

GENETIC ALTERATION	JEKO1	JVM2	MAVER1	GRANTA519	MINO	REC1
<b>t(11;14)</b>	+	+	+	+	+	+
<b>Expression of Cyclin D1</b>	+	weak	+	+	+	+
<b>Expression of Cyclin D2</b>	-	+	-	-	+	-
<b>SOX11</b>	+	-		+	+	+
<b>cMYC (rearrangement 8q24)</b>	+	+	+	+/-	+/-	+/-
<b>RB1</b>	+			+		+
<b>TP53</b>	del/mut	wt/wt	mut/del	wt/wt	del/mut	wt/wt
<b>ATM</b>	amplified	wt	del/nd	wt	mutated	del/nd
<b>CDKN2A (p16)</b>	+	+	del	del	+	+
<b>CDKN1A (p21)</b>	+	+	mut	+	+	-
<b>CDKN1B (p27)</b>	+	-	nd	+	+	+
<b>SR-B1</b>	-	++	+			
<b>BCL2</b>	+	+	+	+		

Supplementary table S2: Characteristics of the different MCL cell lines.

CELLULAR RESPONSE	JEKO1	JVM2	MAVER1
<b>Iromycin IC50 (nM)</b>	12.8	112.6	50.4
<b>Total ROS production (tROS)</b>	-	++	+
<b>Mitochondrial ROS production (mROS)</b>	+	+	-
<b>Cell death</b>	Apoptosis ++ Ferroptosis ++	Apoptosis ++ Ferroptosis +	Apoptosis + Ferroptosis ++
<b>Pro- / anti-apoptotic proteins expression</b>	↓	↑	↑
<b>Oncogene degradation</b>	CCND1 ↓ p27 ↓	CCND1 ↓ CCND2 ↓ p53 ↓	CCND1 ↓ p53 ↑ p21 ↑ p27 ↑
<b>BH3 mimetic priming</b>	Bcl2i Mcl1i Bcl-xLi	Bcl2i	Bcl2i
<b>UPR activation</b>	IRE1 $\alpha$ ++ BiP ++ CHOP +	IRE1 $\alpha$ + peIF2 $\alpha$ ++ CCPG1 ++	IRE1 $\alpha$ ++ XBP1s + BiP ++ ATF4 ++ CCPG +
<b>GPX4</b>	↓	↑	↑
<b>Cell cycle</b>	Sub-G1 G2/M	Sub-G1	G0/G1
<b>FeCl3 supplementation</b>	↑ tROS ↓ mROS	↑ tROS ↑ mROS	= tROS ↓ mROS
<b>Lipid depletion</b>	↑ cell death ↑ lipid peroxidation ↓ tROS	↑ cell death = lipid peroxidation ↑ tROS	↑ cell death ↓ lipid peroxidation ↓ tROS

**Supplementary table S3:** The different cellular effects of iromycin in the three MCL cell lines studied are summarized in the table.