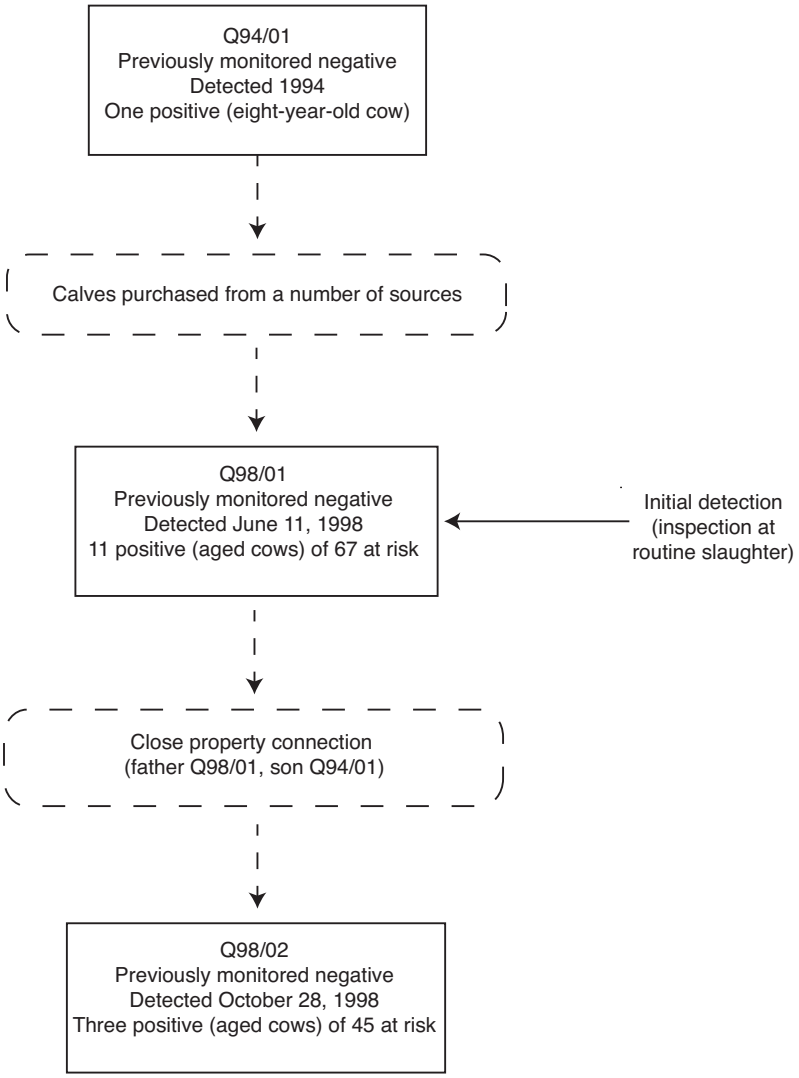
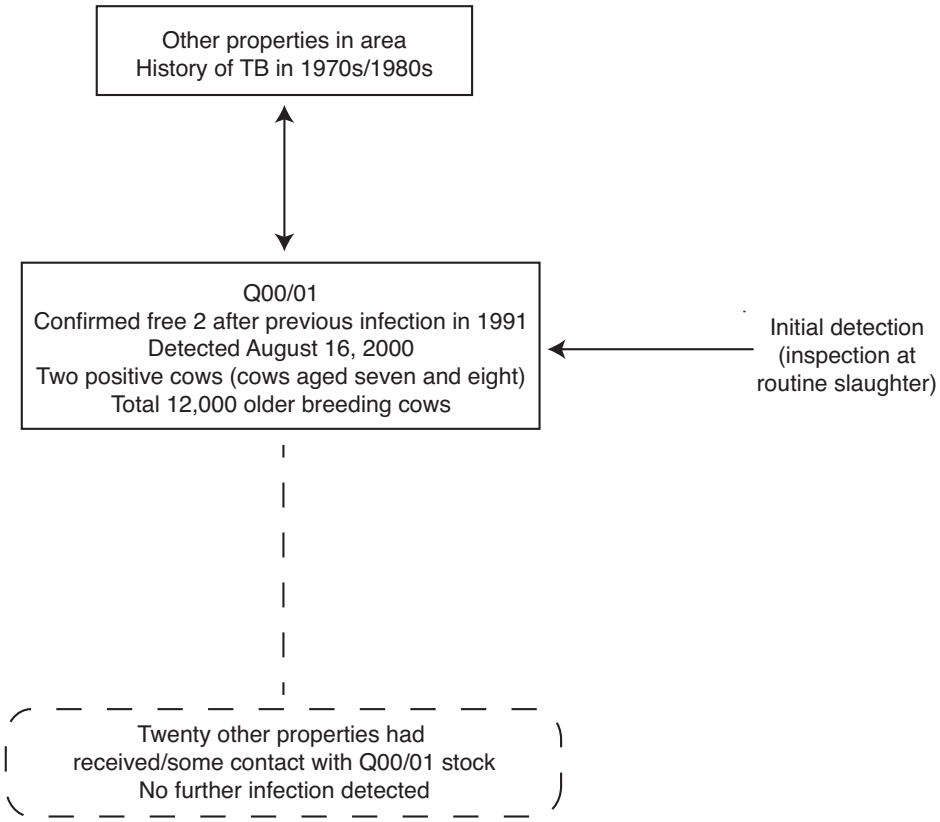
Review

Supplementary Data
Appendix A - Queensland cluster one



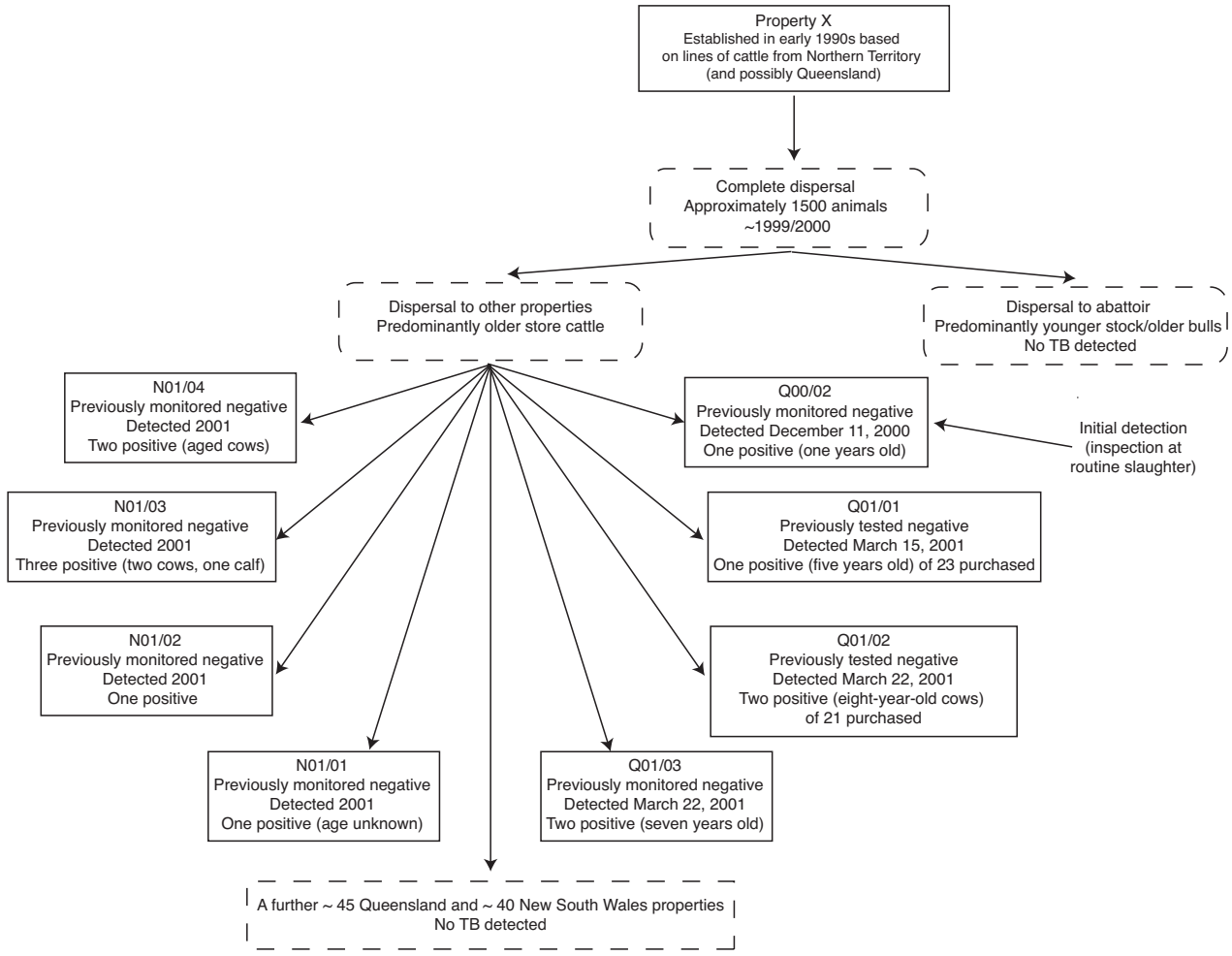
- Disease was detected in Q98/01 cattle during routine slaughter.
- Disease was detected in Q98/02 cattle during trace-forward (destock) slaughter.
- Very high prevalence of infection on Q98/01 (11/67 = 16.4 per cent).
- There was some evidence (although not conclusive) that Q94/01 was the source of infection for Q98/01 based on DNA fingerprinting, management links and presence in the same locality.
- Based on knowledge of management, it is probable that the animals on Q98/02 had become infected while on Q98/01. If so, this would have increased the prevalence on Q98/01 to 14/67 = 20.9 per cent.
- DNA fingerprinting suggested a link to Q94/01, where a single infected eight-year-old cow was found. Q94/01 had been on monitored negative status.

Appendix B - Queensland cluster two



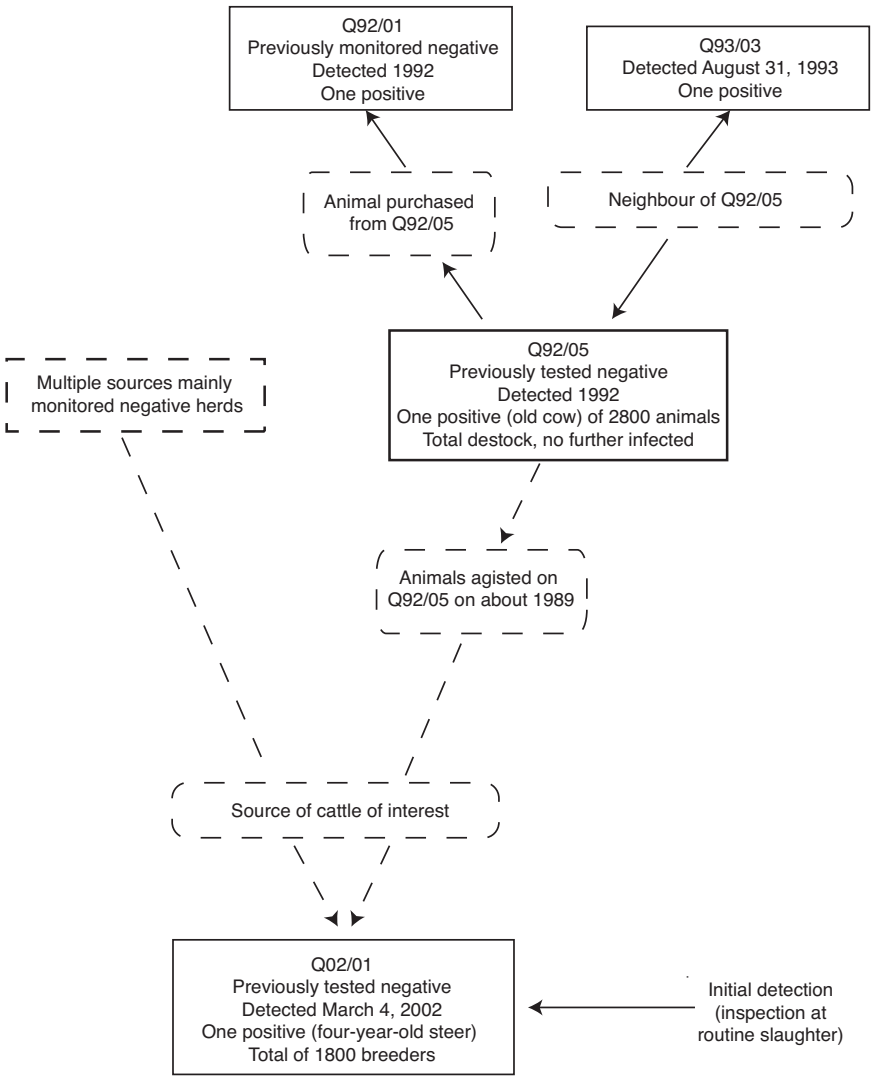
- Disease was detected during routine slaughter of Q00/01 cattle.
- An eradication programme (property testing, extensive area destock) had been implemented on Q00/01 following the previous detection of disease in 1991, and the property had achieved a confirmed free 2 status in 1993.
- Between 1993 and 2000, 5171 cattle were sent to slaughter from this property. A number of granulomas were submitted from these animals under the NGSP, and all were considered negative to tuberculosis.
- Prevalence was extremely low. It was not possible to calculate an exact prevalence figure because the total number of at-risk animals was uncertain (could have been as many as 12,000 older breeding cows; therefore minimum prevalence was 2/12,000 = 0.02 per cent).
- There was evidence of extremely limited transmission of infection. Because the two cows were born after the 1991 eradication programme, infection must have spread to these animals from another animal that had been infected before 1991.
- DNA fingerprinting indicated a common strain, but nonetheless the same strain as that detected on the property in 1991.

Appendix C - Queensland cluster three



- Disease was first detected in a young Q00/02 animal during routine slaughter.
- Disease was later detected in Q01/01, Q01/02, Q01/03, N01/01, N01/02, N01/03 and N01/04 following identification of the link between property X and subsequent trace-forward (destock) slaughter.
- The source of infection at the original property (X) was not established. It is likely that infection had been present at property X since the establishment of this herd in 1990 (via Northern Territory/Queensland purchases or residual infection). At least one of the source properties in Queensland (Y) had been confirmed as infected, however, at the time of the outbreak, property Y had long-since been disbanded.
- There had been no TB testing on property X before herd dispersal.
- At the time of dispersal, prevalence was very low. It was not possible to calculate an exact prevalence figure because the total number of at-risk animals was uncertain (could be as many as 1500 animals; therefore minimum prevalence was 12/1500 = 0.8 per cent).
- More animals may have been infected, although these should have been detected given the intensity of the surveillance effort on all other animals from property X (abattoir surveillance for all animals consigned to slaughter, testing of dispersed animals via testing on all trace-forward properties). Animals on trace-forward properties were probably more likely to be infected than those dispersed directly to an abattoir, based on their age. Consequently, there may have been few infected animals among those consigned from property X directly to slaughter.
- There was very little evidence of transmission of infection following dispersal, apart from infection of a young calf on N01/03. This animal was probably the progeny of an infected cow, although they were slaughtered separately and the dam-progeny linkage was not established with certainty.
- DNA fingerprinting suggested a common strain, and did not assist understanding of source.

Appendix D - Queensland cluster four



- Disease was detected during routine slaughter of Q02/01 cattle.
- The infected animal on Q02/01 was only four years of age.
- The prevalence of disease on Q02/01 was extremely low. It was not possible to calculate an exact prevalence figure because the total number of at-risk animals was uncertain (could be as many as 1800 breeders plus an equal number of progeny; therefore, the minimum expected prevalence in affected groups was 1/3600 = 0.03 per cent).
- Based on available evidence, Q92/05 may have been the source of infection for Q02/01. Q92/05 was a property where some Q02/01 had been agisted in the early 1990s. It was also part of a cluster of infection in the early 1990s. If so, there presumably was an older animal (never identified) which linked the Q02/01 infected animal with this earlier source of infection.
- In the Q92/05 cluster, disease prevalence had been extremely low. On Q92/05, for example, the prevalence was possibly as low as 1/2800 = 0.04 per cent (but would be higher if all animals were not at equal risk of infection).