EXHIBIT AG

Australian National University

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Prof. Carola G Vinuesa, MBBS (LMS), PhD, FAA
NHMRC Principal Research Fellow
Elizabeth Blackburn Fellow

Director, NHMRC Centre of Research Excellence
Centre for Personalised Immunology
John Curtin School of Medical Research
Australian National University
M: +61 432 130 446
carola.vinuesa@anu.edu.au

Canberra ACT 2001, Australia

Re: Report on Whole Exome Sequencing analysis from Kathleen Folbigg

We have performed whole exome sequencing on Kathleen Folbigg's genomic DNA extracted from both buccal swab and saliva. Excellent coverage was obtained from both samples (20-50x).

Analysis of the exome for variants in genes previously shown to cause sudden unexpected death has identified two candidates:

Gene	Mutation (protein)	Inheritance	Frequency	Disease association
CALM2	p.(Gly114Arg)	AD	Novel	Long QT syndrome (LQTS)

The variant in *CALM2* is novel and has not been reported to-date (either in healthy populations or in patients with long QT syndrome). In silico analysis predicts that the amino acid substitution is damaging. Other heterozygous mutations in *CALM2* have been associated LQTS and sudden death in infancy and childhood [1,2].

Gene	Mutation (protein)	Inheritance	Frequency	Disease association
MYH6	p.(Pro82Ser)	AD	0.000008	Atrial septal defect Hypertrophic cardiomyopathy Sick Sinus Syndrome

The variant in *MY6H* is ultra-rare and is not listed in ClinVar. In silico analysis predicts that the mutation is damaging. Other mutations in *MYH6* have been associated with cardiac disease (atrial septal defects, hypertrophic cardiomyopathy and sinus node dysfunction, with early onset, recurrent, and fatal arrhythmias)[3].

Given the associations between heterozygous mutations in both genes and sudden cardiac death, cardiac investigation in Kathleen Folbigg is advisable and genetic investigation in the deceased children is warranted. Additional rare variants have been identified in 8 other genes associated with sudden death.

Further analysis of the contribution of the variants in *CALM2, MYH6* (and possibly others) to the fatal outcome of Kathleen Folbigg's offspring would depend on analysis of paternal and children's exomes.

Sincerely,

Carola G. Vinuesa

References
1. Crotti L et al., Calmodulin mutations associated with recurrent cardiac arrest in infants, Circulation. 2013;127:1009-1017
2. Makita N et al., Novel Calmodulin mutations associated with congenital arrhythmia susceptibility, Circ Cardiovasc Genet. 2014; 7: 466-474
3. Lam L et al., Exome sequencing identifies a novel mutation in the MYH6 gene in a family with early-onset sinus node dysfunction, ventricular arrhythmias, and cardiac arrest. Heart Rhythm Case Reports, Vol 1, No3, May2015.