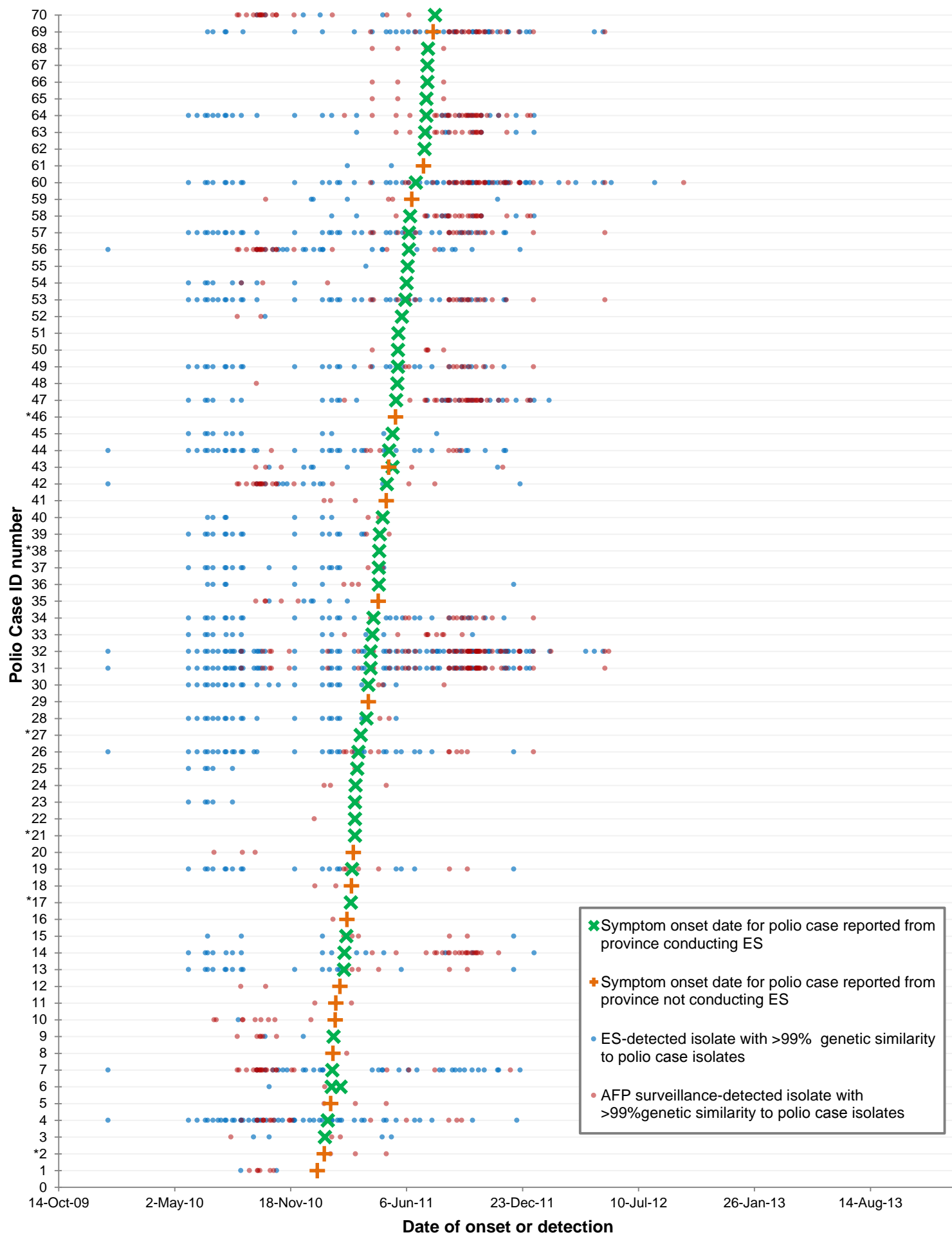
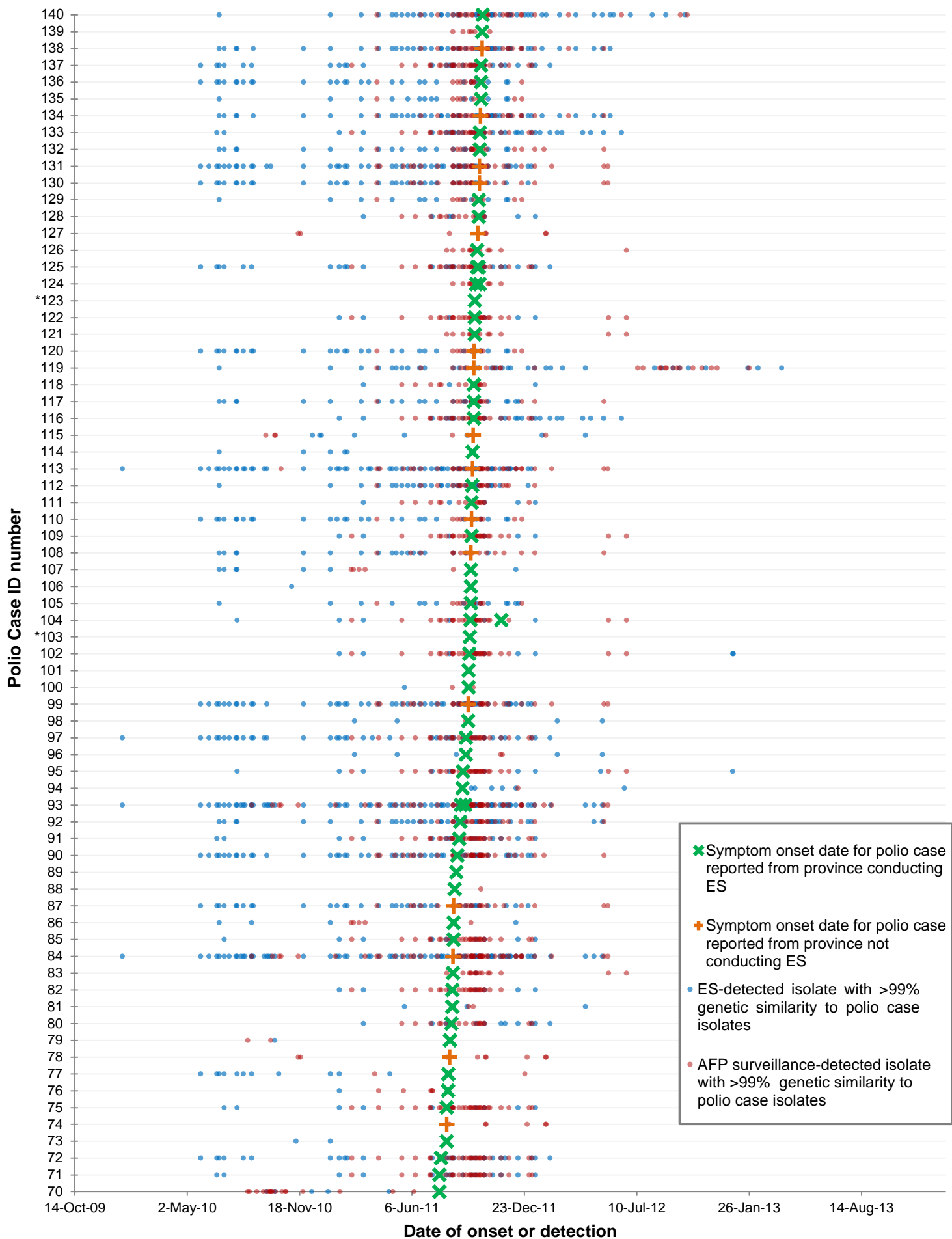


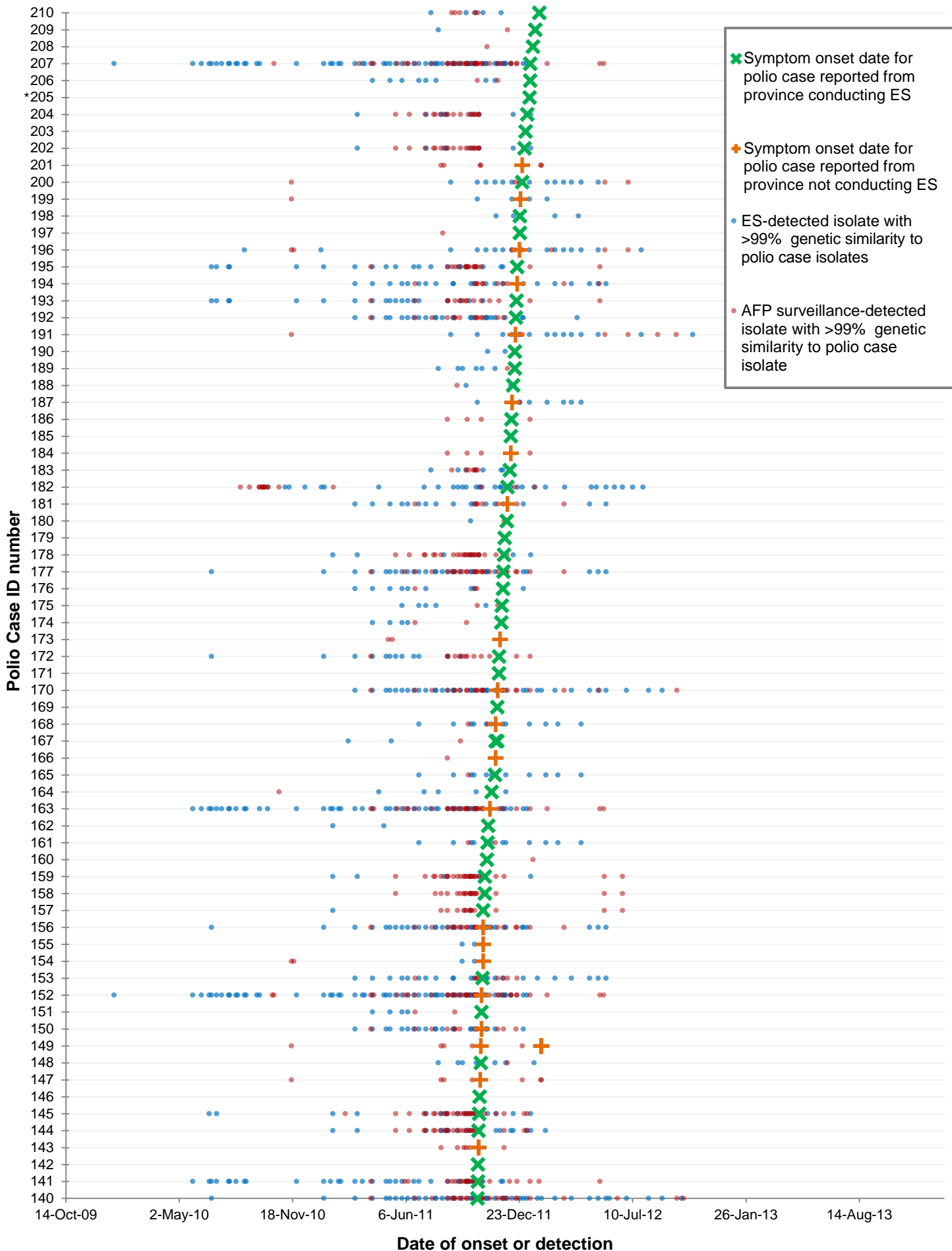
**S3 Fig (Part 1 of 5). Circulation detected by AFP surveillance and Environmental Surveillance for Pakistan polio cases with unique genetic sequences (n=346).** Further descriptions of figure component definitions and calculated measures shown in Tables 4-6 are shown in S2 Fig. Sequence IDs marked with \* are also orphan viruses (no preceding virus detected within 1.5% identity). A phylogenetic tree for a subset of ES and AFP isolates can be found in Figure 3, Alam MM et Al, J Infect Dis, 2014.



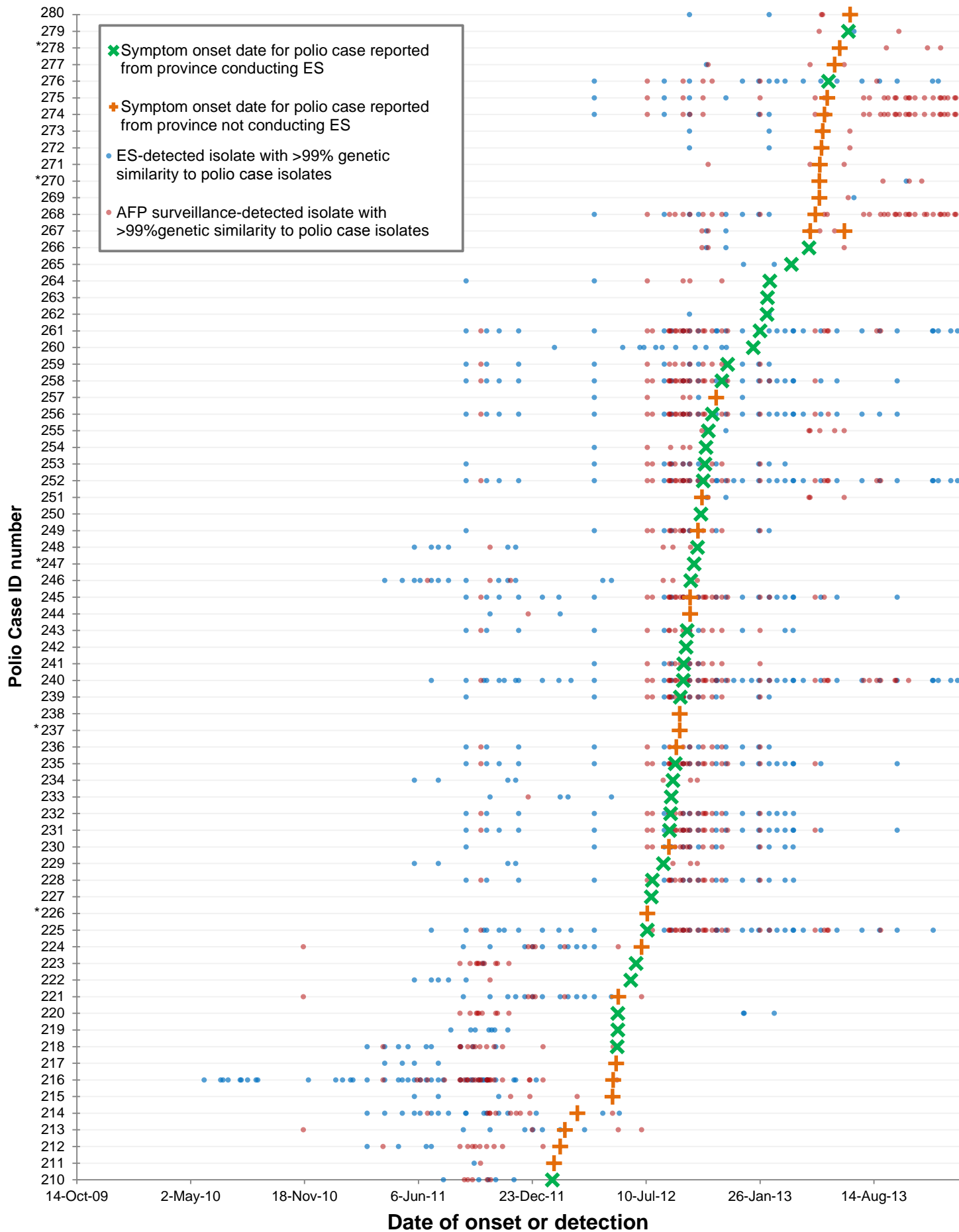
**S3 Fig (Part 2 of 5). Circulation detected by AFP surveillance and Environmental Surveillance for Pakistan polio cases with unique genetic sequences (n=346).** Further descriptions of figure component definitions and calculated measures shown in Tables 4-6 are shown in S2 Fig. Sequence IDs marked with \* are also orphan viruses (no preceding virus detected within 1.5% identity). A phylogenetic tree for a subset of ES and AFP isolates can be found in Figure 3, Alam MM et Al, J Infect Dis, 2014.



**S3 Fig (Part 3 of 5). Circulation detected by AFP surveillance and Environmental Surveillance for Pakistan polio cases with unique genetic sequences (n=346).** Further descriptions of figure component definitions and calculated measures shown in Tables 4-6 are shown in S2 Fig. Sequence IDs marked with \* are also orphan viruses (no preceding virus detected within 1.5% identity). A phylogenetic tree for a subset of ES and AFP isolates can be found in Figure 3, Alam MM et Al, J Infect Dis, 2014.



**S4 Fig (Part 4 of 5). Circulation detected by AFP surveillance and Environmental Surveillance for Pakistan polio cases with unique genetic sequences (n=346).** Further descriptions of figure component definitions and calculated measures shown in Tables 4-6 are shown in S2 Fig. Sequence IDs marked with \* are also orphan viruses (no preceding virus detected within 1.5% identity). A phylogenetic tree for a subset of ES and AFP isolates can be found in Figure 3, Alam MM et al, J Infect Dis, 2014.



**S4 Fig (Part 5 of 5). Circulation detected by AFP surveillance and Environmental Surveillance for Pakistan polio cases with unique genetic sequences (n=346).** Further descriptions of figure component definitions and calculated measures shown in Tables 4-6 are shown in S2 Fig. Sequence IDs marked with \* are also orphan viruses (no preceding virus detected within 1.5% identity). A phylogenetic tree for a subset of ES and AFP isolates can be found in Figure 3, Alam MM et Al, J Infect Dis, 2014.

