Table S2. Prioritized mutations and high level copy number alterations (CNAs) across informative sequenced orbital and ocular adnexal lymphomas (OOALs)

Sample	Subtype	Alteration Type	Location	Gene	Ref.	Var.	AA Change	Var. freq.	CNA	Log_2 CNRatio	Onc/TSG	Epigenetic
IE-37	FL	Mutation	chr1:27087894	*ARID1A*	GGCCACCCA	G	p.727_730del	0.44	N/A	N/A	TSG	Yes
IE-39	DLBCL	Mutation	chr1:27100375	*ARID1A*	C	T	p.Q1363X	0.11	N/A	N/A	TSG	Yes
IE-07	FL	Mutation	chr1:27057736	*ARID1A*	C	T	p.Q482X	0.26	N/A	N/A	TSG	Yes
IE-32	DLBCL	Mutation	chr11:108183151	*ATM*	G	T	p.E1978X	0.49	N/A	N/A	TSG	No
IE-13	DLBCL	Mutation	chr7:55249028	*EGFR*	C	T	p.R776C	0.11	N/A	N/A	Oncogene	No
IE-17	FL	Mutation	chr7:148508728	*EZH2*	A	T	p.Y646N	0.23	N/A	N/A	Oncogene	Yes
IE-11	FL	Mutation	chr7:148508728	*EZH2*	A	T	p.Y646N	0.16	N/A	N/A	Oncogene	Yes
IE-39	DLBCL	Mutation	chr7:148508727	*EZH2*	T	G	p.Y646S	0.37	N/A	N/A	Oncogene	Yes
IE-13	DLBCL	Mutation	chr4:187557927	*FAT1*	G	A	p.R1262X	0.11	N/A	N/A	TSG	No
IE-37	FL	Mutation	chr10:8100362	*GATA3*	G	A	p.W112X	0.11	N/A	N/A	TSG	No
IE-37	FL	Mutation	chr11:533878	*HRAS*	C	T	p.G60S	0.11	N/A	N/A	Oncogene	No
IE-35	FL	Mutation	chr19:36228097	*KMT2B*	C	T	p.Q2495X	0.29	N/A	N/A	TSG	Yes
IE-39	DLBCL	Mutation	chr5:56171042	*MAP3K1*	C	T	p.Q624X	0.14	N/A	N/A	TSG	No
IE-24	MZL	Mutation	chrX:70339260	*MED12*	A	C	p.N46T	0.99	N/A	N/A	Oncogene	No
IE-24	MZL	Mutation	chr3:38182035	*MYD88*	T	C	p.I220T	0.38	N/A	N/A	Oncogene	No
IE-13	DLBCL	Mutation	chr3:38182641	*MYD88*	T	C	p.L265P	0.90	N/A	N/A	Oncogene	No
IE-18	DLBCL	Mutation	chr3:38182641	*MYD88*	T	C	p.L265P	0.48	N/A	N/A	Oncogene	No
IE-32	DLBCL	Mutation	chr3:38182641	*MYD88*	T	C	p.L265P	0.39	N/A	N/A	Oncogene	No
IE-12	MZL	Mutation	chr3:38182641	*MYD88*	T	C	p.L265P	0.52	N/A	N/A	Oncogene	No
IE-15	MZL	Mutation	chr3:38182641	*MYD88*	T	C	p.L265P	0.36	N/A	N/A	Oncogene	No
IE-05	MZL	Mutation	chr3:38182641	*MYD88*	T	C	p.L265P	0.47	N/A	N/A	Oncogene	No
IE-16	DLBCL	Mutation	chr3:38182259	*MYD88*	T	C	p.M232T	0.27	N/A	N/A	Oncogene	No
IE-08	MZL	Mutation	chr3:38182259	*MYD88*	T	C	p.M232T	0.44	N/A	N/A	Oncogene	No
IE-06	DLBCL	Mutation	chr3:38182032	*MYD88*	C	G	p.S219C	0.31	N/A	N/A	Oncogene	No
IE-39	DLBCL	Mutation	chr17:29664869	*NF1*	G	A	p.W2225X	0.10	N/A	N/A	TSG	No
IE-04	MZL	Mutation	chr9:139397775	*NOTCH1*	C	T	p.V1676I	0.61	N/A	N/A	TSG	No
IE-32	DLBCL	Mutation	chr1:115256530	*NRAS*	G	T	p.Q61K	0.20	N/A	N/A	Oncogene	No
IE-39	DLBCL	Mutation	chr5:176675278	*NSD1*	C	T	p.Q1532X	0.11	N/A	N/A	TSG	Yes
IE-16	DLBCL	Mutation	chr10:89624303	*PTEN*	C	T	p.T26I	0.40	N/A	N/A	TSG	No
IE-35	FL	Mutation	chr1:16259360	*SPEN*	C	T	p.Q2209X	0.16	N/A	N/A	TSG	No
IE-16	DLBCL	Mutation	chr1:16260237	*SPEN*	G	A	p.W2501X	0.36	N/A	N/A	TSG	No
IE-38	FL	Mutation	chr17:7577515	*TP53*	GTGA	G	p.255_256del	0.24	N/A	N/A	TSG	No
IE-07	FL	Mutation	chr17:7577550	*TP53*	C	T	p.G244D	0.21	N/A	N/A	TSG	No
IE-06	DLBCL	Mutation	chr17:7578406	*TP53*	C	T	p.R175H	0.36	N/A	N/A	TSG	No
IE-07	FL	Mutation	chr17:7577538	*TP53*	C	T	p.R248Q	0.23	N/A	N/A	TSG	No
IE-13	DLBCL	CNA	chr9	*CDKN2A*	N/A	N/A	N/A	N/A	two copy loss	-3.73	TSG	No
IE-18	DLBCL	CNA	chr9	*CDKN2A*	N/A	N/A	N/A	N/A	two copy loss	-4.26	TSG	No
IE-32	DLBCL	CNA	chr9	*CDKN2A*	N/A	N/A	N/A	N/A	two copy loss	-2.70	TSG	No
IE-29	MZL	CNA	chr9	*CDKN2A*	N/A	N/A	N/A	N/A	two copy loss	-2.37	TSG	No
IE-13	DLBCL	CNA	chr4	*FAT1*	N/A	N/A	N/A	N/A	two copy loss	-1.75	TSG	No
IE-18	DLBCL	CNA	chr10	*PTEN*	N/A	N/A	N/A	N/A	two copy loss	-1.34	TSG	No

All high confidence, prioritized, somatic non-synonymous mutations and and high-level CNAs (see **Methods**) identified across the 36 informative OOALs are shown. For each variant the sample, subtype (follicular lymphoma [FL], diffuse large B-cell lymphoma [DLBCL] and marginal zone lymphoma [MZL], alteration atype, chromosomal location and gene are indicated. For mutations, the (Ref.) and variant (Var.) alleles, amino acid (AA) change and flow corrected variant allele frequency (Var. freq.) are shown. For CNAs, gain or loss and log_2 copy number ratios are shown. Gene type (Oncogene [Onc] vs. Tumor suppressor [TSG]) and known status as an epigenetic regualtor are shown.