Table 1: Detailed method performance breakdown

Step-by-step success rates in the hierarchical detection pipeline

| Pipeline Step | Method Used | Success (n) | Missing (n) | Success Rate | Notes |
| --- | --- | --- | --- | --- | --- |
| qPCR infection detection | Melting curve analysis | 185 | 151 | 55.1% | Primary method for infection presence/absence |
| qPCR species identification | Melting curve patterns | 49 | 287 | 14.6% | Limited by time constraints |
| Amplicon species identification | 18S/28S sequencing | 134 | 202 | 39.9% | Backup method when qPCR species ID unavailable |
| Final species assignment | Hierarchical combination | 169 | 167 | 50.3% | 49 qPCR + 120 amplicon = 169 total |
| Complete data for modeling | Both infection status + species ID | 169 | 167 | 50.3% | Used for downstream random forest validation |