

Table S1 Gene mutation profile

Gene Symbol	cHGVS	pHGVS	Chr	Start	Stop	Ref	Call	MapLoc	VarType	Exln_ID	Function
MYD88	c.794T>C	p.L265P	3	38182640	38182641	T	C	3p22.2	snv	EX5E	missense
BCL6	c.-50+2T>C	.	3	187463195	187463196	A	G	3q27.3	snv	IVS1	splice-5
PIM1	c.4C>T	p.L2F	6	37138354	37138355	C	T	6p21.2	snv	EX1	missense
PIM1	c.29C>T	p.A10V	6	37138379	37138380	C	T	6p21.2	snv	EX1	missense
PIM1	c.63_65delCG	p.A22V	6	37138413	37138416	CGC	TGT	6p21.2	delins	EX1	missense
PIM1	c.68C>T	p.T23I	6	37138418	37138419	C	T	6p21.2	snv	EX1	missense
PIM1	c.83G>A	p.G28D	6	37138548	37138550	GC	AC	6p21.2	snv	EX2	missense
PIM1	c.88G>T	p.E30*	6	37138553	37138554	G	T	6p21.2	snv	EX2	nonsense
PIM1	c.97C>T	p.P33S	6	37138562	37138563	C	T	6p21.2	snv	EX2	missense
PIM1	c.187C>A	p.P63T	6	37138652	37138654	CC	AC	6p21.2	snv	EX2	missense
PIM1	c.202C>T	p.H68Y	6	37138768	37138769	C	T	6p21.2	snv	EX3	missense
PIM1	c.230G>A	p.W77*	6	37138796	37138797	G	A	6p21.2	snv	EX3	nonsense
PIM1	c.286G>A	p.V96M	6	37138945	37138946	G	A	6p21.2	snv	EX4	missense
PIM1	c.376G>A	p.V126M	6	37139035	37139036	G	A	6p21.2	snv	EX4	missense
PIM1	c.403G>A	p.E135K	6	37139062	37139063	G	A	6p21.2	snv	EX4	missense
PIM1	c.412G>A	p.A138T	6	37139071	37139072	G	A	6p21.2	snv	EX4	missense
PIM1	c.418C>T	p.Q140*	6	37139077	37139078	C	T	6p21.2	snv	EX4	nonsense
PIM1	c.594C>G	p.Y198*	6	37139253	37139256	CAC	GAC	6p21.2	snv	EX4	nonsense
PRDM1	c.849_853delTAGAAinsG	p.F283Lfs*27	6	106552883	106552890	TAGA AGA	GGA	6q21	delins	EX5	frameshift
PCLO	c.12601T>C	p.S4201P	7	82544700	82544701	A	G	7q21.11	snv	EX7	missense
PCLO	c.8258A>G	p.D2753G	7	82582010	82582011	T	C	7q21.11	snv	EX5	missense
PCLO	c.1279C>A	p.L427I	7	82784677	82784678	G	T	7q21.11	snv	EX2	missense
FOXO1	c.497C>T	p.A166V	13	41239852	41239853	G	A	13q14.1	snv	EX1	missense
RB1	c.2106+2T>	.	13	49033970	49033972	TA	GA	13q14.2	snv	IVS20	splice-5
CD79B	c.587A>C	p.Y196S	17	62006797	62006798	T	G	17q23.3	snv	EX5	missense
TCF3	c.1142G>A	p.S381N	19	1619803	1619804	C	T	19p13.3	snv	EX14	missense
SMARC	c.3404G>A	p.R1135Q	19	11141426	11141428	GG	AG	19p13.2	snv	EX25	missense

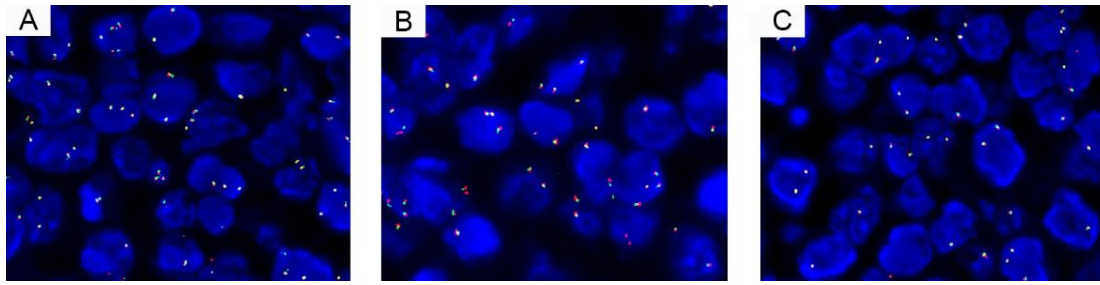


Figure S1 *BCL-2* (A), *BCL-6* (B), and *MYC* (C) gene rearrangements using FISH were all negative.