

# Whole-genome sequencing identifies recurrent somatic *NOTCH2* mutations in splenic marginal zone lymphoma

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**Splenic marginal zone lymphoma (SMZL), the most common primary lymphoma of spleen, is poorly understood at the genetic level. In this study, using whole-genome DNA sequencing (WGS) and confirmation by Sanger sequencing, we observed mutations identified in several genes not previously known to be recurrently altered in SMZL. In particular, we identified recurrent somatic gain-of-function mutations in *NOTCH2*, a gene encoding a protein required for marginal zone B cell development, in 25 of 99 (~25%) cases of SMZL and in 1 of 19 (~5%) cases of nonsplenic MZLs. These mutations clustered near the C-terminal proline/glutamate/serine/threonine (PEST)-rich domain, resulting in protein truncation or, rarely, were nonsynonymous substitutions affecting the extracellular heterodimerization domain (HD). *NOTCH2* mutations were not present in other B cell lymphomas and leukemias, such as chronic lymphocytic leukemia/small lymphocytic lymphoma (CLL/SLL; n = 15), mantle cell lymphoma (MCL; n = 15), low-grade follicular lymphoma (FL; n = 44), hairy cell leukemia (HCL; n = 15), and reactive lymphoid hyperplasia (n = 14). *NOTCH2* mutations were associated with adverse clinical outcomes (relapse, histological transformation, and/or death) among SMZL patients (P = 0.002). These results suggest that *NOTCH2* mutations play a role in the pathogenesis and progression of SMZL and are associated with a poor prognosis.**

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Abbreviations used: CLL/SLL, chronic lymphocytic leukemia/small lymphocytic lymphoma; CSL, CBF1/RBP-Jκ/suppressor of hairless/LAG-1; FL, follicular lymphoma; HCL, hairy cell leukemia; HCS, Hajdu-Cheney syndrome; HD, heterodimerization domain; LNR, Lin-12-*NOTCH* repeat; MALT, mucosa-associated lymphoid tissue; MALT-L, MALT lymphoma; MCL, mantle cell lymphoma; MZL, marginal zone lymphoma; NS, nonsense; PEST, proline/glutamate/serine/threonine; RLH, reactive lymphoid hyperplasia; SMZL, splenic marginal zone lymphoma; SNP, single nucleotide polymorphism; T-ALL, T-acute lymphocytic leukemia; WBC, white blood cell; WGS, whole-genome sequencing

SMZL is an indolent malignancy of splenic B lymphocytes characterized by splenomegaly, peripheral leukocytosis, and cytopenias with a median age of onset of >50 yr (Isaacson et al., 2008). SMZL is the most common primary malignancy of the spleen and represents ~10% of all lymphomas that involve the spleen (Franco et al., 2003). Although the disease course is usually indolent, with many patients surviving beyond 10 yr, some patients present with more aggressive disease and survival between 1 and 2 yr (Chacón et al., 2002). A “watch

and wait” approach to instituting therapy may be considered for patients with favorable clinical prognostic factors (Arcaini et al., 2006); however, as it is difficult to predict subsequent risk of disease aggressiveness or refractoriness, a common first-line therapeutic approach is splenectomy and anti-B lymphocyte biological agents such as the anti-CD20 antibody (rituximab). Refractory cases may then be treated with more toxic chemotherapies, such

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as alkylating agents or purine analogues. In contrast to many other B cell malignancies, SMZL is not associated with recurrent balanced translocations or genetic mutations. Moreover, little is known about the genetic events underpinning the development of aggressive or refractory disease or the transformation to higher grade disease. Therefore, a detailed understanding of SMZL pathogenesis would provide clinically useful insight into patient prognosis and could inform decision-making regarding early therapeutic intervention versus adoption of a “watch and wait” approach.

The NOTCH family of transmembrane receptor proteins is important for mediating cell fate determination and differentiation in a variety of embryonic and adult tissues. During hematopoietic differentiation, NOTCH1 signaling is known to influence cell fate decisions as lymphocytes differentiate into B or T cells (Pui et al., 1999; Radtke et al., 1999; Robey and Bluestone, 2004). Moreover, NOTCH2 is known to control B lymphocyte specification into cells of marginal zone lineage (Saito et al., 2003; Witt et al., 2003). Whereas defects in NOTCH1 signaling have been implicated in oncogenesis in T-acute lymphoblastic leukemia (Weng et al., 2004; Aster et al., 2011), CLL/SLL (Puente et al., 2011; Del Giudice et al., 2012), and MCL (Kridel et al., 2012), comparatively little is known about the potential role of NOTCH2 signaling defects in the development of malignancies affecting cells of B lymphocyte lineage (Aster et al., 2011).

To better understand the pathogenetic mechanisms involved in SMZL, we performed WGS and targeted Sanger gene sequencing and identified recurrent mutations predominantly clustered in the C-terminal portion of the *NOTCH2* gene in SMZL. These mutations are similar to previously defined oncogenic mutations in *NOTCH1* and are markers of poor prognosis in SMZL.

## RESULTS

### Genome sequencing and *NOTCH2* mutation confirmation

To gain insight into the pathogenesis of SMZL, we performed WGS on six index cases of SMZL. WGS yielded a mean of  $350 \pm 10$  million mapped reads per sample with an average of  $97.6 \pm 0.08\%$  genome coverage and  $96.4 \pm 0.3\%$  fully called exome coverage. The median genomic sequencing depth exceeded  $80\times$  in all samples normalized across the entire genome. To enhance our ability to identify somatic alterations that are important in SMZL pathogenesis, we focused on variations that were present in any of the six SMZL genomes and not in the Database of SNPs (dbSNP).

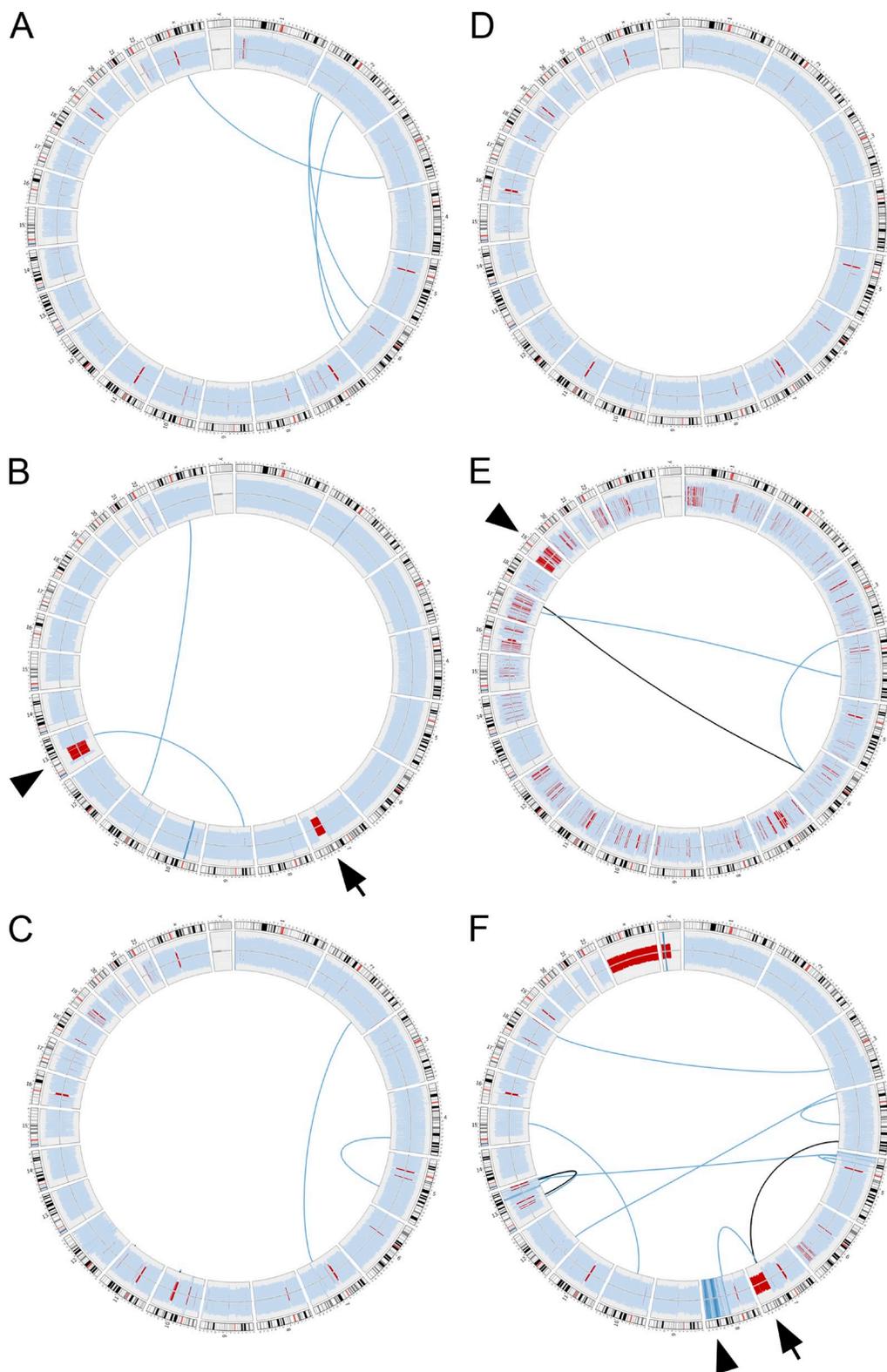
After normalization to publicly available constitutional normal genome sequencing data, relative depth of coverage for distinct chromosomal regions were examined for evidence of recurrent chromosomal gains or losses. Corresponding plots of ploidy for each genome are shown in Fig. 1 (outer data track; light blue indicates regions of euploidy, dark blue indicates region of chromosomal gain, and red indicates region of chromosomal loss). Overall, the SMZL genomes had relatively few large structural alterations

affecting chromosomes (Fig. 1 and Table S1). However, in keeping with previous observations (Mateo et al., 1999; Gruszka-Westwood et al., 2003; Salido et al., 2010; Watkins et al., 2010; Rinaldi et al., 2011) recurrent deletions involving the long arm of chromosome 7 (del7q) were seen in two of the six index genomes (Fig. 1, B and F, arrows). Additionally, one of these genomes also showed a partial loss of genetic elements corresponding to the subcentromeric region of chromosome 13 (del13q; Fig. 1 B, arrowhead).

Individual sequencing reads that mapped to two spatially separated regions of the reference genome were used to identify putative gene fusion or gene disruption events. To reduce the number of candidate structural alterations likely to be pathogenetic, we filtered these data to exclude structural alterations that did not affect coding elements of the involved genes (Fig. 1, inner tracks; light blue lines indicate a single gene involved in structural alteration; black lines indicate that two genes from nonadjacent genomic regions were involved in structural alteration). This analysis revealed no evidence of recurrent chromosomal translocation or chimeric fusions in the six index cases. A complete list of all structural alterations identified through genomic sequencing involving one or more genes is presented in Table S1.

In total, 2,995 candidate genes were identified with at least one previously undocumented single-nucleotide polymorphism (SNP) or small insertion/deletion event (indel) in at least one of the six SMZL genomes (comparison to dbSNP; not shown). Of these, 232 genes showed novel alterations in at least two of the six SMZL index genomes (Table S2). These included mutations in epigenetic modifiers, including *MLL2* and *MLL3*, which have been previously reported to occur in follicular and diffuse large B cell lymphomas, but not in marginal zone lymphomas (Morin et al., 2011; Pasqualucci et al., 2011). Among the recurrently altered genes, we prioritized *NOTCH2* as a candidate gene likely to be important to SMZL pathogenesis based on its known role in murine marginal zone B lymphocyte development (Saito et al., 2003; Witt et al., 2003). In three of six index SMZL cases, variant call analysis identified *NOTCH2* mutations predicted to lead to protein truncation in the distal C-terminal region in the transactivation (TAD) and proline/glutamate/serine/threonine-rich (PEST) domains (Table 1). Two of these cases harbored the same p.R2400X nonsense amino acid substitution mutation, and one case harbored a length-affecting mutation leading to a frameshift at residue p.I2304 (Fig. 2 and Table 2).

These mutations in *NOTCH2* result in deletion of known or predicted degradation motifs that regulate protein stability (Fryer et al., 2004; Chiang et al., 2006; Kopan and Ilagan, 2009). Moreover, NOTCH2 is known to drive development toward the marginal zone B cell lineage (Saito et al., 2003). Therefore, we focused our effort to further characterize *NOTCH2* mutations in SMZL as they are likely to be important to the pathogenesis of this disease. Using Sanger sequencing, we confirmed the presence of



**Figure 1. Structural alterations in index SMZL cases.** Circos diagrams of genomic complexity identified in six index SMZL cases. Outer data track represents the relative sequencing coverage of chromosomal regions normalized to publicly available genome sequencing data of 49 healthy individuals corresponding to ploidy at these regions. Light blue indicates region of euploidy, dark blue indicates region of chromosomal gain and red indicates region of chromosomal loss. Arrows indicate deletion portions of the long arm of chromosome 7 (del7q) in two of the six index genomes. Arrowheads indicate other regions of chromosomal loss or gain. Inner data tracks represent large structural alterations between spatial distinct genomic regions affecting the coding regions of one or more genes. Light blue lines indicate a single gene involved in structural alteration. Black lines indicate two genes involved in structural alteration. The three index genomes with mutations in *NOTCH2* are shown in A–C.

**Table 1.** *NOTCH2* mutations identified in SMZL and MALT-L samples

Cohort	Disease	Identifier	First mutation		Second variation			Confirmed	
			Gene	Protein	Gene	Protein	Consequence	Somatic	
Discovery	SMZL	D-1	c.6909dupC	p.I2304fsX9			FS	Yes	
Discovery	SMZL	D-2	c.7198C>T	p.R2400X			NS	Yes	
Discovery	SMZL	D-3	c.7198C>T	p.R2400X			NS	Yes	
Validation	SMZL	V-1	c.4999G>A	p.V1667I			MS	Yes	
Validation	SMZL	V-2	c.6304A>T	p.K2102X			NS	Yes	
Validation	SMZL	V-3	c.6824C>A	p.A2275D			MS	Yes	
Validation	SMZL	V-4	c.6834delinsGCACG	p.T2280fsX12			FS	Yes	
Validation	SMZL	V-5	c.6853C>T	p.Q2285X			NS	Yes	
Validation	SMZL	V-6	c.6853C>T	p.Q2285X			NS	Yes	
Validation	SMZL	V-7	c.6868G>A	p.E2290X			NS	N/A	
Validation	SMZL	V-8	c.6873delG	p.K2292fsX3			FS	Yes	
Validation	SMZL	V-9	c.6909delC	p.I2304fsX2			FS	N/A	
Validation	SMZL	V-10	c.6909delC	p.I2304fsX2			FS	N/A	
Validation	SMZL	V-11	c.6909delC	p.I2304fsX2	c.7072A>G	p.M2358V	FS/MS	N/A	
Validation	SMZL	V-12	c.6909dupC	p.I2304fsX9			FS	Yes	
Validation	SMZL	V-13	c.6910delinsCCC	p.I2304fsX3			FS	Yes	
Validation	SMZL	V-14	c.6973C>T	p.Q2325X			NS	N/A	
Validation	SMZL	V-15	c.7198C>T	p.R2400X			NS	Yes	
Validation	SMZL	V-16	c.7198C>T	p.R2400X			NS	Yes	
Validation	SMZL	V-17	c.7198C>T	p.R2400X			NS	Yes	
Validation	SMZL	V-18	c.7198C>T	p.R2400X			NS	Yes	
Validation	SMZL	V-19	c.7198C>T	p.R2400X			NS	Yes	
Validation	SMZL	V-20	c.7198C>T	p.R2400X			NS	Yes	
Validation	SMZL	V-21	c.7198C>T	p.R2400X			NS	N/A	
Validation	SMZL	V-22	c.7231G>T	p.E2411X			NS	Yes	
Specificity	MALT-L	S-1	c.7198C>T	p.R2400X			NS	N/A	

All *NOTCH2* mutations identified through either whole genomic sequencing (discovery cohort) or targeted Sanger sequencing (validation and specificity cohorts) of the exonic regions of the *NOTCH2* gene C terminus are shown. Where constitutional tissue was available for sequencing, somatic acquisition of each mutation was confirmed. One sample from the validation cohort of SMZL samples had two separate mutations. All other mutations were heterozygous. NS, non-sense; MS, missense; FS, frameshift. N/A indicates that constitutional tissue was not available for a given sample.

these mutations in the index tumor samples (Fig. 2, SMZL) and their somatic acquisition by testing matched constitutional tissues (Germline).

### Prevalence of *NOTCH2* mutations in SMZL

To establish the prevalence of *NOTCH2* mutations among a larger SMZL cohort, targeted Sanger sequencing of the region comprising all domains known to be important for intracellular NOTCH family signaling (exons 25 through 34; Fig. 3) was performed. We focused on this region based on the location of mutations in *NOTCH2* identified in our initial screen and the analogous location of gain-of-function mutations known to contribute to other mature B cell lymphoproliferative disorders such as CLL/SLL (Del Giudice et al., 2012) and MCL (Kridel et al., 2012), as well as T-acute lymphocytic leukemia (T-ALL; Weng et al., 2004). These exons comprise three Lin-12-NOTCH repeat (LNR) domains (prevent ligand-independent activation), the HD (regulates ligand-independent activation), a single-pass trans-membrane region, RBP-J $\kappa$ -associated module

domain (binds the CBF1/RBP-J $\kappa$ /suppressor of hairless/LAG-1 [CSL] transcription factor), six ankyrin repeats (bind CSL and Mastermind), the TAD, and the PEST domain important for regulating degradation of the NOTCH2 intracellular domain (NICD2; Fig. 4 A).

In total, 93 additional SMZL cases were screened by Sanger sequencing for mutations in *NOTCH2*. A total of 11 novel mutations, 7 additional p.R2400X, and 5 additional frameshift mutations affecting the p.I2304 residue were discovered in these SMZL cases (Fig. 4 A and Fig. 5 and Table 1). These mutations were largely truncating mutations (either frameshift or nonsense mutations) confined to the distal TAD and PEST domains and are predicted to eliminate degradation signals in the PEST domain, thereby increasing the stability of the NICD2. A single missense mutation (p.V1667I) located in the HD is analogous to the p.V1722I *NOTCH1* mutation in T-ALL associated with ligand-independent NOTCH1 activation (Malecki et al., 2006; Gordon et al., 2007). Overall, 25 of



**Table 2.** Patient and disease characteristics of SMZL patients according to *NOTCH2* mutational status

	Total			Positive			Negative			Student's <i>t</i> test
	Average	St Dev	<i>n</i>	Average	St Dev	<i>n</i>	Average	St Dev	<i>n</i>	P-value
Percent male	35%		71	22%		18	40%		53	0.19
Age at diagnosis	62	12	71	63	9	18	61	13	53	0.63
Age at splenectomy	63	12	71	65	10	18	63	12	50	0.62
Stage at diagnosis	3.7	0.8	56	3.5	1.1	13	3.8	0.7	43	0.39
International Prognostic Index/Follicular Lymphoma International Prognostic Index	2.4	0.9	43	2.3	1.0	9	2.5	0.9	34	0.68
Hemoglobin, g/deciliter	11.8	2.0	51	11.7	1.7	11	11.9	2.1	40	0.77
Lactate dehydrogenase (U/liter)	328	154	42	321	122	8	330	162	34	0.89
Albumin (g/deciliter)	4.2	0.5	19	4.4	0.4	4	4.2	0.5	15	0.63
White blood cell (K/mm <sup>3</sup> )	18.7	23.9	21	11.2	6.8	5	21.0	26.9	16	0.44
Platelet (K/mm <sup>3</sup> )	201	109	19	160	50	4	213	119	15	0.41
β2-microglobulin (mg/liter)	3.8	1.5	19	3.5	1.9	4	3.9	1.4	15	0.68

Summary of available clinical, histopathological, and laboratory parameters for SMZL patients is shown according to *NOTCH2* mutational status. No statistically significant differences were noted. St Dev, standard deviation.

The mutation affects an amino acid with the N-terminal region of the *MAML2* protein known to mediate protein–protein interactions with *NOTCH* family members. We therefore sought to assess the prevalence of additional *MAML2* mutations in our validation cohort. This identified a single additional somatic mutation in *MAML2* (p.A11S) in a genome without an identified *NOTCH2* mutation. Overall, the prevalence of putative impactful somatic mutations in *MAML2* was therefore 2 out of 99 cases (2.0%). The identification of mutations affecting *MAML2* is intriguing and warrants further investigation. No mutations were found in *FBW7* or other *NOTCH* pathway–related genes in the discovery cohort.

### Specificity of *NOTCH2* mutations

Having established the frequency of *NOTCH2* mutations in SMZL, we next sought to assess the specificity of these mutations for SMZL. We performed targeted Sanger sequencing on CLL/SLL, FL, HCL, MCL, and reactive lymphoid hyperplasia (RLH) samples. No evidence of *NOTCH2* mutations was identified in any of 103 cases of CLL/SLL, FL, HCL, MCL or RLH (95% confidence interval 0–2.9%; Fig. 3 and Fig. 6 A). Given the relatively small number of non-SMZL cases examined here for each disease category, low prevalence of *NOTCH2* mutations in these other disease entities cannot be ruled out.

In addition to assessing 99 SMZL cases, we also assessed 19 nodal and extranodal marginal zone lymphomas for the presence of *NOTCH2* mutations and identified one sample (an extranodal marginal zone B cell lymphoma of the breast mucosa-associated lymphoid tissue lymphoma [MALT-L]) that

also harbored a heterozygous p.R2400X mutation (Fig. 6 A). These data indicate a high frequency of *NOTCH2* mutations in SMZLs and a lower (5.3%) frequency in nonsplenic MZL. Collectively, these data indicate a high predilection of activating mutations in *NOTCH2* among MZLs.

### Impact of *NOTCH2* mutations on clinical outcome

Having demonstrated the presence of *NOTCH2* mutations in a subset of SMZL cases, we next sought to determine whether the presence of these mutations influenced clinical outcomes. Time to adverse outcome, defined from tissue diagnosis to relapse, transformation, or death was compared between patients harboring *NOTCH2* mutations and those with wild-type *NOTCH2*. Survival data were available for 46 patients from this study, including 11 patients with *NOTCH2* mutations and 35 patients with wild-type *NOTCH2* with a median follow up of 40 mo (range: 0.7–177 mo). Patients with *NOTCH2* mutations had significantly shorter time to adverse outcome compared with patients with wild-type *NOTCH2* (the median time to adverse outcome was 32.6 mo in *NOTCH2*-mutated patients versus 107.2 mo in patients without *NOTCH2* mutations ( $P = 0.002$ ; Fig. 6 B). After controlling for patient gender, performance status, age and stage at diagnosis, harboring a *NOTCH2* mutation is associated with shorter time to adverse outcome (hazard ratio = 5.57;  $P = 0.057$ ). Furthermore, patients with *NOTCH2* mutations also had significantly shorter relapse-free survival, defined from tissue diagnosis to relapse or death ( $P = 0.031$ ; Fig. 6 C). Altogether, these results demonstrate that the presence of *NOTCH2* mutation at diagnosis indicates worse patient outcome.

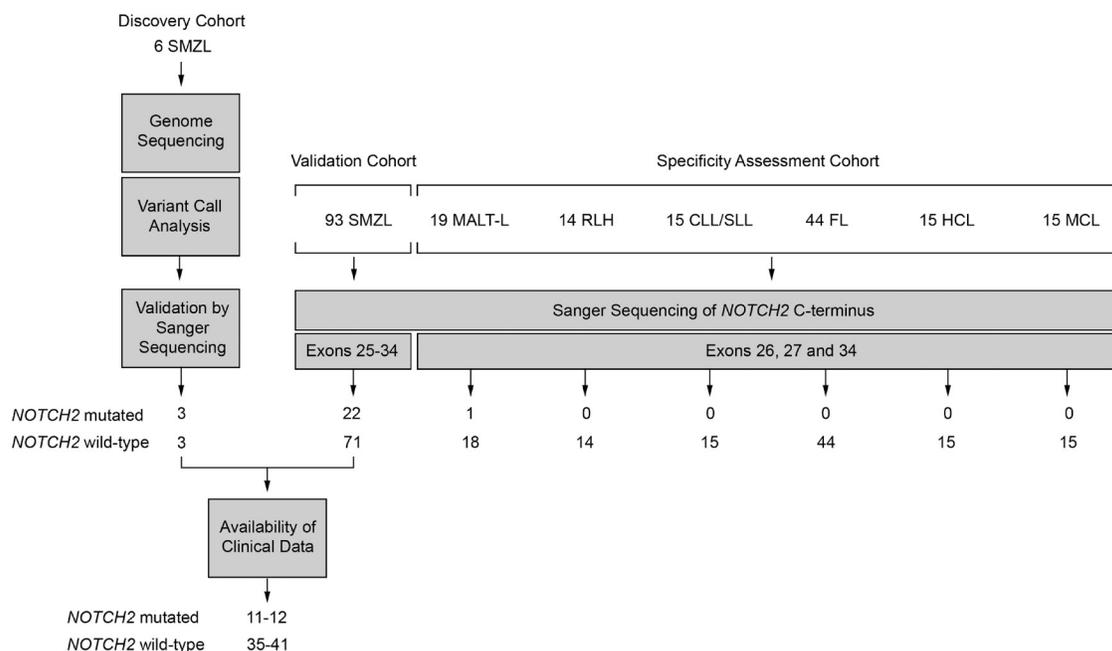
## DISCUSSION

We performed WGS in six cases of SMZL and identified *NOTCH2* mutations in half of these cases. Sanger sequencing of 93 additional SMZLs and 103 other types of B cell lymphoma or leukemia or reactive lymphoid hyperplasia showed *NOTCH2* mutations in 22 additional SMZL patients, yielding an overall frequency of 25.3%. No mutations were identified in other non-MZL B cell lymphomas and leukemias analyzed. Moreover, in 19 patients with *NOTCH2*-mutated SMZL, constitutional DNA was available for assessment and was confirmed to be wild-type, thus indicating somatic acquisition of *NOTCH2* mutation in SMZL.

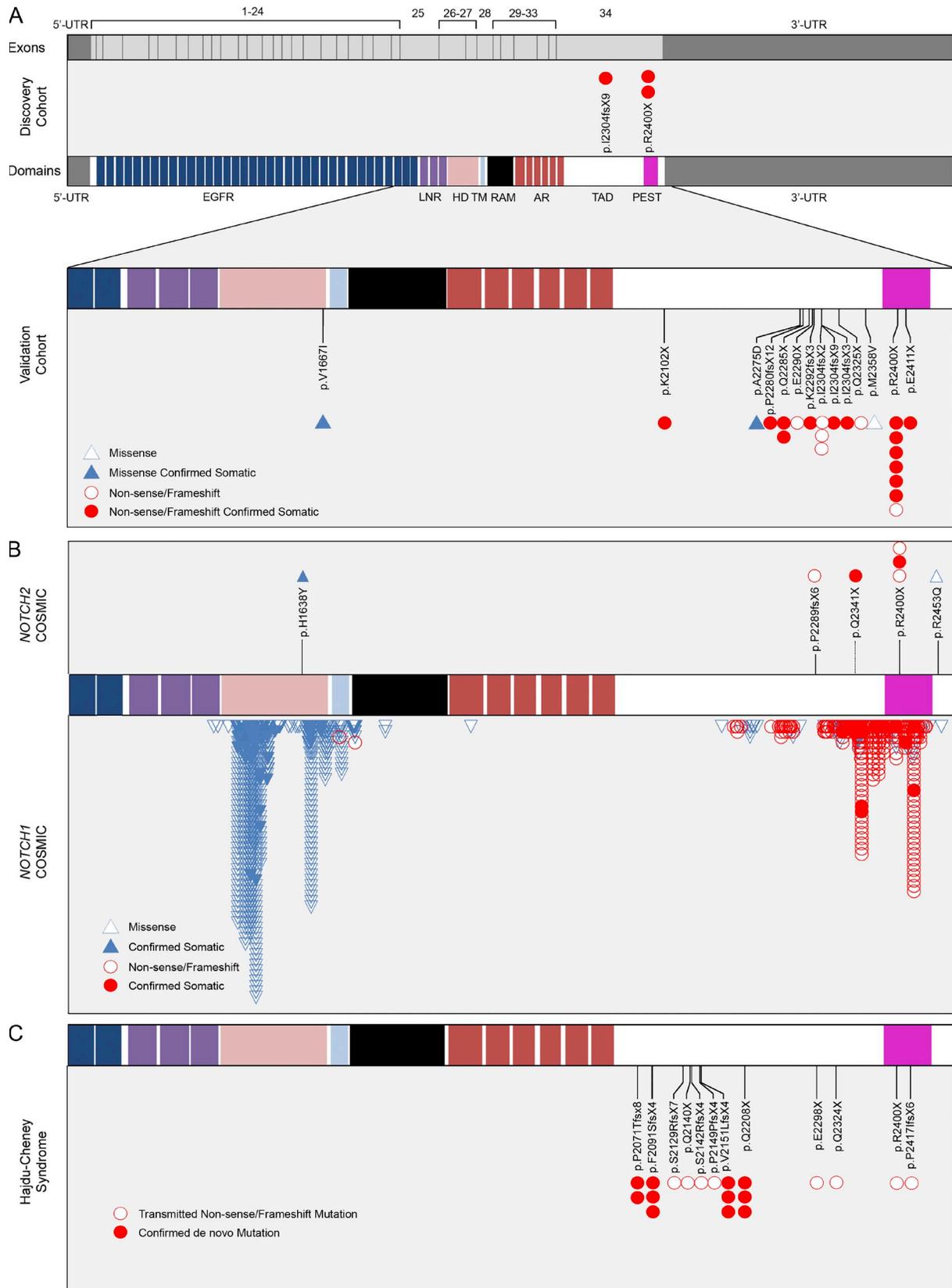
In total, we identified 26 *NOTCH2* mutations in 25 SMZL patients. These mutations represented six unique types of nonsense mutations, five unique types of frameshift mutations, and three unique types of missense mutations. 25 of these mutations affected the TAD or PEST domains, with 23 predicted to yield protein truncation at or upstream of the PEST domain. The remaining case harbored a somatic p.V1667I mutation in the HD. All of these mutations were identified in the same protein domains as have been reported for *NOTCH1* in T-ALL, CLL/SLL, and MCL. However, *NOTCH1* mutations in T-ALL are more prevalent in the HD than the TAD and PEST domain (Fig. S3). Disruption of the C-terminal PEST domain renders NOTCH less

susceptible to regulation by ubiquitin-mediated proteolysis, and thus results in increased activation of the NOTCH pathway (Gupta-Rossi et al., 2001; Oberg et al., 2001; Wu et al., 2001). Using reporter assays for assessment of NOTCH activation, we confirmed that representative mutations affecting either the PEST or HD indeed resulted in NOTCH2 transcriptional hyperactivation (not depicted).

Interestingly, in contrast to the activating effect in SMZL and other lymphoid malignancies, recent studies have suggested that the NOTCH pathway can also function as a tumor suppressor. Loss-of-function mutations in the NOTCH pathway (NCSTN, MAML1, APH1A, and NOTCH2) were recently identified in chronic myelomonocytic leukemia (Klinakis et al., 2011). Other studies have identified oncogenic mutations within the epidermal growth factor repeat region of NOTCH1 in head and neck cancer (Agrawal et al., 2011; Stransky et al., 2011). Loss-of-function mutations affecting NOTCH family and pathway genes have also been implicated in skin and lung cancers (Wang et al., 2011). Finally animal and in vitro studies suggest a tumor suppressor role in hepatocellular carcinoma (Viatour et al., 2011), pancreatic carcinoma (Mazur et al., 2010), and neuroblastoma (Zage et al., 2012). In contrast, mutations identified in lymphoid malignancies (T-ALL, B-CLL/SLL, mantle cell, and diffuse large B cell lymphoma) have all been gain-of-function



**Figure 3. Discovery, validation, and specificity assessment of *NOTCH2* mutations in SMZL and other B cell lymphomas.** A summary of the experimental design and results illustrates initial *NOTCH2* mutation discovery in three of six index SMZL cases through WGS, all of which were confirmed as somatic mutations by traditional Sanger sequencing. Sanger sequencing of the C-terminal of *NOTCH2* comprising exons 25–34 was performed in 93 additional SMZL cases comprising the validation cohort to establish the rate of recurrence of *NOTCH2* mutations in SMZL. In total, 22 additional SMZL cases harbored mutations in the HD and PEST domains of NOTCH2. To assess the specificity of *NOTCH2* mutations among other abnormal B cell proliferations, Sanger sequencing of *NOTCH2* regions with recurrent mutations identified in discovery and validation samples of SMZL (exons 26, 27 and 34) was performed for 19 cases of nonsplenic marginal zone lymphoma (MALT-L), 14 cases of RLH, 15 chronic lymphocytic lymphoma (CLL/SLL), 44 low-grade follicular cell lymphoma (grade 1–2; FL), 15 HCL, and 15 MCL. To assess the consequences of *NOTCH2* mutation on disease characteristics, clinical data were collected on a total of 46–53 SMZL cases including 11–12 cases with *NOTCH2* mutation.



**Figure 4. NOTCH2 mutations in SMZL.** (A, top) The 34 exons of *NOTCH2* are shown as gray boxes flanked by the 5'- and 3'-untranslated (UTR) regions of exons 1 and 34, respectively, above the protein domain structure of *NOTCH2* including 36 epidermal growth factor-like repeats (EGFR, blue);

mutations confined to the C-terminal region extending from exon 25 to exon 34, as was the case in our initial study.

Pathogenic germline mutations in the TAD/PEST domain of *NOTCH2* have been reported in Hajdu-Cheney syndrome (HCS), a rare autosomal dominant skeletal disorder characterized by facial anomalies, acroosteolysis, and osteoporosis (Isidor et al., 2011; Simpson et al., 2011). The *NOTCH2* mutations in HCS include one report of a transmitted p.R2400X mutation (Simpson et al., 2011; Fig. 4 C). No predilection for lymphoma or B lymphocyte dysfunction in HCS patients has been reported to date. Interpretation of the significance of this is confounded by the extreme rarity of this disease. Nonetheless, it is reasonable to speculate that additional genetic alterations may be required for SMZL development.

With regard to neoplasia, isolated *NOTCH2* mutations have been reported in a single case of SMZL and a single case of extranodal MZL in a previous study (Trøen et al., 2008), as well as in a small proportion of cases of diffuse large B cell lymphoma (Lee et al., 2009) or Richter's transformation (Fabbri et al., 2011), but no evidence for prognostic implications for *NOTCH2* mutations was presented in any of these studies. *NOTCH2* shares significant homology with *NOTCH1*, and transforming capacity has been demonstrated for truncated alleles of both proteins (Ellisen et al., 1991; Rohn et al., 1996; Capobianco et al., 1997). Intriguingly, loss-of-function mutations affecting *NOTCH* family and pathway genes have recently been implicated in the pathogenesis of myeloid (Klinakis et al., 2011) and epithelial malignancies (Mazur et al., 2010; Agrawal et al., 2011; Stransky et al., 2011; Viatour et al., 2011; Wang et al., 2011), as well as in neuroblastoma (Zage et al., 2012). These studies highlight the context-dependent roles of *NOTCH* and its signaling partners, which upon mutation, may contribute to the pathogenesis of neoplasia via different mechanisms in diverse cell types. Altogether, these findings suggest that the 26 *NOTCH2* mutations we identified are likely to be pathogenic events contributing to aberrant *NOTCH2* signaling in malignant SMZL cells.

Examination of *NOTCH2* mutational status in non-splenic MZLs revealed mutation in ~5% of cases analyzed. The *NOTCH2* mutation identified in a single case of extranodal MZL of the breast was a p.R2400X nonsense mutation.

This mutation was also identified in 9 of 99 (9.1%) SMZL cases. The selectivity of *NOTCH2* mutations for malignancies of marginal zone B cells is in keeping with the known role of *NOTCH2* in marginal zone cell fate determination (Saito et al., 2003; Witt et al., 2003). It is noteworthy that *NOTCH1* dictates T cell fate and that supraphysiological *NOTCH1* signaling induces T-ALL (Weng et al., 2004). We speculate that because *NOTCH2* specifies marginal zone B cell fate, supraphysiological *NOTCH2* signaling may analogously play a role in the pathogenesis of MZL.

Somatic mutations affecting specific genes that impact SMZL prognosis are largely unknown. Although previous studies have implicated a role for mutations targeting genes in the NF- $\kappa$ B pathway in a subset of SMZL (Rossi et al., 2011), only TP53 alterations affecting a small minority of cases have been demonstrated to impact SMZL prognosis (Salido et al., 2010; Rinaldi et al., 2011). TP53 mutations were not identified in our initial WGS screen of six index cases of SMZL. We have found that the presence of *NOTCH2* mutations in SMZLs at time of diagnosis predicted an adverse disease course characterized either by refractoriness to therapy, histological transformation to higher grade disease, or an otherwise aggressive clinical course. Assessment of *NOTCH2* mutation status in cases of SMZL may thus be useful to predict the risk of aggressive disease. This finding may also inform clinical decision-making at diagnosis, with the presence of *NOTCH2* mutation being an indication for more aggressive therapy. By analogy with pathogenetic mechanisms of *NOTCH1* mutation in T-ALL, it is tempting to speculate that similar downstream targets promoting proliferation, survival and deregulated metabolic pathways are also deregulated in SMZL. In addition to predicting a more aggressive disease course with an increased tendency to relapse, there is a trend toward reduced overall survival (i.e., time to death) among patients with *NOTCH2*-mutated SMZL (Fig. 6 D). However, this trend in overall survival did not reach the level of statistical significance, presumably because of the small sample size in this study ( $P = 0.16$ ).

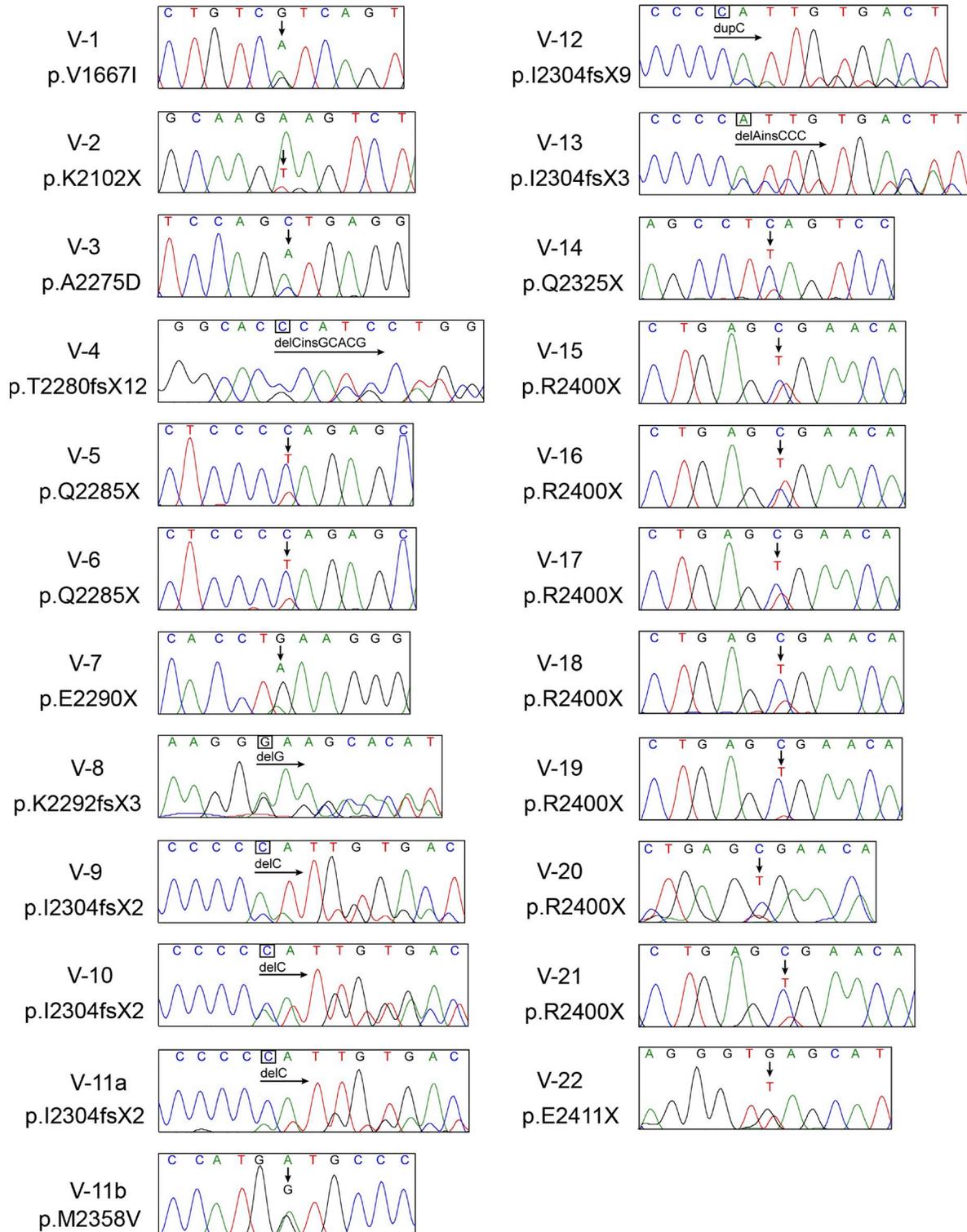
In summary, we used WGS to reveal high-frequency recurrent somatic mutations involving *NOTCH2* in SMZL. *NOTCH2* mutations appear to be specific for marginal zone lymphomas as compared with other B cell leukemias and

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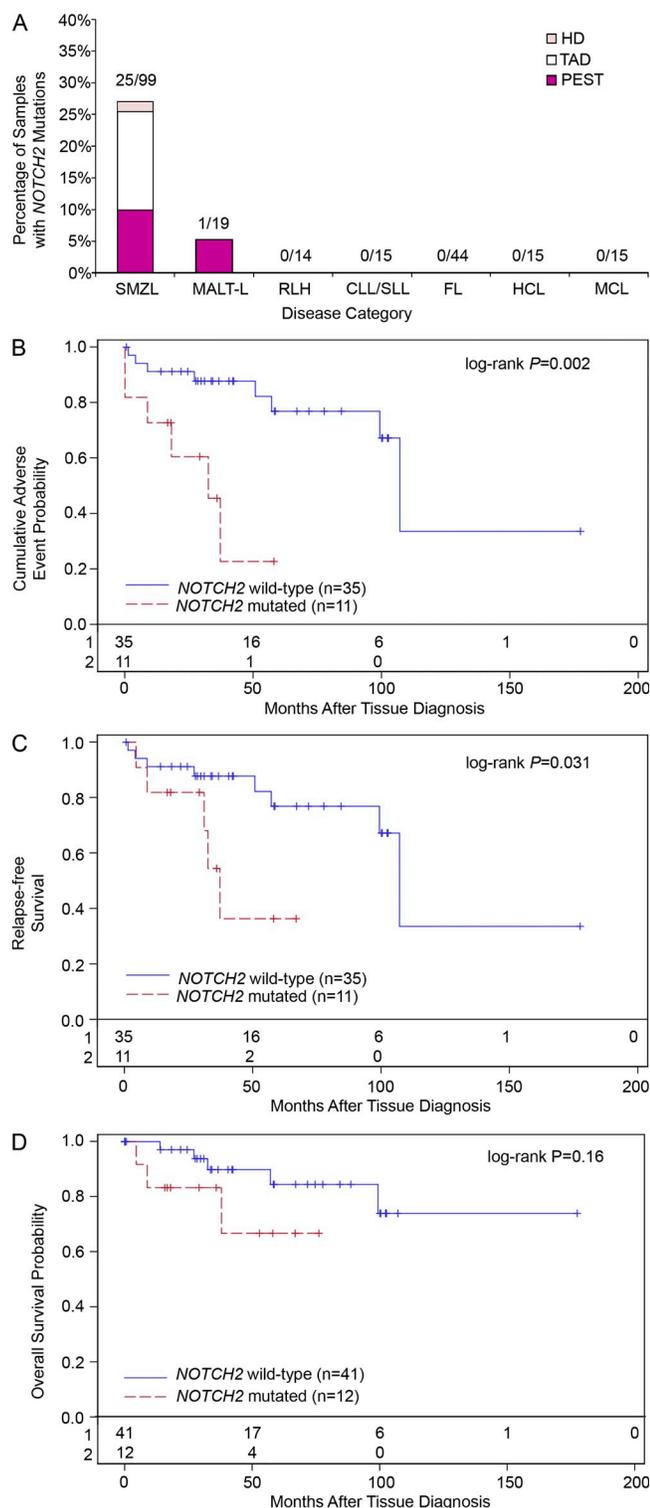
mediates ligand binding), three LNR domains (purple; prevents ligand-independent activation), the HD (pink; prevents ligand-independent activation), a single-pass transmembrane region (TM, light blue), RBP-J $\kappa$ -associated module (RAM, black; required for *NOTCH* signaling), six ankyrin repeats (AR, red; bind the CSL transcription factor), the transactivation domain (TAD, white), and the proline-, glutamate-, serine- and threonine-rich domain (PEST, magenta). (A, Middle) Three mutations in the TAD and the PEST domain downstream of the AR region were identified in the SMZL discovery cohort. (A, Lower) Targeted Sanger sequencing of the SMZL validation cohort uncovered the same as well as additional missense (blue triangles), nonsense and frameshift (red circles) mutations in the HD, TAD and PEST domains. Constitutional tissue from a total of 19 patients confirmed somatic acquisition of these mutations in all samples (solid symbols). Sanger sequencing confirmation was performed in at least two independent replicates. (B) The locations of mutations in hematolymphoid malignancies in the *NOTCH2* (7 total; top) and *NOTCH1* (>800 total; bottom) genes in the COSMIC database are displayed adjacent to *NOTCH2* and *NOTCH1* amino acid sequence alignment. Mutations within both genes cluster in the HD and TAD/PEST domains. Specific amino acid residues and the predicted consequence of all *NOTCH2* mutations in COSMIC are also displayed. (C) Mutations in HCS are confined to the C-terminal of the *NOTCH2* protein and cluster within the TAD and PEST domains. The p.R2400X mutation seen in 9 cases of SMZL is also present in at least one case of HCS as an inherited mutation (open symbol). De novo mutations are displayed as solid symbols.

lymphomas. Additionally, our initial studies indicate an adverse outcome for patients with *NOTCH2*-mutated SMZL. Therefore, we have identified a biomarker specific for a subset

of SMZL patients that may have value in both diagnosis and prognosis of patients with SMZL. Our findings therefore expand the spectrum of recurrent genetic alterations affecting



**Figure 5. Sanger sequencing identification of *NOTCH2* mutations in SMZL validation cohort.** Sanger sequencing results for each *NOTCH2*-mutated sample are shown. Arrows indicate site of nucleotide change. Amino acid change predicted for each mutation is indicated below sample label. Traces shown are representative of at least two independent amplification and sequencing reactions.



**Figure 6. Impact of *NOTCH2* mutations on clinical outcome in SMZL.** (A) Frequency of *NOTCH2* mutations in SMZL, MALT-L, and other B cell proliferative disorders divided among the different domains of the *NOTCH2* protein (color corresponds to domain in which mutations were located). For each separate disease, the number of samples with *NOTCH2* mutations compared with total number of samples analyzed is displayed above each bar. (B) Cumulative probability of relapse, transformation or

genes in the *NOTCH* pathway in human malignancy and suggest potential therapies targeting *NOTCH2* in the treatment of SMZL. Our studies further underscore the ability of unbiased large-scale screening approaches to uncover novel molecular mechanisms in neoplasia.

## MATERIALS AND METHODS

**Patients and samples.** Six SMZL samples from the University of Michigan were selected as index cases for WGS. To assess the prevalence of *NOTCH2* mutations in SMZL, an additional 93 SMZL cases were obtained from the University of Texas MD Anderson Cancer Center (31 cases), the University of Utah Health Sciences Center (25 cases), the Southern California Permanente Medical Group (20 cases), the University of Michigan (15 cases), and the University of Wisconsin (2 cases). Approval from the University of Michigan Hospital institutional review board (HUM00023256) was obtained for these studies. To assess the specificity of *NOTCH2* mutations in SMZL, genomic DNA was extracted from additional tissues representing non-SMZL diseases, including 15 cases of CLL/SLL, 15 cases of MCL, 44 cases of grade 1–2 FL, 15 cases of HCL, and 14 cases of RLH. In addition, 19 cases of nonsplenic MZL (i.e., nodal and extranodal/mucosa-associated lymphoid tissue lymphoma) were analyzed.

**Pathology review.** All specimens were reviewed independently and confirmed by consensus among three hematopathologists (MSL, NGB, and KEJ) according to World Health Organization classification criteria (Isaacson et al., 2008) without knowledge of *NOTCH2* mutational status. Only cases containing adequate neoplastic tissue were included in subsequent analyses.

**WGS and targeted *NOTCH2* DNA sequencing.** From each of six index SMZL cases, 10  $\mu$ g of high-molecular-weight genomic DNA was extracted from fresh frozen tumor tissue using the QIAamp DNA extraction kit (QIAGEN) and subjected to WGS by Complete Genomics, Inc. (CGI; Mountain View, CA). CGI performs massively parallel short-read sequencing using a combinatorial probe-anchor ligation (cPAL) chemistry coupled with a patterned nanoarray-based platform of self-assembling DNA nanoballs (Drmanac et al., 2010). Library generation, read-mapping to the NCBI reference genome (Build 37, RefSeq Accession nos. CM000663–CM00686), local de novo assembly and variant-calling protocols were performed as previously described (Drmanac et al., 2010; Roach et al., 2010). Initial read mapping and variant calling were performed using CGATools v1.3.0 (<http://cgatools.sourceforge.net/docs/1.3.0/>). Additional downstream bioinformatic analyses were performed using custom designed PERL sequencing routines. Targeted sequencing of the *NOTCH2* C-terminal coding exons 25 to 34 was performed using Sanger sequencing for the SMZL samples in the validation cohort. For all other samples, sequencing was confined to exons 26, 27, and 34, where all confirmed mutations in SMZL samples occurred. Somatic acquisition of each mutation was also assessed when matched constitutional tissue was available for analysis. Genomic DNA from index cases and genomic DNA corresponding to matched constitutional tissue were subjected to Sanger sequencing of regions of the *NOTCH2* where mutations were observed through WGS. For targeted sequencing of exons 25–34 in the *NOTCH2* C-terminal region in the validation and specificity cohort samples, genomic DNA was extracted using both the QIAGEN BioRobot EZ1 and QIAamp FFPE DNA extraction kits (QIAGEN). For all Sanger sequencing reactions, PCR amplification was performed using Phusion DNA

death from time of tissue diagnosis for patients with *NOTCH2*-mutated (red lines) and *NOTCH2*-wild-type (blue lines) SMZL. (C) Relapse-free survival from tissue diagnosis. (D) Overall survival from tissue diagnosis. The total number of patients in each analysis is displayed along the x-axes of each graph.

polymerase (New England Biolabs) followed by conventional Sanger sequencing technology using BigDye version 3.1 chemistry run on an Applied Biosystems 3730xl DNA Sequencer at the University of Michigan DNA sequencing Core. All sequencing reactions were performed using nested sequencing primers. Sequencing trace analysis was performed using Mutation Surveyor software. All mutations were verified in at least two independent PCR amplification and sequencing reactions. cDNA nucleotide numbering of coding sequence is based on GenBank accession NG\_008163.1. Protein amino acid numbering is based on GenBank accession NP\_077719.2. Detailed primer sequences for targeted exon sequencing can be found in Table S3–S4.

**Statistical analysis of clinical outcomes.** Clinical outcomes data (time to transformation, relapse or death) were analyzed using standard survival analysis. Survival plots were generated using Kaplan–Meier method and Log-rank tests were used to compare survival times between patients with *NOTCH2* mutations and patients with wild-type *NOTCH2*. Cox-proportional hazards regression analysis was conducted to compare the two groups of patients after adjusting for age, gender, performance status, and stage at diagnosis. Statistical analyses were performed with SAS version 9.3.

**Online supplemental material.** Table S1 details genes involved in large scale structural alterations identified by whole genomic sequencing of six index SMZL cases. Table S2 details genes with novel alterations identified in two or more of the index SMZL genomes by genomic sequencing. Tables S3 and S4 detail the primer sequences used for Sanger sequencing confirmation of *NOTCH2* mutations. Online supplemental material is available at <http://www.jem.org/cgi/content/full/jem.20120910/DC1>.

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