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Supporting Information

Supplementary table

This appendix was part of the submitted manuscript and has been peer reviewed. It is posted as supplied by the authors.

Appendix to: De Silva DL, James PA, Mann GB, Lindeman GJ. Universal genetic testing of patients with newly diagnosed breast cancer — ready for prime time? *Med J Aust* 2021; doi: 10.5694/mja2.51317.

Classification scheme for management of variants of uncertain significance*

Class	Description	Probability of pathogenicity	Counselling and management
Class 5	Definitely pathogenic	> 0.99	Consider as “mutation detected” and manage appropriately. Can be used for genetic testing of at-risk relatives.
Class 4	Likely pathogenic	0.95–0.99	Consider as “mutation detected” and manage appropriately. Can be used for genetic testing of at-risk relatives.
Class 3	Uncertain	0.05–0.949	Consider as “no mutation detected”. Not to be used for predictive testing in at-risk relatives. Personal management will depend on clinic pathological features and family history.
Class 2	Likely not pathogenic or of little clinical significance	0.001–0.049	Consider as “no mutation detected”. Not to be used for predictive testing in at-risk relatives.
Class 1	Not pathogenic or of no clinical significance	< 0.001	Consider as “no mutation detected”. Not to be used for predictive testing in at-risk relatives.

* This classification system has been recommended by the International Agency for Research on Cancer (Plon SE, Eccles DM, Easton D, et al. Sequence variant classification and reporting: recommendations for improving the interpretation of cancer susceptibility genetic test results. *Hum Mutat* 2008; 29: 1282–1291) and has been widely adopted as a framework for managing variants of uncertain significance. Class 1 and 2 variants are usually not reported.