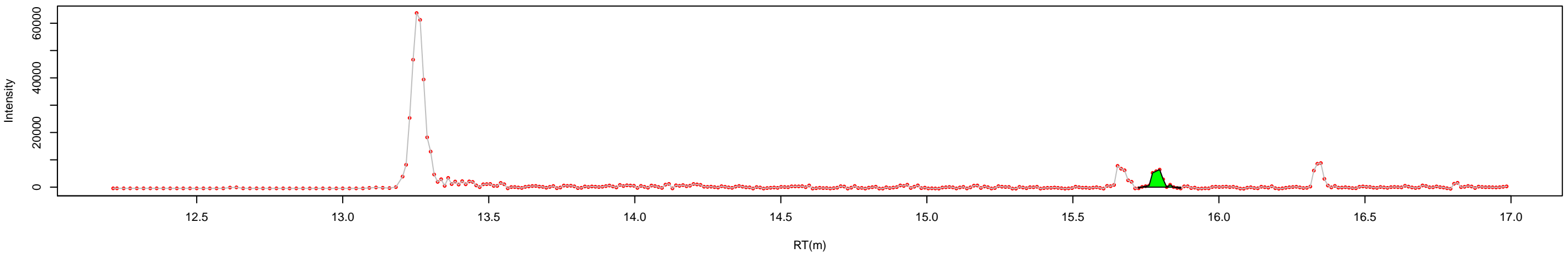
raw chromatogram | batch: 4 sample: std5-10ul-4 conc: 0.05 function: 1 mass: 375.35>375.35



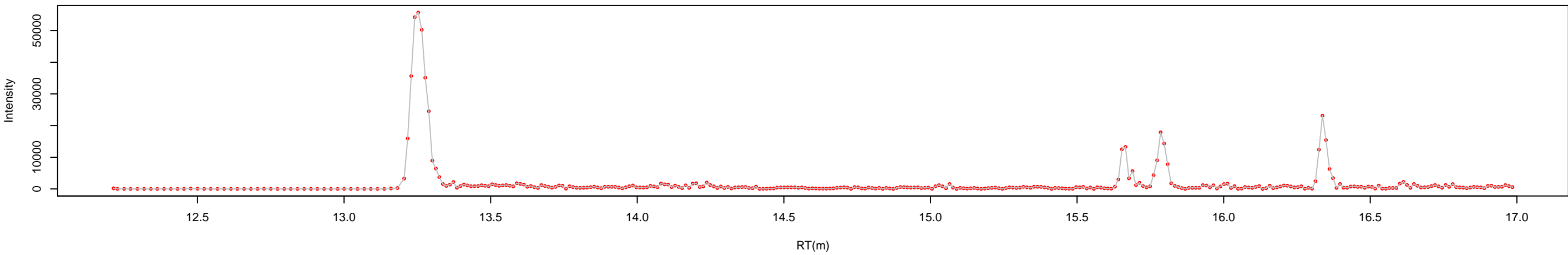
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 16.9 BLine: yes



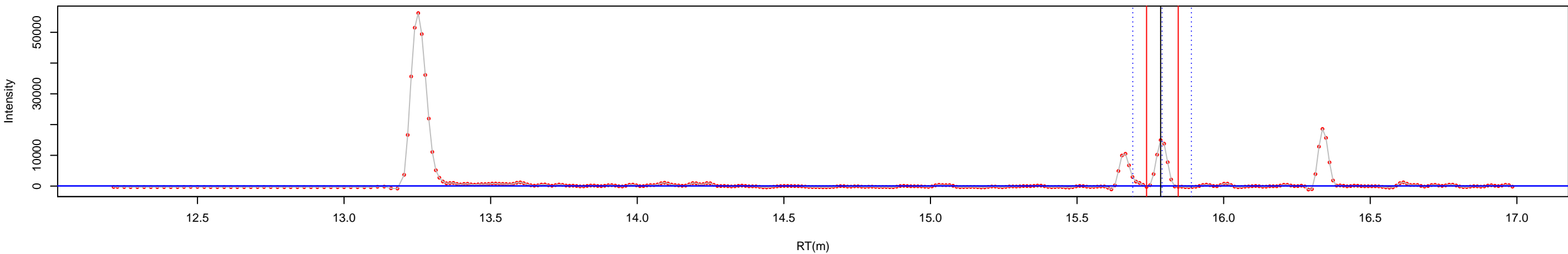
peak area | window size:3 BLine: yes



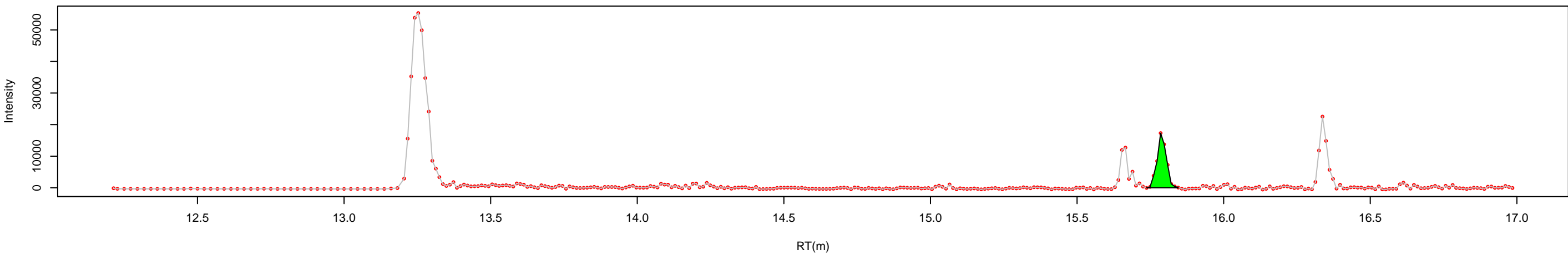
raw chromatogram | batch: 4 sample: std6-10ul-4 conc: 0.1 function: 1 mass: 375.35>375.35



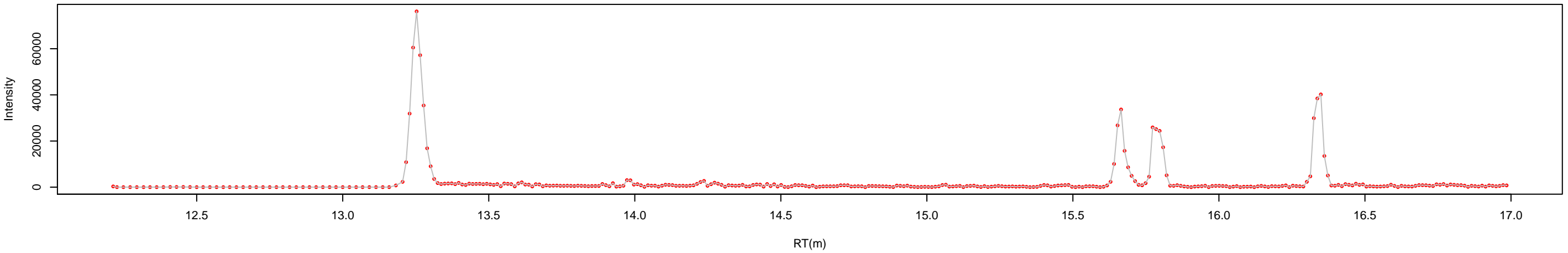
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 9.02 BLine: yes



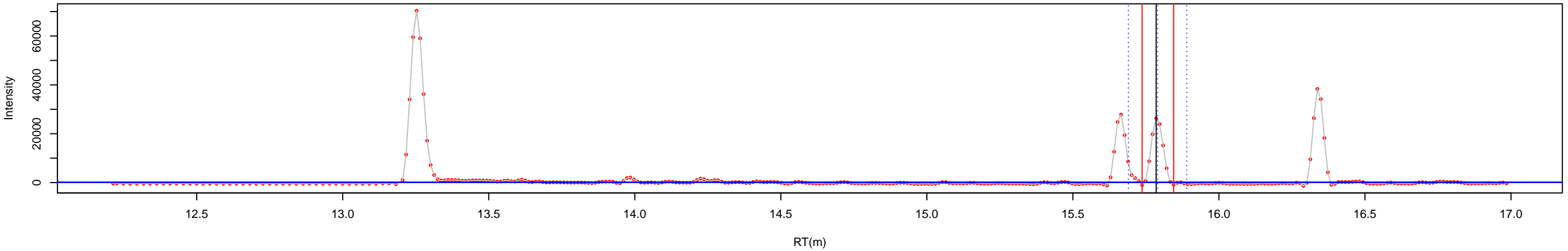
peak area | window size:3 BLine: yes



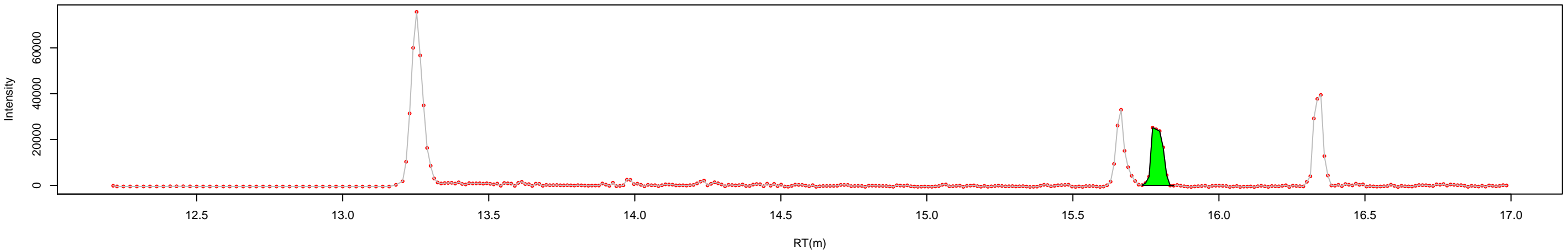
raw chromatogram | batch: 4   sample: std7-10ul-4   conc: 0.2   function: 1   mass: 375.35>375.35



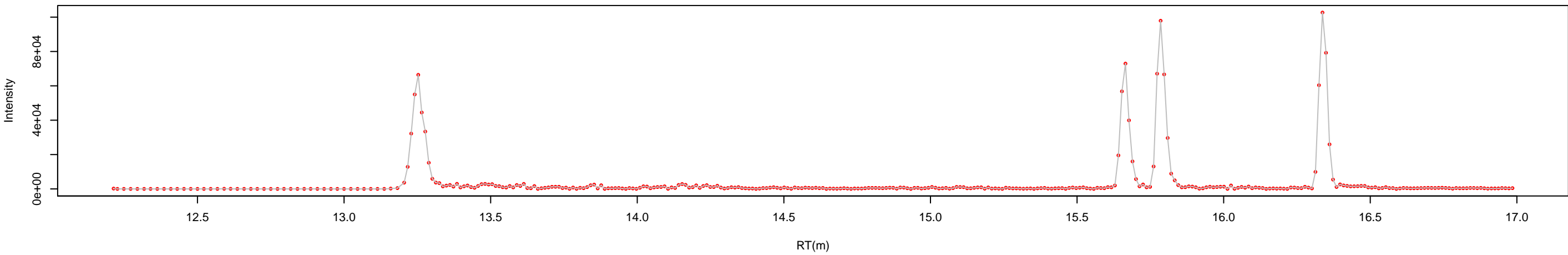
peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 21.8   BLine: yes



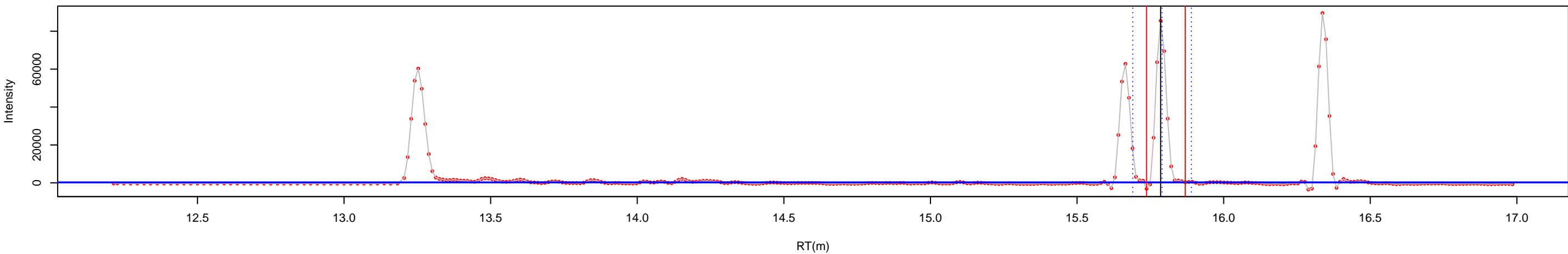
peak area | window size:3   BLine: yes



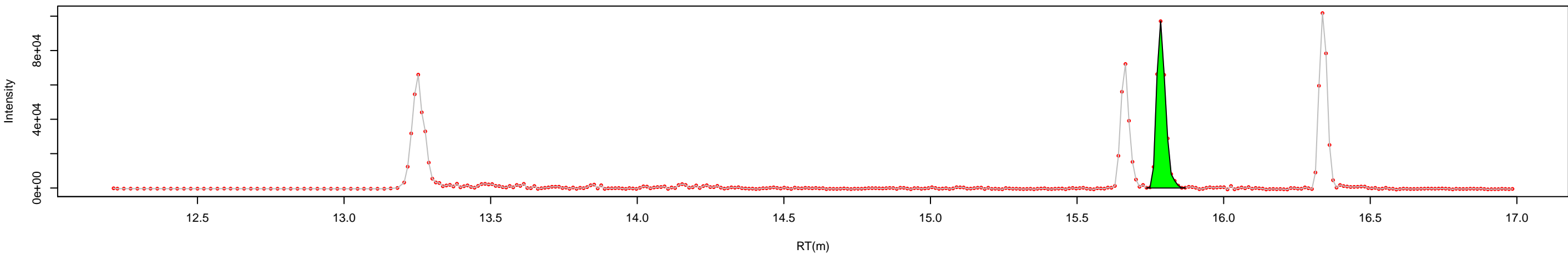
raw chromatogram | batch: 4 sample: std8-10ul-4 conc: 0.5 function: 1 mass: 375.35>375.35



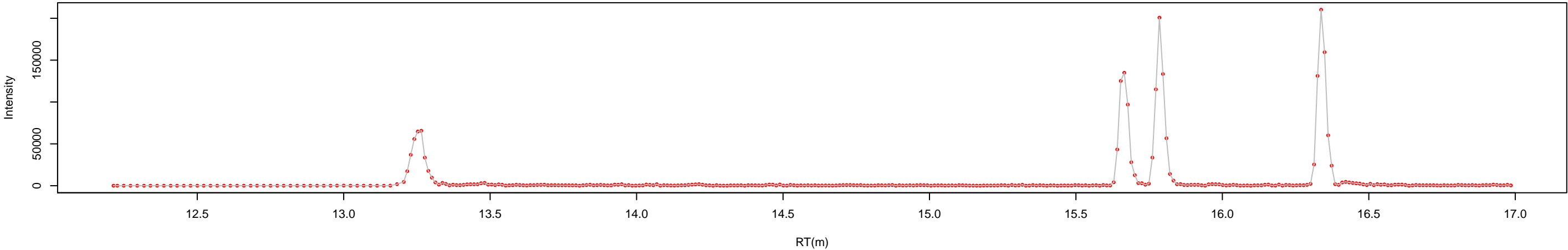
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 45.2 BLine: yes



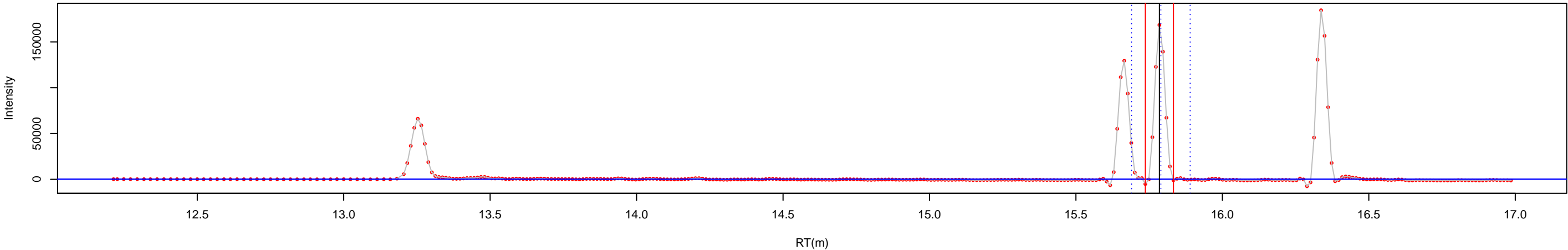
peak area | window size:3 BLine: yes



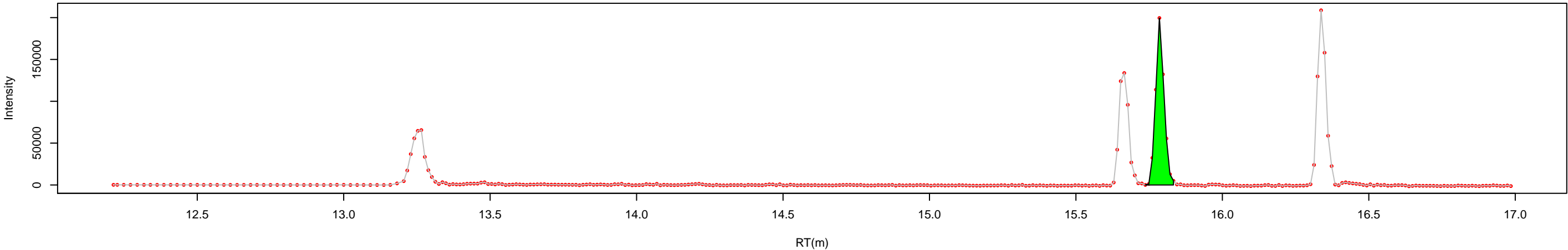
raw chromatogram | batch: 4   sample: std9-10ul-4   conc: 1   function: 1   mass: 375.35>375.35



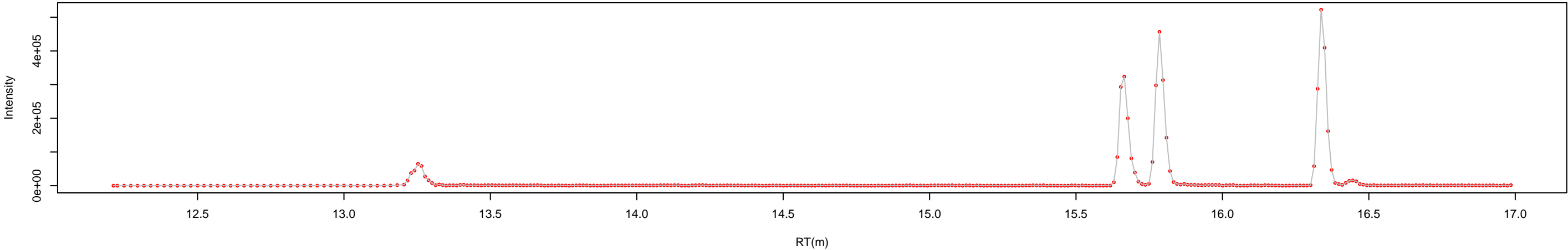
peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 27.4   BLine: yes



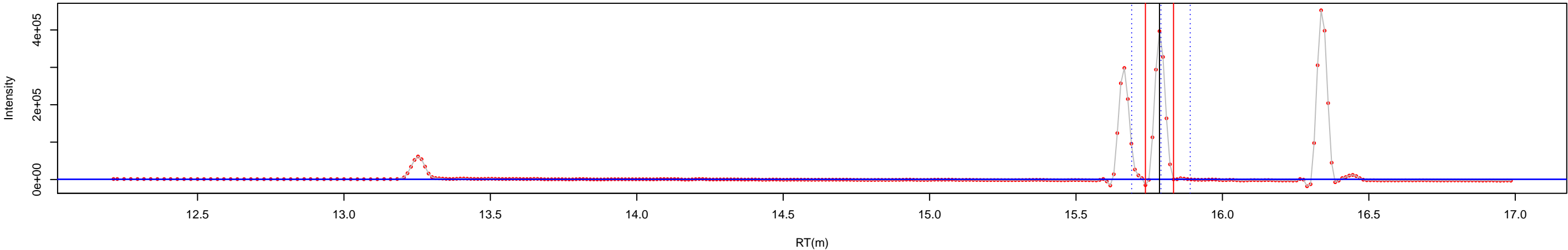
peak area | window size:3   BLine: yes



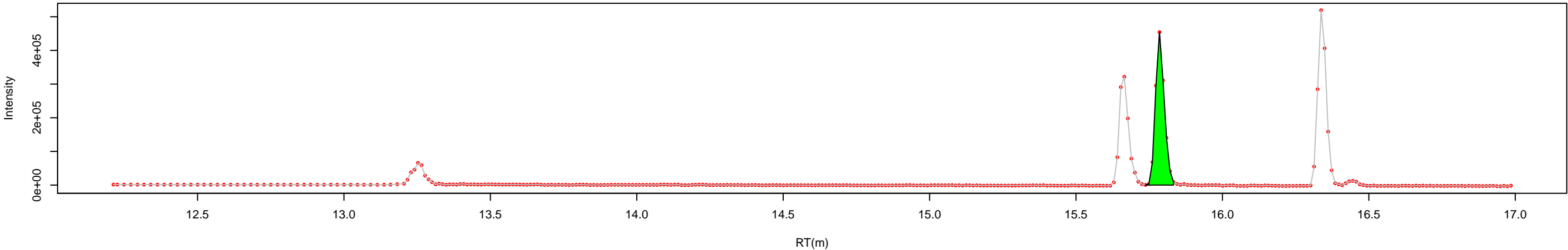
raw chromatogram | batch: 4   sample: std10-10ul-4   conc: 2   function: 1   mass: 375.35>375.35



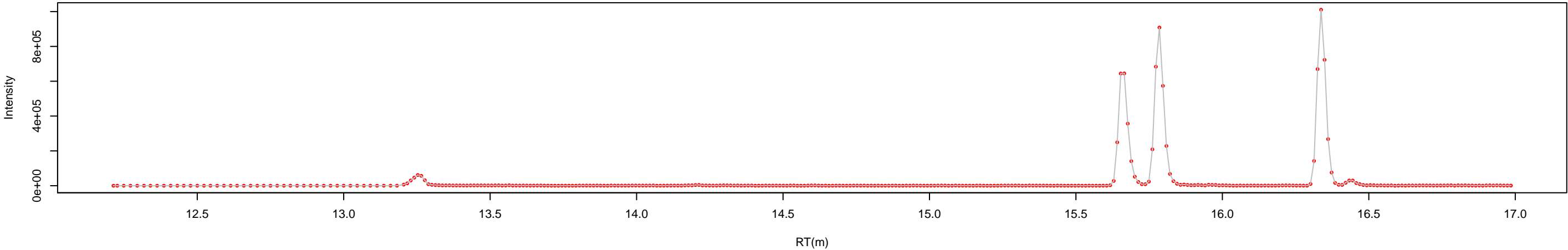
peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 117   BLine: yes



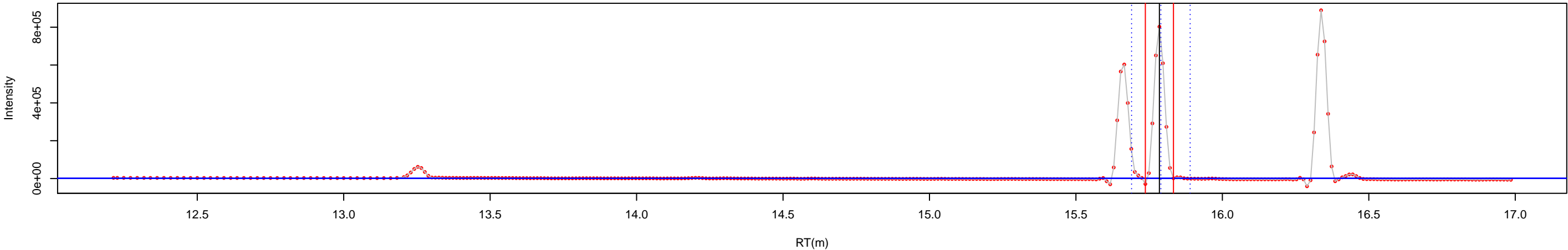
peak area | window size:3   BLine: yes



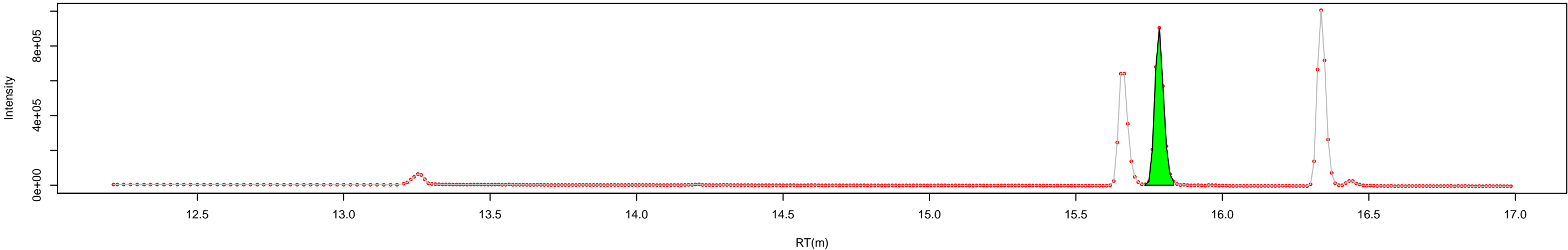
raw chromatogram | batch: 4   sample: std11-10ul-4   conc: 5   function: 1   mass: 375.35>375.35



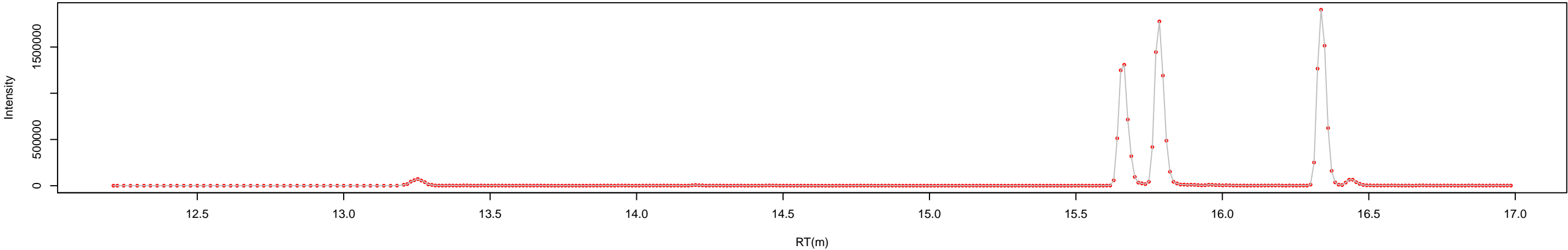
peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 253   BLine: yes



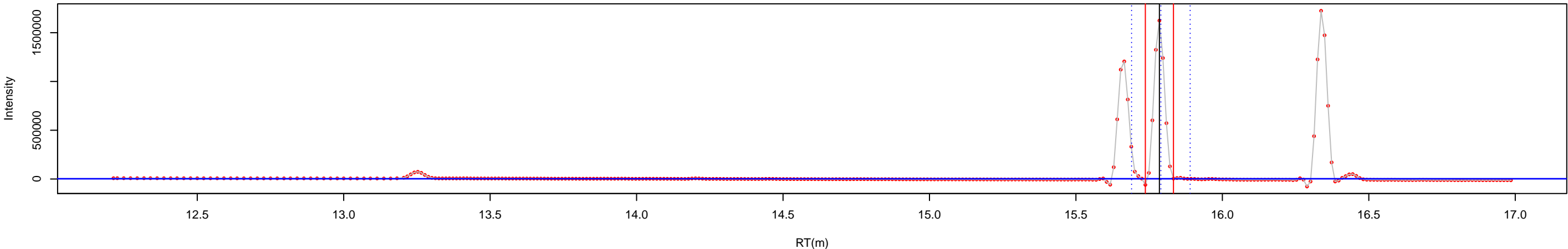
peak area | window size:3   BLine: yes



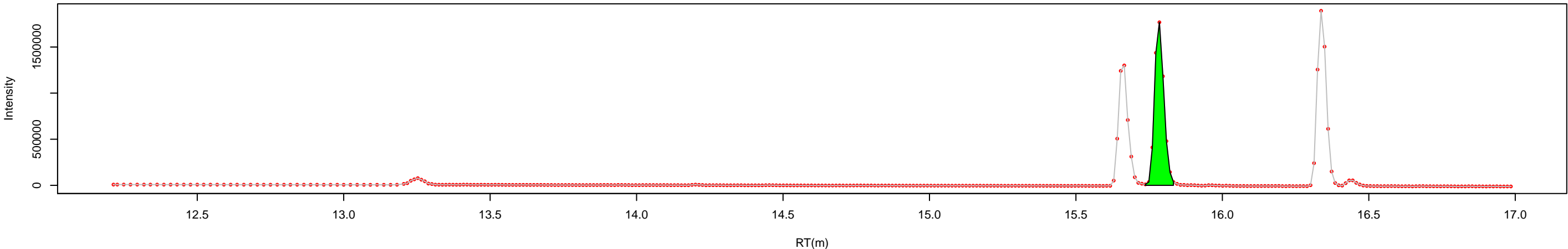
raw chromatogram | batch: 4   sample: std12-10ul-4   conc: 10   function: 1   mass: 375.35>375.35



peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 479   BLine: yes

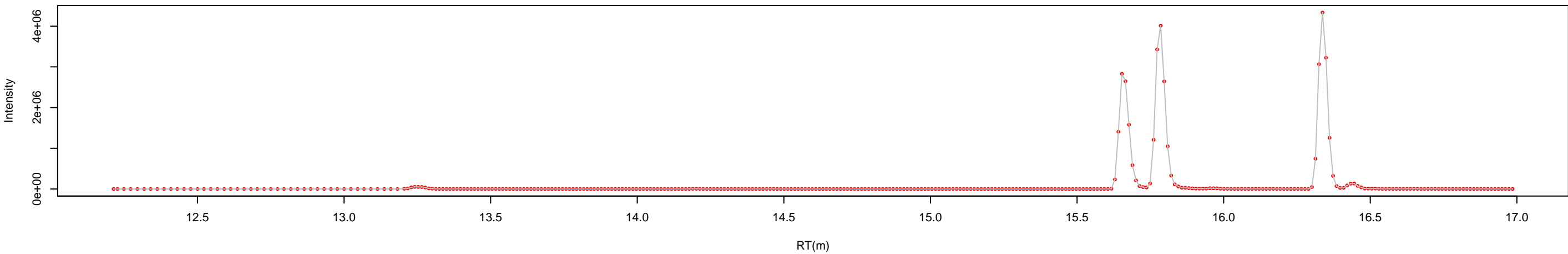


peak area | window size:3   BLine: yes

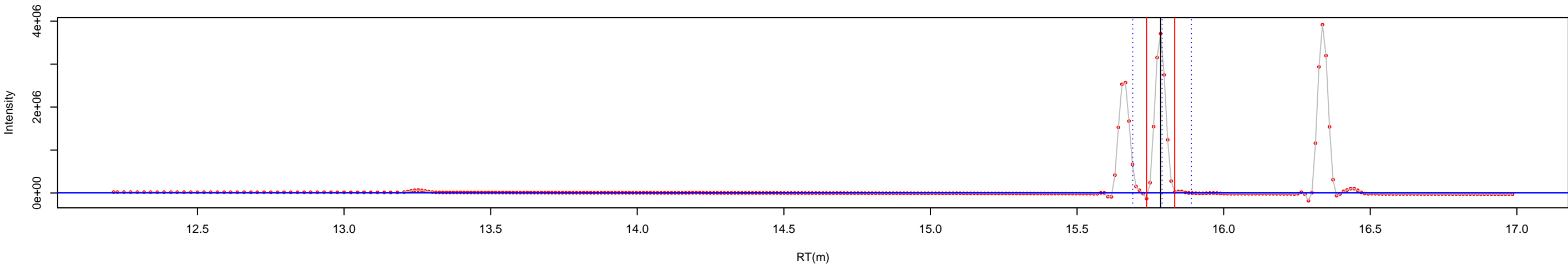




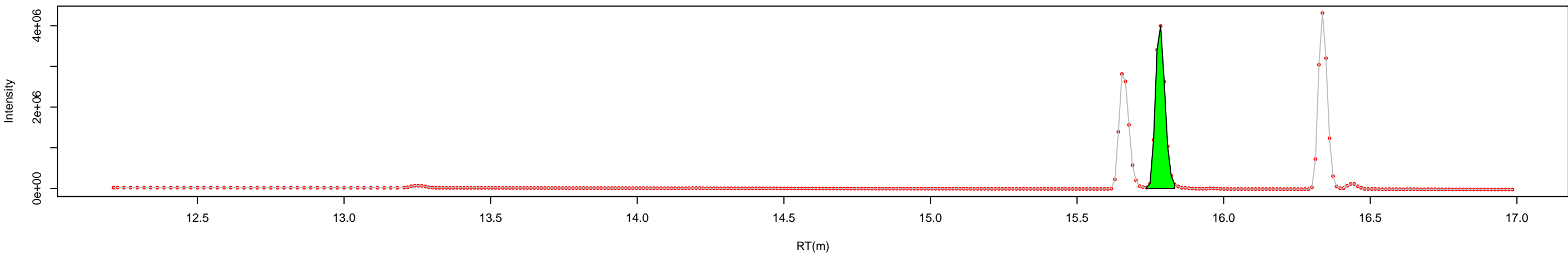
raw chromatogram | batch: 4 sample: std13-10ul-4 conc: 20 function: 1 mass: 375.35>375.35



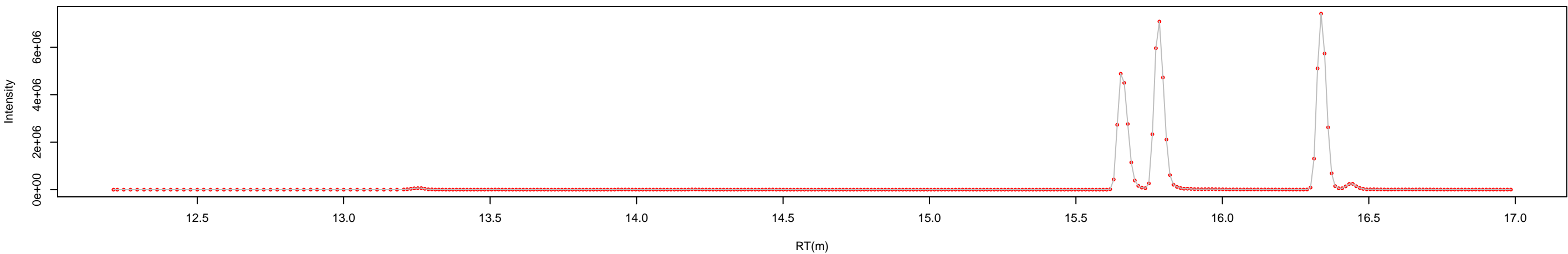
peak picking | window size: 7 iteration: 5 lp: 1 rp: 1 snr: 10 peak location: Nearest noise: 1170 BLine: yes



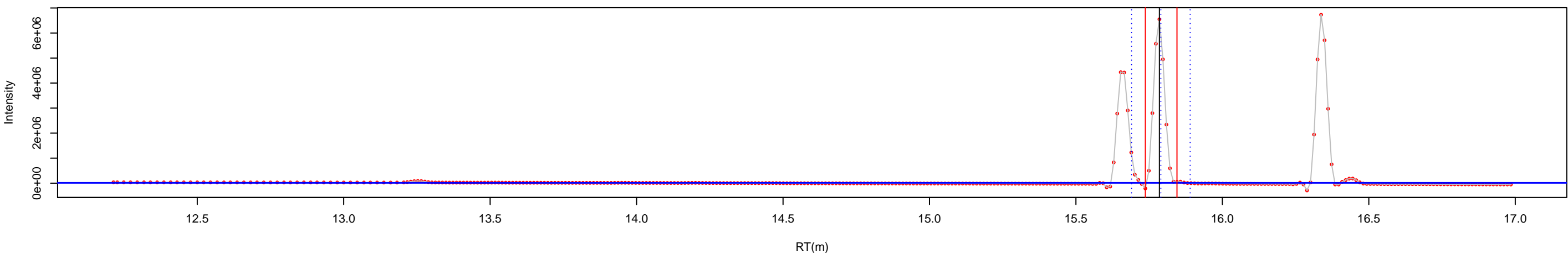
peak area | window size:3 BLine: yes



raw chromatogram | batch: 4   sample: std14-10ul-4   conc: 50   function: 1   mass: 375.35>375.35



peak picking | window size: 7   iteration: 5   lp: 1   rp: 1   snr: 10   peak location: Nearest   noise: 2200   BLine: yes



peak area | window size:3   BLine: yes

