

Table S1

Sequences of oligonucleotide primers

Real-time RT-PCR	
AID _{right}	AGC CGT TCT TAT TGC GAA GA
AID _{left}	TGA TGA ACC GGA GGA AGT TT
PKA _{left}	AGT ACC TGG CCC CTG AGA TT
PKA _{right}	TAG ATC TGG ATG GGC TGG TC
GL _μ _{left}	TGC TGA AGA CAG GAC TGT GG
GL _γ _{right}	TTC GGG GAA GTA GTC CTT GA
GL _α _{right}	GAT GAC CAC GTT CCC ATC TG
GL _α _{left}	AGC AGC CTG ACC AGC ATC
GL _ε _{right}	CAC ATC CAC AGG CAC CAA AT
GL _ε _{left}	AGG GAA TGT TTT TGC AGC AG
BCL6-RNA _{left}	TGG GGT TCT TAG AAG TGG TGA
BCL6-RNA _{right}	GAA GAA CAT CAC TGG CAT GG
GAPDH _{right}	TGT GGT CAT GAG TCC TTC CA
GAPDH _{left}	GCC AAA AGG GTC ATC ATC TC
CD19 _{right}	TCG CTT TCT TTT CCT CCT CA
CD19 _{left}	TAC TAT GGC ACT GGC TGC TG
RT-PCR of the AID coding region	
AID-cod _{right}	TCA AAG TCC CAA AGT ACG AAA TG
AID-cod _{left-ext}	AGC CTC TTG ATG AAC CGG AGG A
AID-cod _{left-int}	TGA TGA ACC GGA GGA AGT TT
PCR of Ig heavy chain variable region, BCL6, PAX5, MYC and RhoH/TF	
VH4 leader	CTC CTG GTG GCA. GCT CCC AGA T
BCL6-DNA _{left}	GCA GTG GTA AAG TCC GAA GC
BCL6-DNA _{right}	GGA GCA AGG AAA GCA GTT TG
PAX5 _{left}	AAC AGT GCT CAC TGC ACA CC
PAX5 _{right}	TAA CTG CGG CGT GTT TGT TA
MYC _{left}	AAA AGC CAA ATG CCA ACT TC
MYC _{right}	GAG GCT ATT CTG CCC ATT TG
RhoH/TF _{left}	AGC CCA GAT CTT CCT GAC AA
RhoH/TF _{right}	GGG GTG AGT GTT GCT TTG AT
RT-PCR of circle transcripts	
C _γ	CGC TGC TGA GGG AGT AGA GT
C _γ _{int}	AGT TCC ACG ACA CCG TCA C
I _α	CTC TTG GCA GGC AGC CAG
I _α _{int}	AGG GTG GAC CTG CCA TGA
I _ε F1 (ref. 23)	GGG AGC TGT CCA GGA ACC CGA CAG AGC
I _ε F2 (ref. 23)	GGC CAC ACA TCC ACA GGC
C _γ R (ref. 23)	CCA ACT CTC TTG TCC ACC TTG G
RT-PCR of mature Ig transcripts	
FR2a (ref. 24)	TGG (AG)TC CG(AC) CAG (GC)C(CT) (CT)C(AGCT) GG
IgG _{ext}	CGC TGC TGA GGG AGT AGA GT
IgE _{ext}	TGG TGG CAT AGT GAC CAG AG
IgE _{int}	AGT GAC CAG AGA GCG TGA GG

Table S2

Relative AID mRNA expression and immunohistochemical / immunocytochemical AID staining in PMBL

case no.	AID expression	
	mRNA	protein
1	6.02	+++
2	9.65	+++
3	2.24	++
4	32.41	+++
5	1.09	+
6	14.13	+++
7	2.63	++
8	0.58	n.a.
9	1.37	++
10	0.01	-
11	1.01	+
12	7.53	+++
13	0.28	+
14	1.18	++
15	21.64	+++
16 (PT)	2.12	++
MedB-1	1.42	+
Karpas1106P	23.15	+++
GC Tonsil I	6.94	+++ (DZ)
GC Tonsil II	5.62	n.a.
GC Tonsil III	4.82	n.a.
GC Tonsil IV	4.74	n.a.
GC Tonsil V	4.31	n.a.

+++ , strong staining; ++, intermediate staining; +, weak staining; -, negative; n.a., not analyzed; GC, germinal center; PT, parental tumor of MedB-1; DZ, dark zone