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Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Research policies, see our Editorial Policies and the Editorial Policy Checklist.

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For	ali statisticai an	lalyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.			
n/a	Confirmed				
	The exact	sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement			
	A stateme	ent on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly			
	The statistical test(s) used AND whether they are one- or two-sided Only common tests should be described solely by name; describe more complex techniques in the Methods section.				
	A descript	cion of all covariates tested			
	A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons				
	A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)				
	For null hypothesis testing, the test statistic (e.g. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted <i>Give P values as exact values whenever suitable.</i>				
\boxtimes	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings				
	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes				
	\square Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated				
Our web collection on <u>statistics for biologists</u> contains articles on many of the points above.					
Software and code					
Policy information about <u>availability of computer code</u>					
Da	ata collection	PerkinElmer Vectra Automated Multispectral Imaging System			
Da	ata analysis	GraphPad Prism version 7.00 (California USA); R package "meta ", 4.15-1; R version 3.6.1.			
For m	nanuscripts utilizing	g custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and			

Data

Policy information about <u>availability of data</u>

All manuscripts must include a <u>data availability statement</u>. This statement should provide the following information, where applicable:

reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

All sequencing data are deposited to European Genome-phenome Archive which are available upon request to corresponding author

Field-spe	cific reporting		
Please select the or	ne below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.		
\(\sum_{\text{life sciences}}\)	Behavioural & social sciences Ecological, evolutionary & environmental sciences		
For a reference copy of t	he document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf		
Life scier	ices study design		
All studies must dis	close on these points even when the disclosure is negative.		
Sample size	The sample size was the maximum number of cases and controls available for analysis.		
Data exclusions	Cases were excluded if a mutation in BRCA1 or BRCA2 was detected.		
Replication	not applicable		
Randomization	Tases and controls were not randomized. Cases were women with a personal and family history of breast cancer. Controls were cancer free women from the general population.		
Blinding	There was no blinding. The data generated was sequencing data to determine the presence or absence of a mutation. The mutation calling was performed by an automated pipeline for both cases and controls. This is not influenced by interpretation biases.		
We require informatic system or method list Materials & exp n/a Involved in th Antibodies Eukaryotic Palaeontolo Animals an Human reso Clinical date	ChIP-seq cell lines Flow cytometry by and archaeology MRI-based neuroimaging d other organisms earch participants		
Antibodies			
Antibodies used	NTHL1 antibody (Abcam, Branford, Connecticut, USA), AE1/AE3 antibody (multi-cytokeratin antibody, Leica Biosystems, Wetzlar, Germany), HRP-labelled anti-rabbit antibody (PerkinElmer Waltham, Massachusetts, USA) and anti-mouse antibody (PerkinElmer, Waltham, Massachusetts, USA).		
Validation	Antibodies have been validated by the manufacturing companies.		
Human resea	arch participants		
Policy information a	about studies involving human research participants		
Population charac	The cases study participants were all female with a personal and family history of breast cancer and over the age of 18. The		

controls were women in the Lifepool cohort (www.lifepool.org) who were above 40 years old and cancer-free as of May

2016

Recruitment The cases were recruited through familial cancer centres in Australia and the controls were recruited through breast screen Victoria.

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Ethics oversight the Human Research Ethics Committee at the Peter MacCallum Cancer Centre

Note that full information on the approval of the study protocol must also be provided in the manuscript.