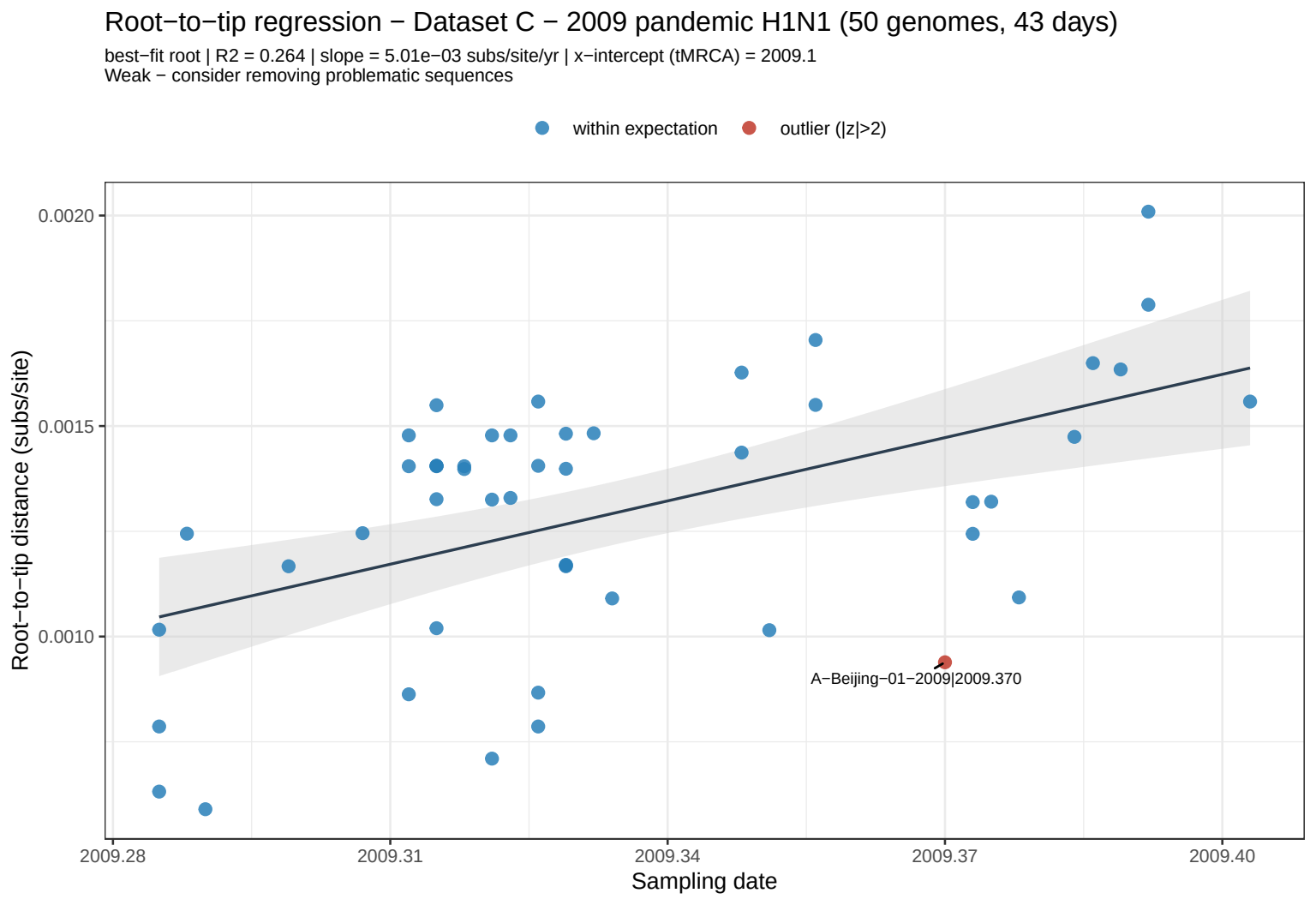

Root−to−tip regression − Dataset C − 2009 pandemic H1N1 (50 genomes, 43 days)
best−fit root | R2 = 0.264 | slope = 5.01e−03 subs/site/yr | x−intercept (tMRCA) = 2009.1
Weak − consider removing problematic sequences
within expectation
outlier (|z|>2)
Root−to−tip distance (subs/site)
0.0020
0.0015
0.0010
A−Beijing−01−2009|2009.370
2009.28
2009.31
2009.34
2009.37
2009.40
Sampling date