

Table S1. Sample size and genotype arrays used for each NHL GWAS.

Study	No. of Subjects in Analysis					Genotyping Platform	No. of Autosomal SNPs
	CLL	DLBCL	FL	MZL	Controls		
NCI*	2,140	2,621	2,085	808	6,105	OmniExpress/Omni2.5	554,315
GELA/EPIC		547			525	HumanHap 610K/660W	486,277
GEC	387				294	Affymetrix 6.0	604,007
Mayo		393			172	HumanHap 660W	492,020
SCALE			371		790	HumanHap 317K	289,632
UCSF2*	213	253	209		745	HumanCNV370-Duo	289,900
UCSF1/NHS			119		340	OmniExpress	554,430
Utah	321				403	HumanHap 610K	483,331
<b>Total</b>	<b>3061</b>	<b>3814</b>	<b>2784</b>	<b>808</b>	<b>9374</b>		

\* The same set of controls was used for the different NHL subtypes in the study; however, quality control metrics were applied separately to each set of cases and controls, resulting in small differences in the number of controls and SNPs in the analysis.

**Table S2.** Characteristics of cases and controls included in each NHL subtype analysis.

Study	No. of Subjects		% Female		Mean Age ( $\pm$ SD)	
	Cases	Controls	Cases	Controls	Cases	Controls
<b>CLL</b>						
NCI NHL	2,140	6,105	44.4%	27.3%	65.6 ( $\pm$ 9.7)	66.0 ( $\pm$ 10.4)
USCF2	213	746	36.2%	42.4%	63.9 ( $\pm$ 11.2)	61.5 ( $\pm$ 13.0)
GEC	387	294	34.9%	36.7%	61.3 ( $\pm$ 11.1)	62.5 ( $\pm$ 11.2)
Utah	321	403	40.2%	43.9%	63.0 ( $\pm$ 10.3)	64.1 ( $\pm$ 10.8)
<b>FL</b>						
NCI NHL	2,085	6,105	54.2%	27.3%	60.3 ( $\pm$ 12.1)	66.0 ( $\pm$ 10.4)
USCF2	209	745	47.4%	42.4%	60.9 ( $\pm$ 11.9)	61.5 ( $\pm$ 13.0)
SCALE	371	790	50.4%	68.2%	57.0 ( $\pm$ 9.5)	50.8 ( $\pm$ 11.6)
UCSF1/NHS	119	340	48.7%	100.0%	58.8 ( $\pm$ 12.9)	62.6 ( $\pm$ 8.6)
<b>DLBCL</b>						
NCI NHL	2,621	6,105	51.1%	27.3%	60.7 ( $\pm$ 14.0)	66.0 ( $\pm$ 10.4)
USCF2	253	745	44.3%	42.4%	62.4 ( $\pm$ 13.9)	61.5 ( $\pm$ 13.0)
Mayo	393	172	47.3%	61.6%	61.7 ( $\pm$ 14.4)	51.1 ( $\pm$ 13.8)
GELA/EPIC	547	525	43.0%	55.1%	58.7 ( $\pm$ 16.7)	58.5 ( $\pm$ 9.5)
<b>MZL</b>						
NCI NHL	808	6,102	59.7%	27.3%	64.0 ( $\pm$ 12.1)	66.0 ( $\pm$ 10.4)

**Table S3.** Individual GWAS and combined association results for the risk of each NHL subtype with FROH and F3.

	Study	FROH					F3				
		$\beta$	SE	p-value	I <sup>2</sup>	p <sub>het</sub>	$\beta$	SE	p-value	I <sup>2</sup>	p <sub>het</sub>
<b>CLL</b>	NCI	18.85	4.73	6.73x10 <sup>-5</sup>			27.45	3.47	2.82x10 <sup>-15</sup>		
	GEC	50.61	19.64	0.01			33.84	10.61	0.001		
	UCSF2	20.81	21.81	0.34			43.03	12.16	4.01x10 <sup>-4</sup>		
	Utah	33.78	21.83	0.12			-0.41	13.99	1.0		
	<i>Combined</i>	21.1	4.41	1.59x10 <sup>-6</sup>	0.0%	0.42	27.5	6.51	2.44x10 <sup>-5</sup>	49.7%	0.11
<b>DLBCL</b>	NCI	14.17	4.78	0.003			14.12	3.35	2.55x10 <sup>-5</sup>		
	Mayo	7.96	35.21	0.82			-6.15	19.04	0.75		
	UCSF2	-3.98	20.47	0.85			12.41	11.83	0.29		
	GELA/EPIC	-15.71	7.80	0.04			-15.53	6.53	0.02		
	<i>Combined</i>	0.0	10.89	1.0	72.5%	0.01	2.0	9.57	0.84	82.4%	0.001
<b>FL</b>	NCI	6.72	5.12	0.19			5.42	3.62	0.13		
	UCSF1/NHS	5.15	34.26	0.88			-18.04	22.07	0.41		
	UCSF2	35.13	18.54	0.06			21.75	11.68	0.06		
	SCALE	20.05	10.45	0.06			28.64	9.04	0.002		
	<i>Combined</i>	11.4	5.82	0.02	5.3%	0.37	13.2	8.01	0.10	64.2%	0.04
<b>MZL</b>	NCI	-0.87	7.88	0.91			6.4	5.2	0.22		

\* Estimates of the log odds ( $\beta$ ), standard error (SE), and p-value are provided for the association between FROH and F3 and each subtype, adjusted for age, sex (except UCSF1/NHS), percentage of missing SNPs, and principal components and combined using random effects meta-analysis. The I<sup>2</sup> statistic provides an estimate of heterogeneity in association estimates across GWAS, and Phet is the p-value for heterogeneity among studies.

**Table S4.** Sensitivity analysis of the risk of each NHL subtype associated with FROH and F3 after removing individual studies from the meta-analysis \*.

	Study Removed <sup>†</sup>	FROH			F3		
		$\beta$	SE	p-value	$\beta$	SE	p-value
CLL	NCI	36.19	12.13	0.003	26.58	12.14	0.03
	GEC	19.57	4.52	1.49x10 <sup>-5</sup>	25.08	9.32	0.007
	UCSF2	26.29	8.98	0.003	23.83	7.42	0.001
	Utah	23.25	7.62	0.002	29.09	3.19	6.25x10 <sup>-20</sup>
DLBCL	NCI	-13.31	7.13	0.06	-4.68	9.75	0.63
	Mayo	-0.78	12.08	0.95	3.36	10.89	0.76
	UCSF2	0.83	13.11	0.95	-1.37	12.30	0.91
	GELA/EPIC	13.14	4.62	0.004	13.43	3.18	2.34x10 <sup>-5</sup>
FL	NCI	22.46	8.80	0.01	18.22	10.37	0.08
	UCSF1/NHS	14.14	7.04	0.04	16.67	8.41	0.05
	UCSF2	9.23	4.56	0.04	10.35	10.30	0.32
	SCALE	10.12	6.72	0.13	7.38	6.97	0.29

\* Estimates of the log odds ( $\beta$ ), standard error (SE), and p-value are provided for the association between FROH and F3 and each subtype, adjusted for age, sex (except UCSF1/NHS), percentage of missing SNPs, and principal components and combined using random effects meta-analysis. <sup>†</sup> This column indicates the specific study removed from the meta-analysis. The estimates presented are from the random effects meta-analysis after excluding this study.