

Table S4. All results of gene-based association using germline pathogenic variants

	No. of pathogenic variant carrier (%)				^a Model 1					^b Model 2				
	Lymphoma (N = 1,982)		Control (N = 37,592)		OR (95% CI)				P value	OR (95% CI)				P value
<i>APC</i>	0	(0.00)	3	(0.01)	NA	NA	–	NA	NA	NA	NA	–	NA	NA
<i>ATM</i>	8	(0.40)	59	(0.18)	2.58	(1.23	–	5.40)	1.21×10^{-2}	2.63	(1.25	–	5.51)	1.06×10^{-2}
<i>BARD1</i>	1	(0.05)	19	(0.05)	1.00	(0.13	–	7.46)	0.999	1.03	(0.14	–	7.74)	0.974
<i>BMPR1A</i>	0	(0.00)	0	(0.00)	NA	NA	–	NA	NA	NA	NA	–	NA	NA
<i>BRCA1</i>	8	(0.40)	26	(0.07)	5.86	(2.65	–	12.95)	1.27×10^{-5}	5.88	(2.65	–	13.02)	1.27×10^{-5}
<i>BRCA2</i>	12	(0.61)	79	(0.21)	2.89	(1.57	–	5.32)	6.29×10^{-4}	2.94	(1.60	–	5.42)	5.25×10^{-4}
<i>BRIP1</i>	0	(0.00)	50	(0.13)	NA	NA	–	NA	NA	NA	NA	–	NA	NA
<i>CDH1</i>	0	(0.00)	5	(0.01)	NA	NA	–	NA	NA	NA	NA	–	NA	NA
<i>CDK4</i>	0	(0.00)	1	(0.00)	NA	NA	–	NA	NA	NA	NA	–	NA	NA
<i>CDKN2A</i>	0	(0.00)	3	(0.01)	NA	NA	–	NA	NA	NA	NA	–	NA	NA
<i>CHEK2</i>	1	(0.05)	35	(0.09)	0.54	(0.07	–	3.96)	0.546	0.55	(0.08	–	4.04)	0.559
<i>EPCAM</i>	1	(0.05)	8	(0.02)	2.37	(0.30	–	18.97)	0.416	2.66	(0.33	–	21.36)	0.359
<i>HOXB13</i>	0	(0.00)	9	(0.02)	NA	NA	–	NA	NA	NA	NA	–	NA	NA
<i>MLH1</i>	0	(0.00)	2	(0.01)	NA	NA	–	NA	NA	NA	NA	–	NA	NA
<i>MSH2</i>	1	(0.05)	3	(0.01)	6.33	(0.66	–	60.84)	0.110	7.00	(0.72	–	67.54)	0.093

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<i>MSH6</i>	0	(0.00)	16	(0.04)	NA	NA	–	NA	NA	NA	NA	–	NA	NA
^c <i>MUTYH</i>	0	(0.00)	0	(0.00)	NA	NA	–	NA	NA	NA	NA	–	NA	NA
<i>NBN</i>	1	(0.05)	50	(0.13)	0.38	(0.05	–	2.75)	0.337	0.39	(0.05	–	2.80)	0.346
<i>NF1</i>	0	(0.00)	17	(0.05)	NA	NA	–	NA	NA	NA	NA	–	NA	NA
<i>PALB2</i>	2	(0.10)	20	(0.05)	1.90	(0.44	–	8.12)	0.388	1.98	(0.46	–	8.47)	0.359
<i>PMS2</i>	0	(0.00)	17	(0.05)	NA	NA	–	NA	NA	NA	NA	–	NA	NA
<i>PTEN</i>	0	(0.00)	8	(0.02)	NA	NA	–	NA	NA	NA	NA	–	NA	NA
<i>RAD51C</i>	0	(0.00)	14	(0.04)	NA	NA	–	NA	NA	NA	NA	–	NA	NA
<i>RAD51D</i>	11	(0.56)	122	(0.33)	1.71	(0.92	–	3.18)	0.088	1.72	(0.92	–	3.19)	0.088
<i>SMAD4</i>	0	(0.00)	3	(0.01)	NA	NA	–	NA	NA	NA	NA	–	NA	NA
<i>STK11</i>	0	(0.00)	2	(0.01)	NA	NA	–	NA	NA	NA	NA	–	NA	NA
<i>TP53</i>	3	(0.15)	10	(0.03)	5.70	(1.57	–	20.72)	8.25×10^{-3}	5.22	(1.43	–	19.02)	1.23×10^{-2}

^aModel 1: unadjusted in a logistic regression model.

^bModel 2: adjusted by sex and age at entry in a logistic regression model

^cGermline pathogenic variant status was defined as an individual with biallelic pathogenic variants.

Abbreviations: CI, confidence interval; NA, not available; OR, odds ratio.