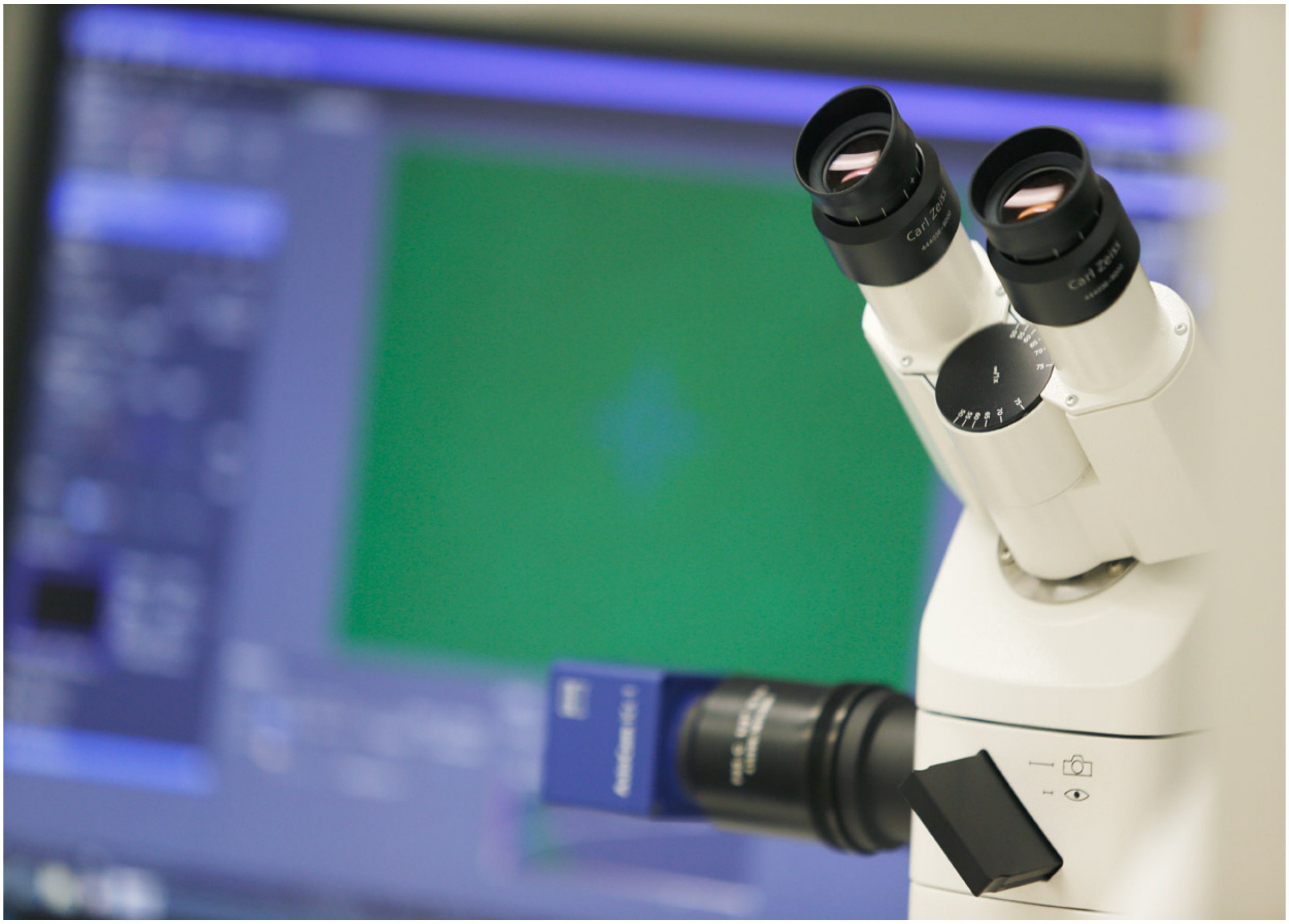
Measles Molecular Epidemiology: Australia 2014



Victorian Infectious Diseases Reference Laboratory

Summary Report

VIDRL
Victorian Infectious Diseases Reference Laboratory

Doherty Institute
A joint venture between the University of Melbourne and the Royal Melbourne Hospital

Measles Molecular Epidemiology in Australia 2014

Between January and December 2014 measles genotyping was attempted on 224 samples with genotyping possible from 209 cases. The remaining 16 cases had a virus load (ct ≥ 36) that was too low for genotyping (untypable). The breakdown of genotyped samples by state and territory was: Victoria 73, New South Wales 41, Australian Capital Territory 4, Northern Territory 61, Western Australia 37, South Australia 1 and Tasmania 7. An additional 46 genotyping results were submitted directly to the WHO Measles Nucleotide Surveillance database by Queensland Health Scientific Services.

Measles cases were detected in 47 of the 52 reporting weeks (Figure 1) with measles circulation identified in all Australian states and Territories (Figure 3). At least 14 countries were identified as possible sources with the majority of cases linked to importation or were import-related. Seven measles virus genotypes were identified: A (vaccine), B3, D4, D8, D9, G3, and H1.

Genotype B3, the most common type detected (n=155), circulated after at least 24 separate cases were introduced from the Philippines (Figure 2), where a large outbreak has been occurring since October 2013. This Asian phylogenetic lineage of B3 was also imported from Indonesia, Vietnam, Hong Kong, Singapore and Papua New Guinea (Figure 4). A single case of genotype B3 with African lineage was also imported from Somalia (Figure 4). Although it may appear that there was sustained transmission of this genotype for 35 weeks, from 1/2014 to 35/2014, phylogenetic and epidemiological analysis reveals that this was not the case. In this example, chains of transmission were not continuous, with prolonged circulation of this genotype the result of multiple importations (Figure 2).

Forty-five cases of genotype D8 were detected in New South Wales, Western Australia, Victoria, Tasmania, Australian Capital Territory and the Northern Territory. There were 3 phylogenetic lineages of genotype D8 identified (Figure 5). Cases from lineage 1 and lineage 2 were predominately imported from south-east Asia (Indonesia and Viet Nam respectively). The third lineage of D8 was of European origin.

The genotype D9 samples (n=23) MVN-450 sequences formed 4 distinct phylogenetic lineages. Cases from 2 of the lineages were imported from Indonesia with the origins of the remaining 2 lineages from Thailand and the Philippines. The majority of D9 cases were detected in Queensland and Victoria.

Twelve cases of genotype H1, forming 2 discrete lineages, were imported from Viet Nam, Singapore and Thailand. There was also a single case of genotype G3 from a traveller returning from Indonesia.

Measles-vaccine associated cases were detected in 18 individuals all of which shared an identical N450 sequence to the vaccine strain (1 nucleotide different to wild-type Edmonston strain).

Figure 1. Distribution of measles genotypes identified at VIDRL by epi-week, Jan-Dec 2014.

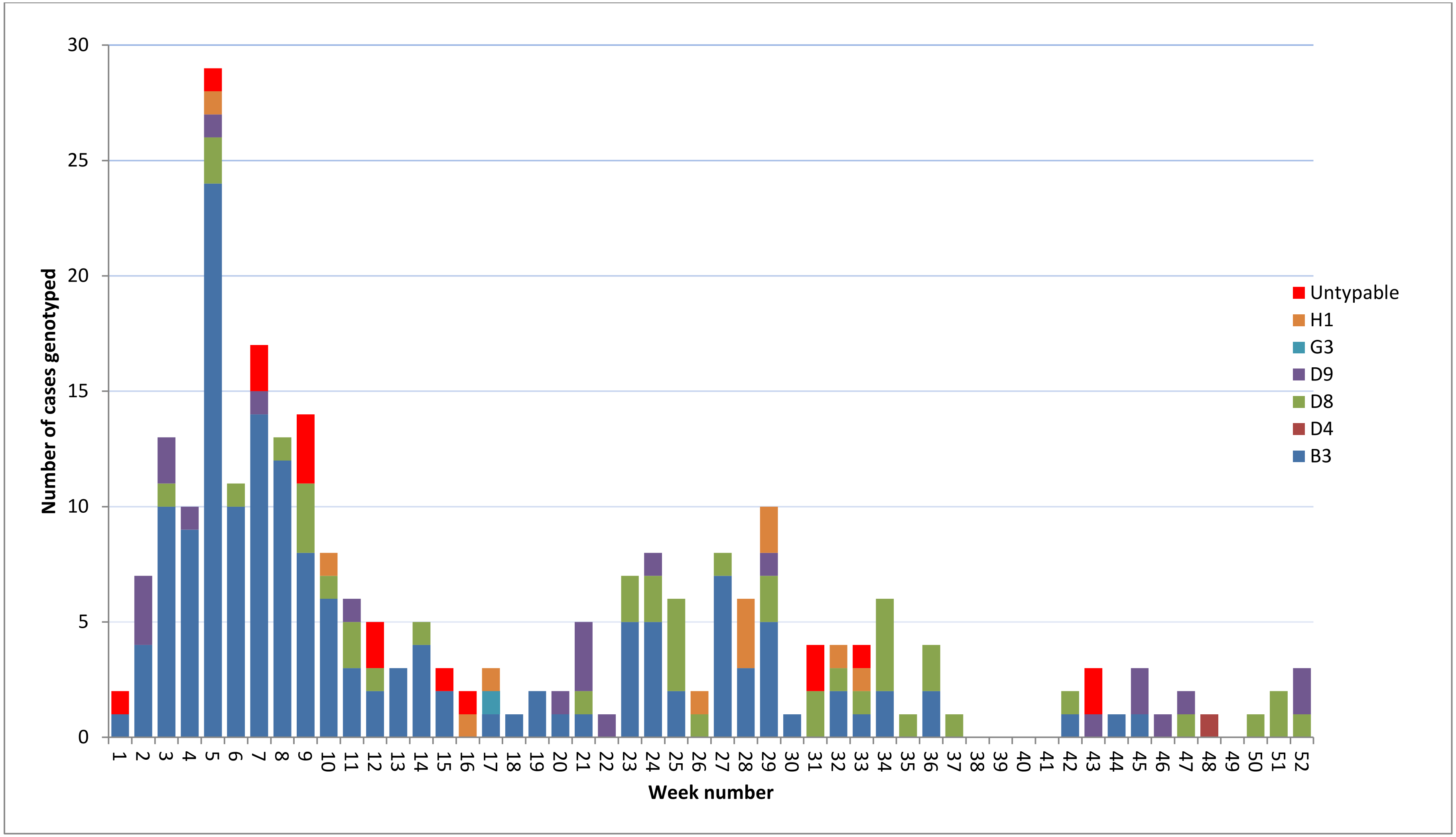
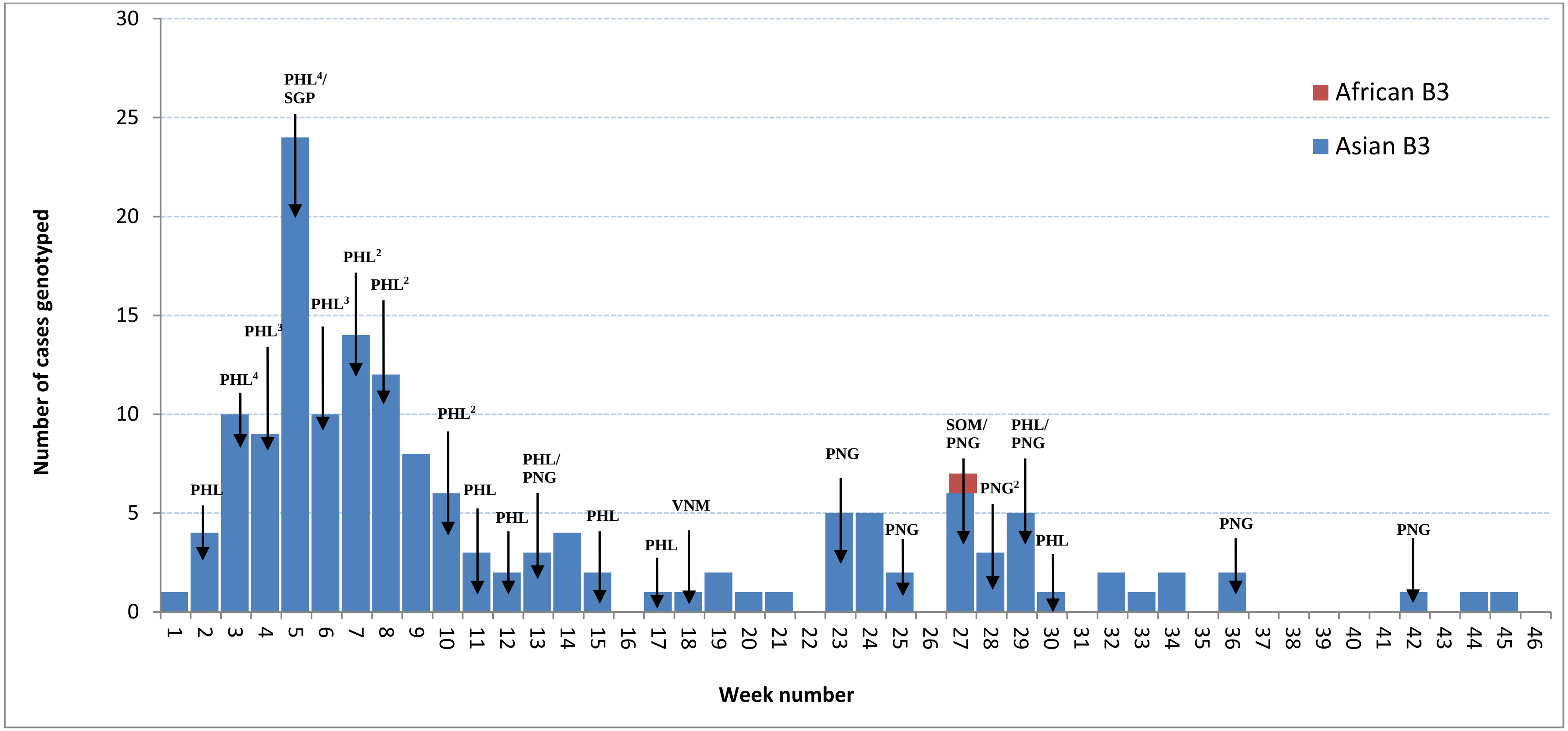
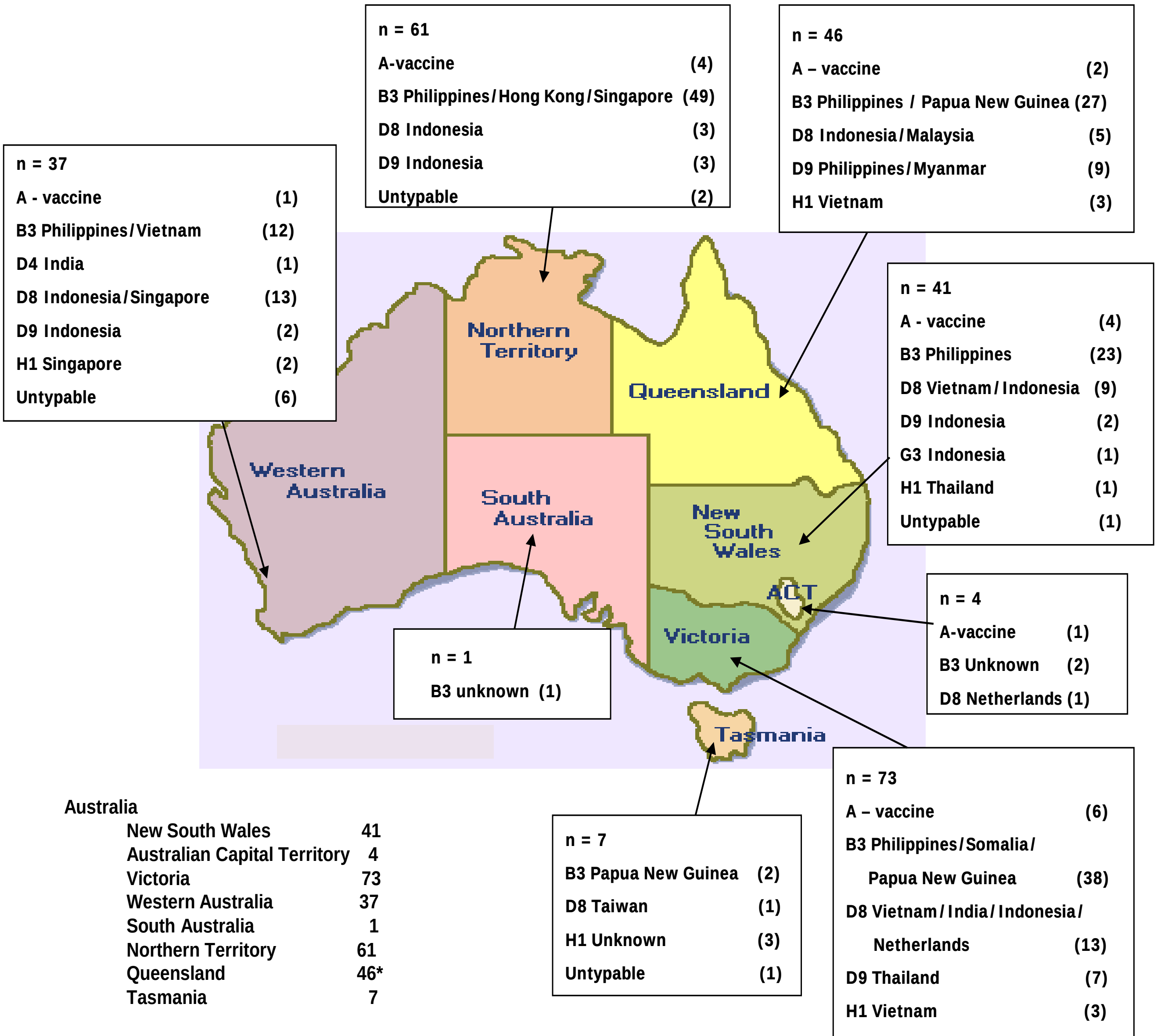


Figure 2. Distribution of measles genotype B3 identified at VIDRL by epi-week, Jan-Dec 2014.



Country codes of importation assiociated with clusters are indicated (THA = Thailand; KHM = Cambodia; PHL = Philippines; SGP = Singapore; PNG = Papua New Guinea; VNM = Viet Nam; SOM = Somalia. Superscripted numbers denote number of importations

Figure 3. Measles virus genotypes imported into Australian states and territories (January to December 2014 inclusive). The countries of importation are indicated (unknown = source of infection not determined). The source country of each confirmed measles case is based on the travel history provided to VIDRL and may not necessarily represent the 'true' country of origin for that genotype, since contact with the measles virus may have occurred in transit.



n = 37
A - vaccine (1)
B3 Philippines/Vietnam (12)
D4 India (1)
D8 Indonesia/Singapore (13)
D9 Indonesia (2)
H1 Singapore (2)
Untypable (6)

n = 61
A-vaccine (4)
B3 Philippines/Hong Kong/Singapore (49)
D8 Indonesia (3)
D9 Indonesia (3)
Untypable (2)

n = 46
A – vaccine (2)
B3 Philippines / Papua New Guinea (27)
D8 Indonesia/Malaysia (5)
D9 Philippines/Myanmar (9)
H1 Vietnam (3)

n = 41
A - vaccine (4)
B3 Philippines (23)
D8 Vietnam/Indonesia (9)
D9 Indonesia (2)
G3 Indonesia (1)
H1 Thailand (1)
Untypable (1)

n = 4
A-vaccine (1)
B3 Unknown (2)
D8 Netherlands (1)

n = 1
B3 unknown (1)

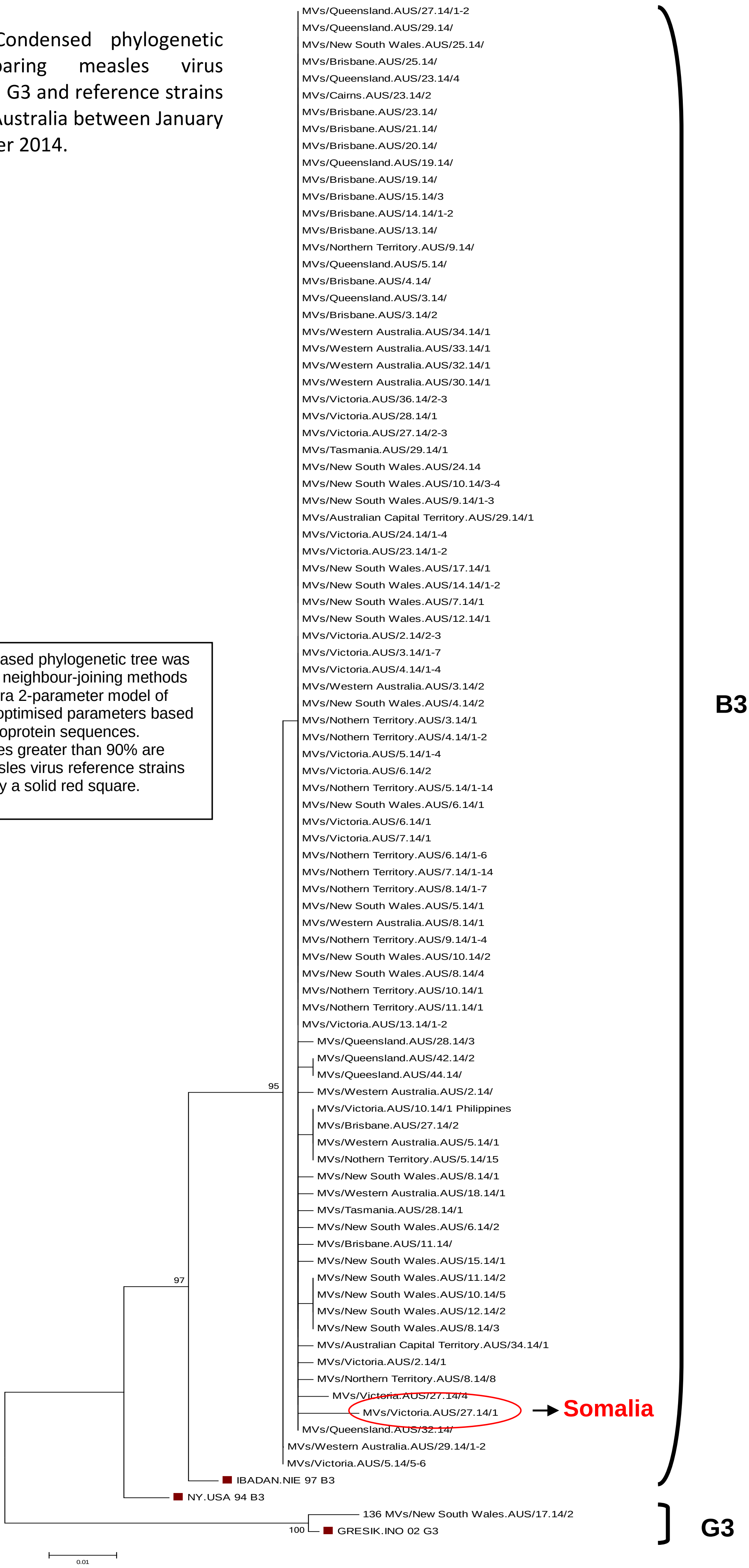
n = 7
B3 Papua New Guinea (2)
D8 Taiwan (1)
H1 Unknown (3)
Untypable (1)

n = 73
A – vaccine (6)
B3 Philippines/Somalia/Papua New Guinea (38)
D8 Vietnam/India/Indonesia/Netherlands (13)
D9 Thailand (7)
H1 Vietnam (3)
Untypable (6)

Australia	
New South Wales	41
Australian Capital Territory	4
Victoria	73
Western Australia	37
South Australia	1
Northern Territory	61
Queensland	46*
Tasmania	7

* Forty-six N-450 sequences were provided by QHL

Figure 4. Condensed phylogenetic tree comparing measles virus genotype B3, G3 and reference strains detected in Australia between January and December 2014.



The distance-based phylogenetic tree was constructed by neighbour-joining methods using the Kimura 2-parameter model of evolution with optimised parameters based on 450nt nucleoprotein sequences. Bootstrap values greater than 90% are indicated. Measles virus reference strains are indicated by a solid red square.

Figure 5. Phylogenetic tree comparing measles virus genotype D4, D8, D9, H1 and reference strains detected in Australia between January and December 2014.

The distance-based phylogenetic tree was constructed by neighbour-joining methods using the Kimura 2-parameter model of evolution with optimised parameters based on 450nt nucleoprotein sequences. Bootstrap values greater than 90% are indicated. Measles virus reference strains are indicated by a solid red square.