Supplementary Tables.

Supplementary Table 1: *IGVH* gene mutational status in MCL patients

Patient	*IGVH* family	Mutational Status	Homology %
iMCL1	V_H2-70	Hypermutated	93
iMCL2	V_H4-34	Hypermutated	94
iMCL3	V_H4-59	Hypermutated	94
iMCL4	V_H4-31	Hypermutated	94.3
iMCL5	V_H3-23	Hypermutated	93.6
iMCL6	V_H1-2	Hypermutated	91
iMCL7*	V_H3-23	Hypermutated	94
iMCL8*†	V_H3-23	Mutated	95.4
iMCL9†‡	V_H4-34	Unmutated	≥ 98
iMCL10†	V_H3-21	Unmutated	≥ 98
cMCL1	V_H5-51	Unmutated	≥ 98
cMCL2	V_H1-8	Unmutated	≥ 98
cMCL3	V_H4-4	Unmutated	≥ 98
cMCL4	V_H3-33	Unmutated	≥ 98
cMCL5	V_H1-8	Unmutated	≥ 98
cMCL6	V_H4-39	Mutated	95
cMCL7	V_H1-3	Hypermutated	93
cMCL8	V_H4-61	Hypermutated	94
cMCL9	V_H3-23	Unmutated	≥ 98
cMCL10	V_H4-34	Unmutated	≥ 98
cMCL11	V_H4-34	Unmutated	≥ 98
cMCL12	V_H1-46	Hypermutated	92.4
cMCL13	V_H5-51	Unmutated	≥ 98
cMCL14	V_H3-48	Mutated	95.6
cMCL15	V_H1-2	Mutated	96

* The sample analyzed was obtained from tumoral spleen.
†Not studied by expression array
cMCL indicates conventional mantle cell lymphoma; iMCL indicates indolent mantle cell lymphoma.
‡ This case had a second IGHV rearrangement that was not productive. The family used was VH3-13 and showed also ≥98% homology

Supplementary Table 2. Summary of pUPD identified in MCL cases determined by SNP arrays

pUPD region	MCL cases*	Germinal/Somatic
3q26.6	cMCL3	Germinal
4q13.2-q13.2	cMCL12	n.a.
4q32.3-qter	iMCL6	Somatic
6p11.1-q12	iMCL6	Germinal
6q24.1-24.2	cMCL14	Germinal
6q25.2-q25.3	iMCL3	Germinal
7q32.2-q34	iMCL2	Germinal
12p11.21-q12	cMCL1	n.a.
16q22.2-q23.3	cMCL3	Germinal
17pter-p11.2*	cMCL13	n.a.
17pter-p12	cMCL1	n.a.
17pter-p13.1*	cMCL3	Somatic
20p12.3-p12.2	cMCL2	Germinal
20q11.22-qter	cMCL14, cMCL15	Somatic

*Cases with TP53 mutation (cMCL3 527G>T; cMCL13 659A>G)
n.a.: not available due to the lack of constitutional DNA. pUPD: partial uniparental disomy

Supplementary Table 3: List of differentially expressed genes between iMCL and cMCL cases

Gene	Description	Probe set	GMI iMCL	GMI cMCL	GMI Ratio	P value
RNGTT	RNA guanylyltransferase and 5´-phosphatase	211849_s_at	138.15	814.45	0.17	6.20×10^{-6}
HDGFRP3	Hepatoma-derived growth factor, related protein 3	209524_at	10.66	265.27	0.04	1.23×10^{-5}
FARP1	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	239246_at	16.53	160.82	0.10	1.51×10^{-5}
HMGB3	High-mobility group box 3	225601_at	20.86	130.16	0.16	1.57×10^{-5}
LGALS3BP	Lectin, Galactoside-binding, soluble, 3-binding protein	200923_at	58.71	385.44	0.15	4.69×10^{-5}
PON2	Paraoxonase 2	210830_s_at	16.13	183.59	0.09	4.93×10^{-5}
CDK2AP1	CDK2-associated protein 1	201938_at	239.26	1008.01	0.24	5.16×10^{-5}
DBN1	Drebrin 1	202806_at	13.78	110.52	0.12	8.40×10^{-5}
CNR1	Cannabinoid receptor 1	1560225_at	88.01	911.88	0.10	0.00014
CNN3	Calponin 3	201445_at	15.98	139.98	0.11	0.00026
SETMAR	SET domain and mariner transposase fusion gene	206554_x_at	52.50	150.67	0.35	0.00027
SOX11	SRY (sex determining region Y)-box 11	204913_s_at	33.52	691.44	0.05	0.00027
CSNK1E	Casein kinase 1, epsilon	202332_at	158.63	342.79	0.46	0.00030

GMI: Geometric Mean of Intensities