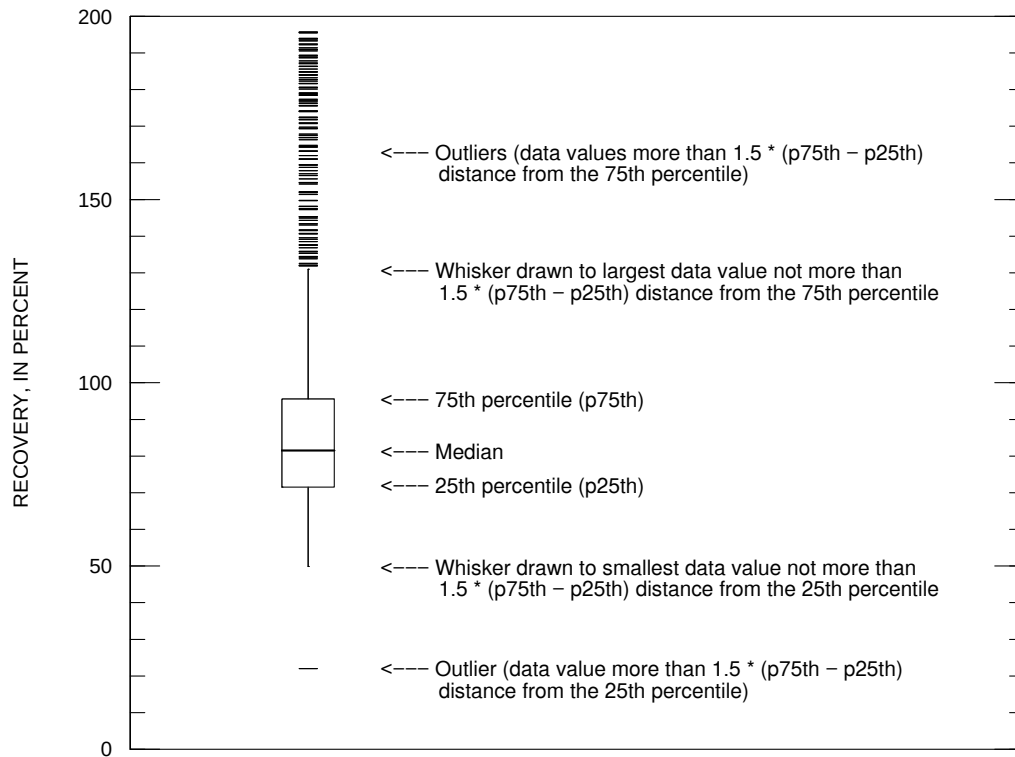
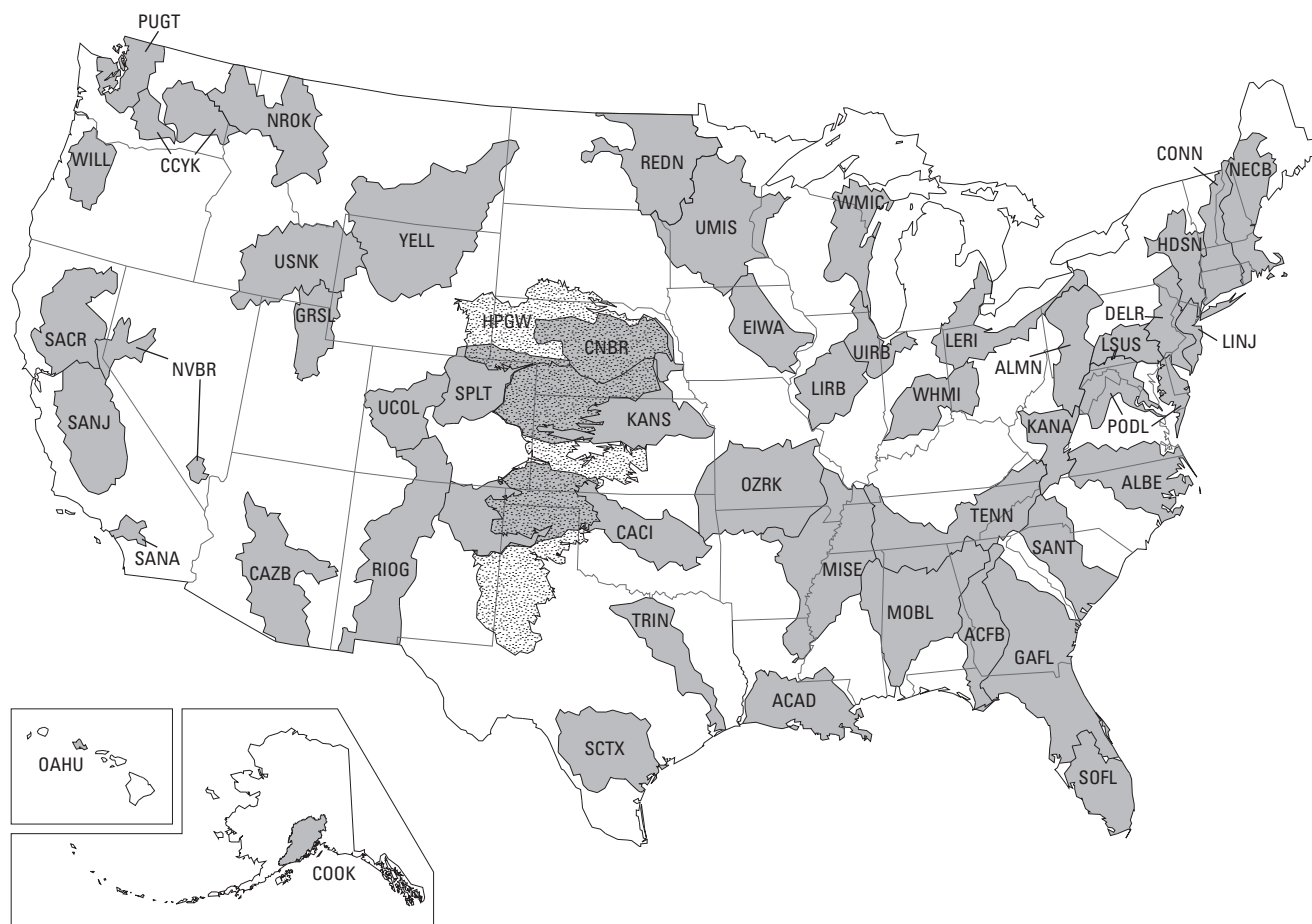


## Appendix 6. Distribution of residual errors in models of recovery by NAWQA Study Unit.



**Explanation of boxplots used to depict distributions of recovery.** Outliers are not shown in this appendix. In some figures, the number of measurements is shown at the top or bottom of the boxplot.



### Study Units

|      |                                                 |      |                                                               |
|------|-------------------------------------------------|------|---------------------------------------------------------------|
| ACAD | Acadian-Pontchartrain Drainages                 | NROK | Northern Rockies Intermontane Basins                          |
| ACFB | Apalachicola-Chattahoochee-Flint River Basin    | NVBR | Las Vegas Valley Area and the Carson and Truckee River Basins |
| ALBE | Albemarle-Pamlico Drainage Basin                | OAHU | Island of Oahu                                                |
| ALMN | Allegheny and Monongahela River Basins          | OZRK | Ozark Plateaus                                                |
| CACI | Canadian-Cimarron River Basins                  | PODL | Potomac River Basin and Delmarva Peninsula                    |
| CAZB | Central Arizona Basins                          | PUGT | Puget Sound Basin                                             |
| CCYK | Central Columbia Plateau - Yakima River Basin   | REDN | Red River of the North Basin                                  |
| CNBR | Central Nebraska Basins                         | RIOG | Rio Grande Valley                                             |
| CONN | Connecticut, Housatonic and Thames River Basins | SACR | Sacramento River Basin                                        |
| COOK | Cook Inlet Basin                                | SANA | Santa Ana Basin                                               |
| DELR | Delaware River Basin                            | SANJ | San Joaquin-Tulare Basins                                     |
| EIWA | Eastern Iowa Basins                             | SANT | Santee River Basin and Coastal Drainages                      |
| GAFL | Georgia-Florida Coastal Plain                   | SCTX | South-Central Texas                                           |
| GRSL | Great Salt Lake Basins                          | SOFL | Southern Florida                                              |
| HDSN | Hudson River Basin                              | SPLT | South Platte River Basin                                      |
| HPGW | High Plains Regional Ground Water Study         | TENN | Tennessee River Basin                                         |
| KANA | Kanawha - New River Basins                      | TRIN | Trinity River Basin                                           |
| KANS | Kansas River Basin                              | UCOL | Upper Colorado River Basin                                    |
| LERI | Lake Erie - Lake Saint Clair Drainages          | UIRB | Upper Illinois River Basin                                    |
| LINJ | Long Island - New Jersey Coastal Drainages      | UMIS | Upper Mississippi River Basin                                 |
| LIRB | Lower Illinois River Basin                      | USNK | Upper Snake River Basin                                       |
| LSUS | Lower Susquehanna River Basin                   | WHMI | White, Great and Little Miami River Basins                    |
| MISE | Mississippi Embayment                           | WILL | Willamette Basin                                              |
| MOBL | Mobile River Basin                              | WMIC | Western Lake Michigan Drainages                               |
| NECB | New England Coastal Basins                      | YELL | Yellowstone River Basin                                       |

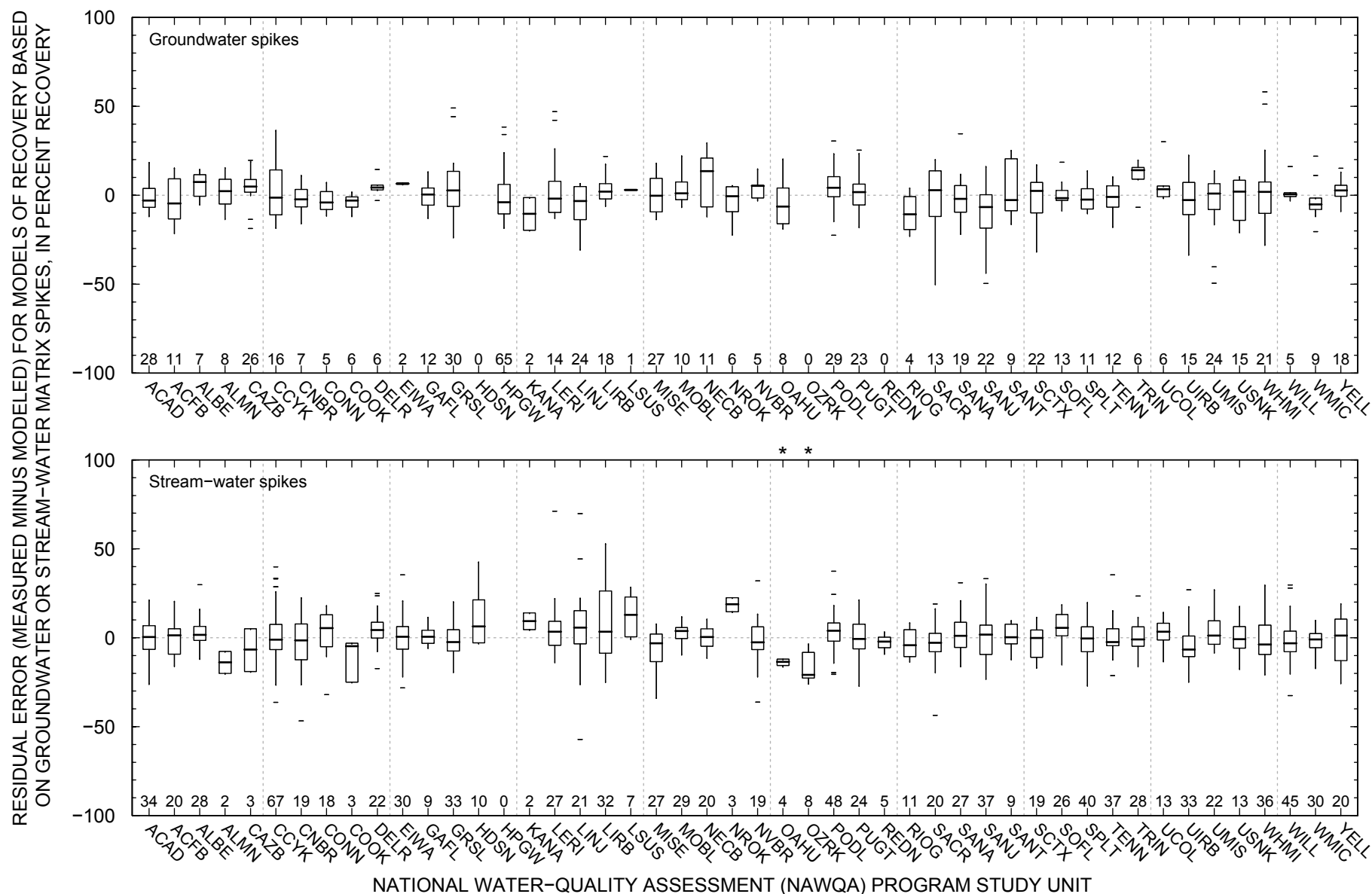


Figure A6-1. Distribution of residual errors in models of recovery of acetochlor by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

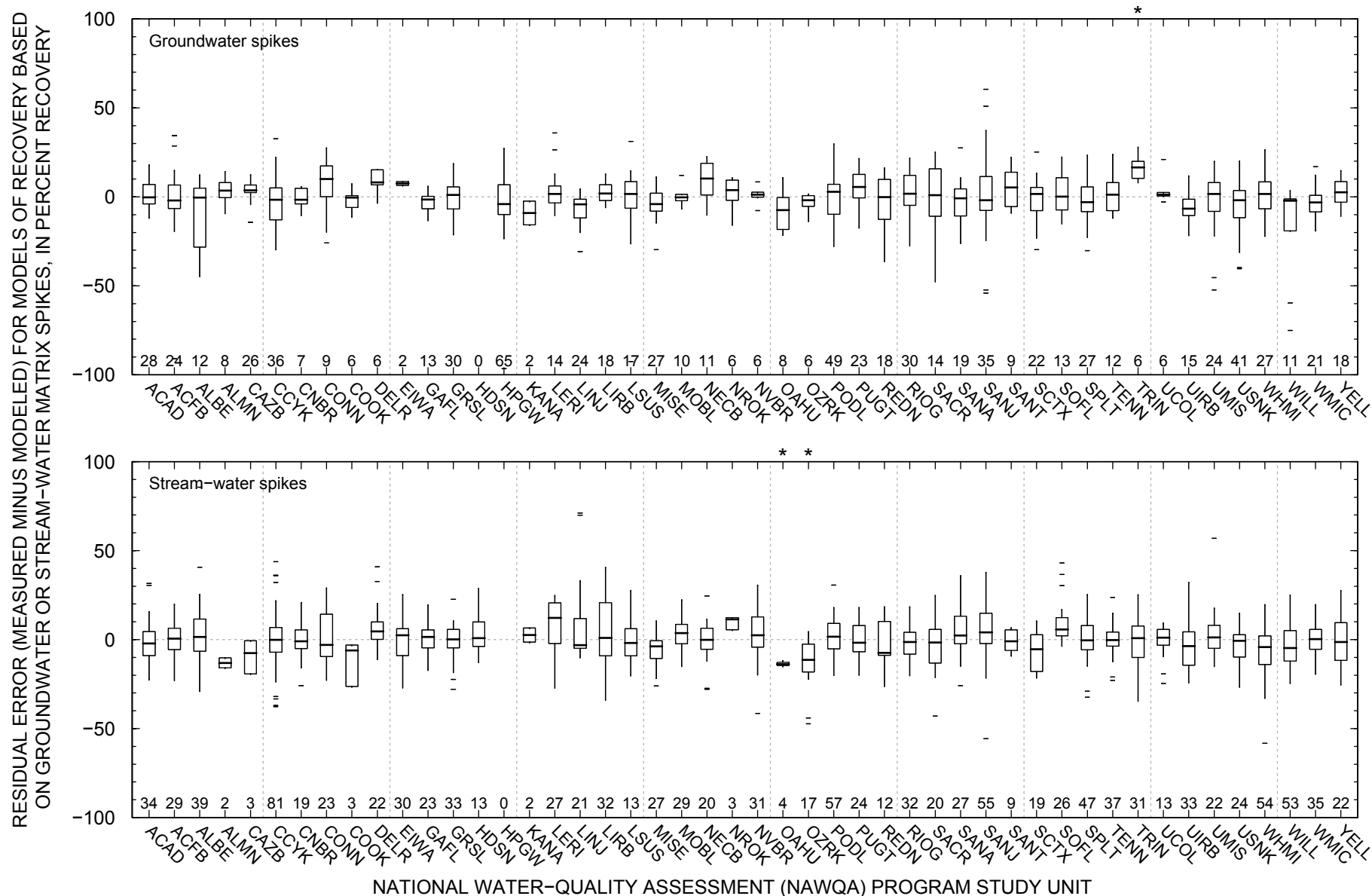


Figure A6-2. Distribution of residual errors in models of recovery of alachlor by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

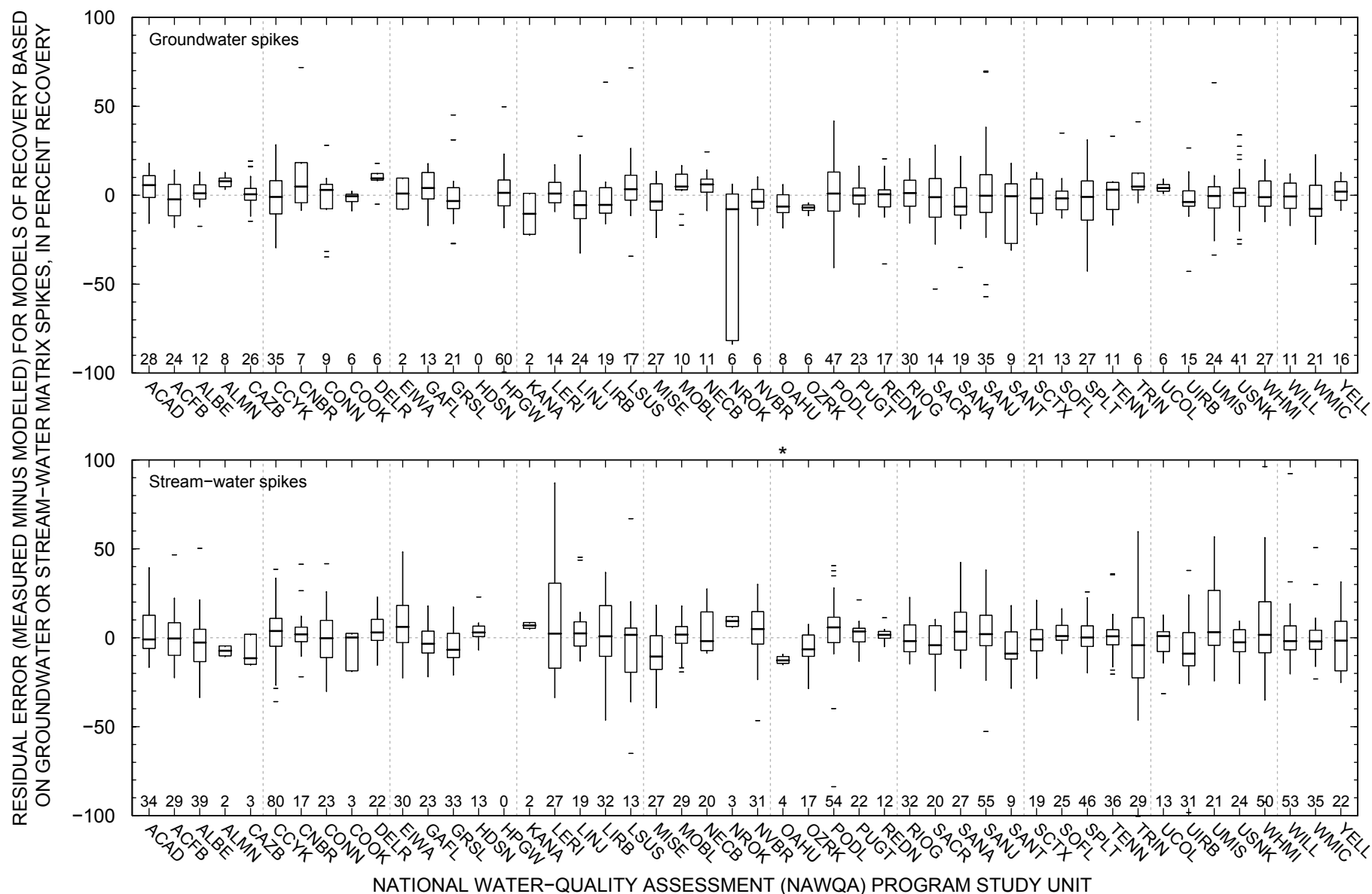


Figure A6-3. Distribution of residual errors in models of recovery of atrazine by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

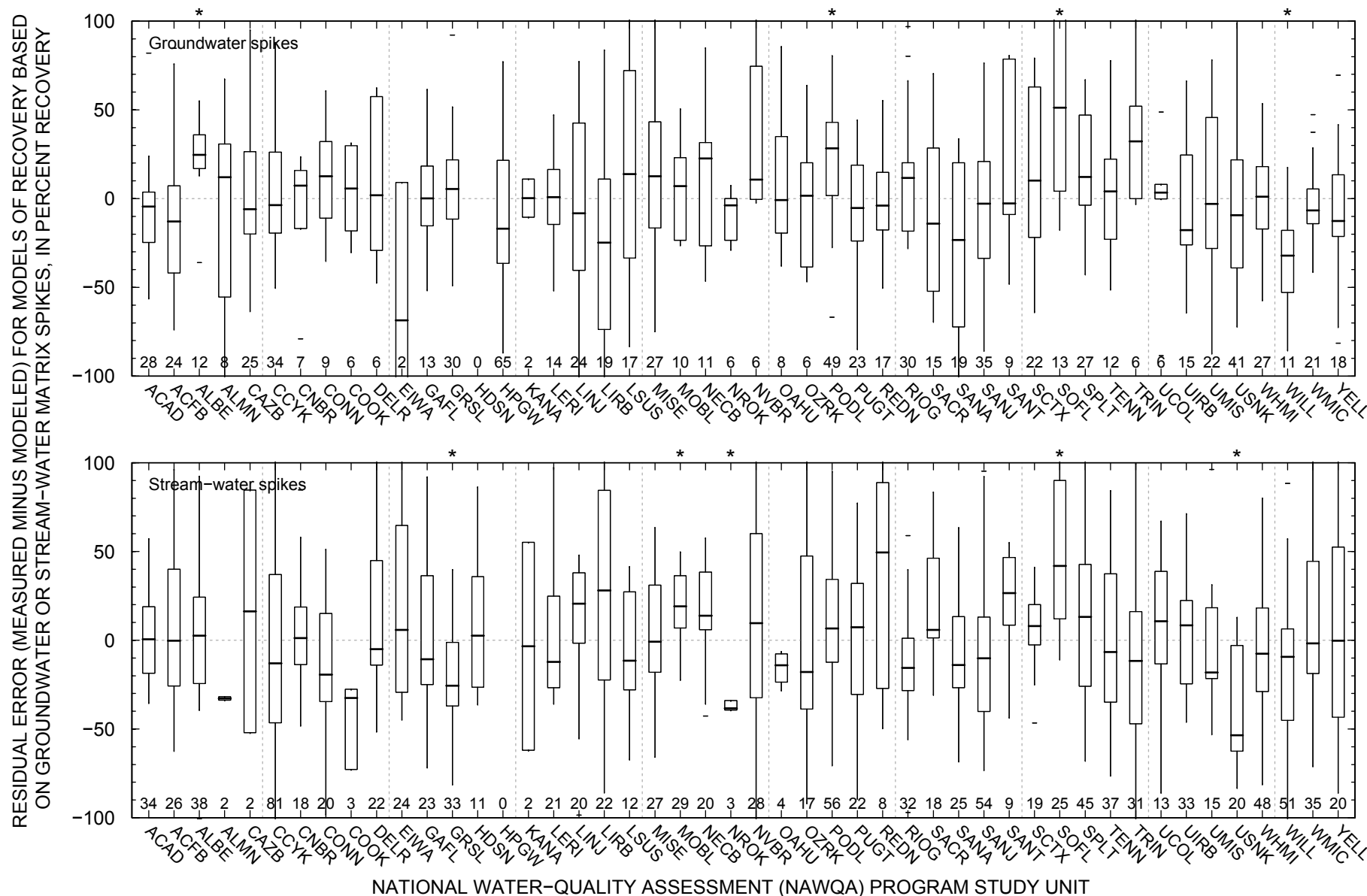


Figure A6-4. Distribution of residual errors in models of recovery of azinphos-methyl by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

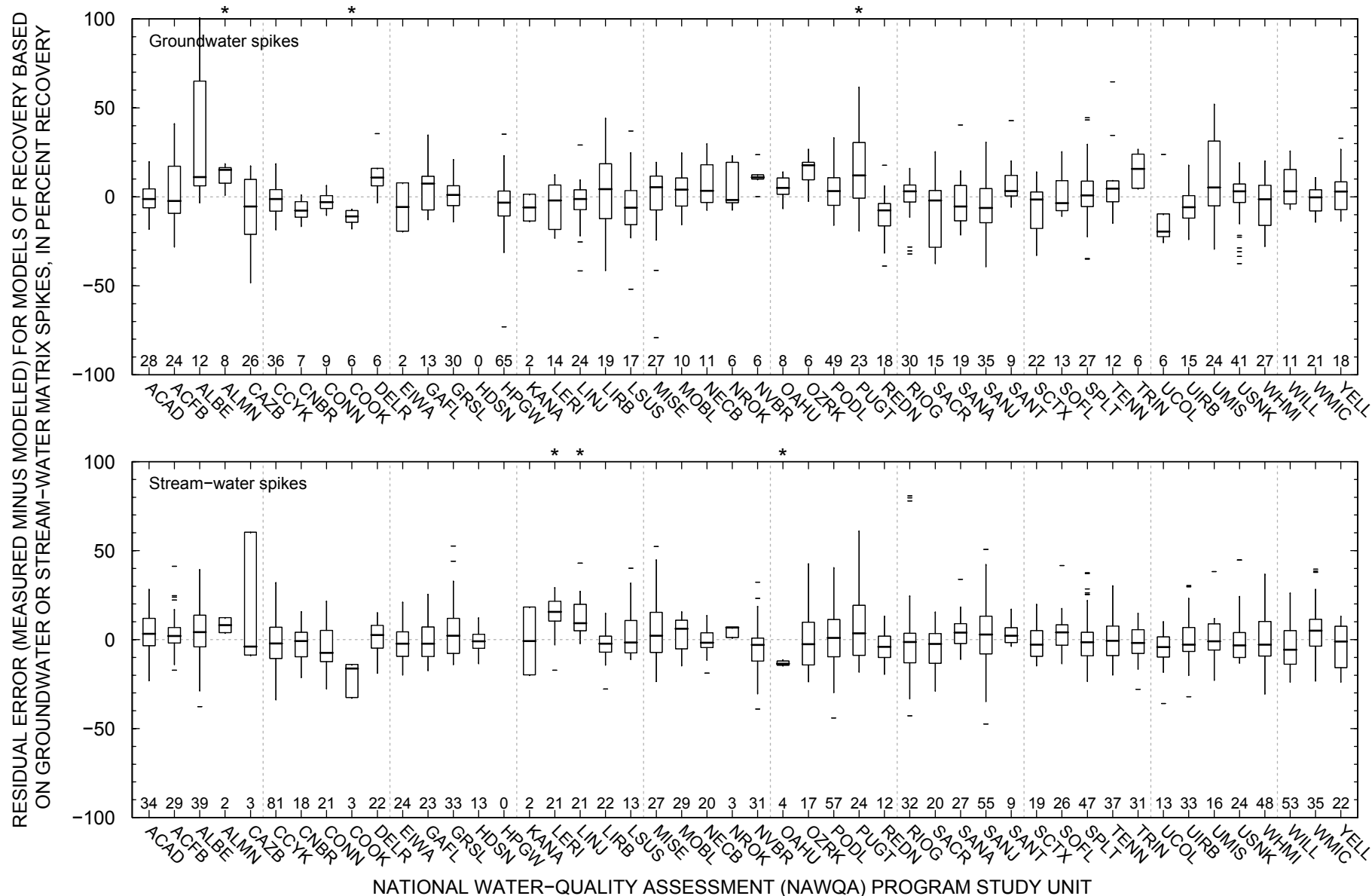


Figure A6-5. Distribution of residual errors in models of recovery of benfluralin by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

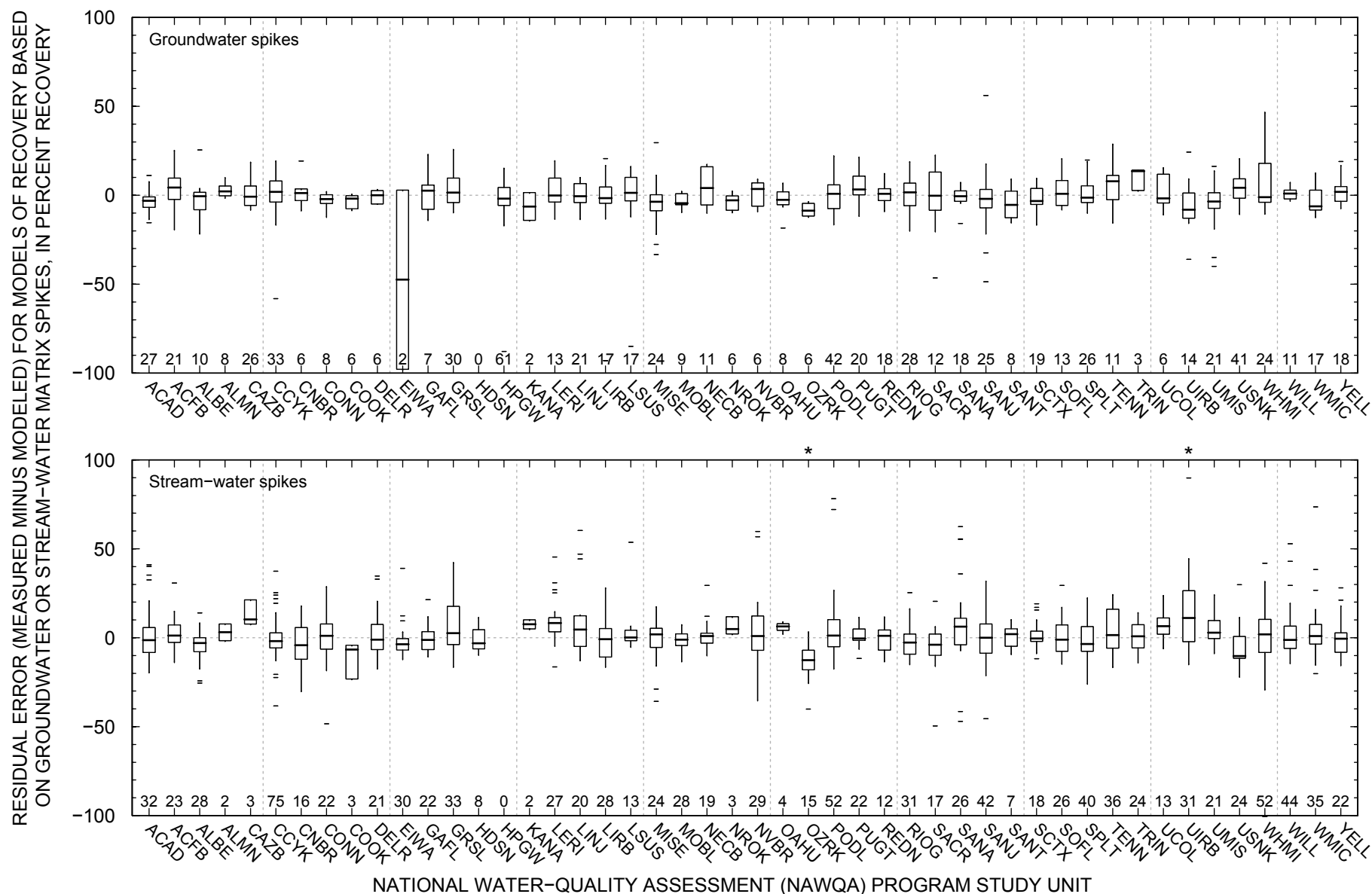


Figure A6-6. Distribution of residual errors in models of recovery of butylate by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).



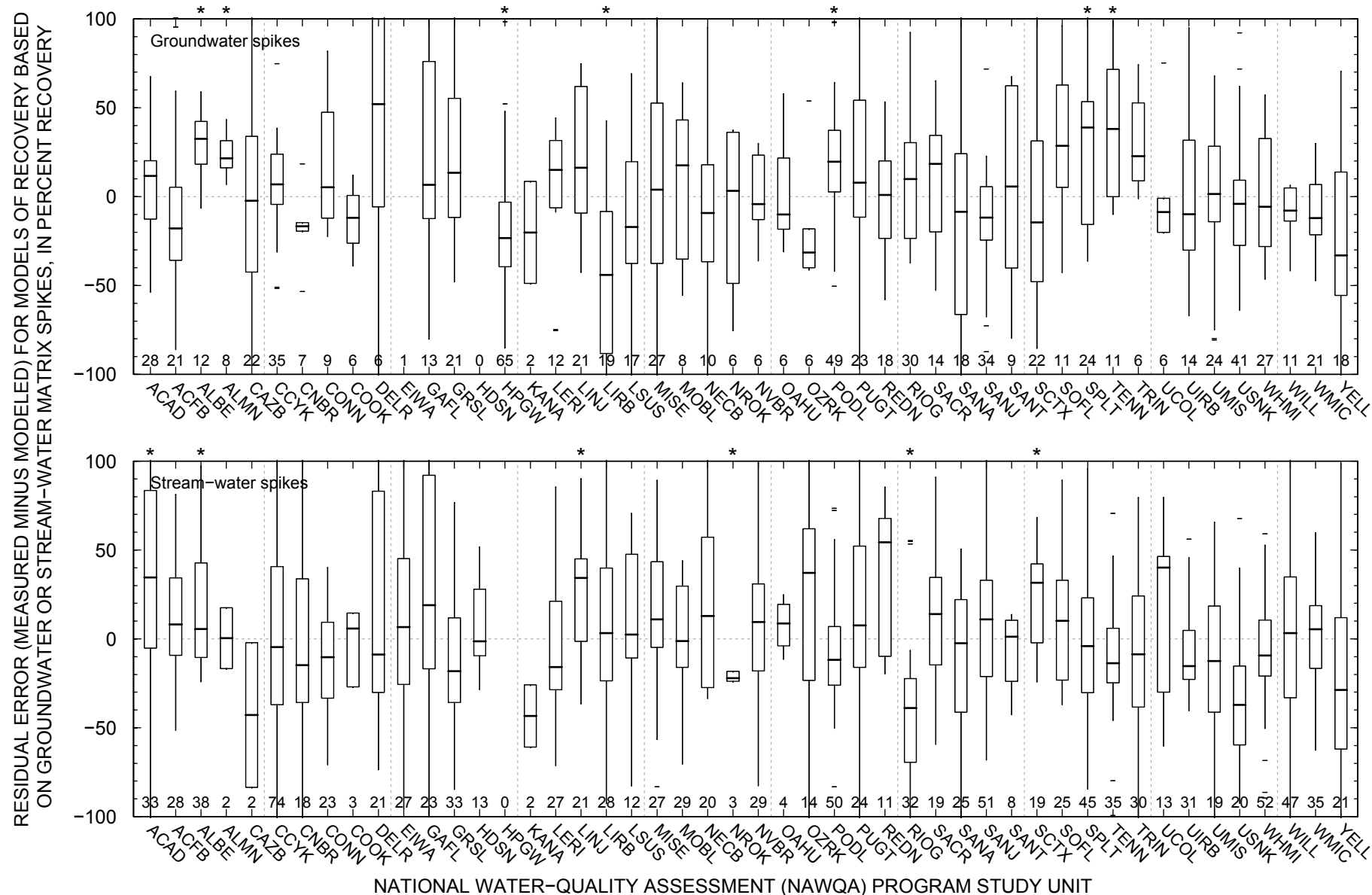


Figure A6-7. Distribution of residual errors in models of recovery of carbaryl by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

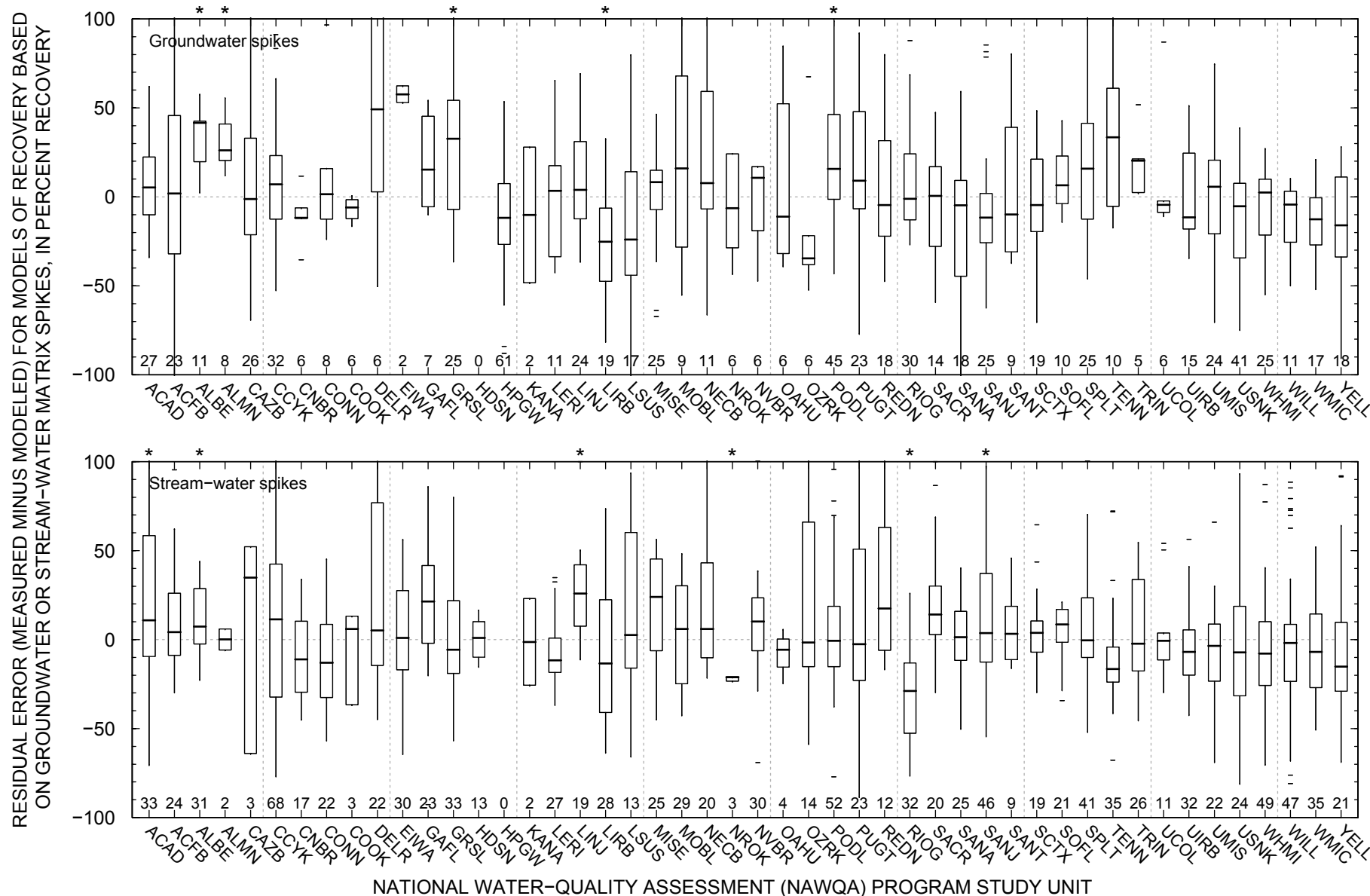


Figure A6-8. Distribution of residual errors in models of recovery of carbofuran by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

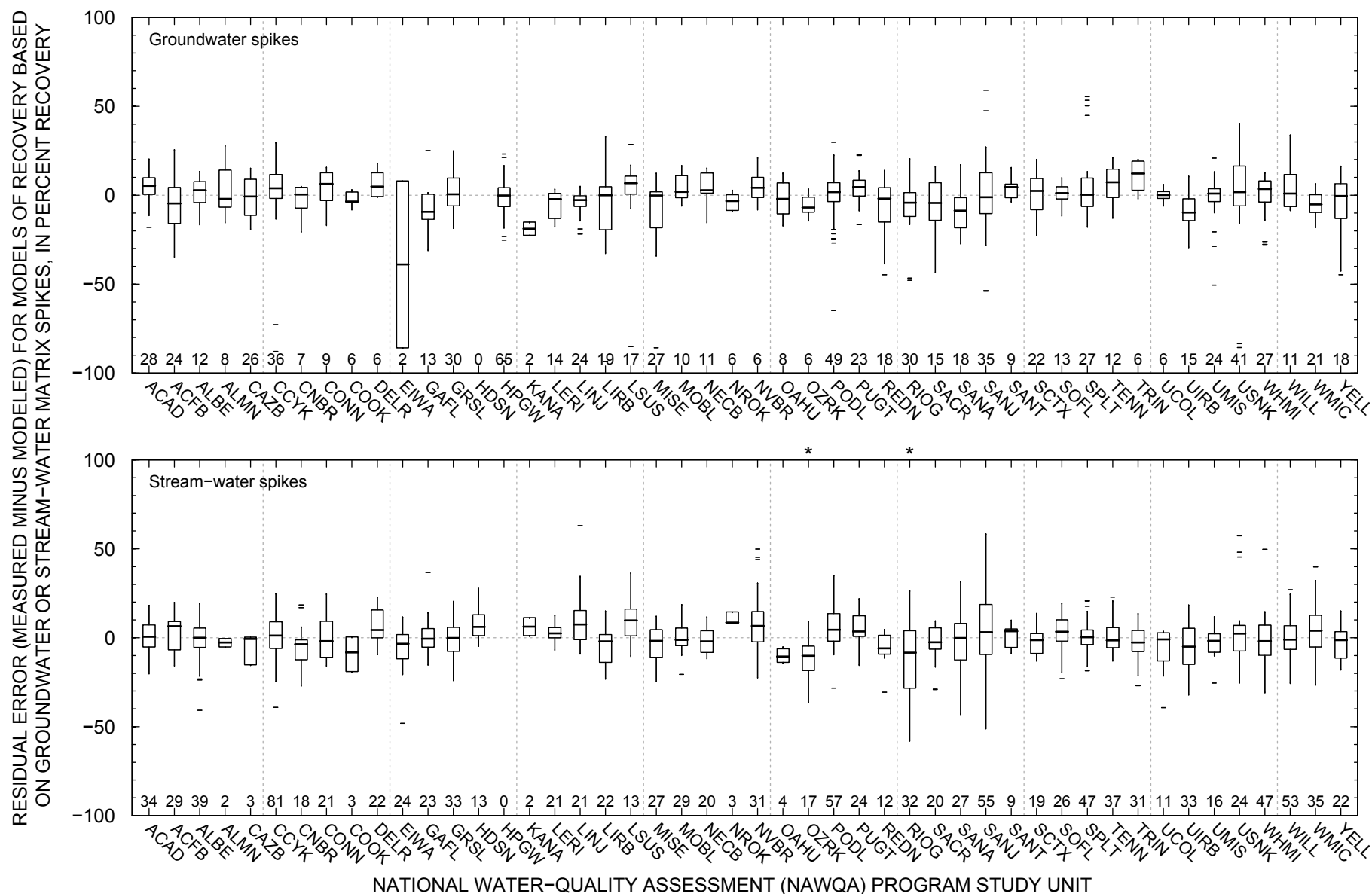


Figure A6-9. Distribution of residual errors in models of recovery of chlorpyrifos by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

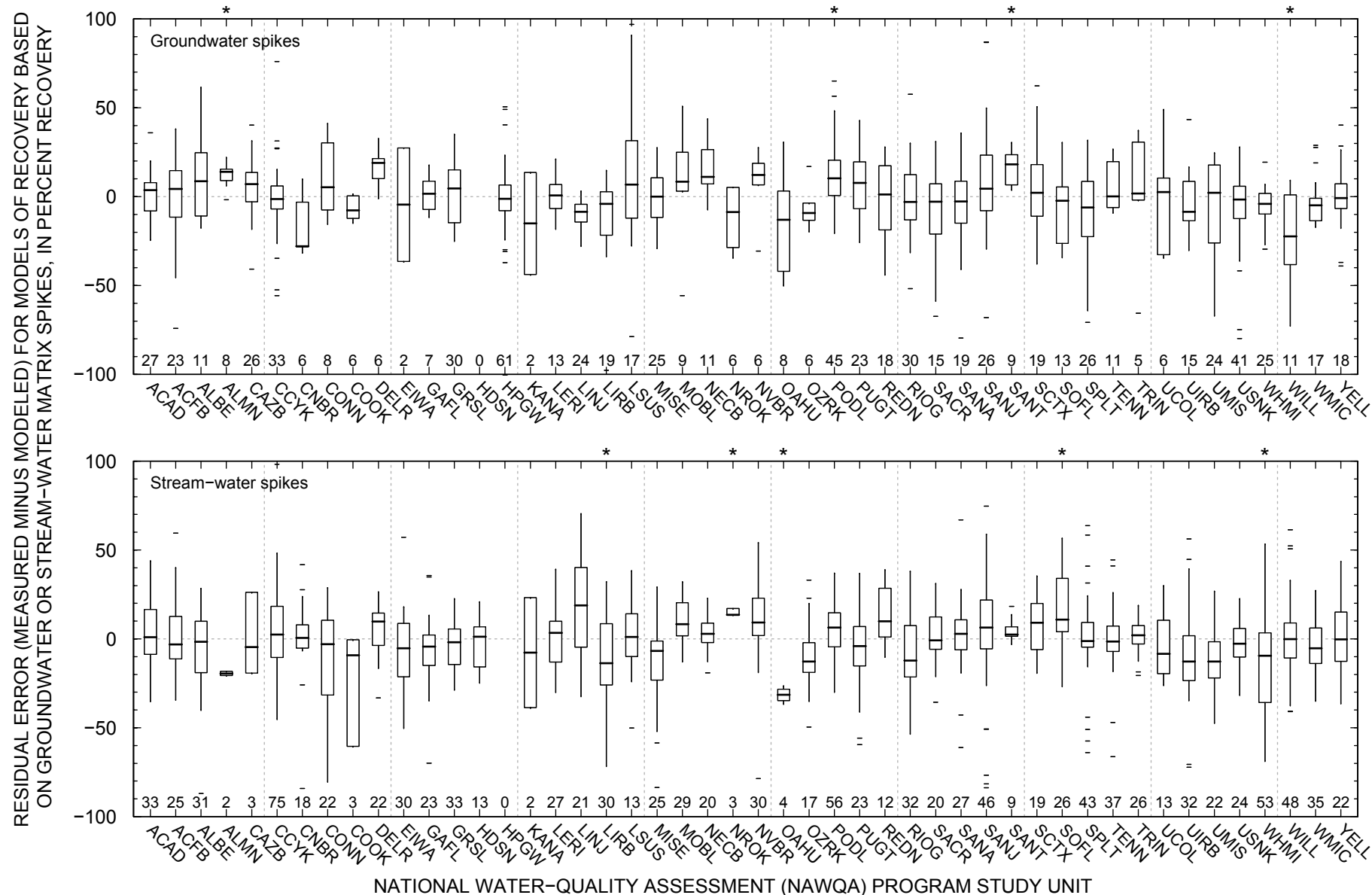


Figure A6-10. Distribution of residual errors in models of recovery of cyanazine by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

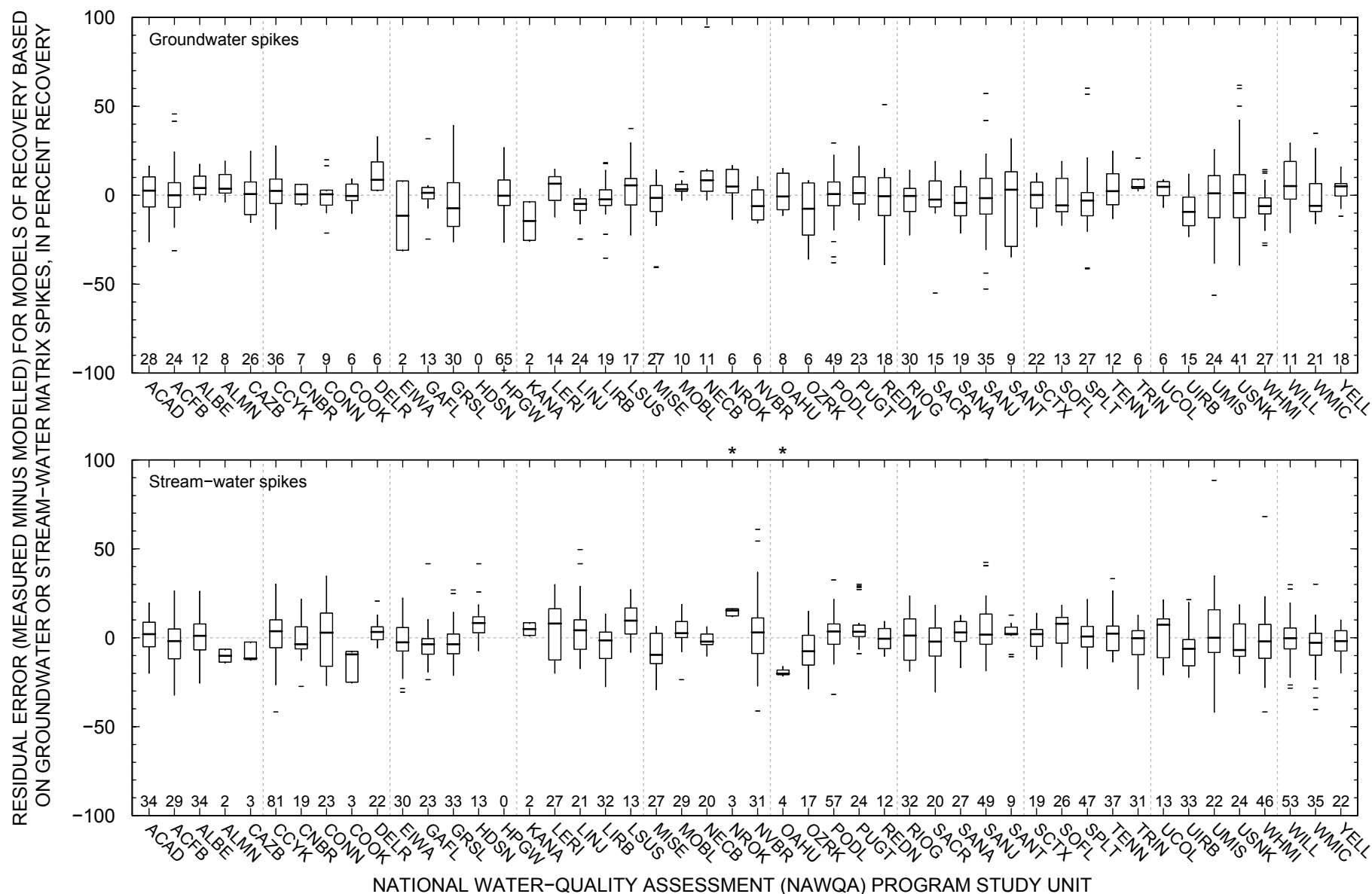


Figure A6-11. Distribution of residual errors in models of recovery of dachthal by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

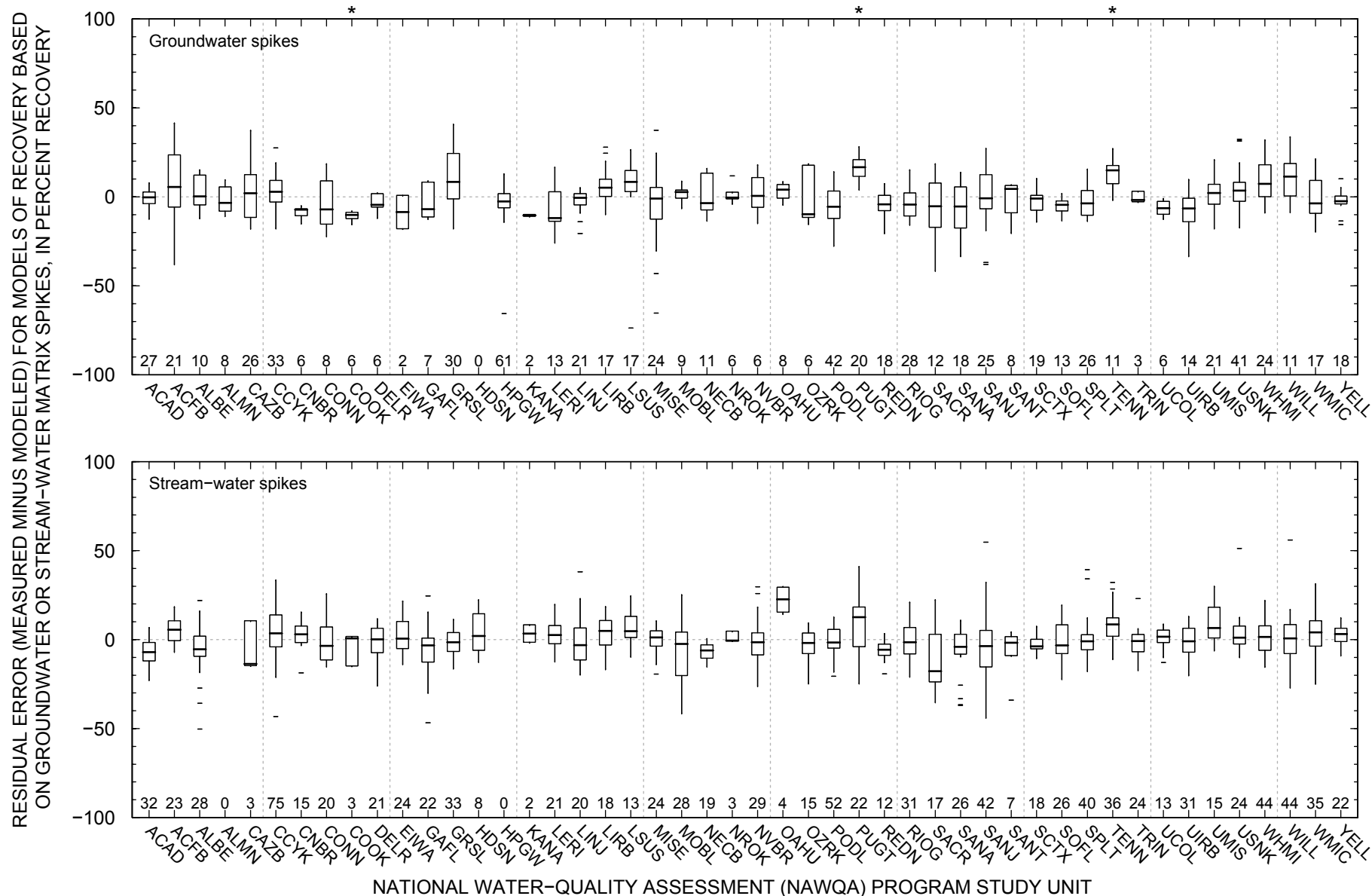


Figure A6-12. Distribution of residual errors in models of recovery of p,p'-DDE by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

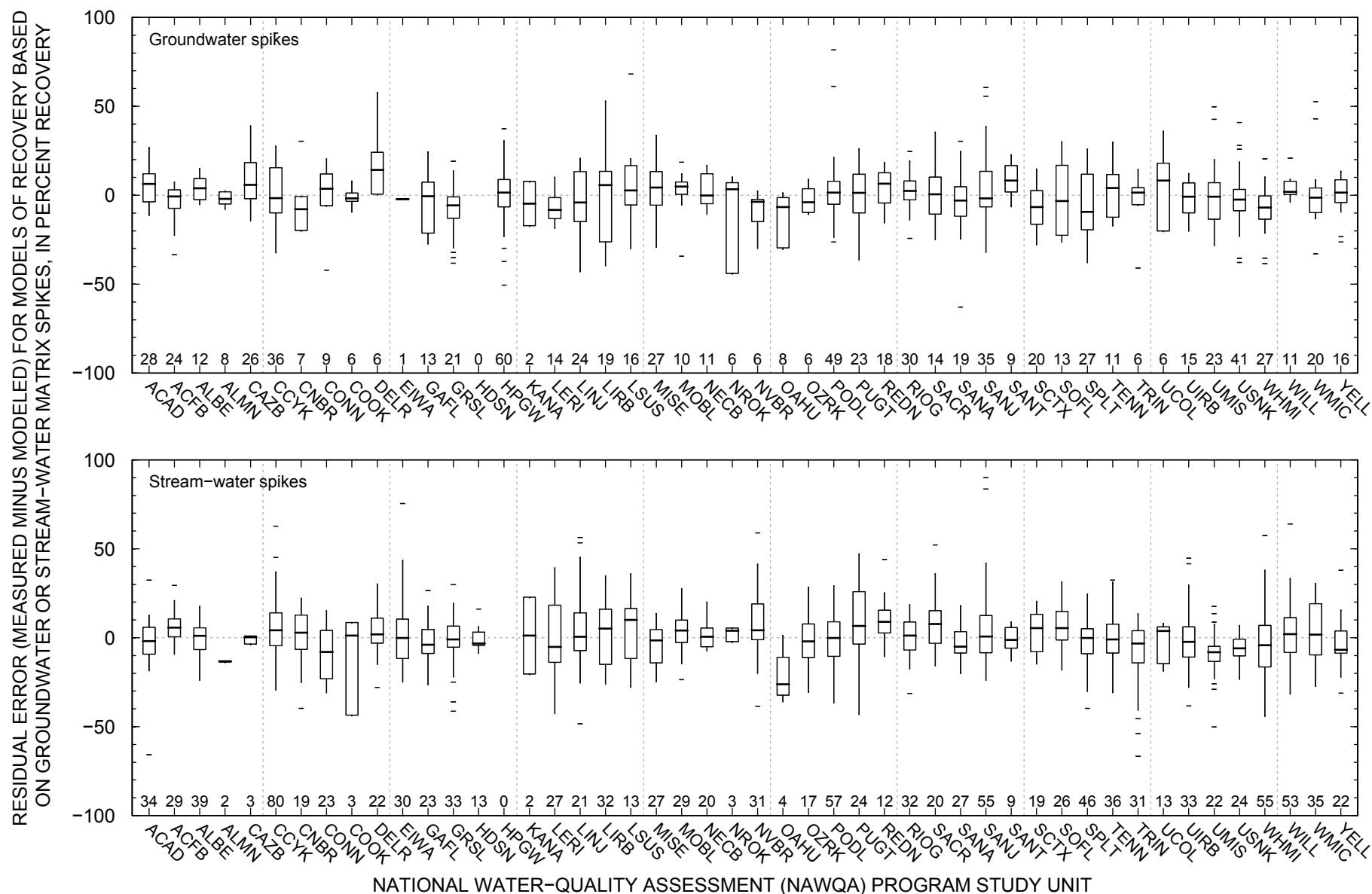


Figure A6-13. Distribution of residual errors in models of recovery of deethylatrazine by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

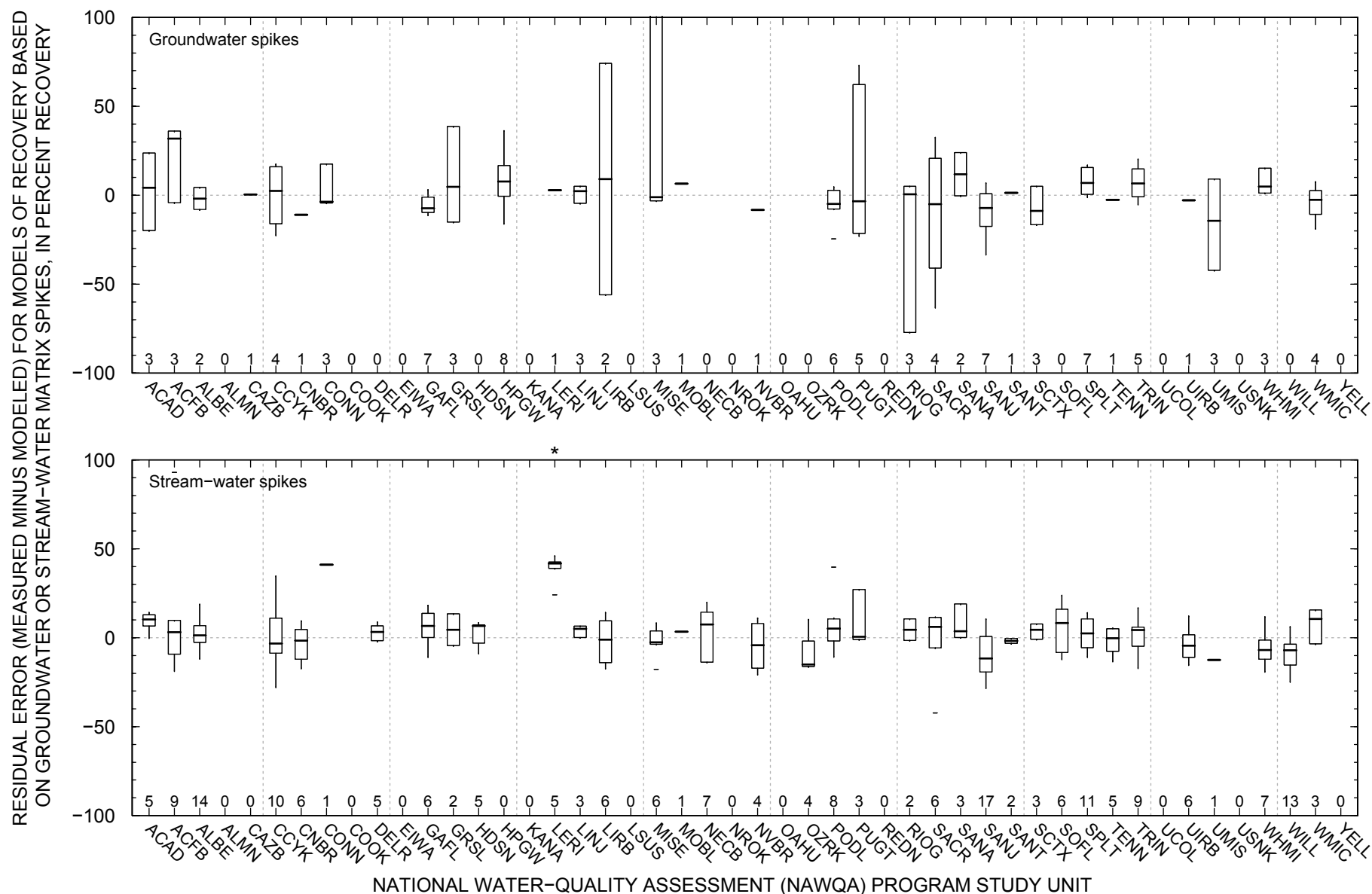


Figure A6-14. Distribution of residual errors in models of recovery of desulfinylfipronil by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).



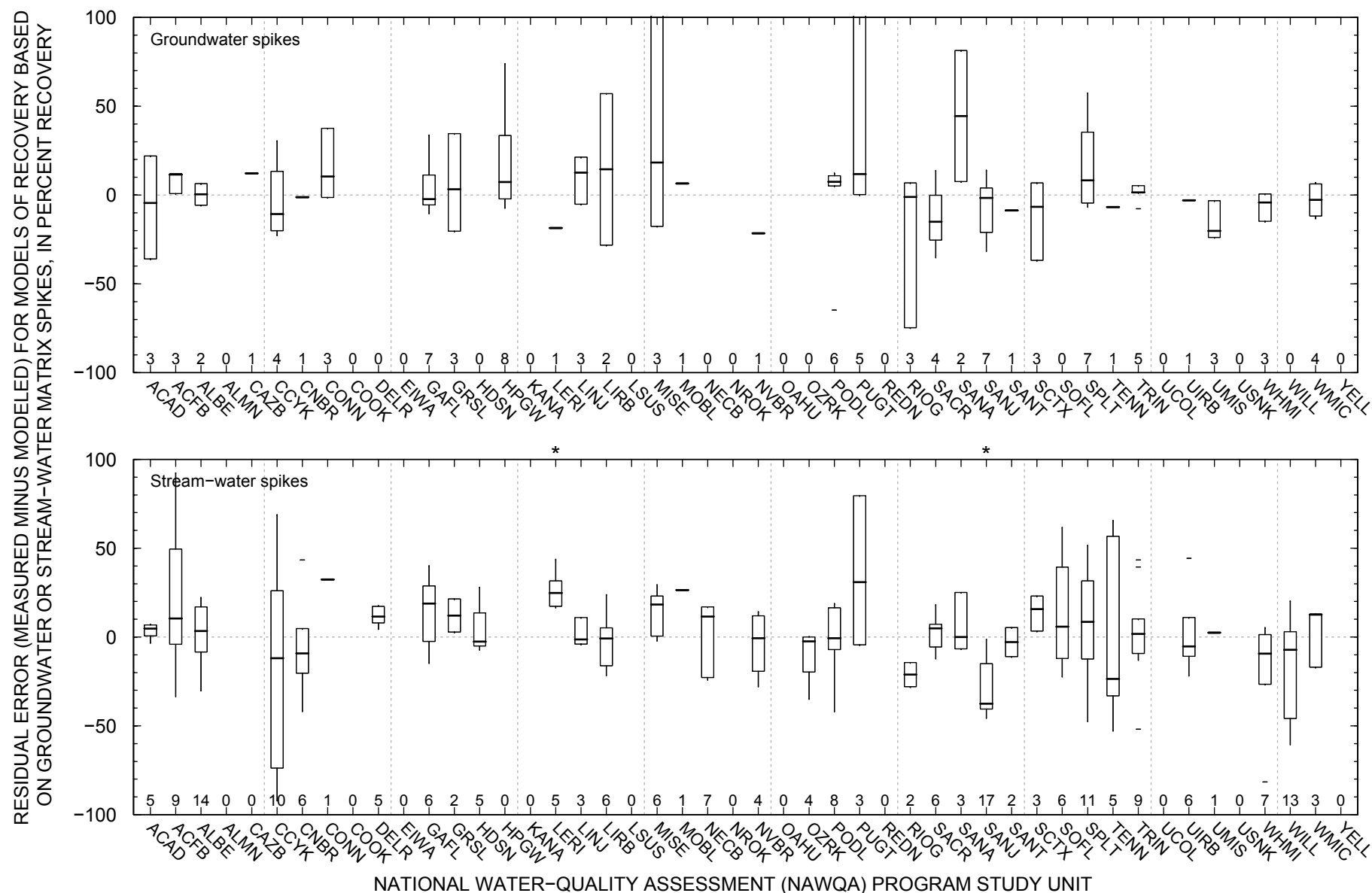


Figure A6-15. Distribution of residual errors in models of recovery of desulfinylfipronil amide by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

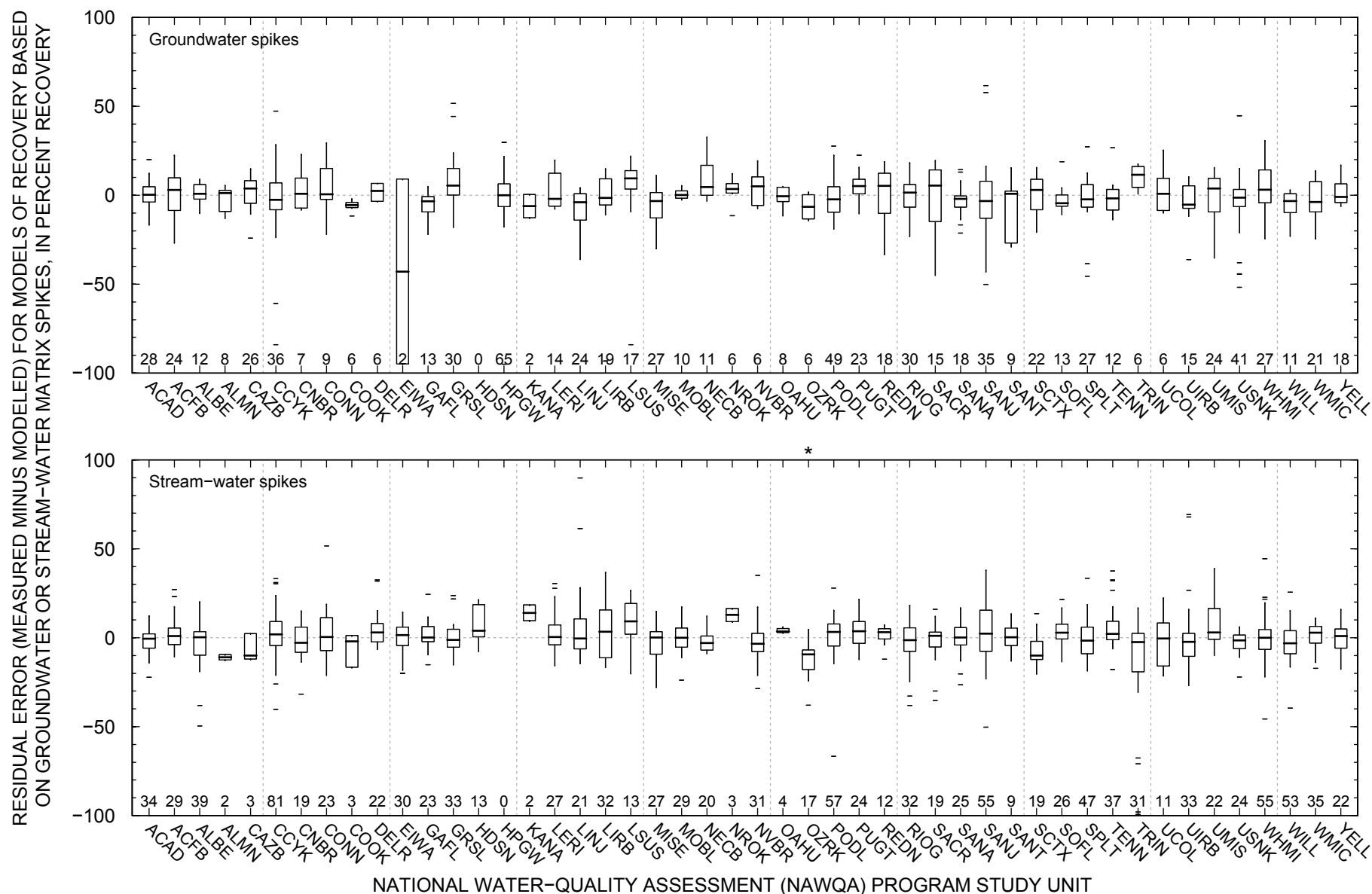


Figure A6-16. Distribution of residual errors in models of recovery of diazinon by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

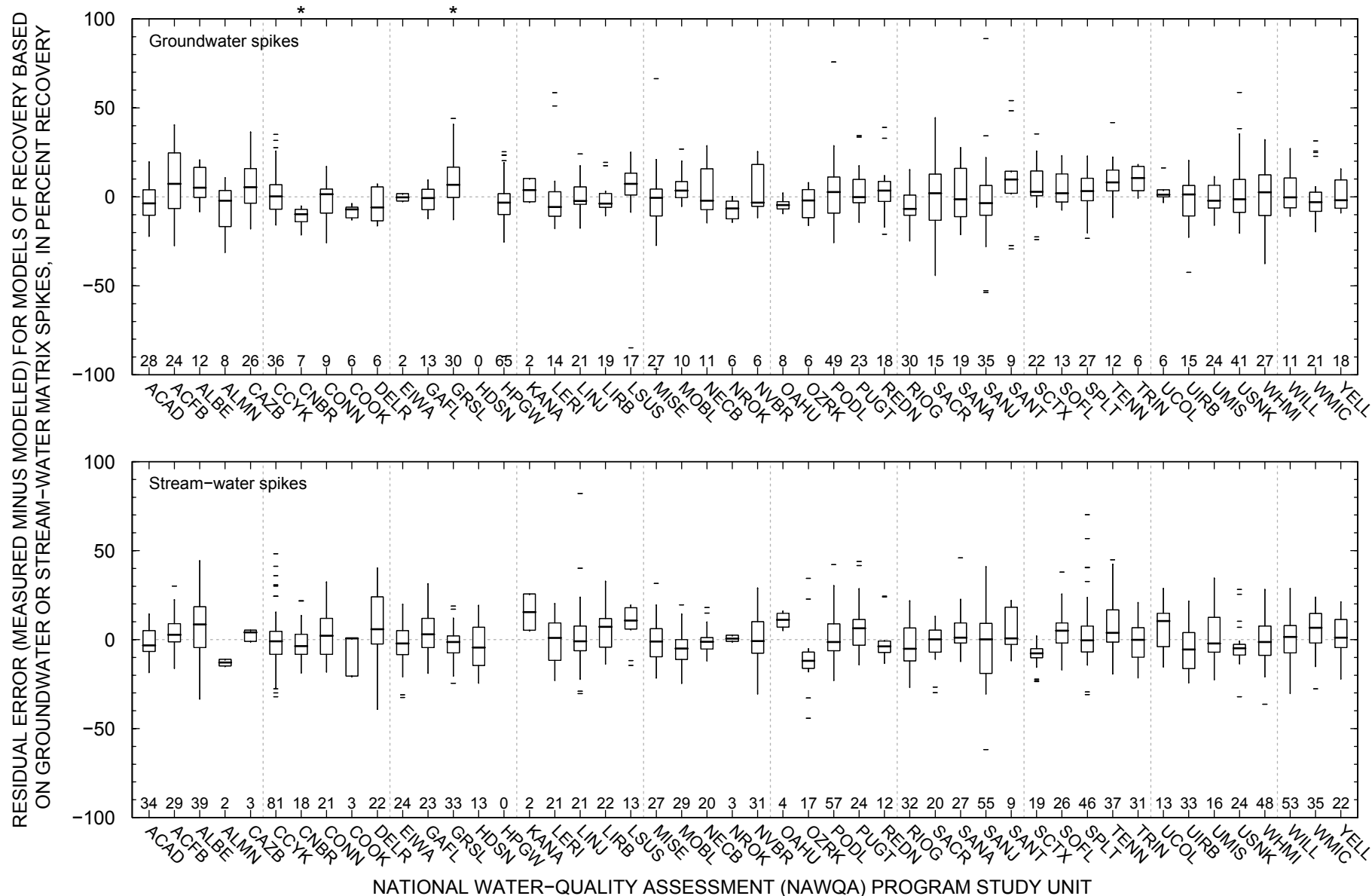


Figure A6-17. Distribution of residual errors in models of recovery of dieldrin by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

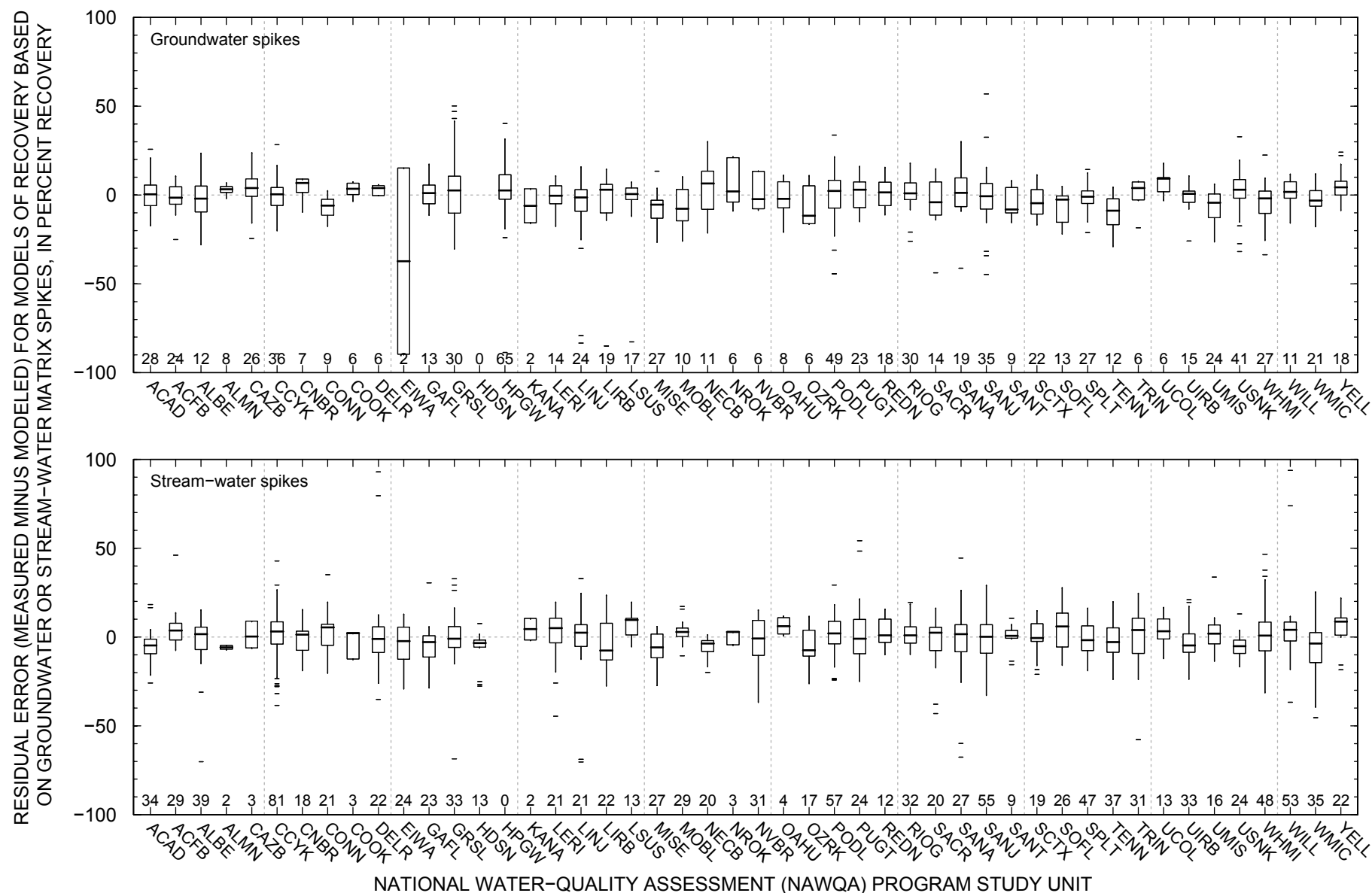


Figure A6-18. Distribution of residual errors in models of recovery of 2,6-diethylaniline by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

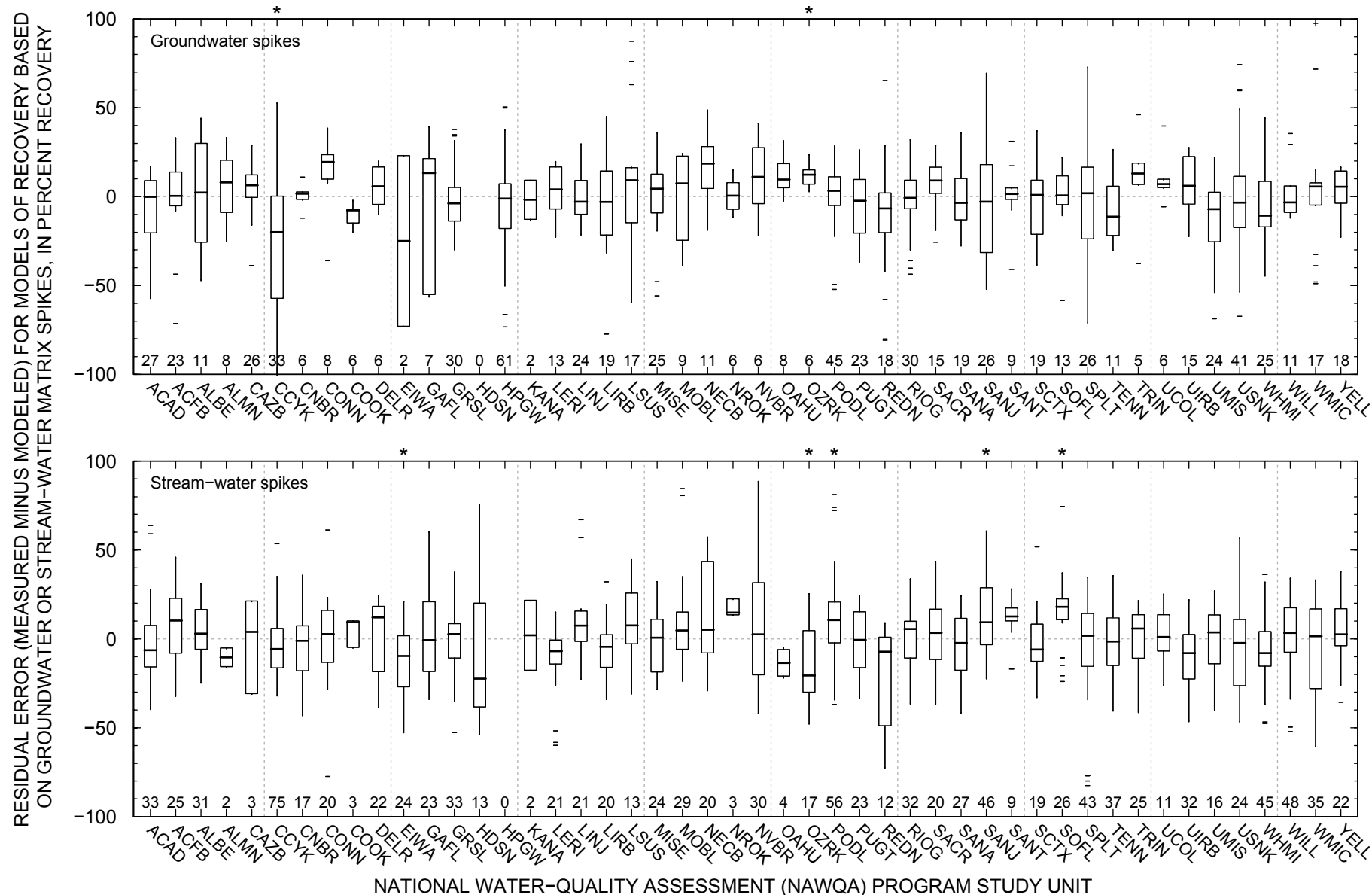


Figure A6-19. Distribution of residual errors in models of recovery of disulfoton by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

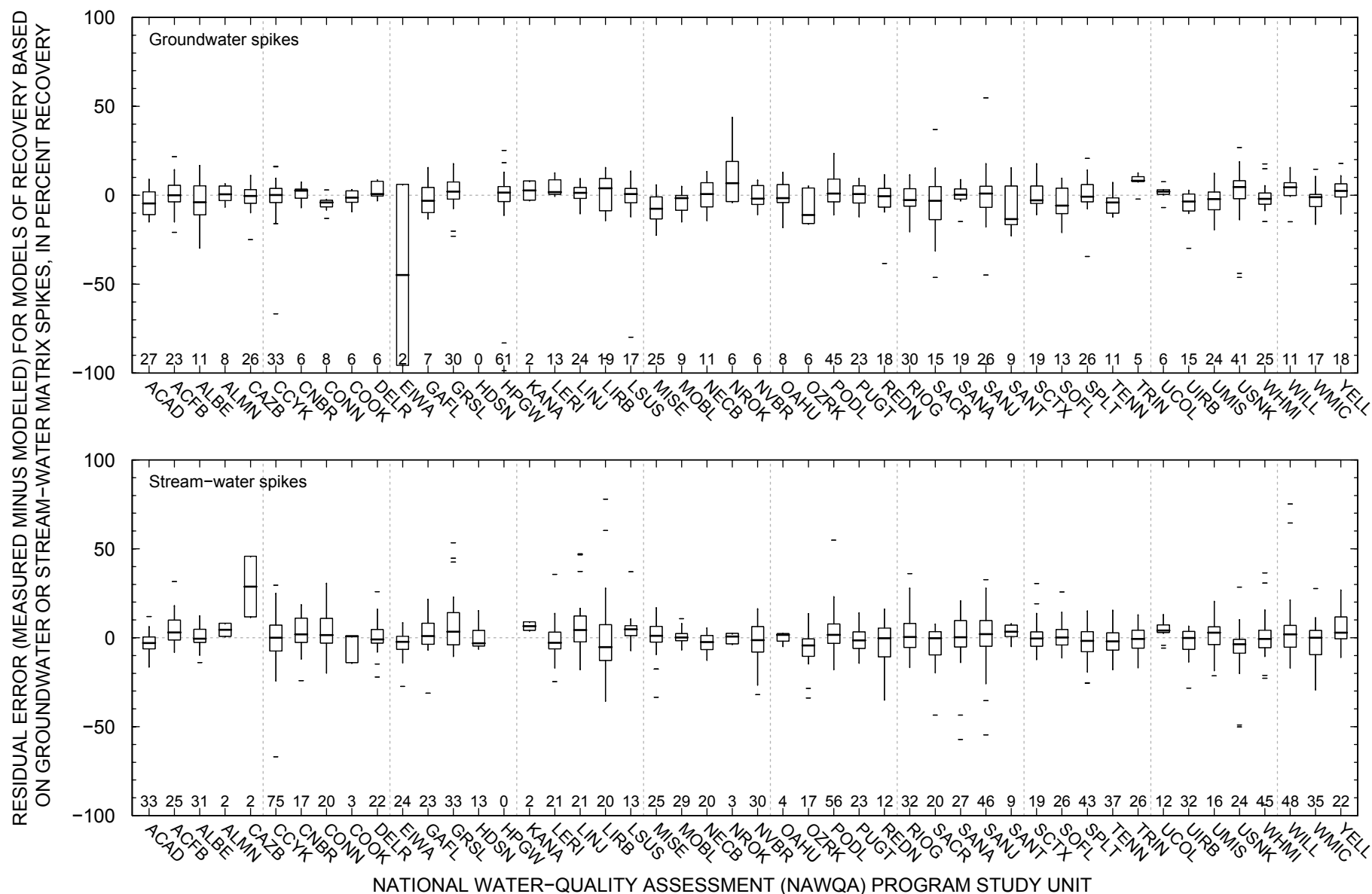


Figure A6-20. Distribution of residual errors in models of recovery of EPTC by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

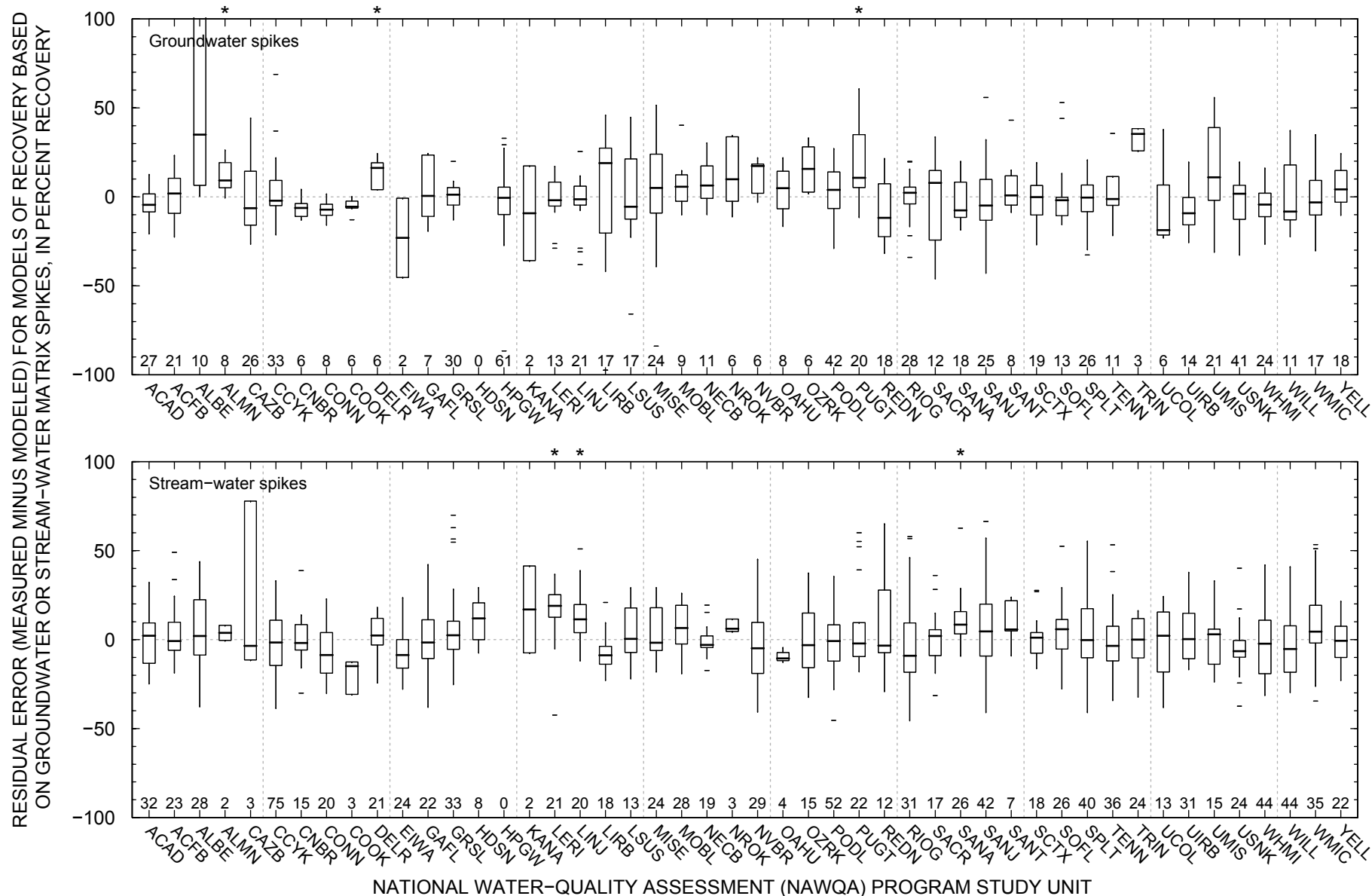


Figure A6-21. Distribution of residual errors in models of recovery of ethalfluralin by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

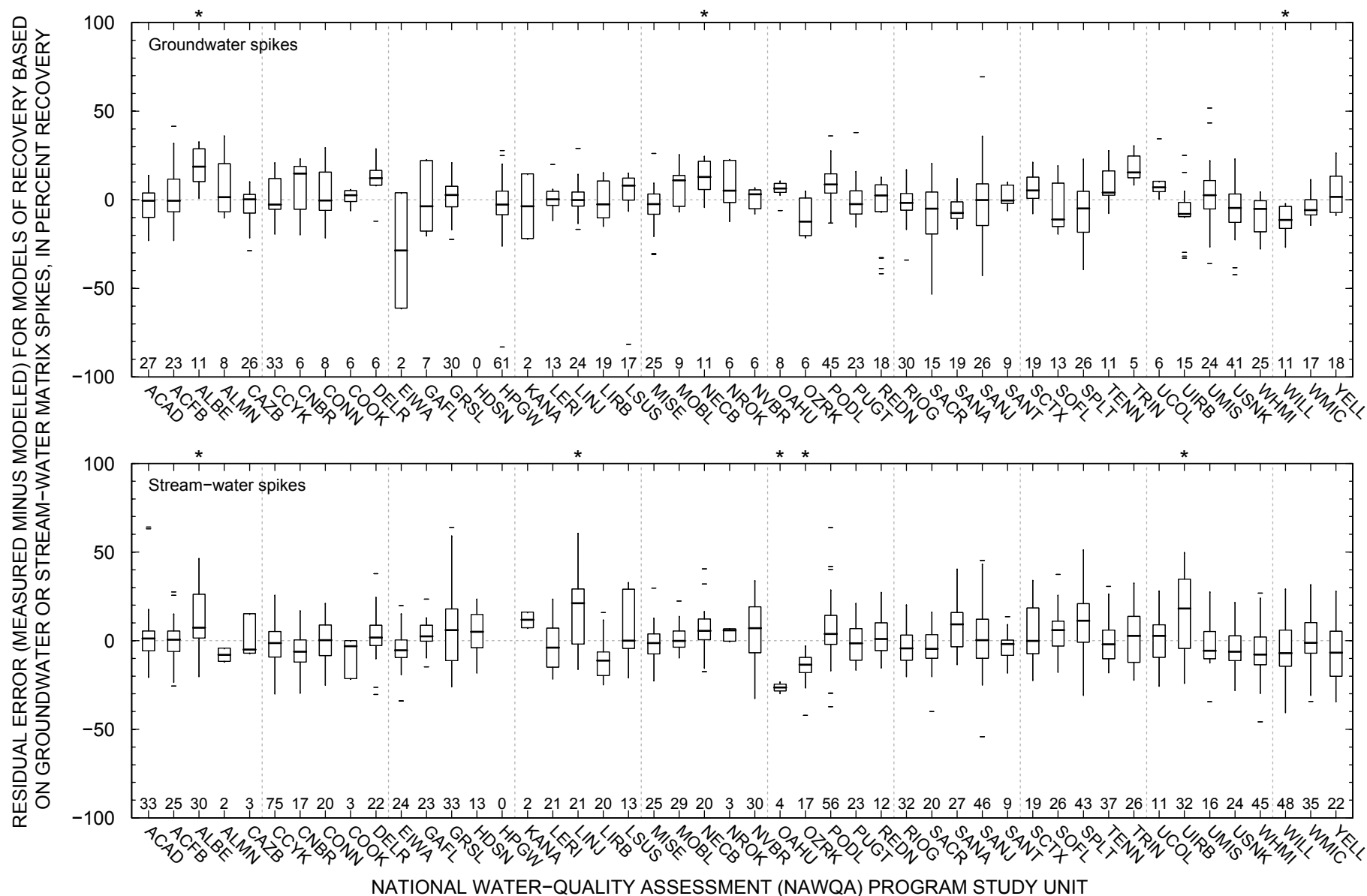


Figure A6-22. Distribution of residual errors in models of recovery of ethoprophos by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).



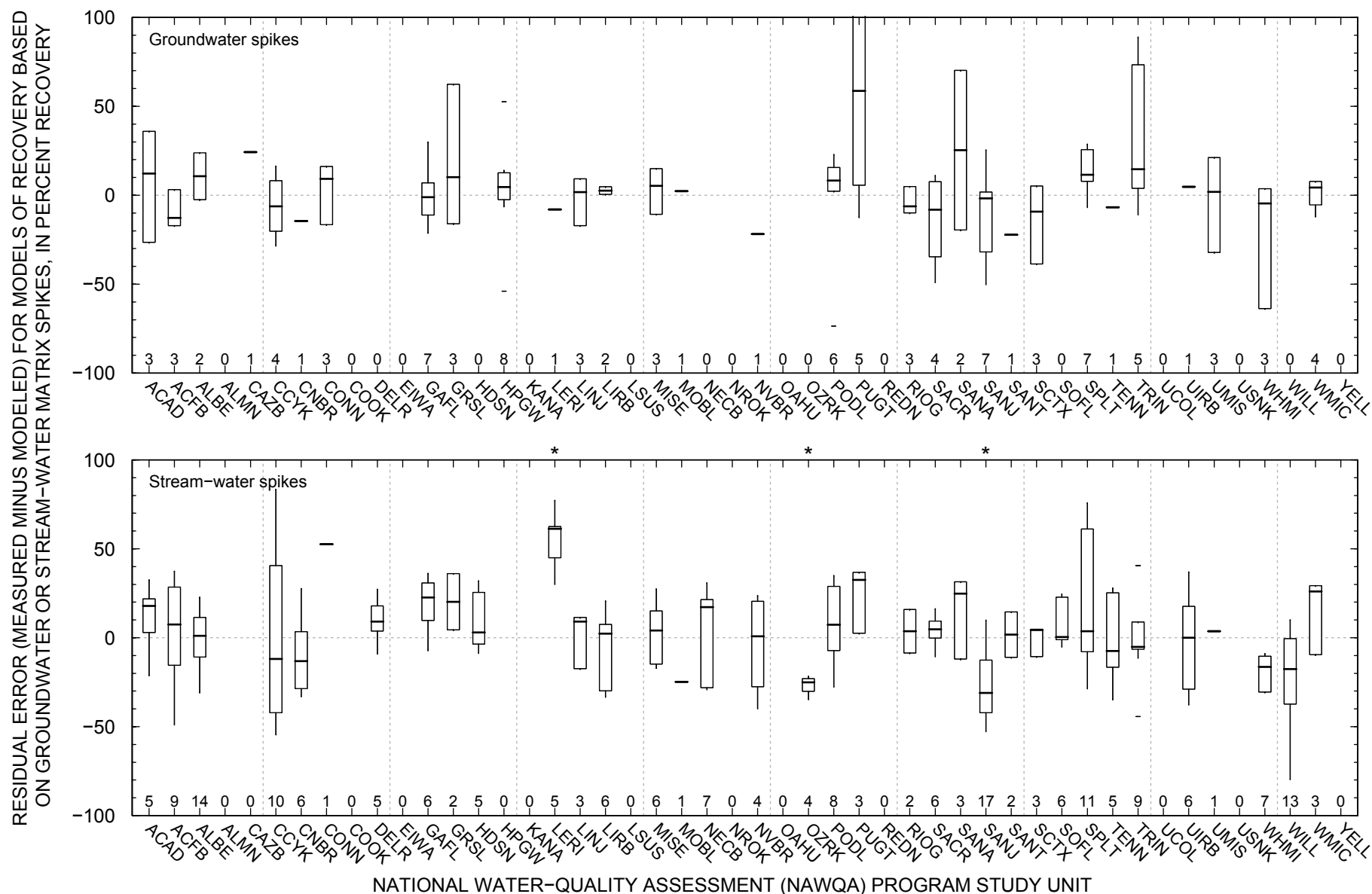


Figure A6-23. Distribution of residual errors in models of recovery of fipronil by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

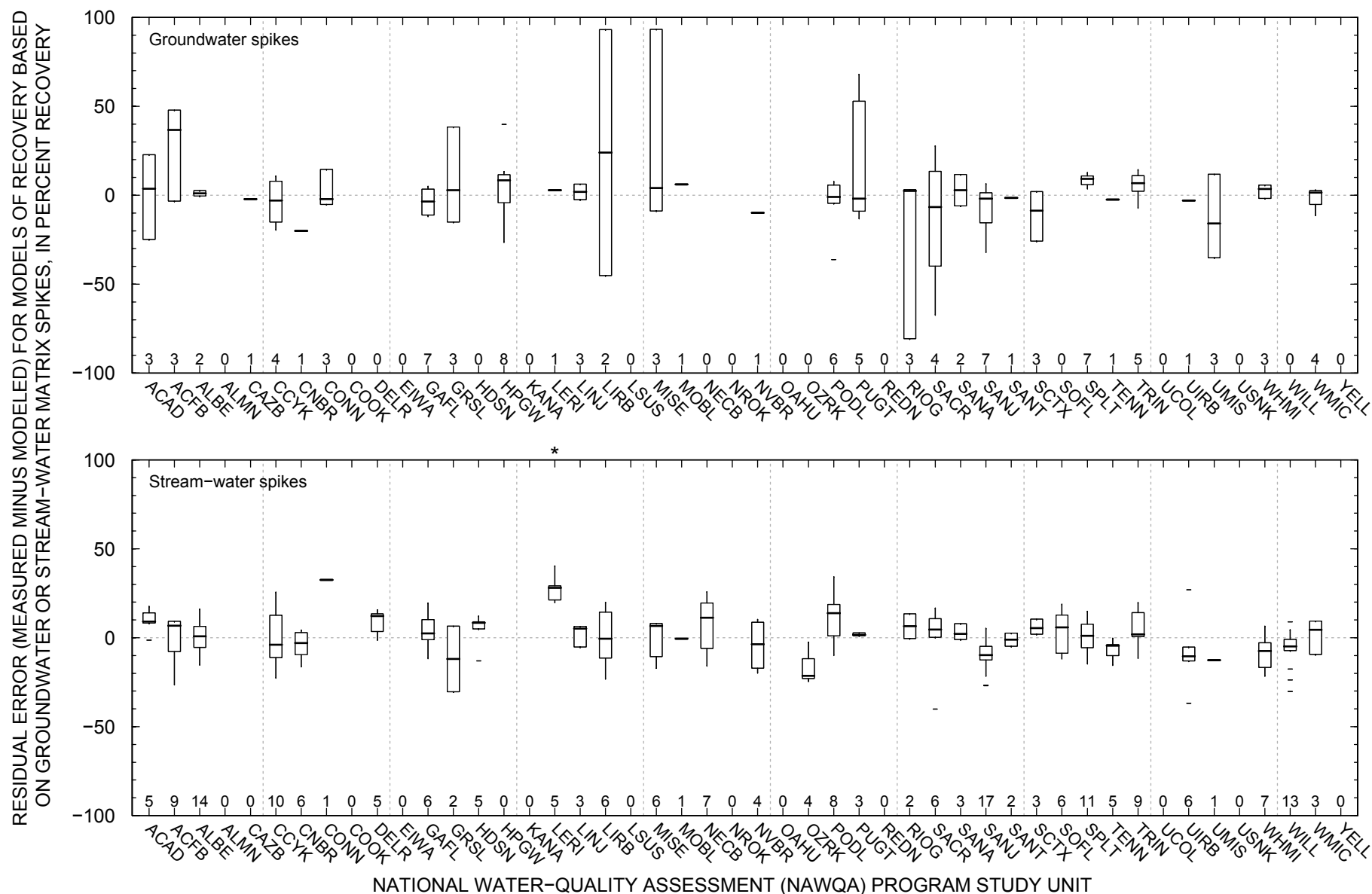


Figure A6-24. Distribution of residual errors in models of recovery of fipronil sulfide by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

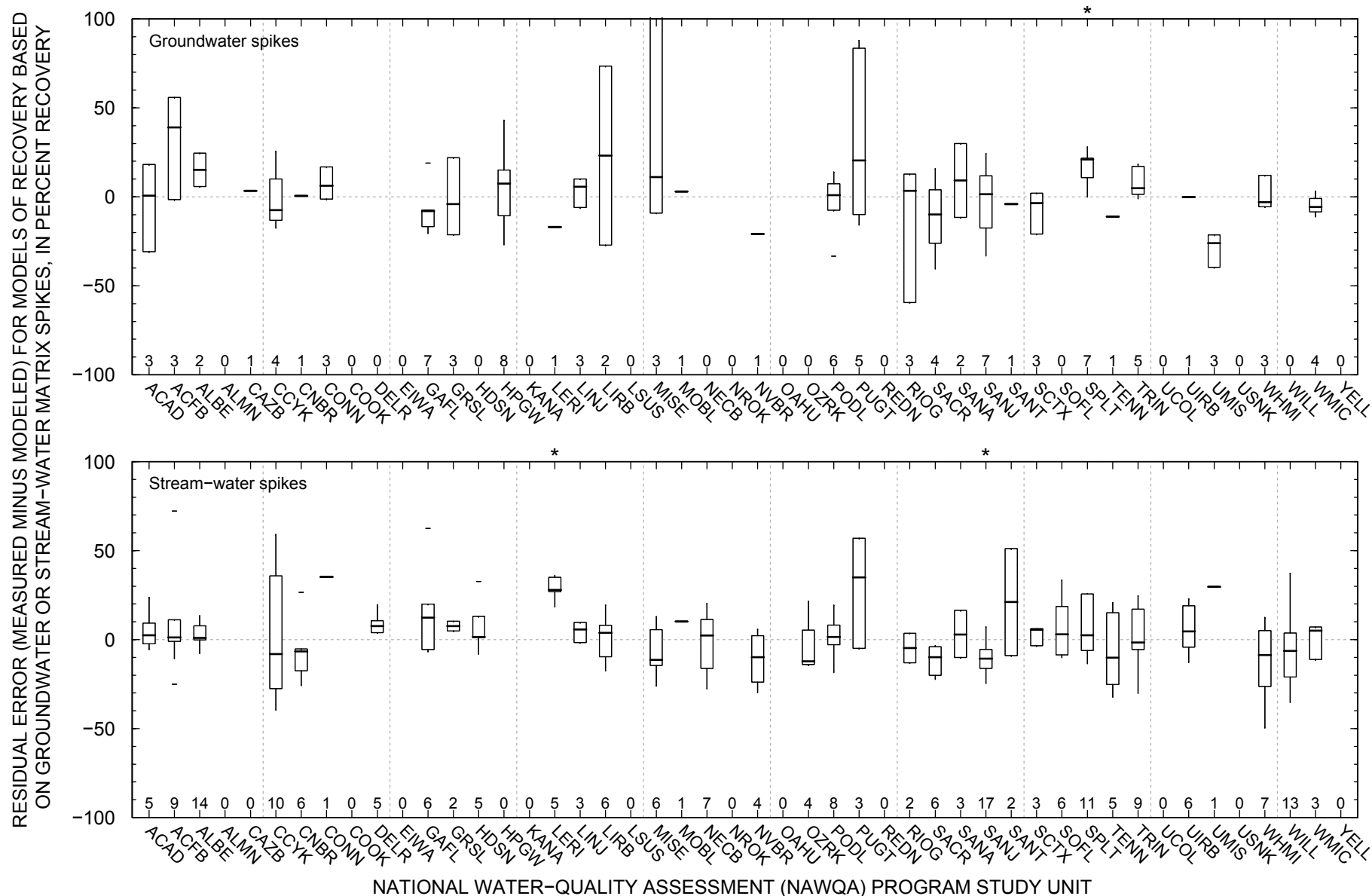


Figure A6-25. Distribution of residual errors in models of recovery of fipronil sulfone by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

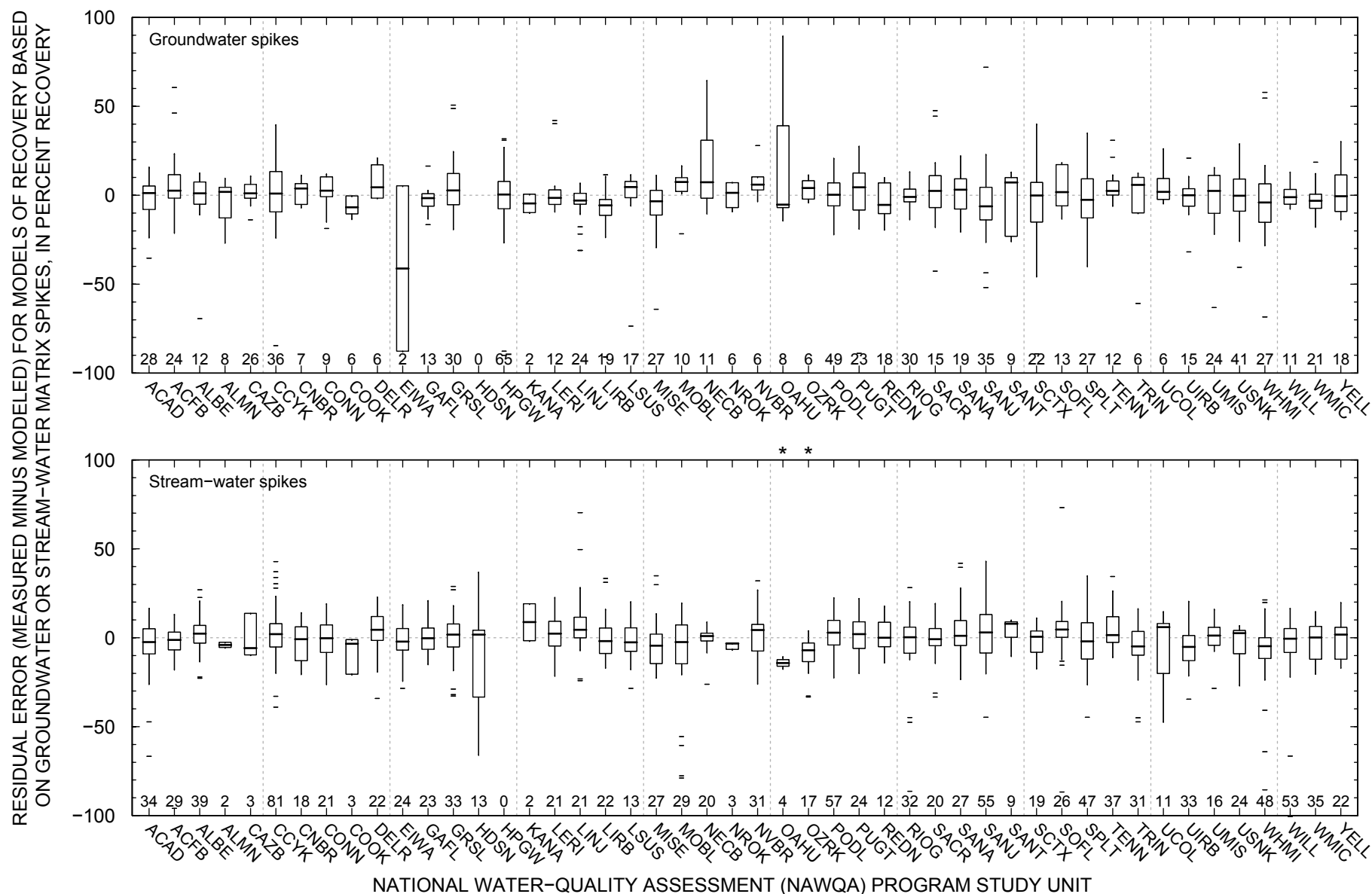


Figure A6-26. Distribution of residual errors in models of recovery of fonofos by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

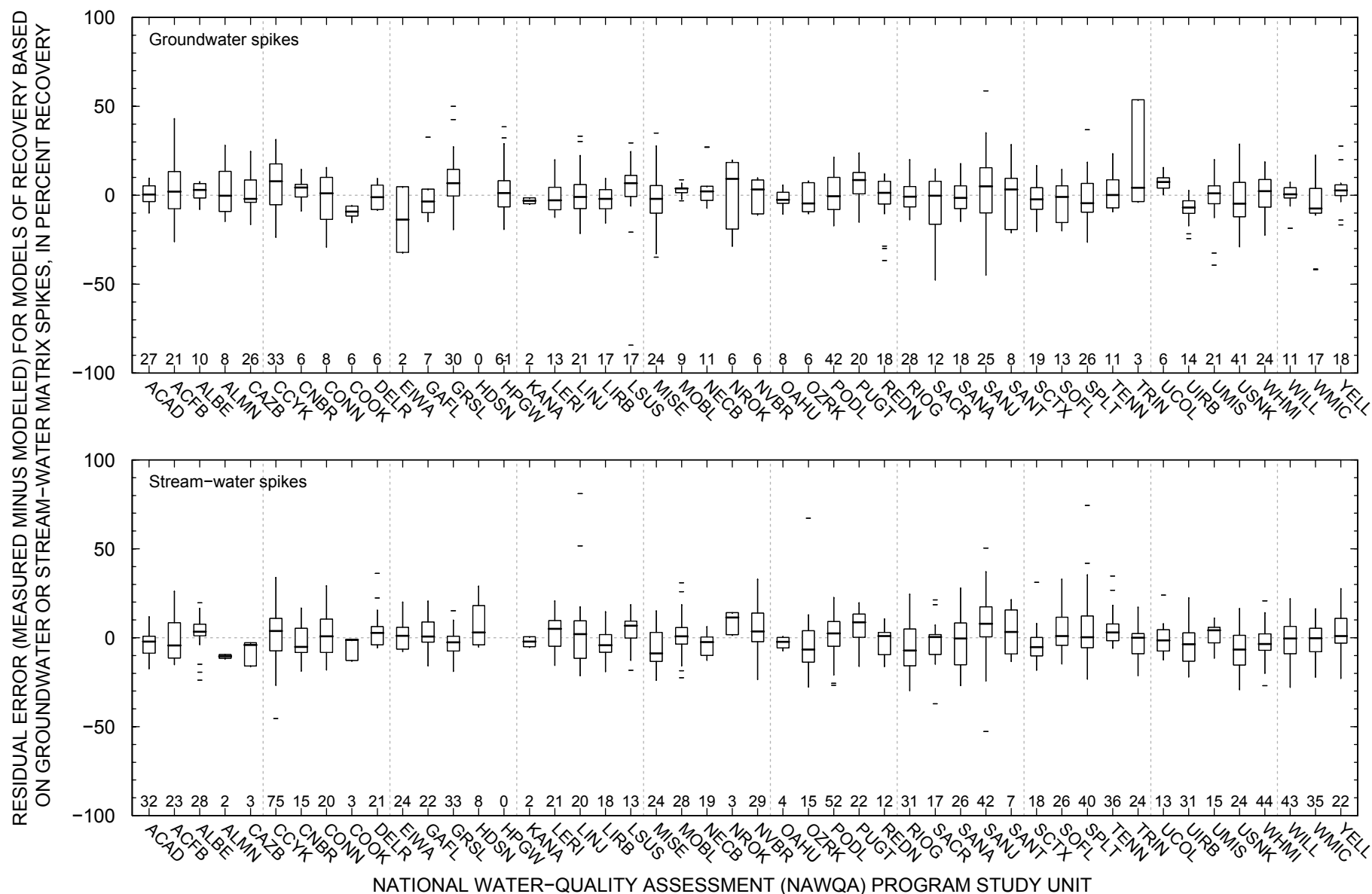


Figure A6-27. Distribution of residual errors in models of recovery of alpha-HCH by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

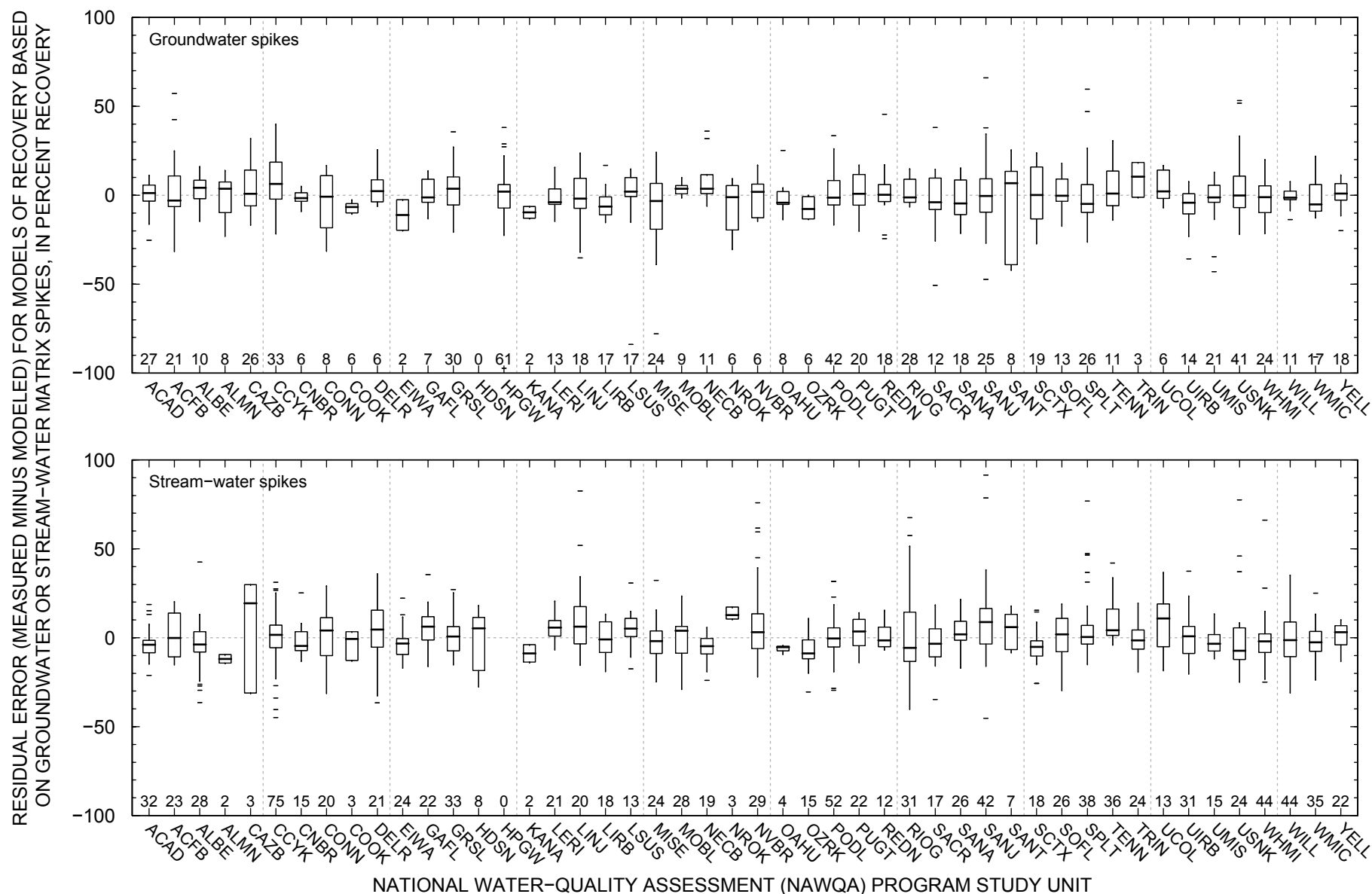


Figure A6-28. Distribution of residual errors in models of recovery of gamma-HCH by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

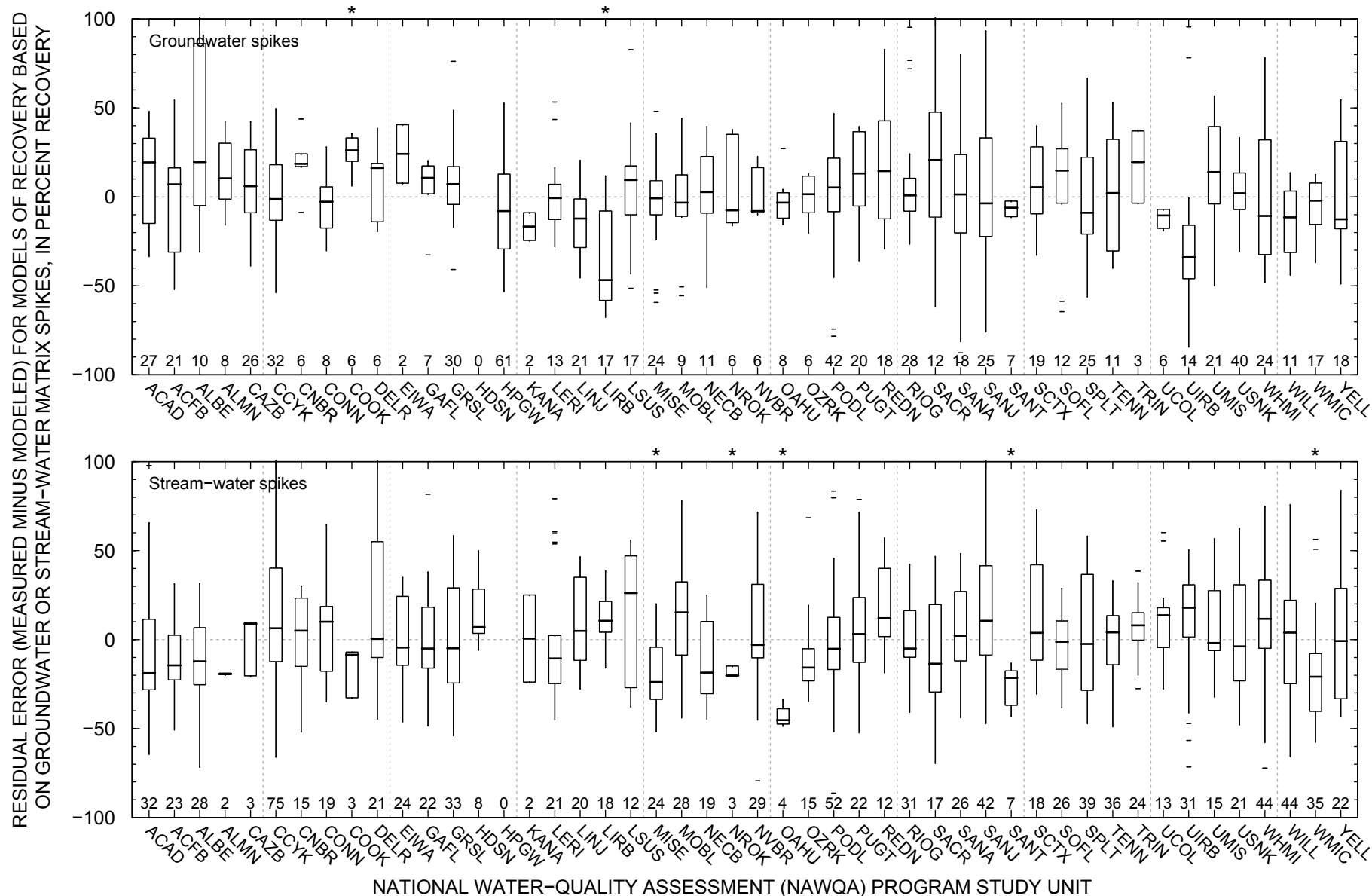


Figure A6-29. Distribution of residual errors in models of recovery of linuron by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

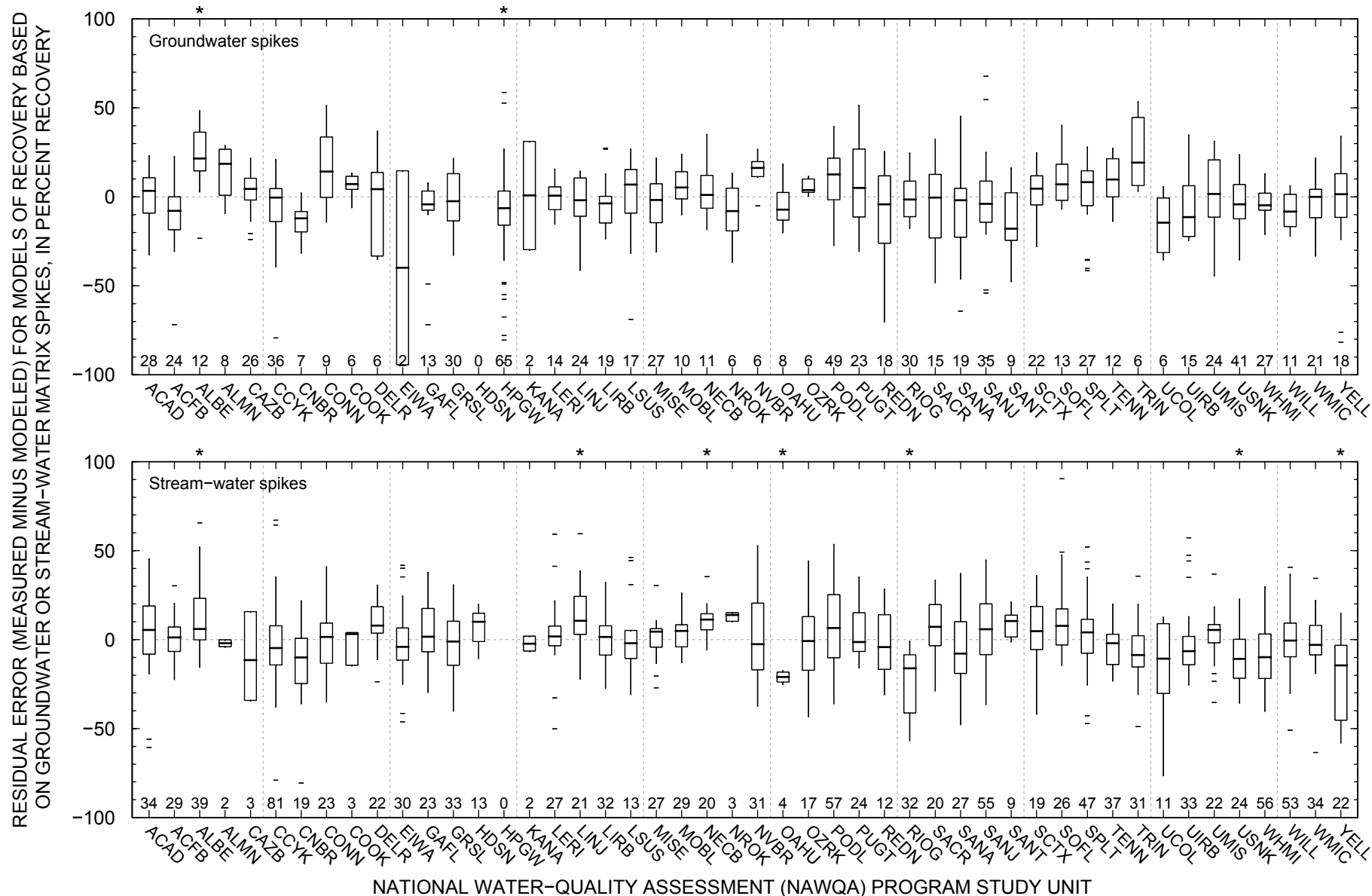


Figure A6-30. Distribution of residual errors in models of recovery of malathion by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).



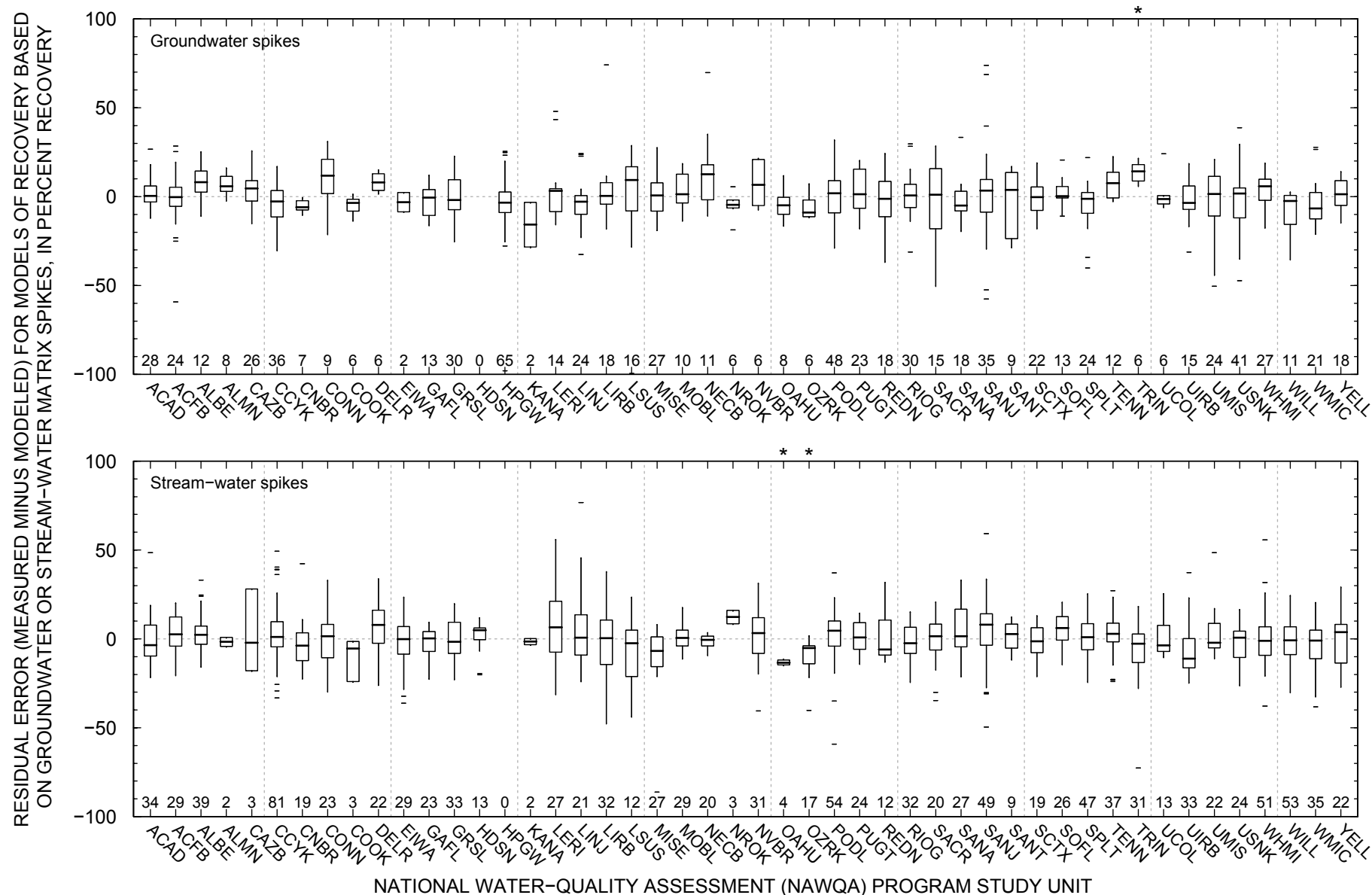


Figure A6-31. Distribution of residual errors in models of recovery of metolachlor by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

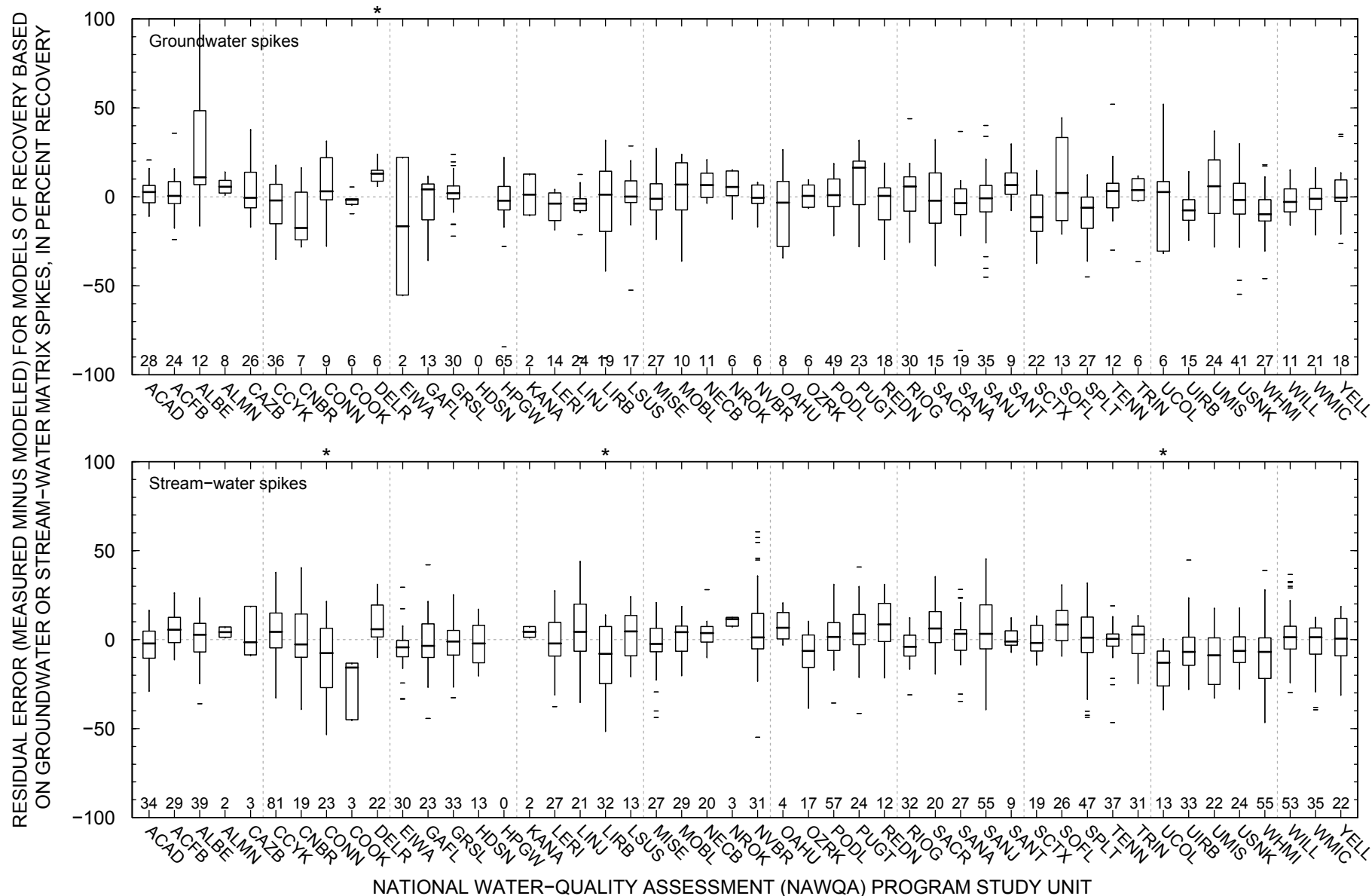


Figure A6-32. Distribution of residual errors in models of recovery of metribuzin by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

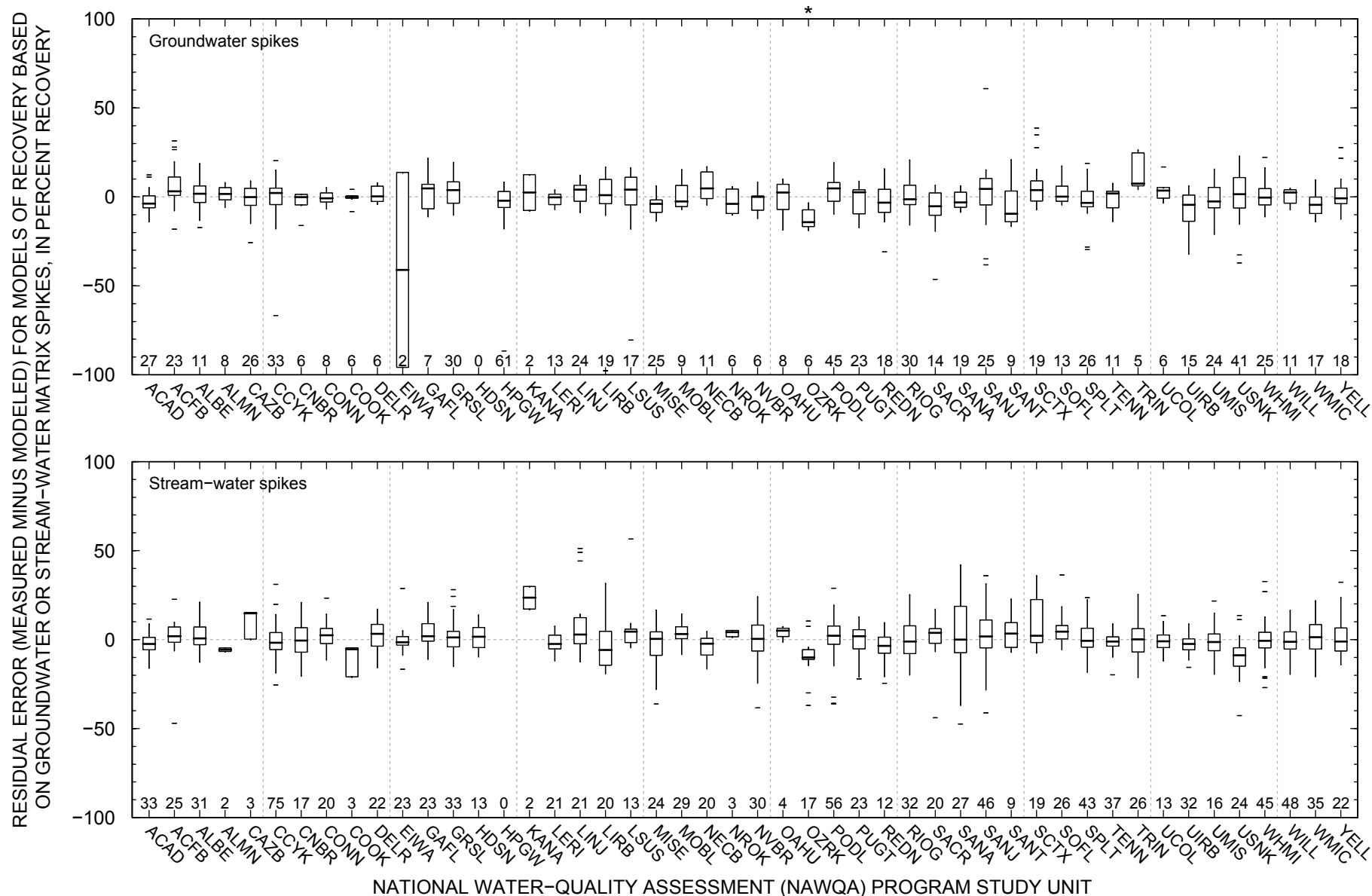


Figure A6-33. Distribution of residual errors in models of recovery of molinate by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

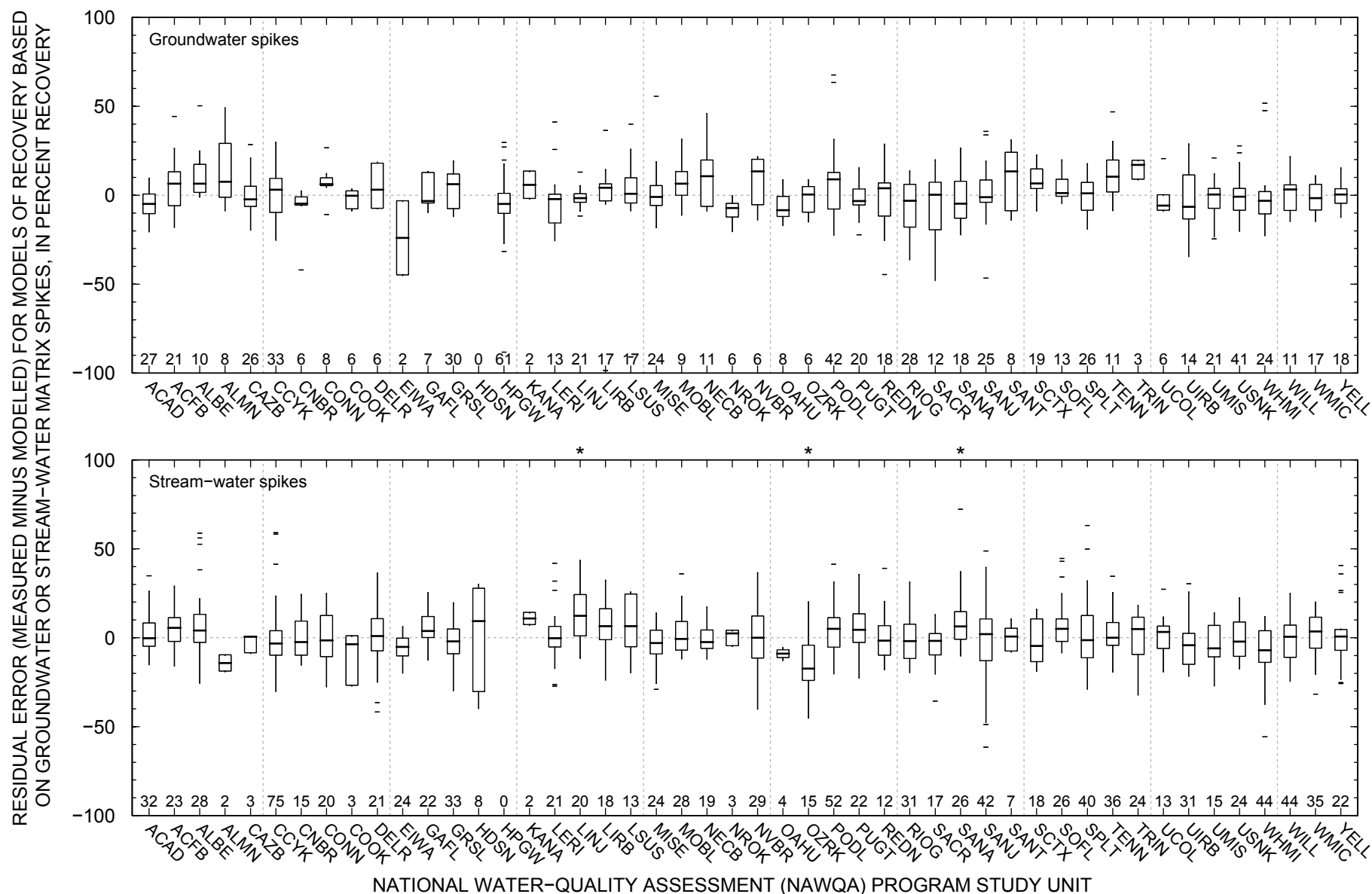


Figure A6-34. Distribution of residual errors in models of recovery of napropamide by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

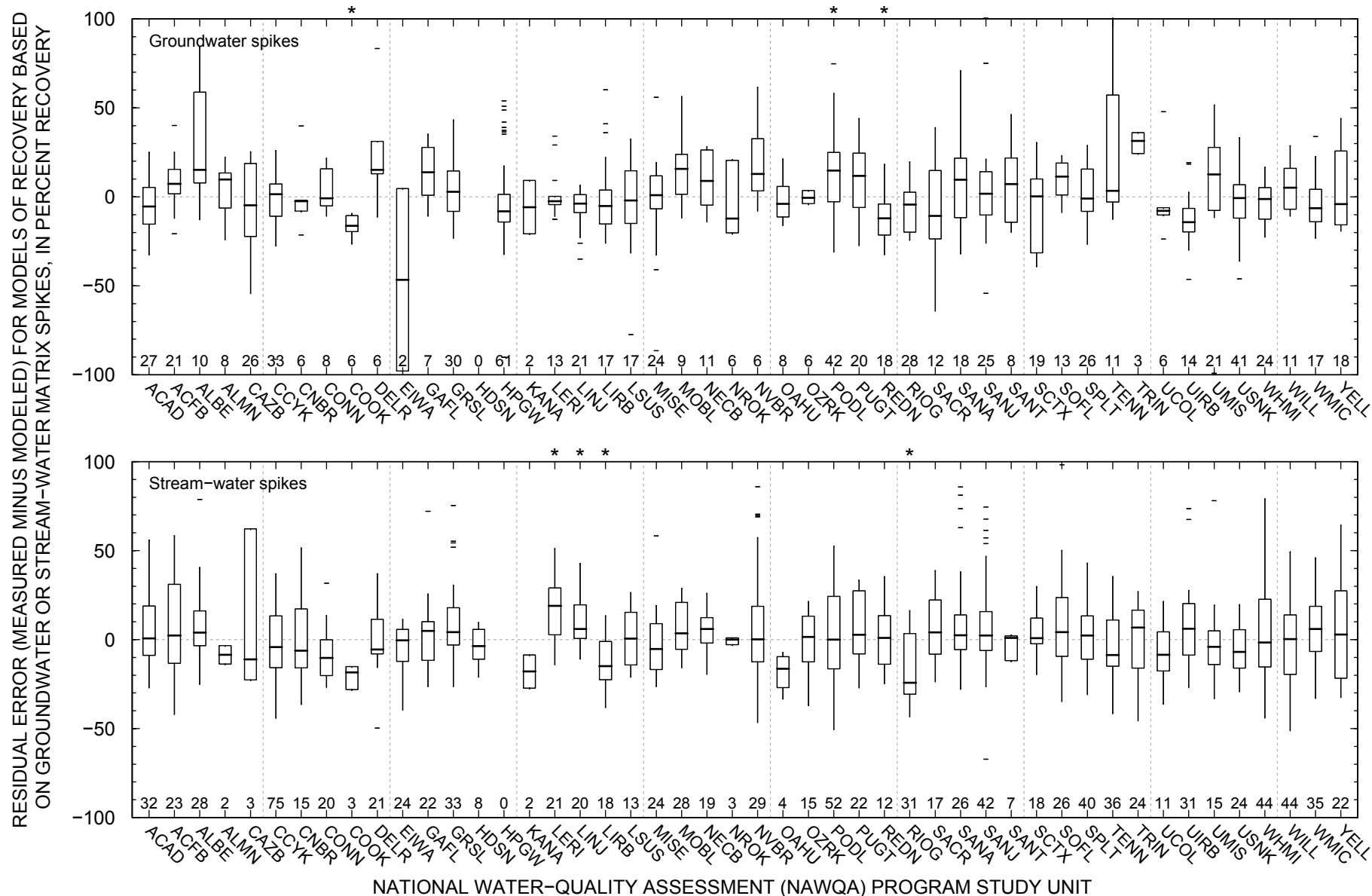


Figure A6-35. Distribution of residual errors in models of recovery of parathion by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

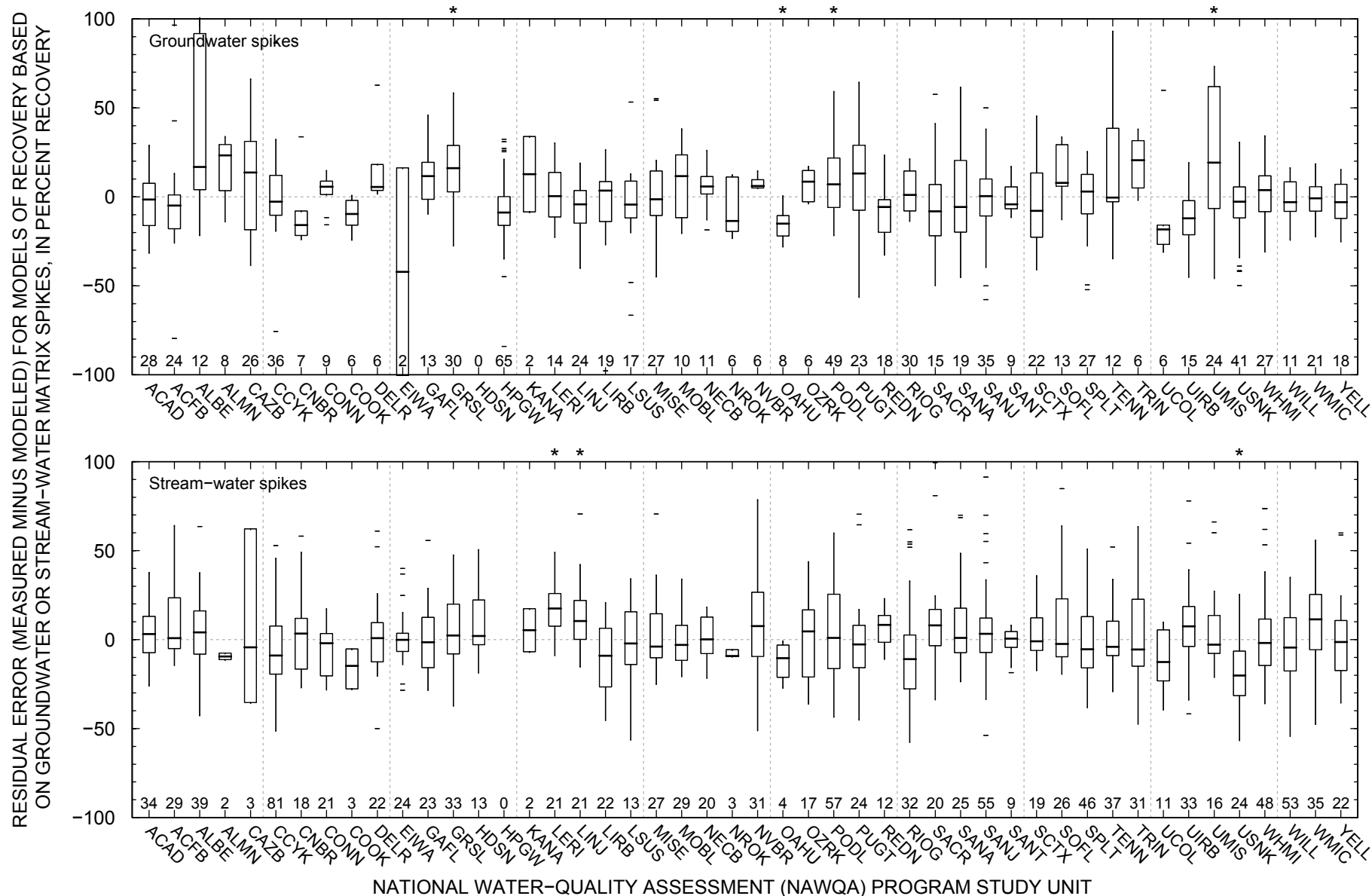


Figure A6-36. Distribution of residual errors in models of recovery of parathion-methyl by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

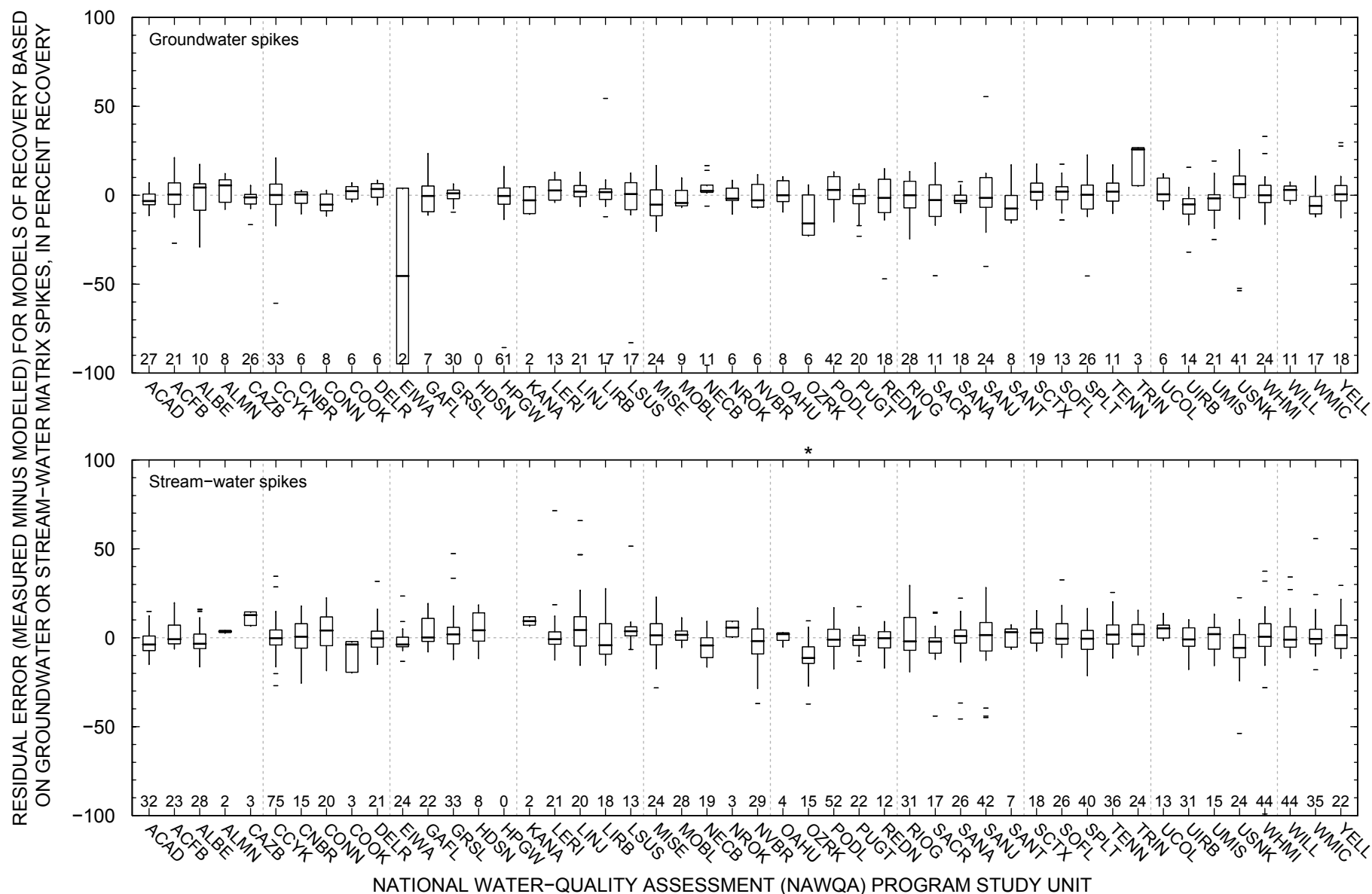


Figure A6-37. Distribution of residual errors in models of recovery of pebulate by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

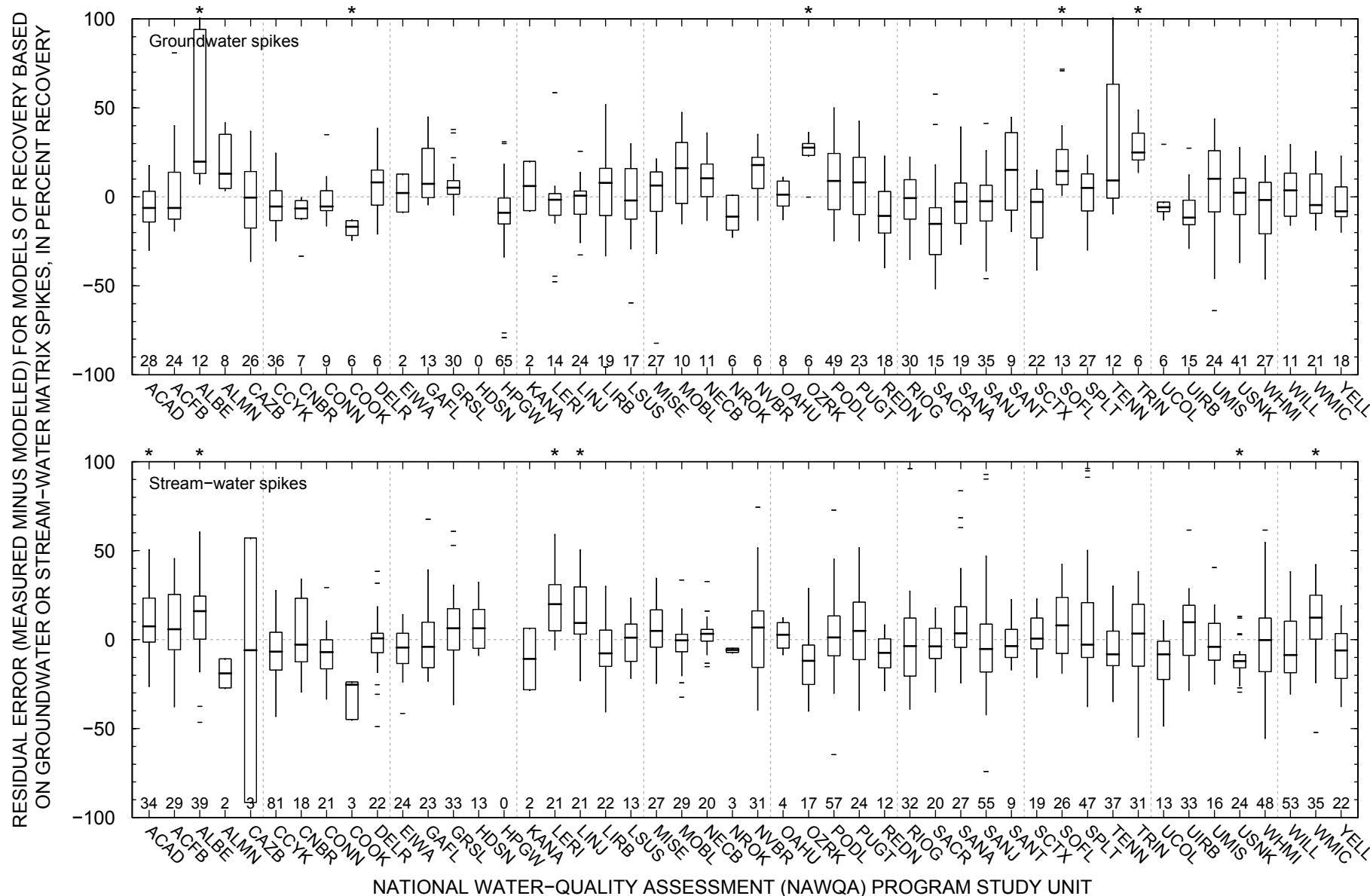


Figure A6-38. Distribution of residual errors in models of recovery of pendimethalin by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).



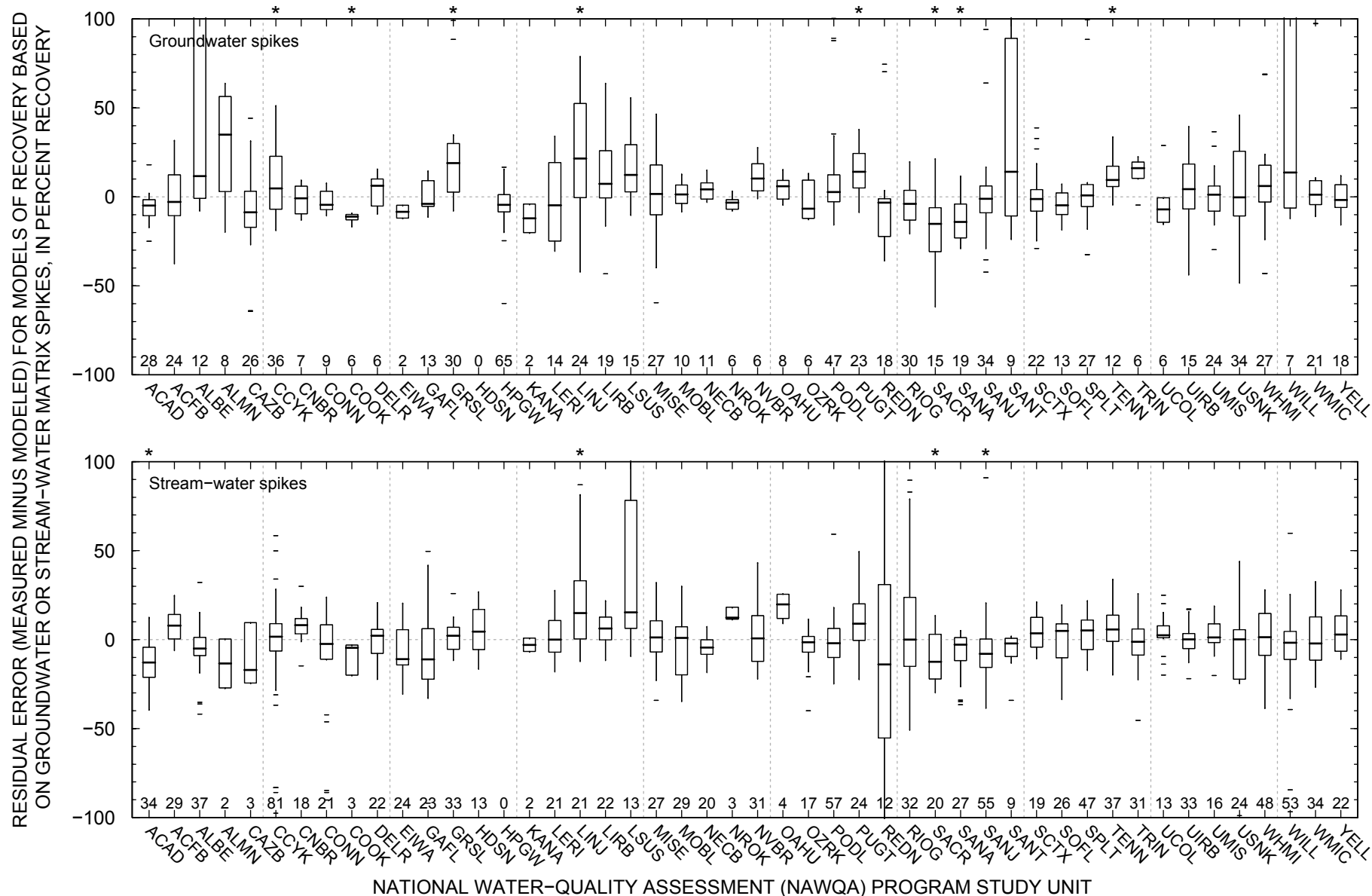


Figure A6-39. Distribution of residual errors in models of recovery of cis-permethrin by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

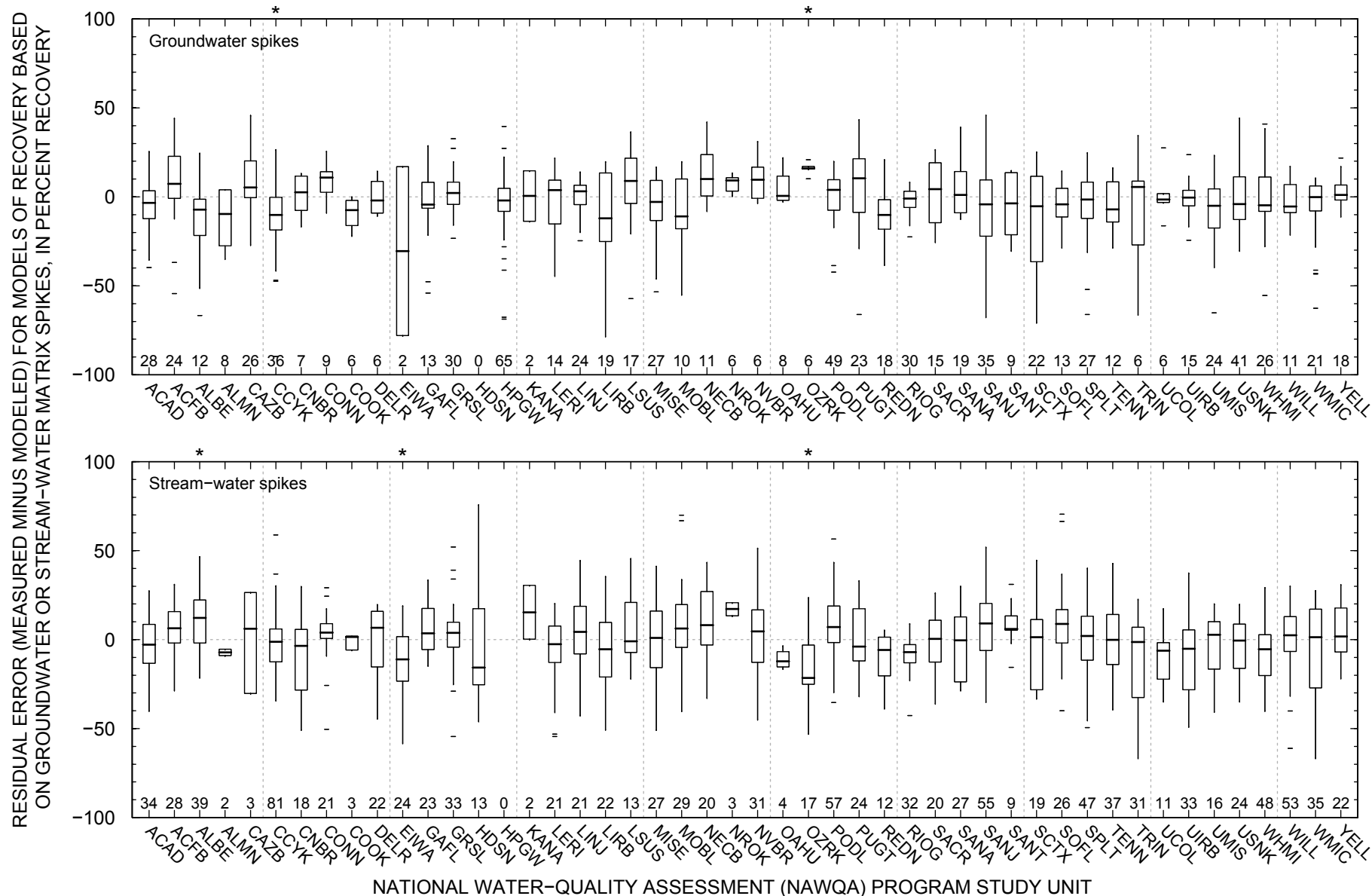


Figure A6-40. Distribution of residual errors in models of recovery of phorate by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

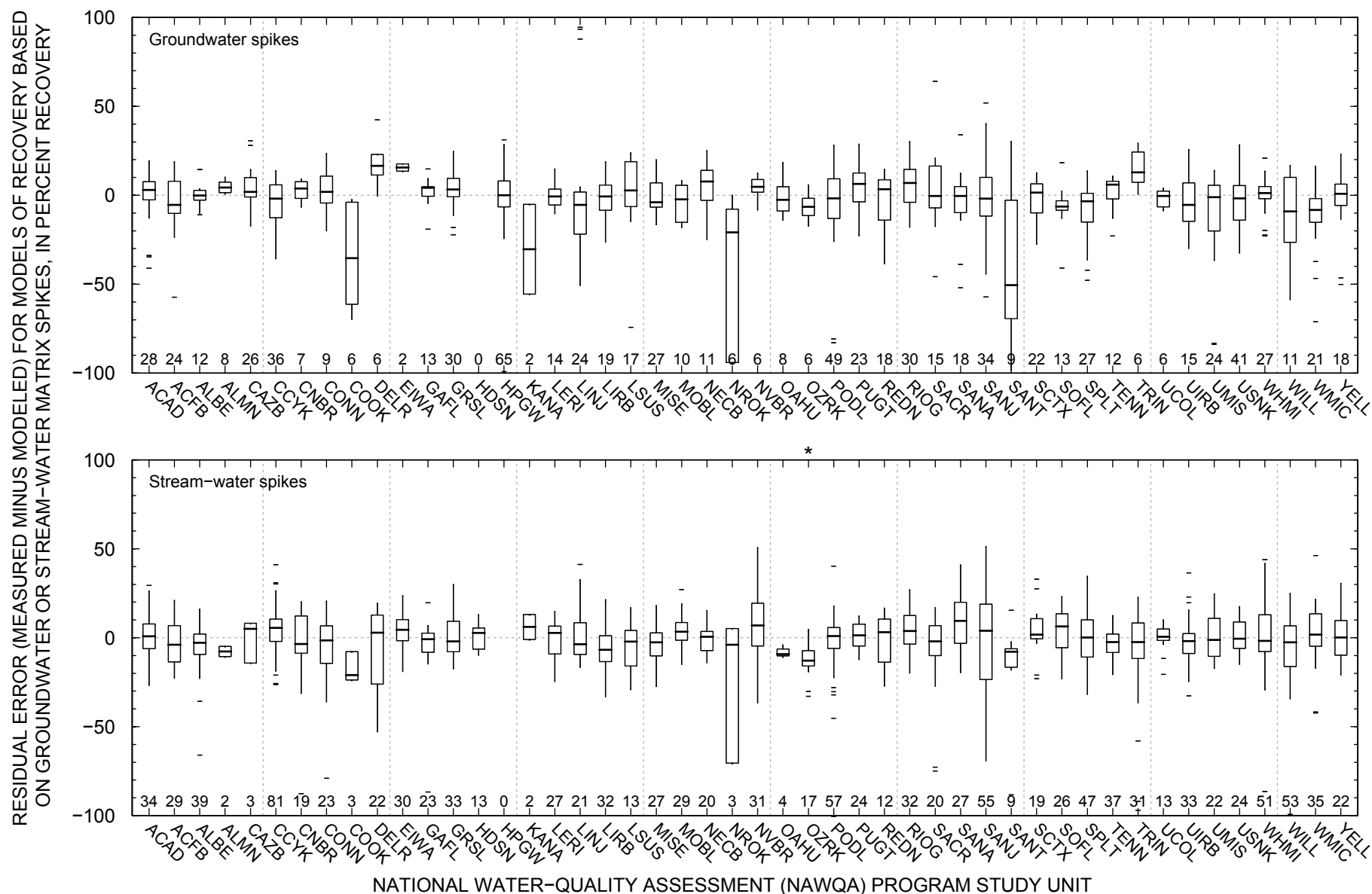


Figure A6-41. Distribution of residual errors in models of recovery of prometon by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

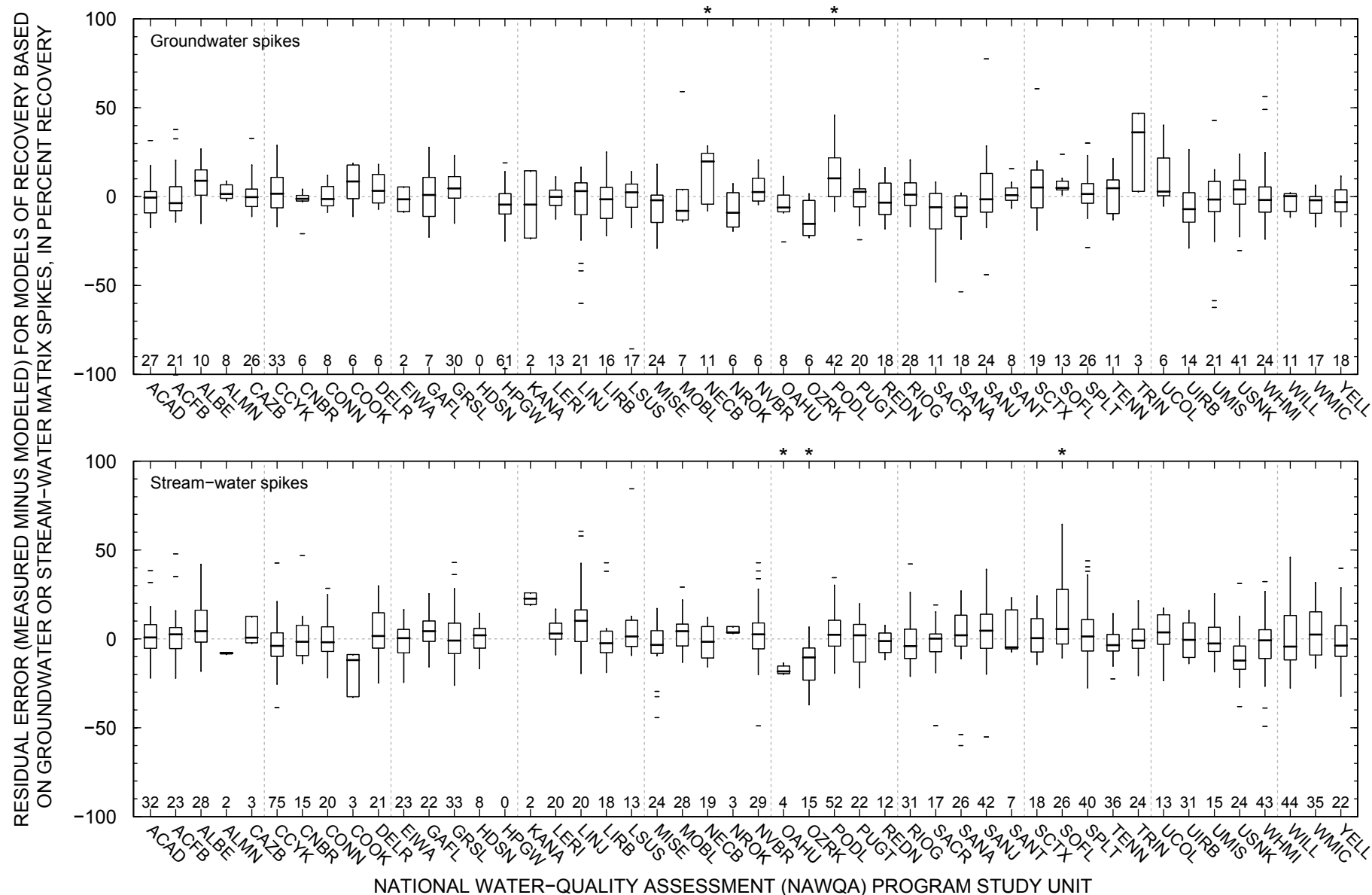


Figure A6-42. Distribution of residual errors in models of recovery of propachlor by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

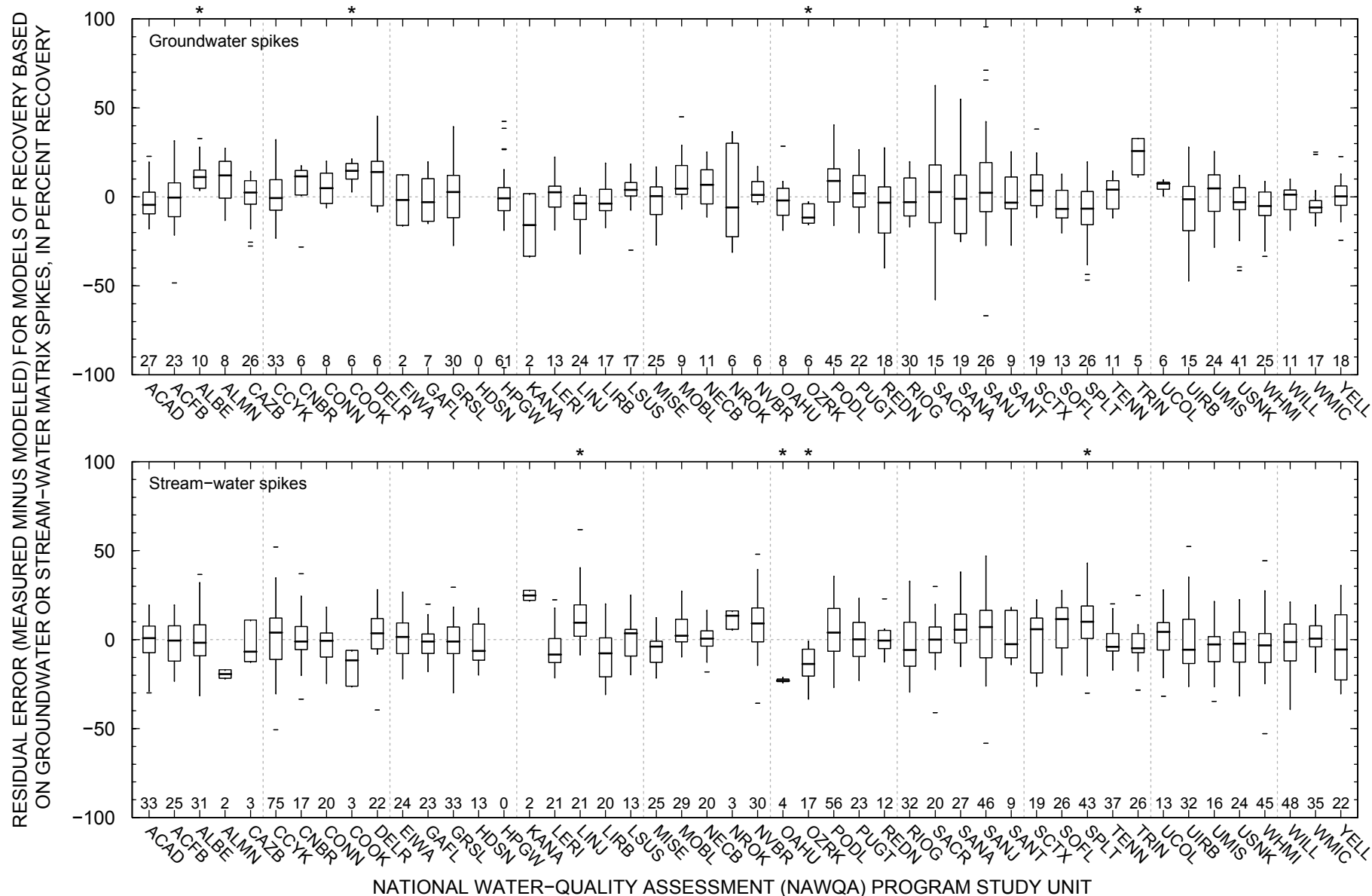


Figure A6-43. Distribution of residual errors in models of recovery of propanil by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

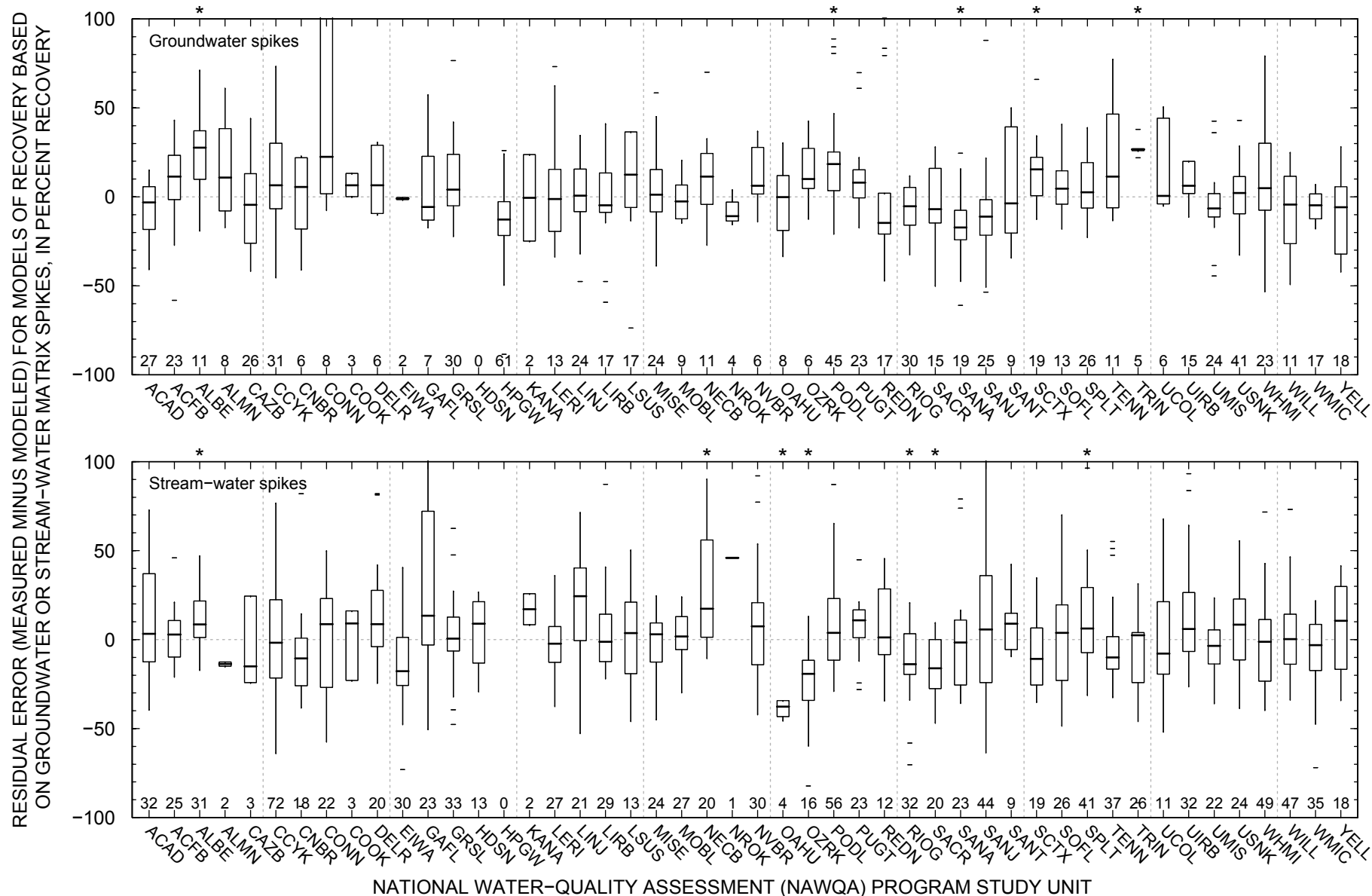


Figure A6-44. Distribution of residual errors in models of recovery of propargite by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

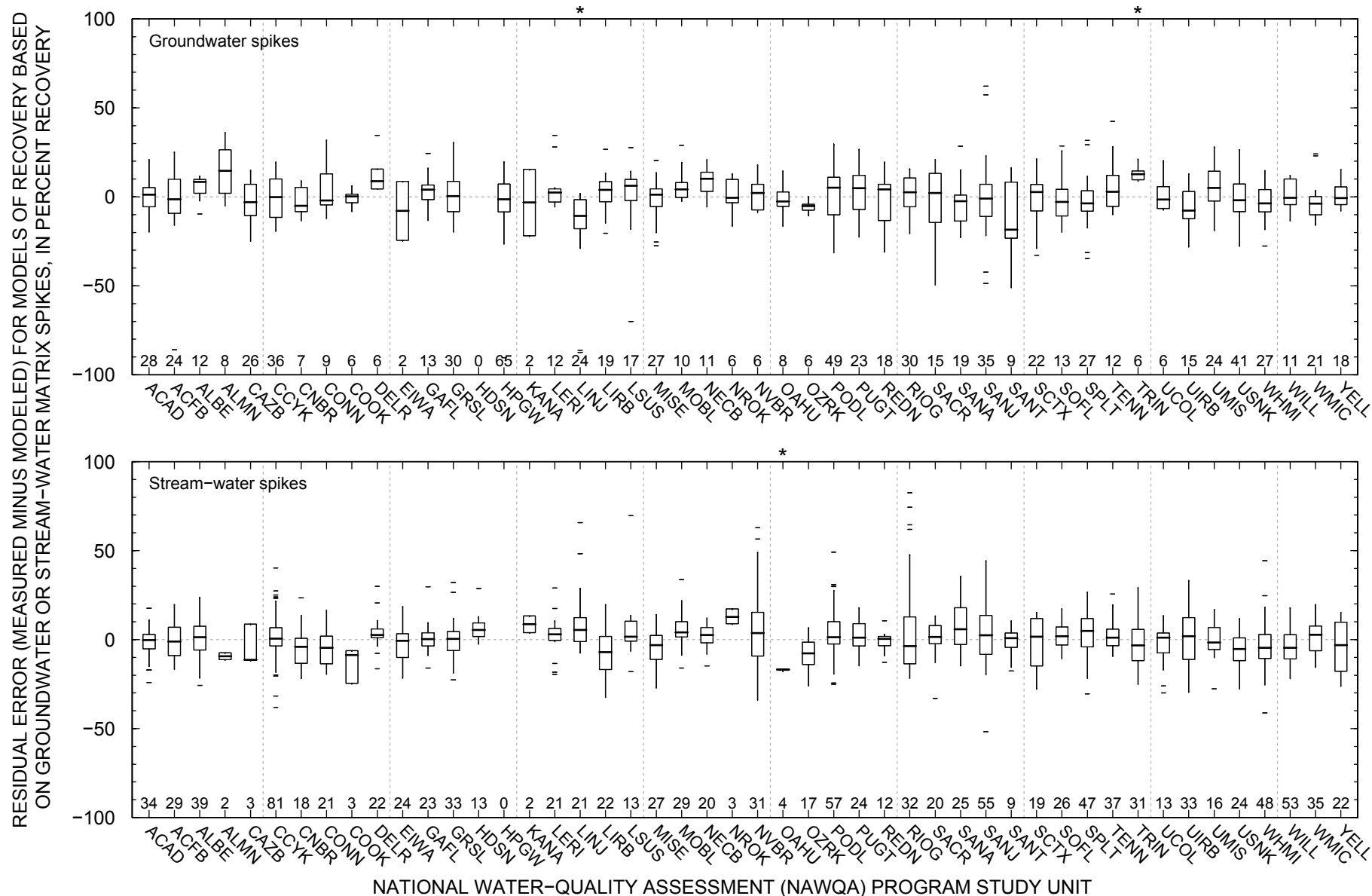


Figure A6-45. Distribution of residual errors in models of recovery of propyzamide by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

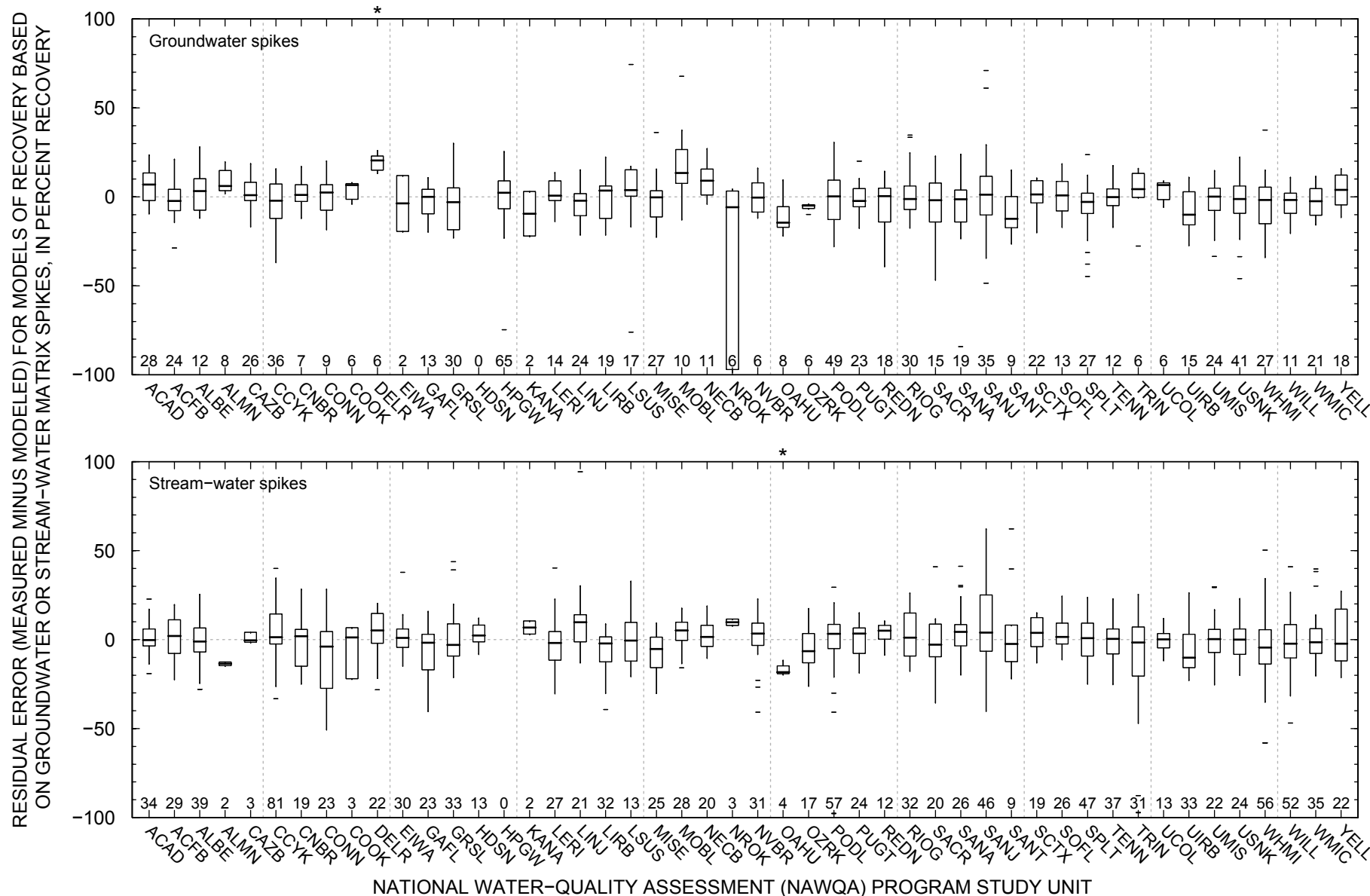


Figure A6-46. Distribution of residual errors in models of recovery of simazine by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).



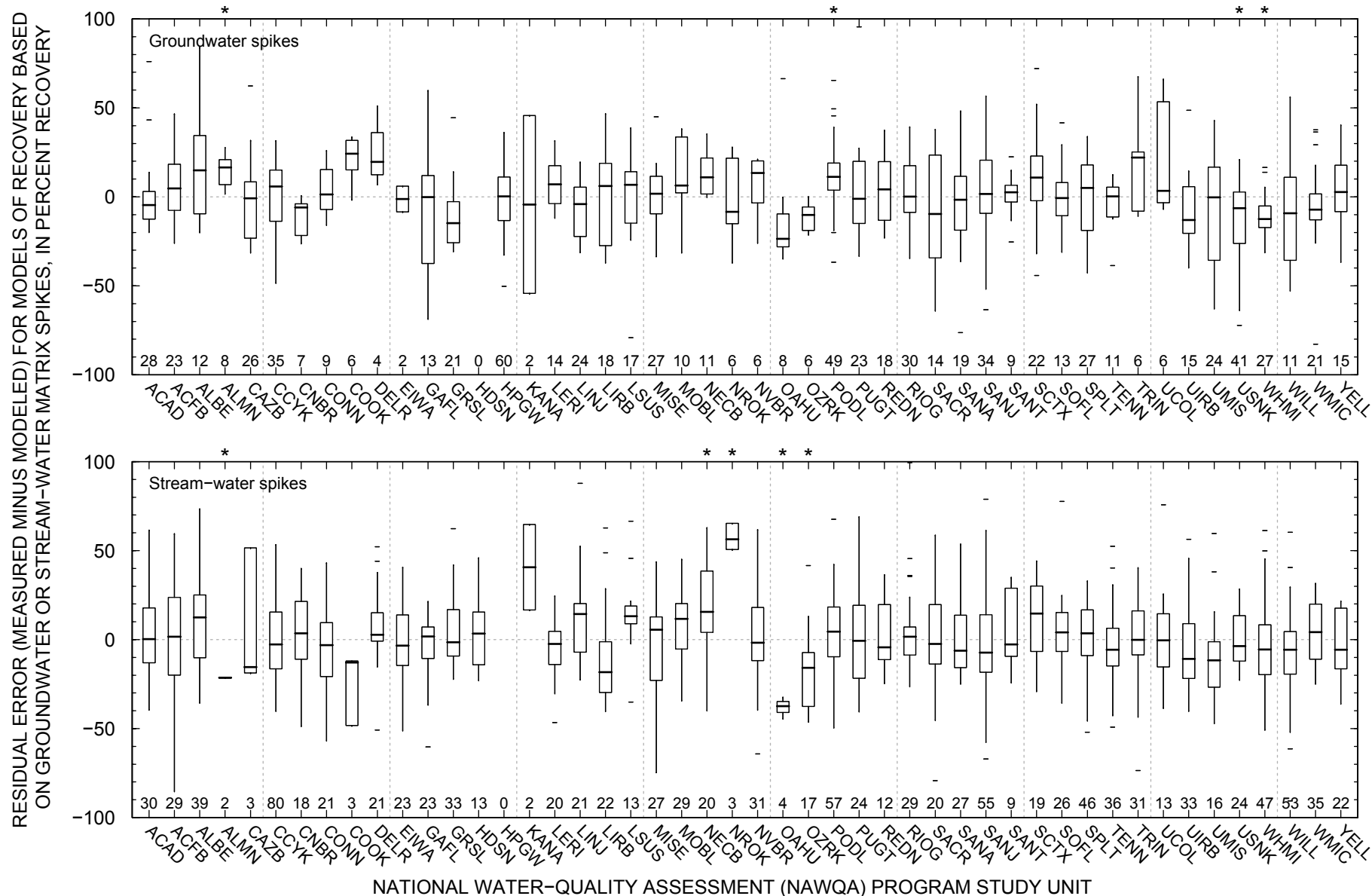


Figure A6-47. Distribution of residual errors in models of recovery of tebuthiuron by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

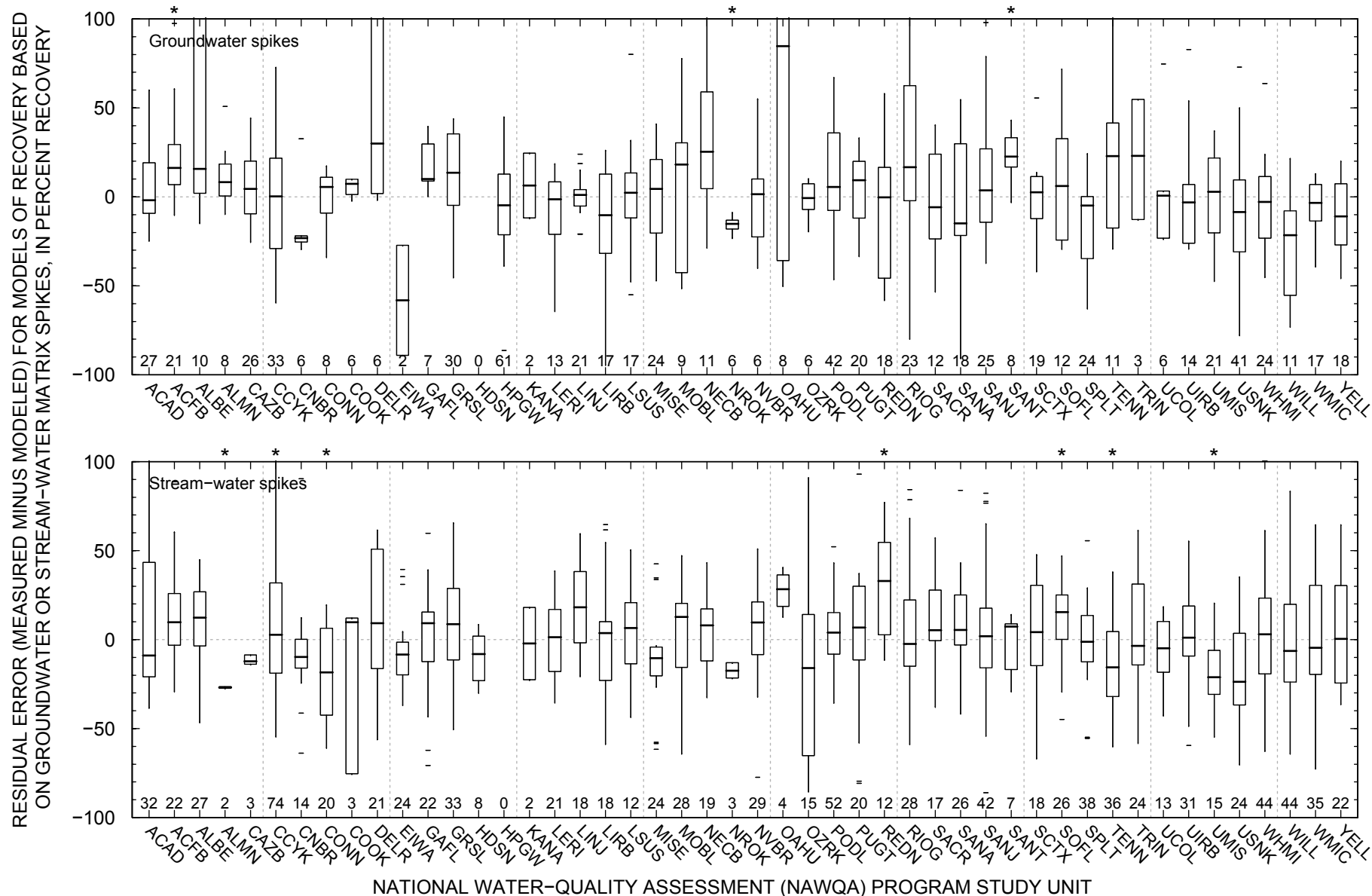


Figure A6-48. Distribution of residual errors in models of recovery of terbacil by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

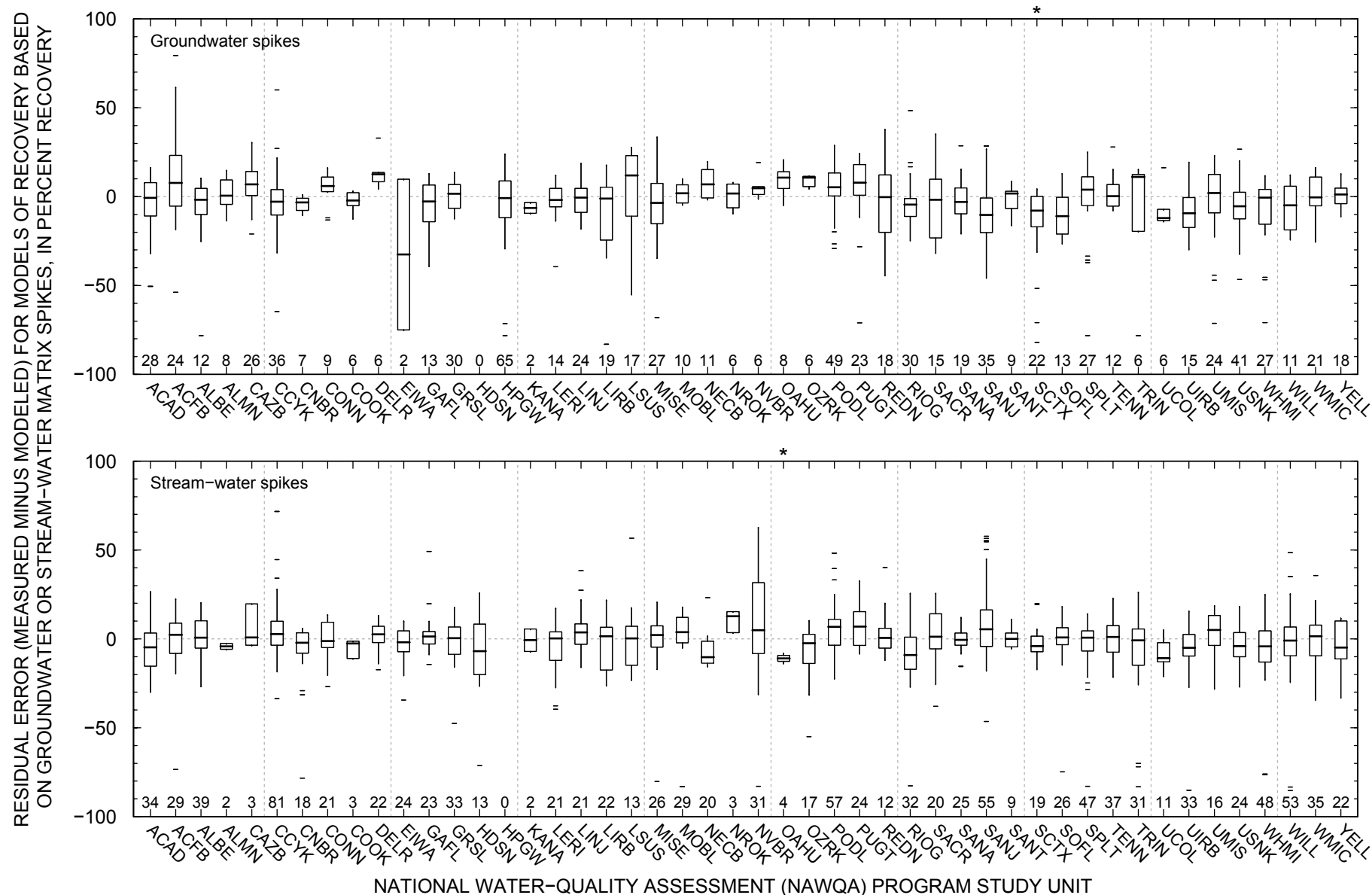


Figure A6-49. Distribution of residual errors in models of recovery of terbufos by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

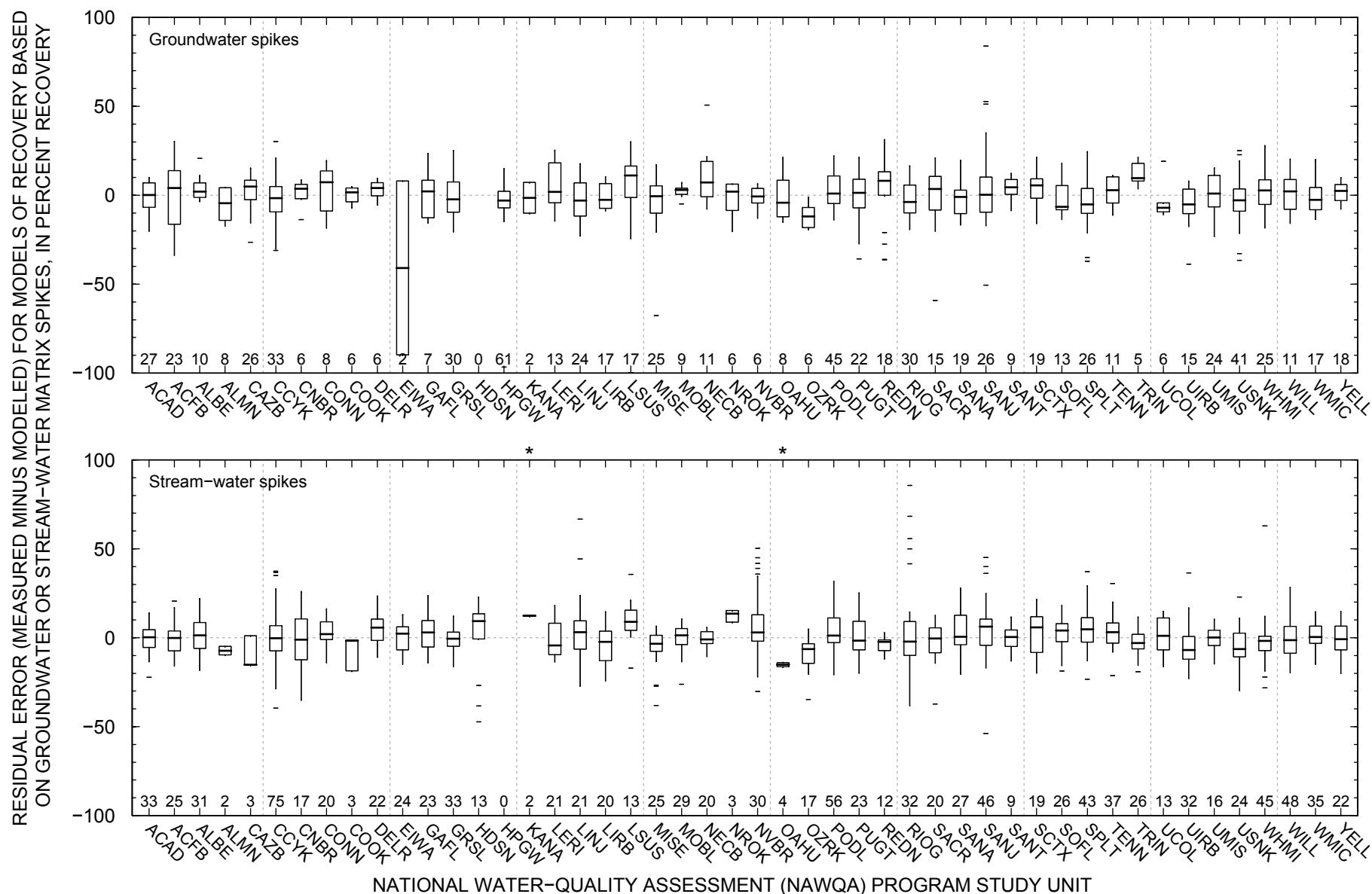


Figure A6-50. Distribution of residual errors in models of recovery of thionocarb by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

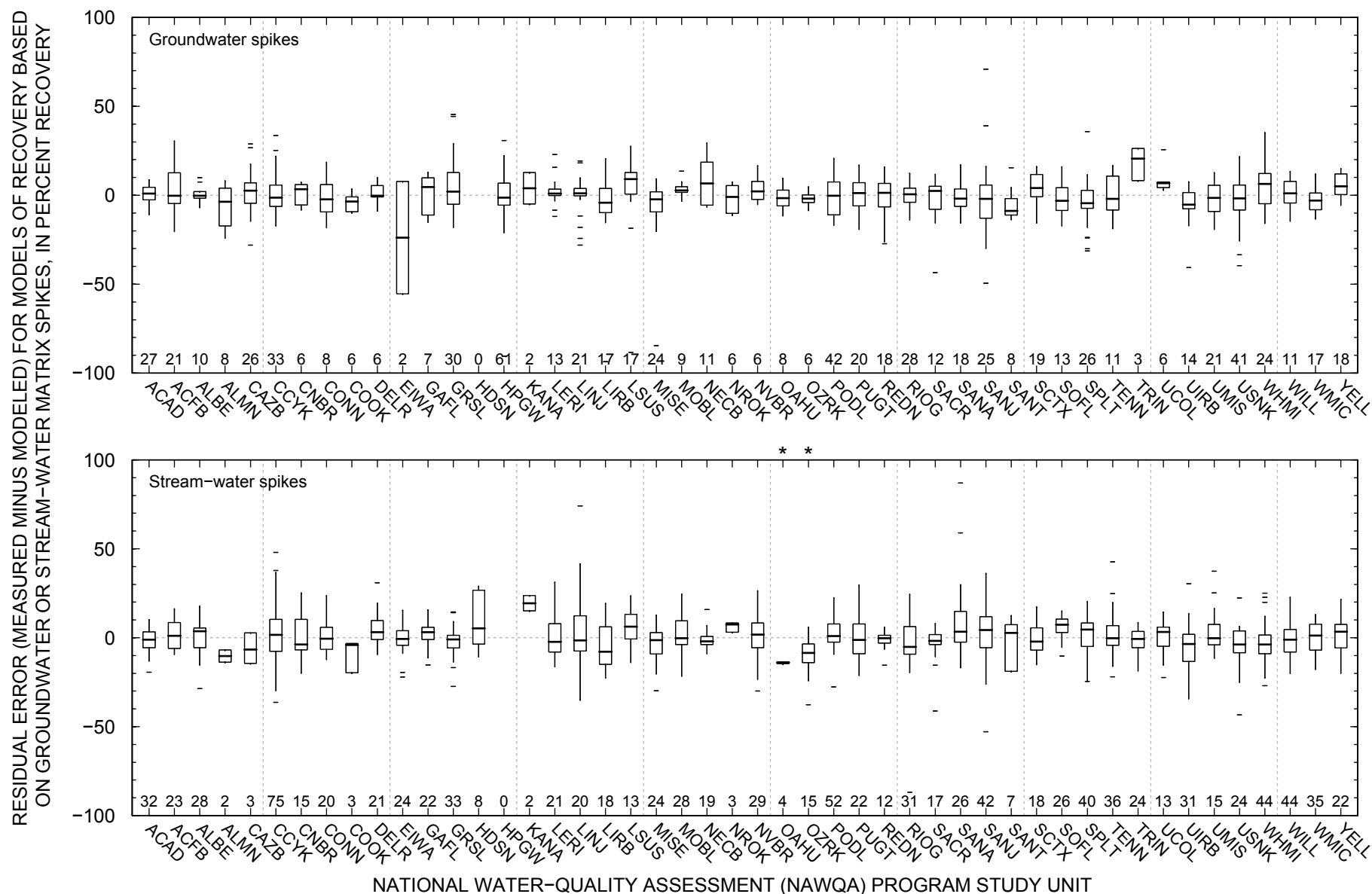


Figure A6-51. Distribution of residual errors in models of recovery of triallate by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).

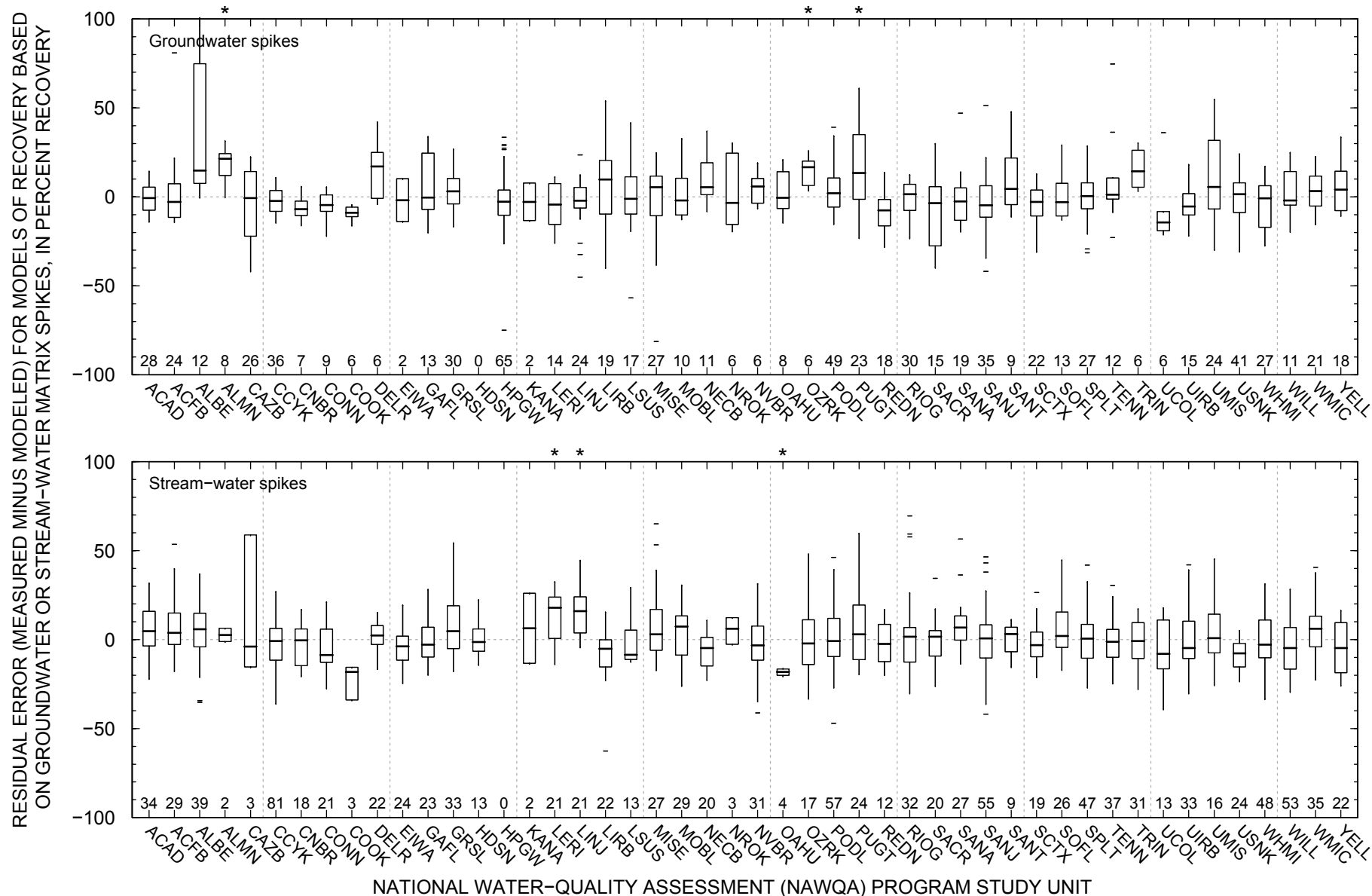


Figure A6-52. Distribution of residual errors in models of recovery of trifluralin by NAWQA Study Unit. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates Study Units where mean residual error (1) is significantly different from 0 ( $p < 0.01$ ) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than -100 percent are not shown).