SUPPLEMENTAL INFORMATION APPENDIX

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MATERIAL AND METHODS

Generation of a transplantation model in immunodeficient mice. Full-length human cDNAs of *MALT1* and *BCL10* genes (kindly provided by Martin Dyer, Leicester, UK) and full length ORF of an exon7-exon8 *API2-MALT1* fusion (kindly provided by Mathijs Baens, Leuven, The Netherlands) were cloned into the pcDNA3.1 vector (primer sequences are listed below). Murine pro-B BaF3 cells were grown in RPMI 1640 medium supplemented with 10% FCS, 10% WEHI-conditioned medium, 2 mM Gln, and penicillin/streptomycin. To simulate the natural conditions of the lymphocytes in patients with MALT lymphoma, cells were BCR-activated by treating them for three days prior and two days after transfection with anti mouse IgM 10 µg/mL (Sigma, St Louis, MO, USA), anti mouse CD40 2 µg/mL (BD Pharmingen, Palo Alto, CA, USA) and recombinant human IL4 10 ng/mL (R&D Systems, Minneapolis, MN, USA). Then, BCR-acicated BaF3 cells were transfected using Nucleofector technology (Amaxa) and selected using 1 mg/mL G418. Clones were isolated by limiting dilution, and stable transfectants were maintained at 500 ng/mL G418. To test IL-3 dependence, transfected and exponentially-growing BaF3 cells were washed twice with PBS and incubated in complete medium with or without 10% WEHI-conditioned medium for the indicated times. Cell viability was determined by the trypan blue exclusion method. Results were measured as the percentage of the living cells grown without versus with WEHI-conditioned medium. To test the oncogenic potential of the different genes *in vivo*, 1 x 10^6 transduced BaF3 cells were inoculated through the tail vein into 4-6-week-old BALB/c nude mice obtained from Charles River Laboratories. For each gene, two independent clones and the pool of transfected cells were used (5 mice per group, a total of 15 mice per gene). Mice were observed for 3 months and survival curves were calculated by the Kaplan-Meier method.

List of primers used for gene cloning, detection of *API2-MALT1* gene fusion and RT-PCR of *MALT1* and *BCL10*.

Primer	Sequence	Technique
MALT1-F	CCTCGAGATGTCGCTGTTGGGGGA	cDNA amplification
MALT1-R	TCATTTTTCAGAAATTCTGAGCCTGTCAGAGAAAC	
API2-MALT1-F	CTCGAGATGAACATAGTAGAAAACAGCATATTCTT	cDNA amplification
API2-MALT1-R	GCGGCCGCAAATCATTTTTCAGAAATTCTGAGC	
API2-1144F	ATTAATGCTGCCGTGGAAAT	Fusion identification
MALT1-1213R	GGTGCTCCCGGTAATTCATA	
BCL10-F	CCTCGAGATGGAGCCCACCGCAC	cDNA amplification
BCL10-R	TCATTGTCGTGAAACAGTACGTGATCTTAAGGGAA	
hMALT1-F	GCGCCTCAGTTGCCTAGACCTG	qPCR
hMALT1-R	GCTCATCTTCAGTGCACTCCAC	
mMALT1-F	CGCAGAGTTCTCCAATGTCA	qPCR
mMALT1-R	GAGTCCCCTTGTTTGCATGT	
m-beta-actin-F	TAGGAATCCATGGCCACTGCCGCATCCTCTTCC	qPCR
m-beta-actin-R	CACGATGGAGGGGCCGGACTCATC	

All primer sequences are listed as 5'-3'.

PCR CONDITIONS:

h-MALT1: (94ºC, 1 min; 56ºC, 1 min; 72ºC 1 min) 40 cycles; 72ºC, 10 min
m-βACTIN: (94ºC, 1 min; 56ºC, 1 min; 72ºC 1 min) 30 cycles; 72ºC, 10 min

Generation of Sca1-MALT1 transgenic mice. Human MALT1 cDNA was inserted into the ClaI site of the pLy6 vector to generate the Sca1-MALT1 vector. Stem cell antigen-1 (Sca-1) is an 18-kDa mouse glycosyl phosphatidylinositol-anchored cell surface protein (GPI-AP) of the *Ly6* gene family. Originally identified as lymphocyte activation protein-6A (Ly-6A), the murine *Ly6* gene family encodes at least 18 highly homologous, cross-hybridizing genes closely linked on mouse chromosome 15, many of which demonstrate greater than 80% sequence similarity with Ly-6A. The Sca-1 antibody recognizes antigens encoded by several members of the Ly-6 multigene family, including Ly-6A and Ly-6E. The lymphocyte activation protein-6A (Ly-6A) is the one expressed in B-lymphocytes. In our study we have used the Ly-6E.1 to direct and limit expression of MALT1 to HSC/progenitor cells. Accordingly, to demonstrate the validity of our strategy, we showed that human MALT1 expression was not detected in more differentiated B cells or in mature B-cell lymphoma cells, indicating that the tumoral phenotype in Sca1-MALT1 mice was most likely due to the restricted expression of the transgene in $Sca1^{+}Lin^{-}$ cells. The transgene

fragment (Figure 1A) was excised from its vector by restriction digestion with NotI, purified for injection (2 ng/mL) and injected into CBAxC57BL/6J fertilized eggs (1). Transgenic mice were identified by Southern blot analysis of tail snip DNA after EcoRI digestion. Malt1 cDNA was used to detect the transgene expression. Total RNA was isolated in two steps using TRIzol (Life Technologies) followed by RNeasy Mini-Kit (Qiagen Inc.) purification, following the manufacturer's RNA clean-up protocol with the optional on-column DNase treatment. The integrity and quality of RNA were verified by electrophoresis and its concentration measured. For RT-PCR analysis, reverse transcription (with random hexamer primers) was performed as described (2). Primer sequences are listed above. β-actin was used as a control to check cDNA integrity. Three independent Sca1-MALT1 transgenic lines were generated and analyzed, showing similar phenotypic features. Heterozygous *p53*$^{+/-}$ mice (3) were bred to Sca1-MALT1 mice to generate compound heterozygotes. F1 animals were crossed to obtain null *p53*$^{-/-}$ mice hemizygous for Sca1-MALT1. Upon signs of disease, mice were sacrificed and subjected to standard necropsy procedures. All major organs were examined under the dissecting microscope. Tissue samples were taken from homogenous portions of the resected organs and used for the different studies. Differences in survival of the different mouse cohorts were evaluated with Kaplan-Meier survival plots using the log-rank (Mantel-Cox) test. All animals were handled and housed in accordance with the Spanish Department of Health Guide for the Care and Use of Laboratory Animals, and the study was approved by the author's Institutional review Boards.

Flow cytometry. Nucleated cells were obtained from total mouse bone marrow (BM), peripheral blood, thymus, liver and spleen. To prepare cells for flow cytometry, contaminating red blood cells were lysed with RCLB lysis buffer and the remaining cells were then washed in PBS with 2% FCS. After staining, all cells were washed once in PBS with 2% FCS containing 2 mg/mL propidium iodide (PI) to allow dead cells to be excluded from both analyses and sorting

procedures. The samples and the data were analyzed in a FACSCalibur device using the CellQuest program (Becton Dickinson). Specific fluorescence of FITC and PE excited at 488 nm (0.4 W) and 633 nm (30 mW), respectively, as well as known forward and orthogonal light scattering properties of mouse cells were used to establish gates. Nonspecific antibody binding was blocked by preincubation of cells with CD16/CD32 Fc-block solution (BD Pharmingen). For each analysis, a total of at least 5,000 viable (PI^-) cells were assessed. To determine the purity of the BM isolated $CD34^+$ cells obtained from patients with MALT lymphoma and healthy donors, samples were processed as above and stained with a human CD34 antibody. Monoclonal antibodies were obtained from BD Pharmingen and are listed below.

Flow cytometry antibodies used in the study.

Lineage marker	Clone
CD3e	145-2C11
CD4	RM4-5
CD8	53-6.7
CD11b (Mac1)	M1/70
CD19	1D3
CD16/CD32 (Fc Block)	2.4G2
CD21	7G6
CD23	B3B4
CD25	PC61
CD45R/B220	RA3-6B2
CD117 (cKit)	2B8
IgD	11-26c.2a
IgM	R6-60.2
Ly-6A/E (Sca1)	E13-161.7
Ly-6G (Gr1)	RB6-8C5
CD34	581-CD34

Cell isolation. For cell sorter separation, BM cells were incubated with anti-Sca1 and anti-lineage marker antibodies (CD4, CD8, B220, Gr1, and Mac1). $Sca1^+Lin^-$ cells were isolated and purified from the BM of Sca1-MALT1 and control mice by fluorescence-activated cell sorting (FACS) (FACSVANTAGE; Becton Dickinson). c-kit (CD117) was not used for stem cell isolation, as previous studies of human and mouse specimens have described down-regulation of c-kit as a feature of leukemia stem cells (4, 5). Sorted cells were then reanalyzed for purity with flow

cytometry (purity >98%) (see Figure S2E). Isolation of human BM hematopoietic stem/progenitor $CD34^+$ cells was carried out in BM samples from six patients with MALT lymphoma and five healthy donors using the AutoMACs automated separation system with CD34 microBeads (Miltenyi-Biotec). Final purity was checked by flow cytometry using a PE mouse anti-human CD34 antibody (BD Pharmigen), being >95% in all cases.

Immunohistochemistry (IHC) and Western blot analysis. Paraffin-embedded tumor xenografts, transgenic mice tissues and human lymphoma samples were incubated with primary antibodies, centrally reviewed by a panel of pathologists, and diagnosed using uniform criteria. For comparative studies, age-matched WT mice were used. In transgenic mouse lymphomas, appropriate positive and negative control tissues were included for each antibody. Control tissues were composed of non-neoplastic, lymphoid mouse tissue (spleen, lymph nodes), were expression of CD20 was limited to B-cell areas, expression of Gcet1, CD10 & Bcl6 limited to germinal centre B-cells, expression of Foxp1 mainly limited to the follicle mantle & marginal zone, and the expression of Mum1 limited to B-cells in the light zone of the B-follicle (and plasma cells). For Western blot analysis, equal amounts of total protein (10-50 μg) were separated on sodium dodecyl sulfate–polyacrylamide gel electrophoresis (SDS-PAGE), and electrotransferred onto nitrocellulose membranes. Membranes were incubated with primary antibodies, followed by secondary antibodies conjugated to horseradish peroxidase, which were detected by chemiluminescence (Applied Biosystems, and Pierce, respectively). IHC and Western blot antibodies used in the study are listed below.

Western blot and immunohistochemistry antibodies used in the study.

For Human samples

Antibody	From	Use
ACTIN	Oncogene Research, Merk	WB
BCL10 (M7260)	Dako Cytomation	WB, IHC
CD20	Dako Cytomation	IHC (1:50)
EGFR (EGFR.113)	Novocastra	IHC
p-IκB	Cell Signaling	WB
IκB	Cell Signaling	WB
LTF (L3262)	Sigma Aldrich	IHC
MALT1	G. Roncador	WB
MALT1 (5745)	Imgenex	IHC

For Mouse samples

Antibody	From	Use
Pax5	Polyclonal anti-Pax5	IHC (1:50)
CD3	Santa Cruz	IHC (1:20)
Foxp1	Abcam	IHC (1:200)
CD20	Santa Cruz	IHC (1:50)
IgM	Serotec	IHC (1:50)
IgD	Monosan	IHC (1:50)
CD10	Santa Cruz	IHC (1:50)
Gcet1	Abcam	IHC (1:100)
Bcl6	Santa cruz	IHC (1:100)
Mum1	Abcam	IHC (1:100)

Blood cell count. Peripheral blood was collected from retro-orbital plexus with a heparinized capillary tube from both Sca1-MALT1 and control mice. The following parameters were estimated using 40 µl peripheral blood with a HEMAVET HV950FS multispecies hematology instruments (Drew Scientific, Inc.): red blood cells (RBC), hemoglobin (HB), hematocrit (HCT), mean corpuscular volume (MCV), mean corpuscular hemoglobin (MCH), mean corpuscular hemoglobin concentration (MCHC), red cell distribution width (RDW), platelet (PLT), and mean platelet volume (MPV). The differences in ranked hemogram parameters that defined the anemia in Sca1-MALT1 mice were analyzed by a one-way Kruskal-Wallis ANOVA. They were statistically significant for the following parameters: red blood cells ($p=0.0003$), hemoglobin ($p<0.0001$) and hematocrit ($p<0.0001$). To evaluate the specific differences between the control mice group and the two Sca1-Malt1 groups we used the Dunn's multiple comparison test.

V(D)J Recombination Analysis of mouse lymphomas. Ig gene rearrangements were amplified by PCR using primers specific for several V gene families in conjunction with reverse J primers, as previously described (6). PCR bands were cloned into a plasmid vector, and 8-10 clones from each purified band were sequenced and analyzed for the presence of somatic hypermutation studies of *Ig* gene sequences.

Southern blot analysis of Ig gene rearrangements. DNA was prepared from the mouse lymphomas using standard procedures. The DNA was digested with EcoRI and analyzed for V(D)J rearrangements at the *Igh* gene locus by Southern blotting using a 3'JH4 probe (1.6-kb HindIII-EcoRI fragment of plasmid JH4.3).

Measurement of MALT1 expression in mouse hematopoietic subpopulations. QRT-PCR analysis of human *MALT1* expression was performed in isolated mouse hematopoietic cell populations in an Eppendorf MasterCycler Realplex machine. Primers and probes used were obtained from Integrated DNA technologies (MALT1 assay Hs.PT.45.3837093). The differences in the Ct values (dCt) between MALT1 and endogenous control (GAPDH) were used to determine the relative expression of the transgene on each sample.

Patient samples. Seventy-five MALT lymphoma biopsies from different territories and biopsies from patients diagnosed with diffuse large-B-cell lymphoma (n=26), follicular lymphoma (n=15) and splenic marginal B-cell lymphoma (n=12) obtained from untreated patients were procured by seven institutions in Europe and North America. Clinical and laboratory data of this series are shown in Table S4. Six patients with pulmonary MALT lymphoma have been previously reported (marked with an asterisk in Table S4) (7). In addition, 13 samples corresponding to normal lymphocyte subpopulations isolated from peripheral blood or non-tumoral tonsils were included in

the study: T-cells, naïve B-cells, centroblasts, memory B-cells, peripheral blood marginal B-cells $IgM^+IgD^+CD27^+$, peripheral blood $CD19^+$ and activated $CD19^+$ cells. $CD19^+$ cells were activated with anti-human IgM 10 μg/mL (Sigma), anti-human CD40 2 μg/mL (R&D Systems) and recombinant human IL4 10 ng/mL (R&D Systems) for 24 hours. In addition, six Spanish patients diagnosed with MALT lymphoma and five healthy individuals were included in the study for BM $CD34^+$ cell isolation and characterization. Informed consent was obtained from the patients and donors in accordance with the Declaration of Helsinki. These studies were approved by the Institutional Research Ethics Committees of the different participating institutions.

Detection of chromosomal translocations by fluorescence in situ hybridization (FISH) and RT-PCR. Human MALT lymphoma specimens were screened for the presence of the t(14;18)(q32;q21) and t(11;18)(q21;q21) chromosomal translocations by FISH and/or RT-PCR. FISH was performed on fixed lymphoma cells from cytogenetic analysis and on a tissue microarray (TMA) composed of 70 lymphoma biopsies, as previously reported (8). Specific probes for *MALT1* (LSI-MALT1 Dual Color Break Apart Probe, Vysis, Molecular Laboratories, Abbott Park, IL, USA) and for *API2-MALT1* (LSI-API2/MALT1 Dual Color Dual Fusion Translocation Color Break Apart Probe, Vysis, Abbott) were used. Primers used for RT-PCR detection of *API2-MALT1* were listed previously, according to a previous report (9).

Gene expression microarray analysis. Human samples were processed following Affymetrix recommendations. The cRNAs were hybridized to the Affymetrix Human Genome U133 Plus 2.0 and GeneChip Human Exon 1.0 ST arrays in the case of human samples. Mouse samples were similarly processed and hybridized to the Affymetrix Mouse Genome 430 2.0. Raw gene expression microarray data files were submitted to GEO and are available under the accession numbers GSE25636, GSE25637, GSE25638, GSE25639 and GSE34015. Background correction

and normalization were done with the Robust Multichip Average (RMA) algorithm (10). R and Bioconductor were used for preprocessing and statistical analyses (11).

Validation of gene expression microarray data by QRT-PCR. A number of differentially expressed genes identified in the gene expression microarray analyses of human lymphoma samples and normal hematopoietic subpopulations were selected for validation using QRT-PCR: *FCRL4*-Irta1, *LTF, MEIS1, PBX1, ETV6, FZD7* and *FOXO3* genes. For RT reactions, 0.5 µg of total RNA were retrotranscribed using the MMLV-RT (Invitrogen). qPCRs were performed in an ABI PRISM 7500 device (Applied Biosystems, Weitersadt, Germany) using Taqman® Gene Expression assays. Measurement of *GAPDH* or *HPRT* genes product expression was used as an endogenous control. All samples were run in triplicate. The comparative CT Method (ΔΔCt) was used to calculate relative expression of these genes in patient samples. The change in threshold cycle (ΔCt) of each sample was calculated as the Ct value of the tested gene (target) minus the Ct value of GAPDH (endogenous control). The ΔΔCt of each sample was obtained by subtracting the ΔCt value of the reference from the ΔCt value of the sample. The ΔCt reference value used was the ΔCt obtained from normal tonsil or lymph node samples depending on the gene studied. The fold change in the two groups, calculated as $2^{-\Delta\Delta Ct}$ sample, was compared. Difference in mRNA expression between MALT lymphoma patients and the rest of lymphoma patients was analyzed using one-way Kruskal-Wallis ANOVA. Differences between specific groups were evaluated using the Dunn's multiple comparison test.

Differential expression analysis and identification of gene signatures. LIMMA (Linear Models for Microarray Data Analysis) was used to identify the probe sets with significant differential expression between experimental conditions (12). The B-statistic (lods or B), which is the log-posterior odds of differential expression, adjusted for multiple testing, was used using a cut-off

value of B>0. The Prediction Analysis for Microarrays (PAM) was used to classify the different human lymphoma subgroups and to identify genes that were associated with each specific class (13). This algorithm ranked genes using a penalized t-statistic and identified a gene set for classification with soft-thresholding. The number of genes was controlled by a thresholding parameter, which was determined with a 10-fold cross-validation. The molecular signature obtained by PAM was confirmed with consensus clustering (14). Hierarchical pair-wise average-linkage clustering was performed on the basis of the gene expression, with Pearson correlation used as a similarity metric. Data sets were obtained by sub-sampling, whereby 80% of the original samples were randomly selected, and 1,000 iterations were run for each signature. The consensus matrices were built for a number of clusters equal to the number of classes considered by the classifier.

Functional and pathway analysis of microarray data. Biological knowledge extraction was carried out using Ingenuity Pathway Analysis (Ingenuity Systems, www.ingenuity.com). In order to determine the biological meaning of the results, enrichment tests with respect to sets of related genes was carried out. To this end, the Gene Set Enrichment Analysis (GSEA) software was used, selecting the signal-to-noise metric and 1,000 permutations of the phenotype or gene set, when more or fewer than 7 samples per phenotype were studied, respectively (15). The q-values for each gene-set were computed on the basis of 1,000 iterations and false discovery rate (FDR) <25% including multiple hypothesis testing correction. (16).

High-resolution comparative genomic hybridization (aCGH) to microarray analysis of mouse lymphomas.

Genomic DNA was extracted from isolated B220$^+$ mouse lymphoma cells (n=11) and from WT B220$^+$ splenic B cells (n=2) that were used as normal hybridization controls. Whole genome

analysis was conducted using a commercial 180K oligonucleotide mouse aCGH microchip (AMADID 27411, Agilent Technologies), following a reported protocol (17). Microarray data was extracted and visualized using Feature Extraction software v10.7 and Agilent Genomic Workbench software v5.0 (Agilent Technologies). Regions with DNA copy number abnormalities were detected using ADM-2 (set as 6) statistic provided by DNA Analytics, with a minimum number of 5 consecutive probes. Genomic build mm7 was used for the experiment.

Primary cultures and Annexin V-FITC/PI staining. $B220^{+}$ single-cell suspensions were isolated from the spleen of three Sca1-MALT1, three Sca1-MALT1,$p53^{-/-}$ mice and three normal littermates. To inhibit MALT1 proteolytic activity and NF-κB signaling, $1x10^{4}$ cells were incubated in the absence or presence of the specific MALT1 inhibitor z-VRPR-fmk (75-microM) and of the NF-κB inhibitor Bay 11-7082 (Calbiochem) (5-microM). BaF3-MALT1-expressing cells were used as a positive control. After 48 hours, apoptosis was measured by annexin V-FITC/PI staining. Briefly, cells were washed with PBS and then stained with 500 µl labeling solution containing APC-B220, FITC-labeled annexin V (BD Pharmingen) and 5 µg/mL propidium iodide (PI; Sigma) for 15 min at room temperature in the dark. Subsequently, the samples were analyzed by flow cytometry within 1 hour to determine the percentage of cells displaying annexin V^{+} (early apoptosis) or annexin V^{+}/PI^{+} staining (late apoptosis/necrosis). The differences between experimental variables was determined using the Student *t* test.

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SUPPLEMENTAL FIGURES (S1-S6)

Figure S1. MALT1 overexpression is oncogenic in a transplantation mouse model. (**A**) Increased IκB phosphorylation indicating NF-κB signaling activation was found in isolated single-cell clones and cell pools from activated BaF3 cells transfected with either MALT1, BCL10 or API2-MALT1. (**B**) IL3 dependence of the different transfectants was assessed by plating them in the presence or absence of IL3 and measuring cell number by counting cells by Trypan blue exclusion method. Only MALT1- BaF3 transfectants grew in the absence of IL3. Mean values of three sequential experiments including error bars are shown. (**C**) Kaplan-Meier overall survival (OS) curve using the log-Rank (Mantel-Cox) test in mice transplanted with BA/F3-pcMALT1 cells (median OS, 13 days) *vs.* BaF3-pcBCL10 *vs*. BaF3-pcAIP2-MALT1 *vs*. BA/F3-mock control cells (median OS, not reached). Five mice were injected on each group. The p values for the different comparisons in survival duration shown are: control *vs.* pcAPI2-MALT1, p=0.07; control *vs*. pcBCL10, p=0.6; and control *vs.* pcMALT1 p<0.001. (**D**) Tumors induced in mice by MALT1-expressing cells were composed of large MALT1-expressing lymphocytes with a $CD19^{-}B220^{weak}CD5^{-}IgM^{-}$ phenotype, which involved bone marrow, peripheral blood, lung, lymph nodes and spleen. (**E**) Micro-positron emission tomography (microPET) imaging of control and pcMALT1 transplanted mice at 12 days post-transplantation showed metabolic activity in spleen and lung of mice transplanted with BaF3-MALT1 cells in comparison to control mice.

Figure S2. Generation and Characterization of the Sca1-MALT1 transgenic mice. (**A**) Schematic representation of the genomic structure of the mouse Sca1 locus and the Sca1-MALT1 transgenic vector, indicating *NotI* sites used to excise the transgene fragments and *EcoRI* sites used to examine Southern blots. (**B**) Identification of transgenic mice by Southern blot analysis of tail snip DNA after EcoRI digestion. *MALT1* cDNA was

used to detect the transgene. The Sca1-MALT1 transgene and the endogenous *Malt1* are indicated. (**C**) RT-PCR analysis revealed *MALT1* expression in Sca1^{+}Lin^{-} cells isolated from the BM of Sca1-MALT1 mice but not from WT mice. (**D**) Quantitative Real-Time PCR (QRT-PCR) analysis of human *MALT1* gene was measured in the indicated cell populations from Sca1-MALT1 transgenic mice and normalized to GAPDH mRNA. (**E**) MALT1 immunofluorescence analysis of cells sorted from Sca1-MALT1 mice. MALT1 is shown in green and nuclei counterstained with DAPI in blue. The human MALT1-expressing SSK41 cell line was used as a positive control. (**F**) Immunofluorescence analysis of MALT1 protein in sorted bone marrow (BM) Sca1^{+}Lin^{-} cells and CD23^{-} CD21^{high}B220^{+} splenic marginal-zone B cells isolated from 2-month-old Sca1-MALT1 mice, and B220^{+} B lymphocytes isolated from Sca1-MALT1 transgenic lymphomas developed in older mice. (**G**) Measurement of human MALT1 protein expression by Western blot analysis in T cells from both transgenic and WT mice. The human SSK41 cell line was used as a positive control for MALT1 protein expression. The presence of MALT1 protein was not detected in transgenic T lymphocytes. (**H-I**) Flow cytometry analysis of the hematopoietic cell compartments in the thymus, spleen, lymph nodes, bone marrow and peripheral blood of 2-month-old Sca1-MALT1 mice. Analysis of myeloid cells (determined by Gr1-Mac1 staining), B-cells (determined by B220-IgM-ckit; CD19-B220-ckit; IgD-IgM-B220; CD23-CD21-B220 and CD25-B220-IgM staining), hematopoietic stem cells (determined by Sca1-cKit-Lin staining) and T cells (determined by CD4-CD8 staining) are shown. Representative images from the study in three mice are shown. (**J**) Purity of the isolated stem/progenitor cells population (Sca1^{+}Lin^{-}) was determined by flow cytometry (over 98%). The expression of the characteristic cell surface markers is shown. Antibody staining and FACS were performed as described in the Supplemental Information (Material and Methods). (**K**) Heatmap image showing the

$Sca1^{+}Lin^{-}$ MALT1 transcriptional signature, comprised of genes differentially expressed between BM $Sca1^{+}Lin^{-}$ cells isolated from five Sca1-MALT1 transgenic mice and three WT mice. (**L**) GSEA showed enrichment of NF-κB target genes in $Sca1^{+}Lin^{-}$ cells from transgenic mice. (**M**) Ingenuity Pathway Analysis of the differentially expressed genes in the $Sca1^{+}Lin^{-}$ MALT1 signature. The differentially expressed genes (FC>1.8 and B>0) revealed that the inflammatory response was one of the main features overrepresented in this signature. (**N**). Detection of anemia in diseased Sca1-MALT1 mice. Parameters defining anemia were analyzed in young Sca1-MALT1 mice (n=10; 1.5-4 months old), old Sca1-MALT1 mice (n=30; 14-26 months old) and control mice (n=22; 10-15 months old) as indicated in the Experimental Procedures. All diseased aged Sca1-MALT1 mice showed a significant decrease in the red blood cell count, hemoglobin and hematocrit, but not in the mean corpuscular volume. The corresponding ANOVA p-values are indicated, and the differences were analyzed with the Dunn´s multiple comparison test.

Figure S3. Histopathological, imunohistochemical and genetic analyses of Sca1-MALT1 mouse lymphomas. Intestinal human MALT lymphomas and human-like mouse MALT lymphomas showed similar histopathological pictures including typical lymphoepithelial lesions; these lymphomas expressed the pan-B cell markers CD20 or $Pax5^{+}$. Magnification is 200X in figures **A**) and **C**) and 400X in **B**) and **D**). (**E**) A typical MALT lymphoma is shown, which (**e1**) infiltrates lungs (**e2**) and salivary glands (**e3**), evolving into a high-grade lymphoma resembling human DLBCL involving spleen (**e4**), stomach (**e5**), kidneys (**e6**) and liver (**e7**). (**F**) Representative IHC analysis for CD20, CD3, IgM and IgD stainings in Sca1-MALT1 lymphomas. (**G**) PCR analysis of the VH-to-DJH gene rearrangements in Sca1-MALT1 and Sca1-MALT1,$p53^{-/-}$ lymphomas. Sorted $CD19^{+}$ splenic B-cells and $CD4^{+}$ $CD8^{+}$ thymocytes were used as positive and negative controls, respectively. (**H**) The oligoclonal or clonal origin of several Sca1-

MALT1 and Sca1-MALT1,p53$^{-/-}$ lymphomas was also shown by Southern blot analysis. Tumor DNA was digested with EcoRI and analyzed for V(D)J rearrangements at the *Igh* locus by Southern blotting using a 3´JH4 probe (1.6-kb HindIII-EcoRI fragment of plasmid JH4.3). GL denotes the position of the germline fragment. Each tumor is characterized by the presence of at least two prominent *Igh* DNA bands, demonstrating that the lymphomas are oligoclonal/clonal in origin of V(D)J rearrangements at the *Igh* locus. (**I**) Histopathological and IHC studies of the high-grade lymphomas spontaneously developed in Sca1-MALT1 mice showed that the neoplastic cells expressed CD20 and Foxp1, in the absence of CD10, Gcet1, Mum1 and Bcl6 expression. As such, according to the algorithm by Choi et al. for human DLBCLs, these mouse lymphomas were classified as human-like ABC-DLBCLs. Appropriate positive tissue controls were used to ascertain Bcl6, Mum1/Irf4, CD10 and Gcet1 expression.

Figure S4. Histological and molecular characterization of human MALT lymphoma samples. (**A**) Human MALT lymphoma cases were evaluated for MALT1 and BCL10 expression and for the presence of the t(14;18)(q32;q21) and t(11;18)(q21;q21) translocations. (**A1**) HE-stained section of a MALT lymphoma biopsy showing typical centrocyte-like cells and lymphoepithelial lesions (400X). (**A2**) IHC for MALT1 showing high levels of the protein in the cytoplasm of tumor cells (200X). (**A3-4**) BCL10 protein expression and subcellular localization was evaluated in the tumors. In **A4**, a typical nuclear BCL10 expression in a case with a t(11;18)(q21;q21) translocation is shown (400X). (**A5-6**) FISH analysis showing a t(14;18)(q32;q21) (**A5**), and a t(11;18)(q21;q21) (**A6**). (**B**) Bioinformatic analysis of the gene expression microarray data using Prediction Analysis for Microarrays (PAM) identified 132 genes that distinguished MALT lymphoma from follicular lymphoma, diffuse large B-cell lymphoma and splenic marginal zone lymphoma, thus defining the human MALT lymphoma transcriptional

signature (n=145 probes, 132 genes). The number of genes obtained with PAM was controlled by a thresholding parameter, t, determined with a 10-fold cross-validation. This parameter was manually selected (t = 5) to obtained a compromise between the number of genes and the overall error in the classification. Control samples corresponding to purified B-cell subsets at different maturation stages are also represented. (**C**) Expression profiling validation of the microarray data analysis. A number of differentially expressed genes were selected for validation using QRT-PCR: *FCRL4*-Irta1, *LTF, MEIS1, PBX1, ETV6, FZD7* and *FOXO3* genes. The genes were selected from the human MALT lymphoma transcriptional signature of 132 genes defined by PAM. The genes were selected using biological and functional criteria because of their special interest for lymphoma. A total of 31 MALT lymphoma patient samples (20 of them different of those used for the microarrays) and 20 patients with other lymphomas were used for validation. As indicated in the supplementary material and methods, differences in mRNA expression between MALT lymphoma patients and the rest of lymphoma patients were analyzed using one-way Kruskal-Wallis ANOVA. Differences between specific groups were evaluated using the Dunn's multiple comparison test. In addition, two proteins were selected for IHC analysis because of concerns regarding the cells expressing those genes in the MALT lymphomas. (**D**) IHC study for LTF (**D1**, **D2**) and EGFR (**D3**) proteins revealed that they were not expressed by the B-cell lymphoma cells but by the accompanying inflammatory or epithelial cells in the MALT lymphoma biopsies. We tried to confirm other proteins in this list but lack of appropriate antibodies hampered this effort. (**E**) Gene set enrichment analysis (GSEA) plot showing enrichment of upregulated NF-κB target genes in MALT lymphoma *vs.* DLBCL, FCL and SMZL (gene set S=278 genes; FDR q<0.001). (**F**) Ingenuity Pathway Analysis (IPA) on the differentially expressed genes in the human MALT lymphomas *vs.* all other lymphomas (FC>1.8 and B>0) revealed that one of the

main features overrepresented was inflammatory response. (**G**) Similarly, IPA in Sca1-MALT1 lymphomas compared to WT littermates revealed the inflammatory response revealed the inflammatory response as one of the most prominent functions identified (160 molecules, $p<0.0001$). (**H**) Genes related to plasma cell differentiation were upregulated in $Sca1^{+}Lin^{-}$-sorted cells from transgenic Sca1-MALT1 relative to WT mice (including *Ig* genes, *Xbp1* and *Prdm1).* The XBP1 target gene signature was then studied using GSEA in all datasets, showing significant enrichment in sorted progenitor cells, mice tumors and human MALT lymphomas. (**I-J**) High-resolution aCGH analysis revealed that all nine Sca1-MALT1 mouse lymphomas studied displayed genomic abnormalities including changes syntenic with the characteristic genomic gains and losses observed in human MALT lymphomas.

Figure S5. Histopathological and genetic characterization of lymphomas developed in Sca1-MALT1,p53$^{-/-}$ mice. (**A**) Representative histopathological (HE) staining analysis of the lymphomas developed in Sca1-Malt1,p53$^{-/-}$ mice in comparison to p53$^{-/-}$ and WT mice. (**B-C**) aCGH analysis of two clonal lymphomas developed in Sca1-MALT1,p53$^{-/-}$ mice identified recurrent genomic abnormalities that are frequent in ABC-DLBCL. (**D**) Murine Malt1 mRNA expression was detected in murine lymphomas from spleen and intestine as well as in WT control tissues (n=3 mice, each). (**E**) Total splenic extracts from WT mice or Sca1-MALT1 splenic lymphomas were assayed for MALT1 proteolytic activity over Bcl10. Lane 1 (left): Bcl10 recombinant protein. Lanes 2 and 3: extracts from Sca1-MALT1 splenic lymphomas without or with Bcl10 recombinant protein, respectively. Lanes 4 and 5: extracts from WT spleens without or with Bcl10 recombinant protein, respectively. Endogenous Malt1 proteolytic activity on Bcl10 was detected in cell extracts from Sca1-MALT1 in comparison with WT littermates. Moreover, an increase in the amount of cleaved Bcl10 was detected when His-tagged Bcl10 was added.

(**F**) A representative flow cytometry plot showing the increased apoptosis in MALT1 p53$^{-/-}$ B220^{+} cells treated with Bay11-7082 relative to untreated cells (control), as visualized by Annexin V *vs*. PI staining.

Figure S6. Characterization of human bone marrow CD34^{+} cells isolated from patients with MALT lymphoma. (**A**) To investigate whether the t(11;18)(q21;q21) chromosomal translocation was present in isolated bone marrow CD34^{+} cells (purity >95%) from one patient with gastric MALT lymphoma carrying this genetic abnormality, two-color FISH studies using probes either flanking the MALT1 gene locus or specific probes for detecting API2-MALT1 rearrangement (Vysis) were applied to tumor cells and to CD34^{+} isolated BM cells. Whereas the MALT1 translocation was detected in 67 of 100 lymphoma cells analyzed (left), it was not found in any of the 500 nuclei of the CD34^{+} cells evaluated (right) (patient #6, Table S4A). (**B**) Semi-quantitative RT-PCR of *API2-MALT1* gene rearrangement. RT-PCR experiments were carried out with cDNAs generated from 275 ng of total RNA. An aliquot from each of the samples was removed at 30, 35, 37 and 40 cycles. The size of the amplified product is 250 bp. The housekeeping gene β2-microglobulin (β2M) was run in parallel and used as a control. RT-PCR was applied to the CD34^{+} cells isolated from the bone marrow of a patient with pulmonary MALT lymphoma carrying the t(11;18)(q21;q21) (patient #4) and to the other cases (cases #1, 2, 3 and 5). While the *API2-MALT1* gene fusion was detected in the lymphomas cells of case #4 (left), it was not identified in the CD34^{+} cells. (**C**) Heatmap image of the human CD34^{+} MALT transcriptional signature of the bone marrow CD34^{+} cells from five patients with MALT lymphoma *vs*. five healthy individuals (LIMMA, B>0). (**D**) IPA on the human CD34^{+} MALT transcriptional signature. (**E**) GSEA identified that the CD34^{+} cells from MALT lymphoma patients were enriched in NF-κB signaling molecules (FDR, q<0.0001). **Panels F-I** aim to show how the gene expression

profile of $CD34^+$ cells from the BM of MALT lymphoma patients is related to MALT lymphoma. (**F**) The human $CD34^+$ MALT lymphoma transcriptional signature was also enriched in the human MALT lymphoma dataset, but not in the datasets from other B-cell lymphomas. All lymphomas studied presented enrichment in this signature, but it is only statistically significant for the MALT lymphoma patients. (**G-I**) Gene set enrichment analysis (GSEA) showed that the human $CD34^+$ MALT lymphoma transcriptional signature was significantly enriched in the previously defined human MALT lymphoma dataset (FDR, q=0.012), but not in the datasets from patients with (G) DLBCL (q=0.059), (H) follicular lymphoma (q=0.113) or (I) splenic marginal-zone lymphoma (q=0.357). (**J-K**) The molecular signatures of the $Sca1^+Lin^-$ cells and of the Sca1-MALT1 mouse lymphomas were enriched in the human $CD34^+$ MALT lymphoma dataset.

FIGURE S1. MALT1 overexpression is oncogenic in a transplantation mouse model.

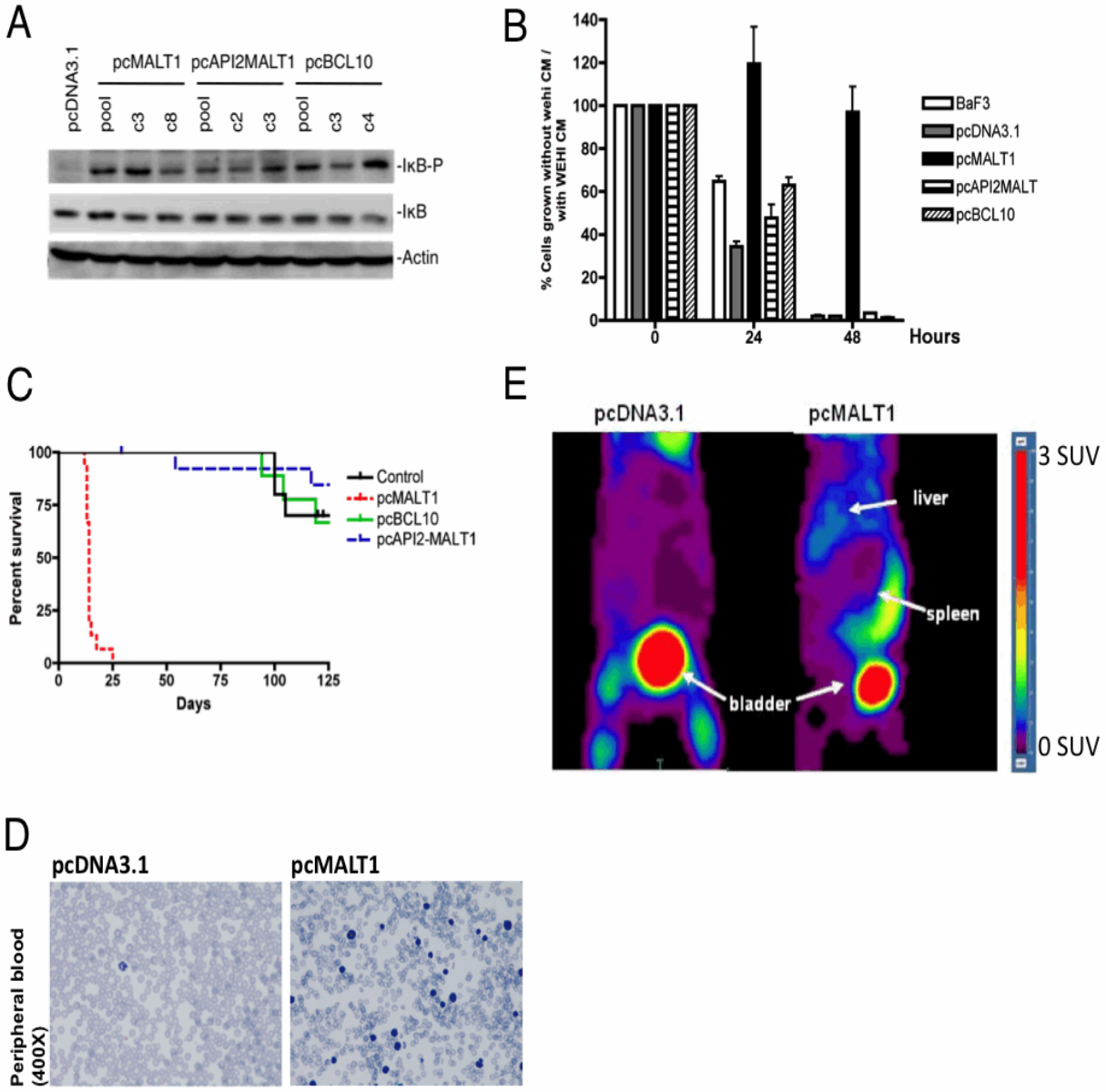
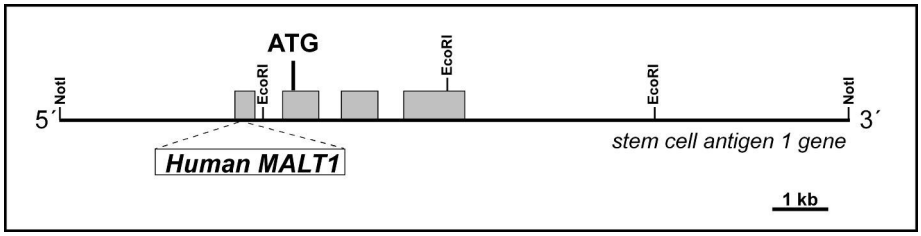


FIGURE S2. Characterization of Sca1-MALT1 transgenic mice.

2A



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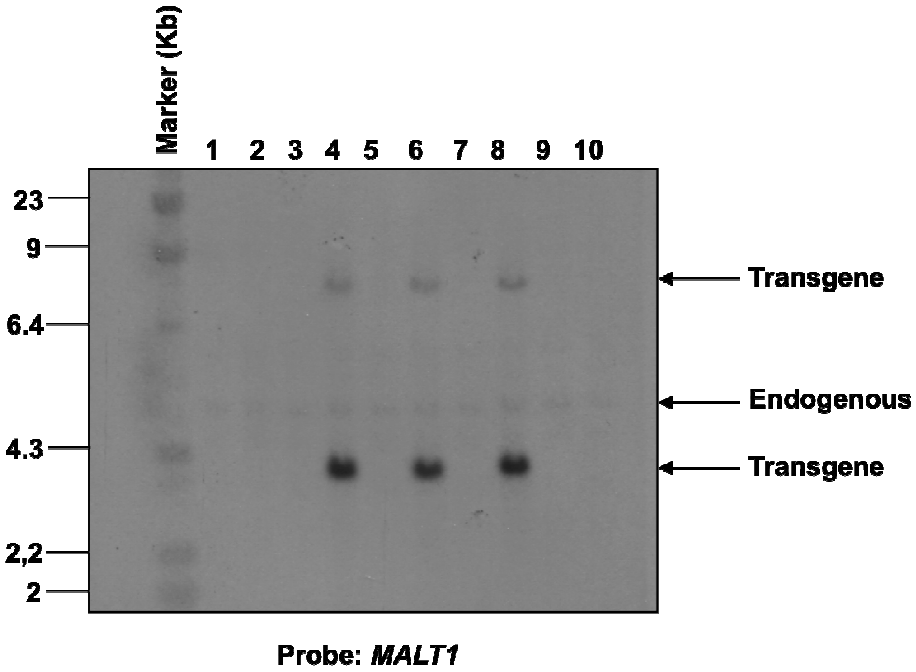

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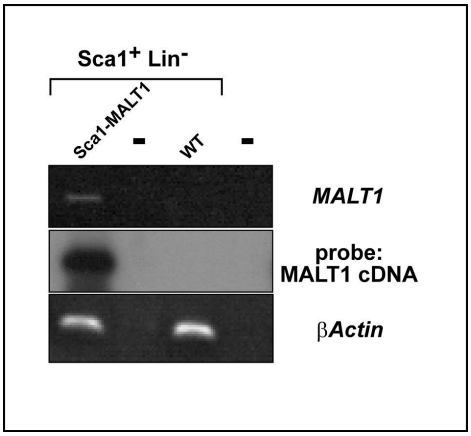
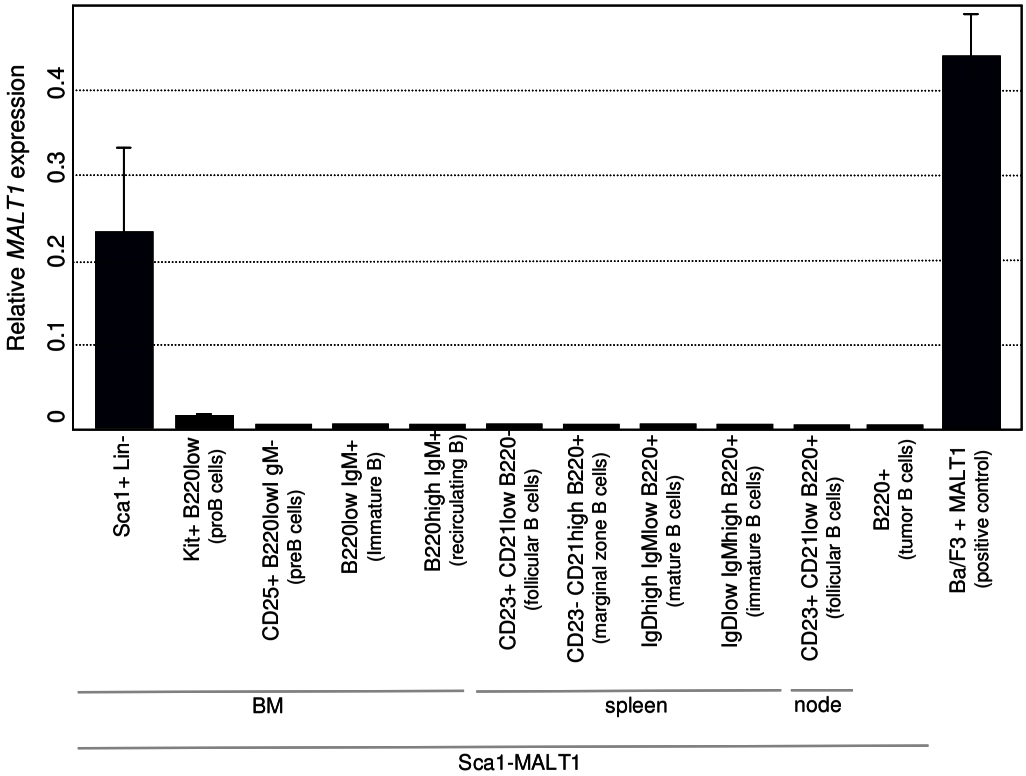
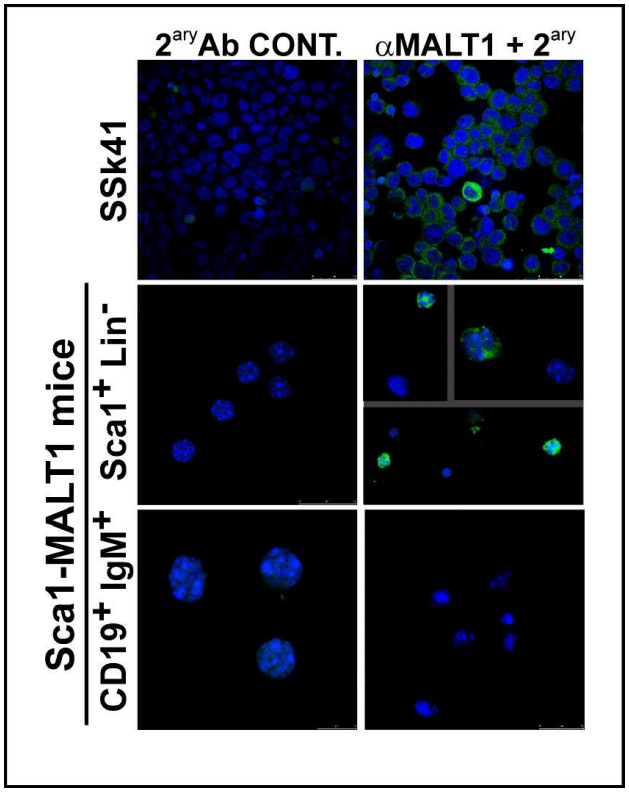


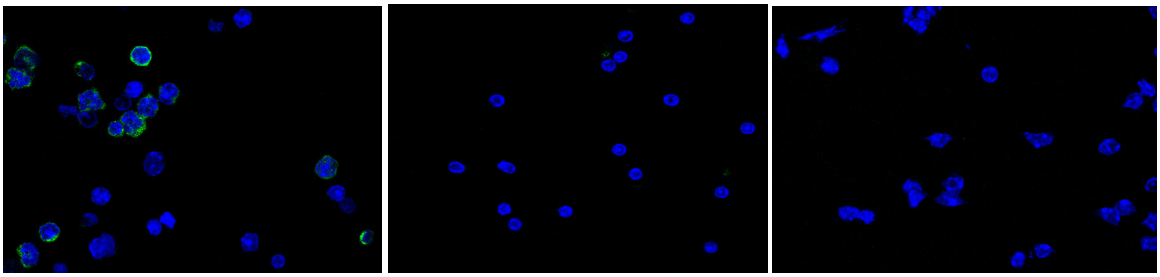
2D


Relative MALT1 expression
0
0.1
0.2
0.3
0.4
Sca1+ Lin-
Kit+ B220low (proB cells)
CD25+ B220lowl gM- (preB cells)
B220low IgM+ (Immature B)
B220high IgM+ (recirculating B)
CD23+ CD21low B220- (follicular B cells)
CD23- CD21high B220+ (marginal zone B cells)
IgDhigh IgMlow B220+ (mature B cells)
IgDlow IgMhigh B220+ (immature B cells)
CD23+ CD21low B220+ (follicular B cells)
B220+ (tumor B cells)
Ba/F3 + MALT1 (positive control)
BM
spleen
node
Sca1-MALT1

2E


Sca1-MALT1 mice
CD19+ IgM+
Sca1+ Lin-
SSk41
2ary Ab CONT.
αMALT1 + 2ary

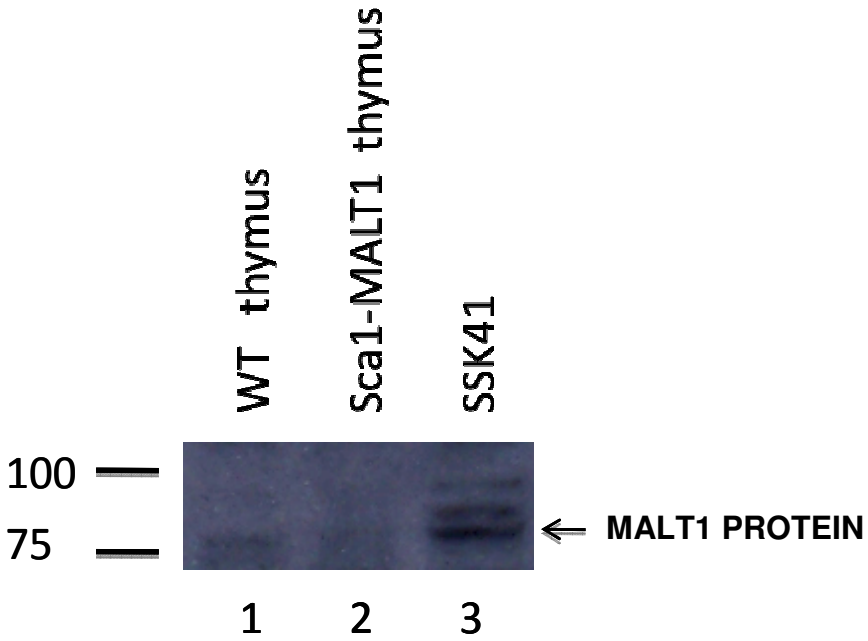
2F



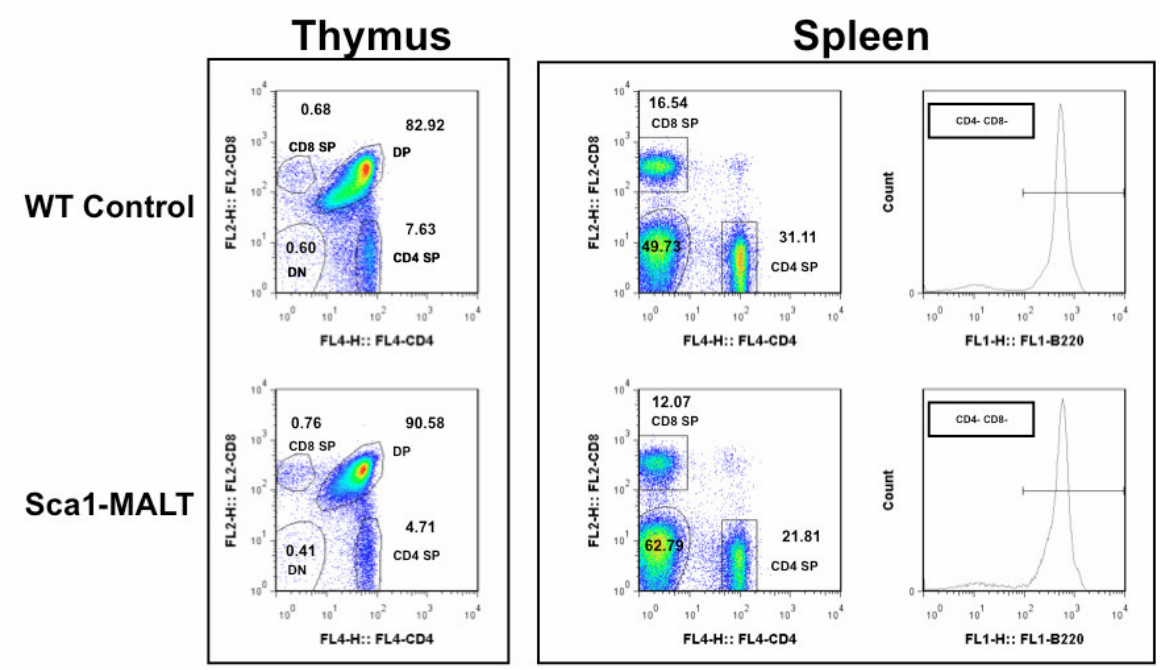
Sca1+Lin- | marginal zone B | tumor B

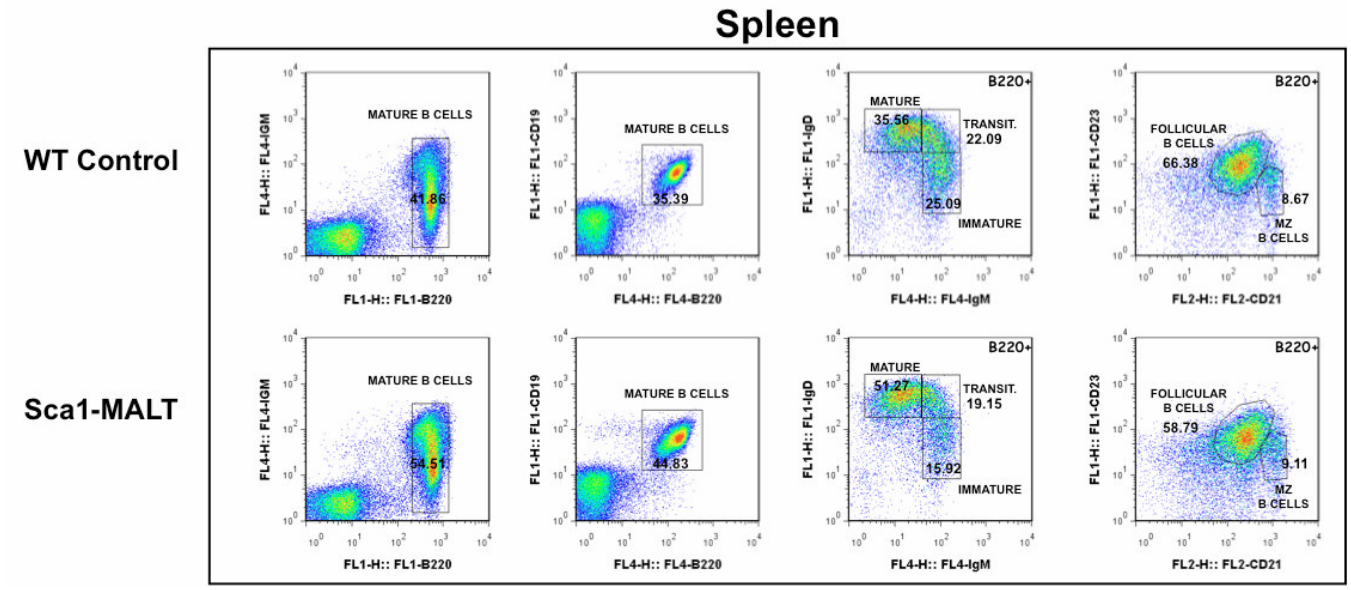
Sca1-MALT1 mice (MALT1 Ab)

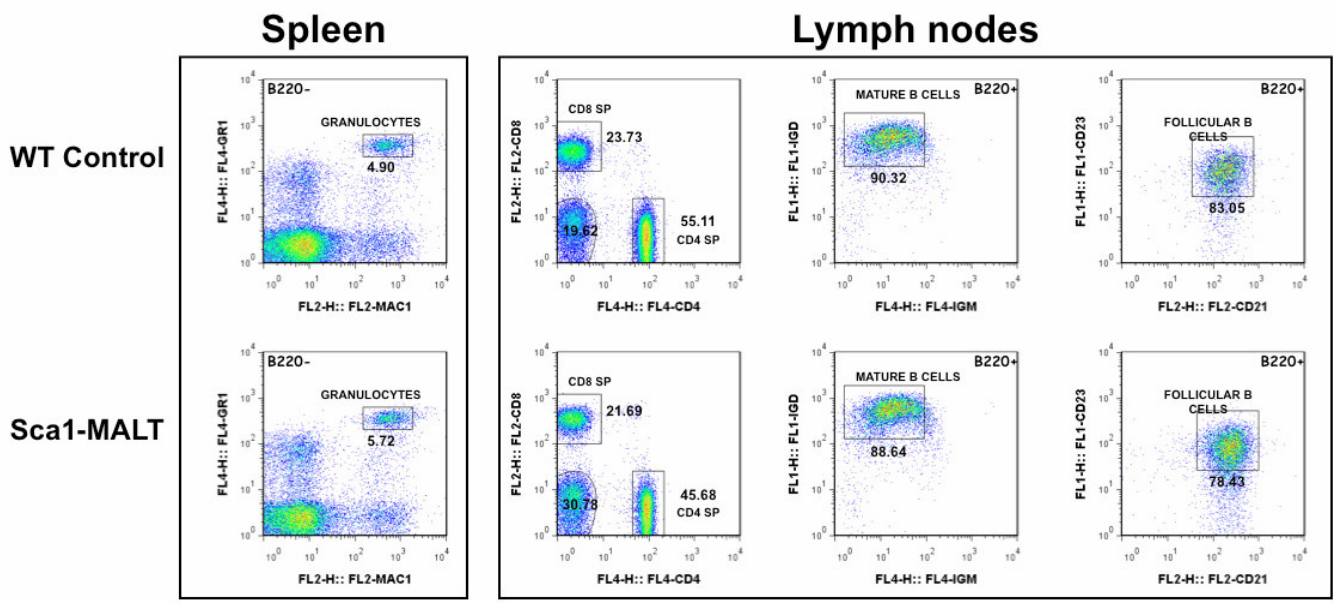
2G

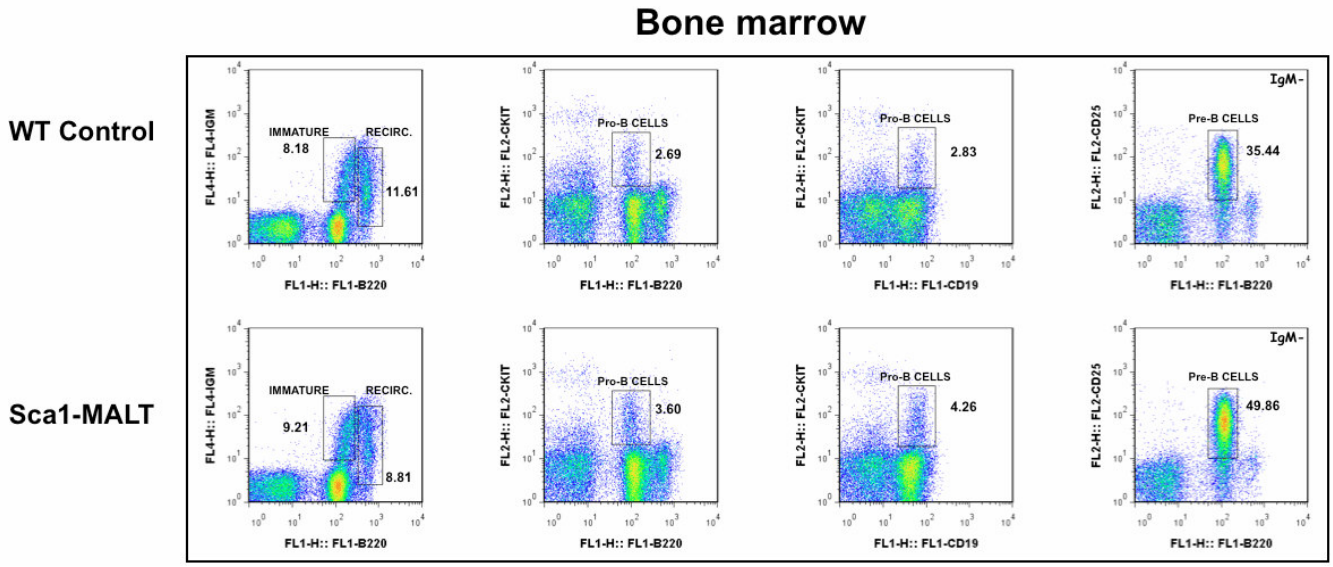


2H

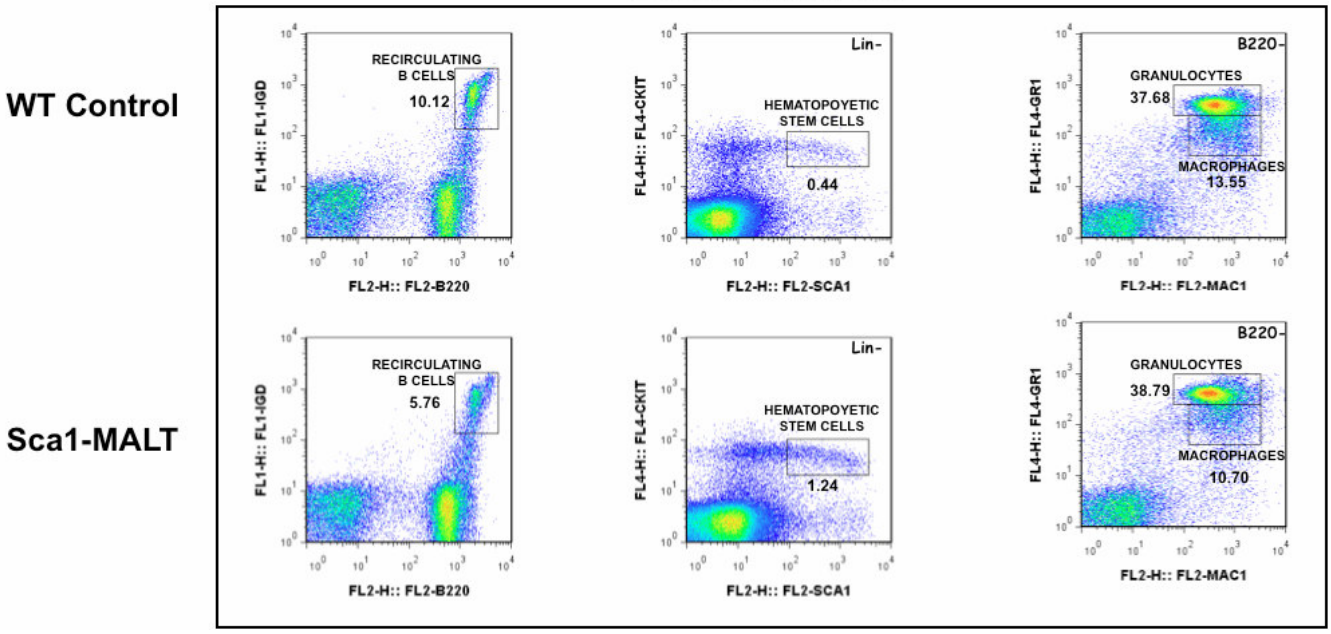

Thymus
Spleen
WT Control
Sca1-MALT
0.68
82.92
CD8 SP
DP
7.63
0.60
DN
CD4 SP
0.76
90.58
4.71
0.41
16.54
49.73
31.11
12.07
62.79
21.81
CD4- CD8-
Count
FL2-H:: FL2-CD8
FL4-H:: FL4-CD4
FL1-H:: FL1-B220


Spleen
WT Control
Sca1-MALT
MATURE B CELLS
41.86
35.39
54.51
44.83
B220+
MATURE
35.56
TRANSIT.
22.09
25.09
IMMATURE
51.27
19.15
15.92
FOLLICULAR
B CELLS
66.38
8.67
MZ
B CELLS
58.79
9.11
FL4-H:: FL4-IGM
FL1-H:: FL1-B220
FL1-H:: FL1-CD19
FL4-H:: FL4-B220
FL1-H:: FL1-IgD
FL4-H:: FL4-IgM
FL1-H:: FL1-CD23
FL2-H:: FL2-CD21

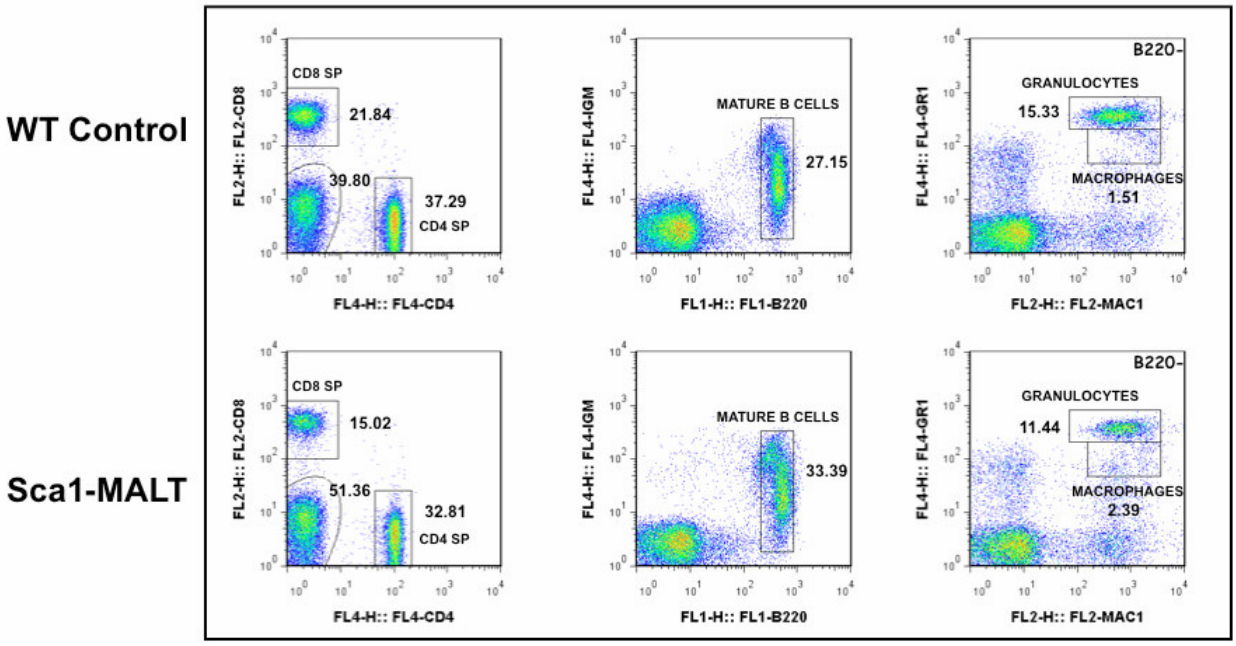

Spleen
Lymph nodes
WT Control
Sca1-MALT
B220-
GRANULOCYTES
4.90
5.72
FL4-H:: FL4-GR1
FL2-H:: FL2-MAC1
CD8 SP
23.73
19.62
55.11
CD4 SP
21.69
30.78
45.68
FL2-H:: FL2-CD8
FL4-H:: FL4-CD4
MATURE B CELLS
B220+
90.32
88.64
FL1-H:: FL1-IGD
FL4-H:: FL4-IGM
FOLLICULAR B CELLS
83.05
78.43
FL1-H:: FL1-CD23
FL2-H:: FL2-CD21


Bone marrow
WT Control
Sca1-MALT
IMMATURE
RECIRC.
8.18
11.61
9.21
8.81
FL4-H:: FL4-IGM
FL1-H:: FL1-B220
Pro-B CELLS
2.69
3.60
FL2-H:: FL2-CKIT
2.83
4.26
FL1-H:: FL1-CD19
IgM-
Pre-B CELLS
35.44
49.86
FL2-H:: FL2-CD25

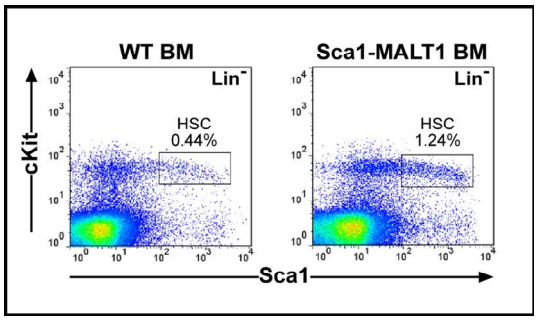
Bone marrow

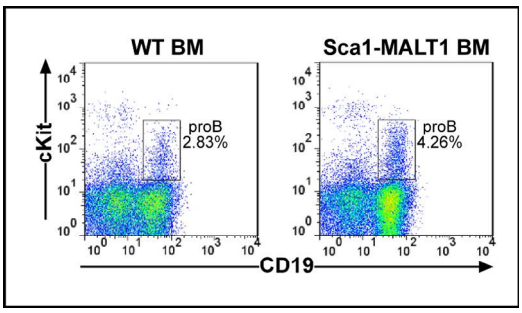


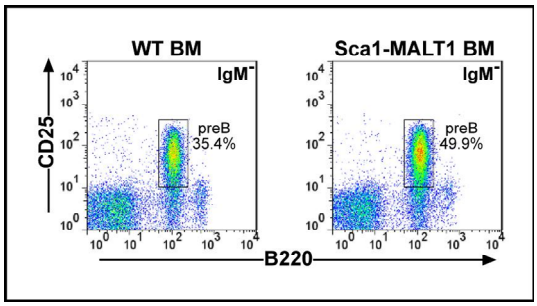
Peripheral Blood

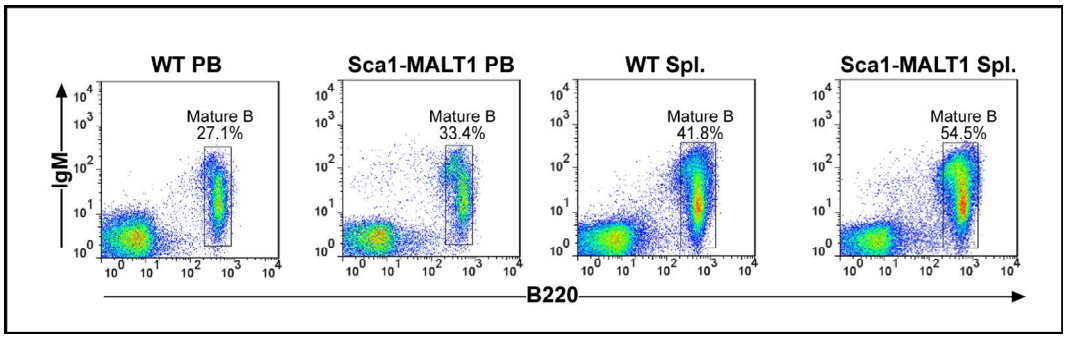


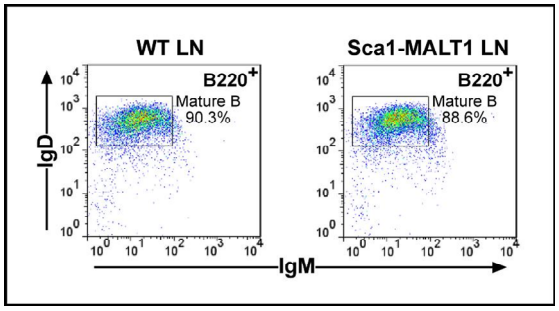
2I


WT BM
Sca1-MALT1 BM
Lin-
HSC
0.44%
HSC
1.24%
cKit
Sca1

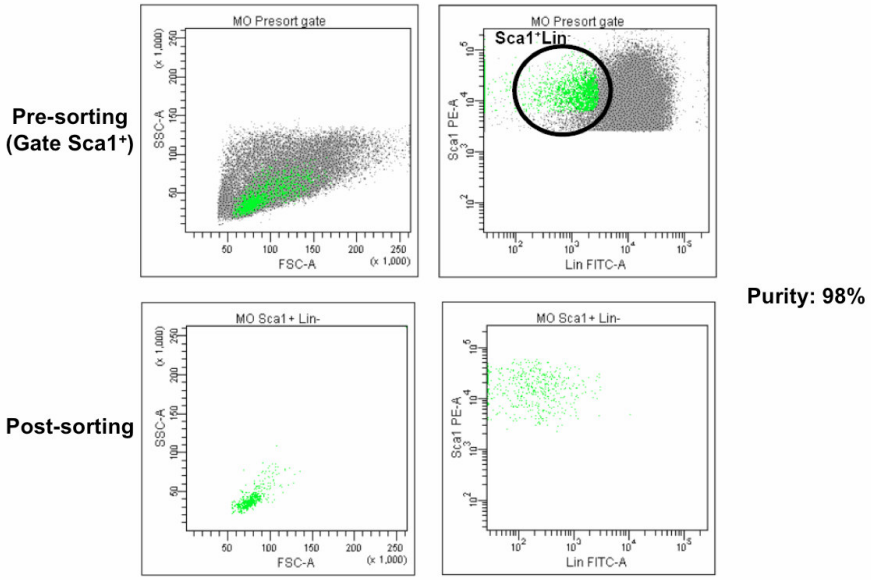

WT BM
Sca1-MALT1 BM
proB
2.83%
proB
4.26%
cKit
CD19


WT BM
Sca1-MALT1 BM
IgM-
preB
35.4%
preB
49.9%
CD25
B220

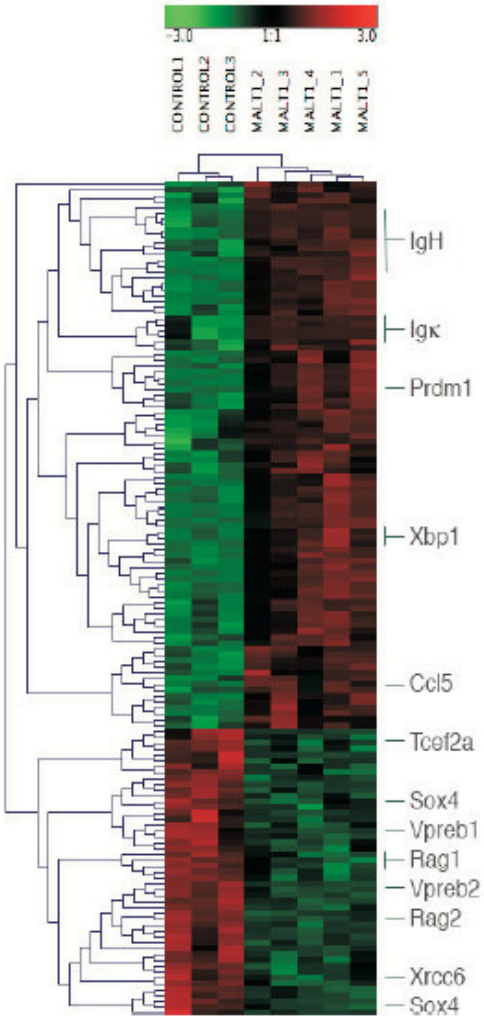

WT PB
Sca1-MALT1 PB
WT Spl.
Sca1-MALT1 Spl.
Mature B
27.1%
Mature B
33.4%
Mature B
41.8%
Mature B
54.5%
IgM
B220


WT LN
Sca1-MALT1 LN
B220+
Mature B
90.3%
B220+
Mature B
88.6%
IgD
IgM

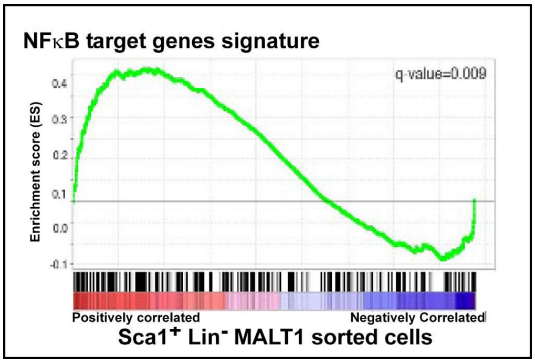
2J


Pre-sorting
(Gate Sca1+)
Post-sorting
MO Presort gate
MO Sca1+ Lin-
Sca1+Lin-
SSC-A
FSC-A
Sca1 PE-A
Lin FITC-A
Purity: 98%

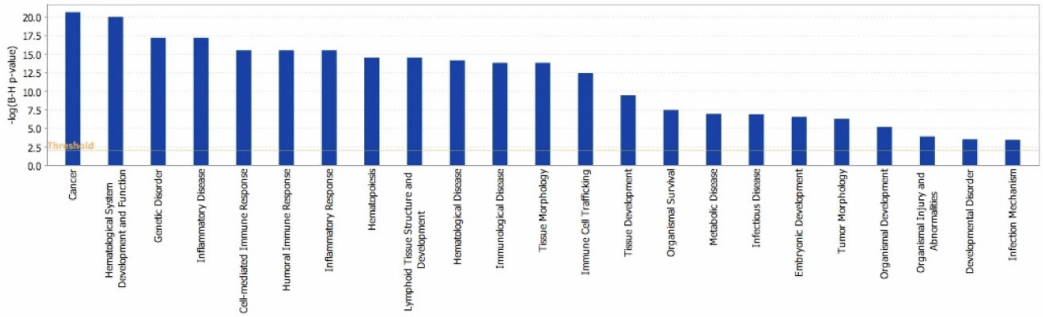
2K


-3.0
1.1
3.0
CONTROL1
CONTROL2
CONTROL3
MALT1_2
MALT1_3
MALT1_4
MALT1_1
MALT1_5
IgH
Igκ
Prdm1
Xbp1
Ccl5
Tcef2a
Sox4
Vpreb1
Rag1
Vpreb2
Rag2
Xrcc6
Sox4

2L


NFκB target genes signature
q-value=0.009
Enrichment score (ES)
0.4
0.3
0.2
0.1
0.0
-0.1
Positively correlated
Negatively Correlated
Sca1+ Lin- MALT1 sorted cells

2M


-log(B-H p-value)
20.0
17.5
15.0
12.5
10.0
7.5
5.0
2.5
0.0
Threshold
Cancer
Hematological System Development and Function
Genetic Disorder
Inflammatory Disease
Cell-mediated Immune Response
Humoral Immune Response
Inflammatory Response
Hematopoiesis
Lymphoid Tissue Structure and Development
Hematological Disease
Immunological Disease
Tissue Morphology
Immune Cell Trafficking
Tissue Development
Organismal Survival
Metabolic Disease
Infectious Disease
Embryonic Development
Tumor Morphology
Organismal Development
Organismal Injury and Abnormalities
Developmental Disorder
Infection Mechanism

2N

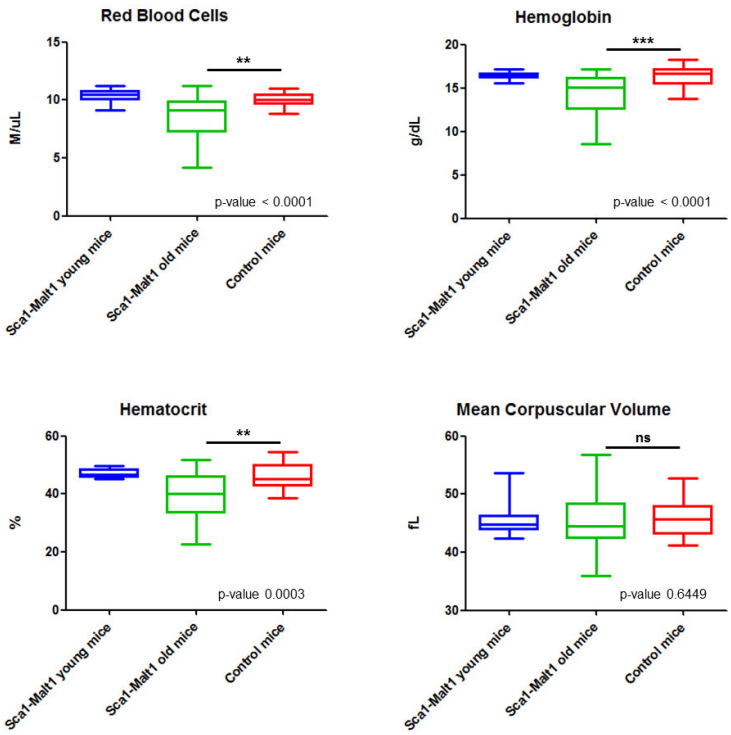
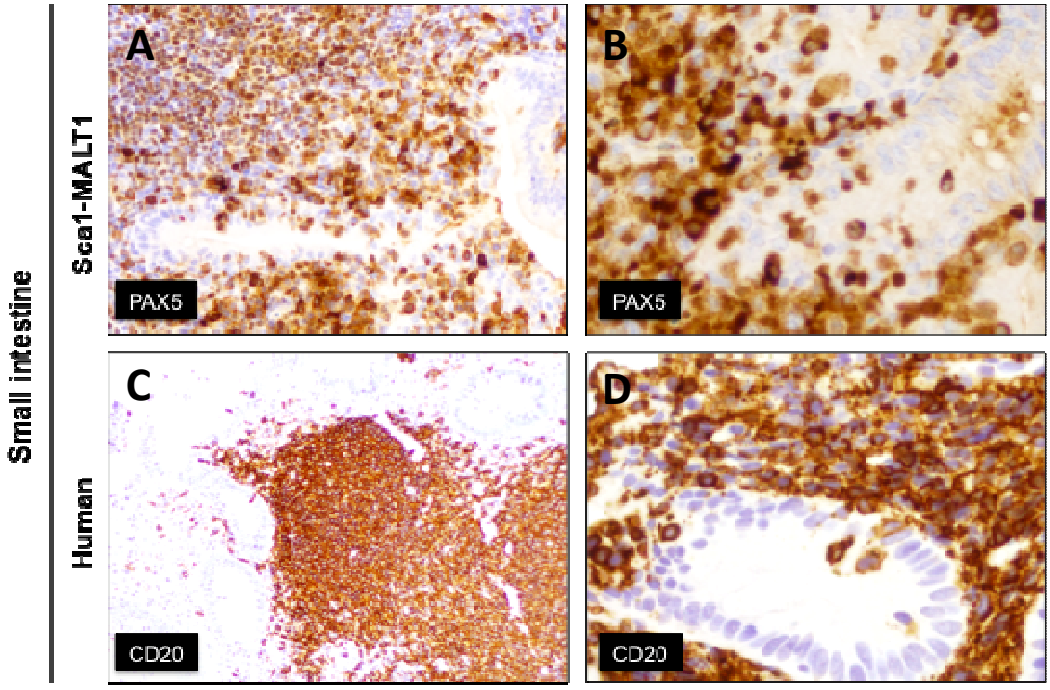
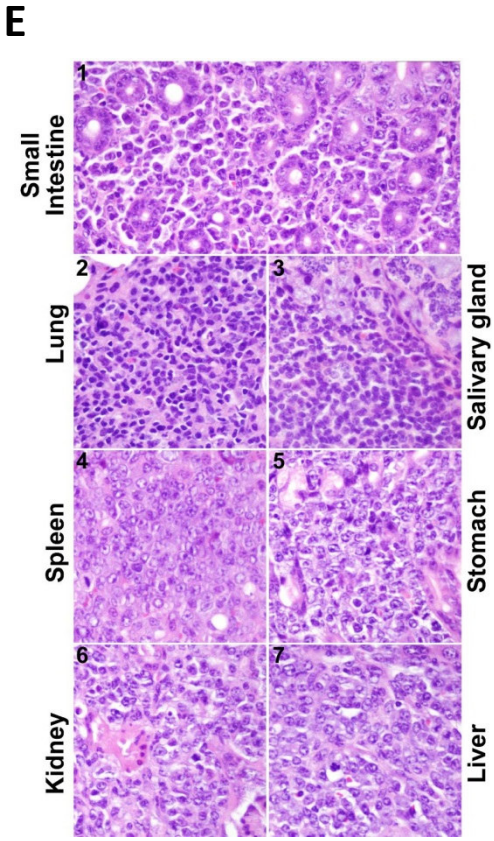
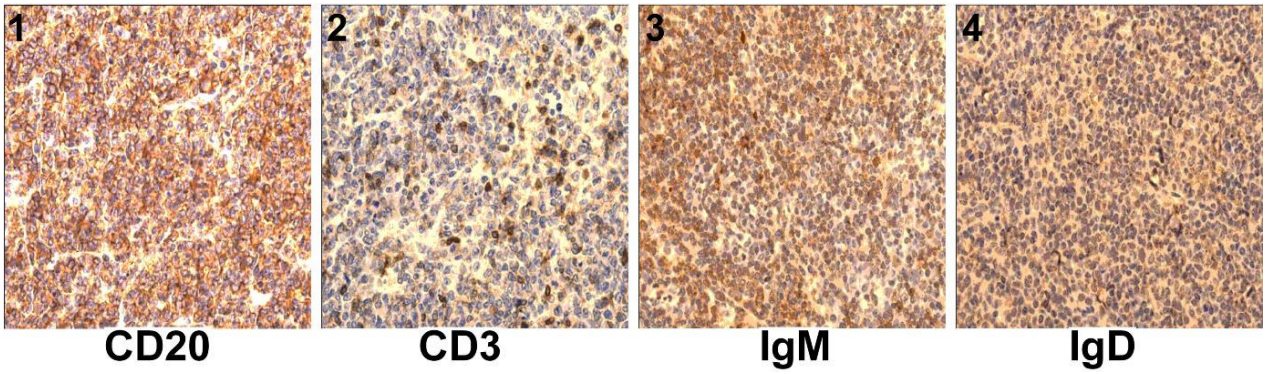

Red Blood Cells
M/uL
**
p-value < 0.0001
Hemoglobin
g/dL
***
p-value < 0.0001
Hematocrit
%
**
p-value 0.0003
Mean Corpuscular Volume
fL
ns
p-value 0.6449
Sca1-Malt1 young mice
Sca1-Malt1 old mice
Control mice

Figure S3. Histopathological, imunohistochemical and genetic analyses of Sca1-MALT1 mouse lymphomas.

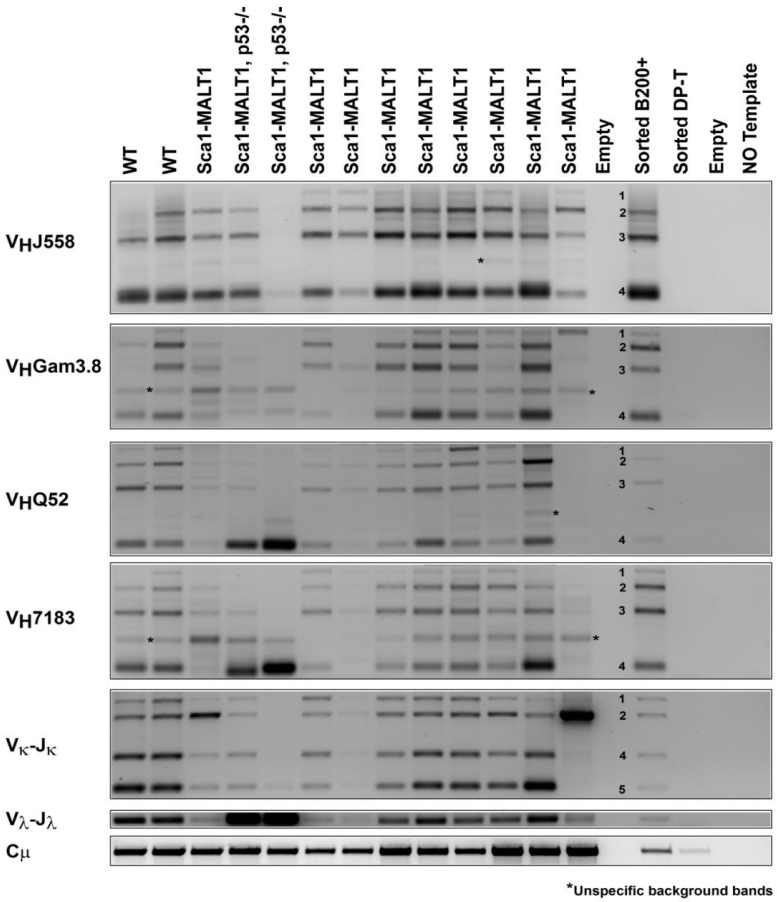




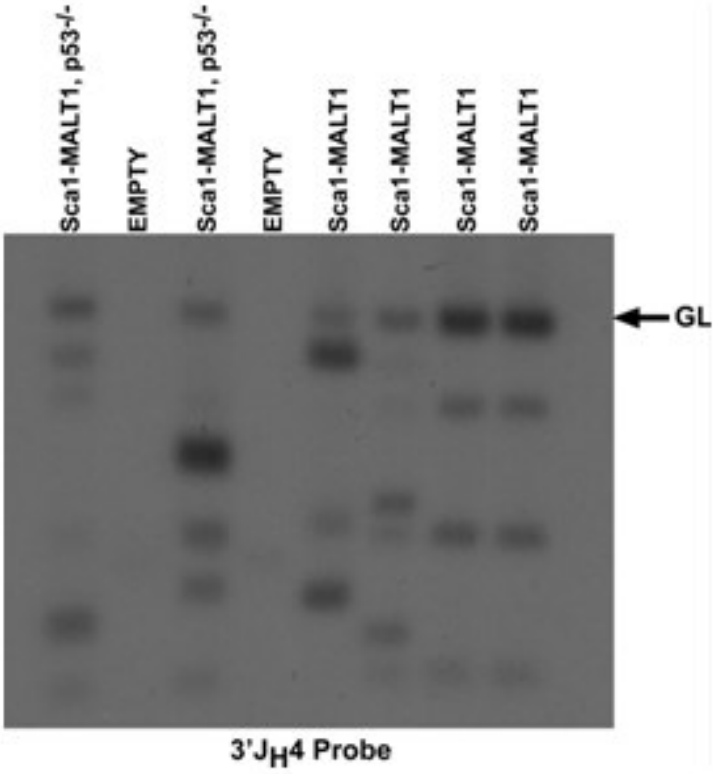
F


1
2
3
4
CD20
CD3
IgM
IgD

G


WT
WT
Sca1-MALT1
Sca1-MALT1, p53-/-
Sca1-MALT1, p53-/-
Sca1-MALT1
Sca1-MALT1
Sca1-MALT1
Sca1-MALT1
Sca1-MALT1
Sca1-MALT1
Sca1-MALT1
Sca1-MALT1
Empty
Sorted B200+
Sorted DP-T
Empty
NO Template
VHJ558
VHGam3.8
VHQ52
VH7183
Vκ-Jκ
Vλ-Jλ
Cμ
*Unspecific background bands

H


Sca1-MALT1, p53-/-
EMPTY
Sca1-MALT1, p53-/-
EMPTY
Sca1-MALT1
Sca1-MALT1
Sca1-MALT1
Sca1-MALT1
GL
3'JH4 Probe

I

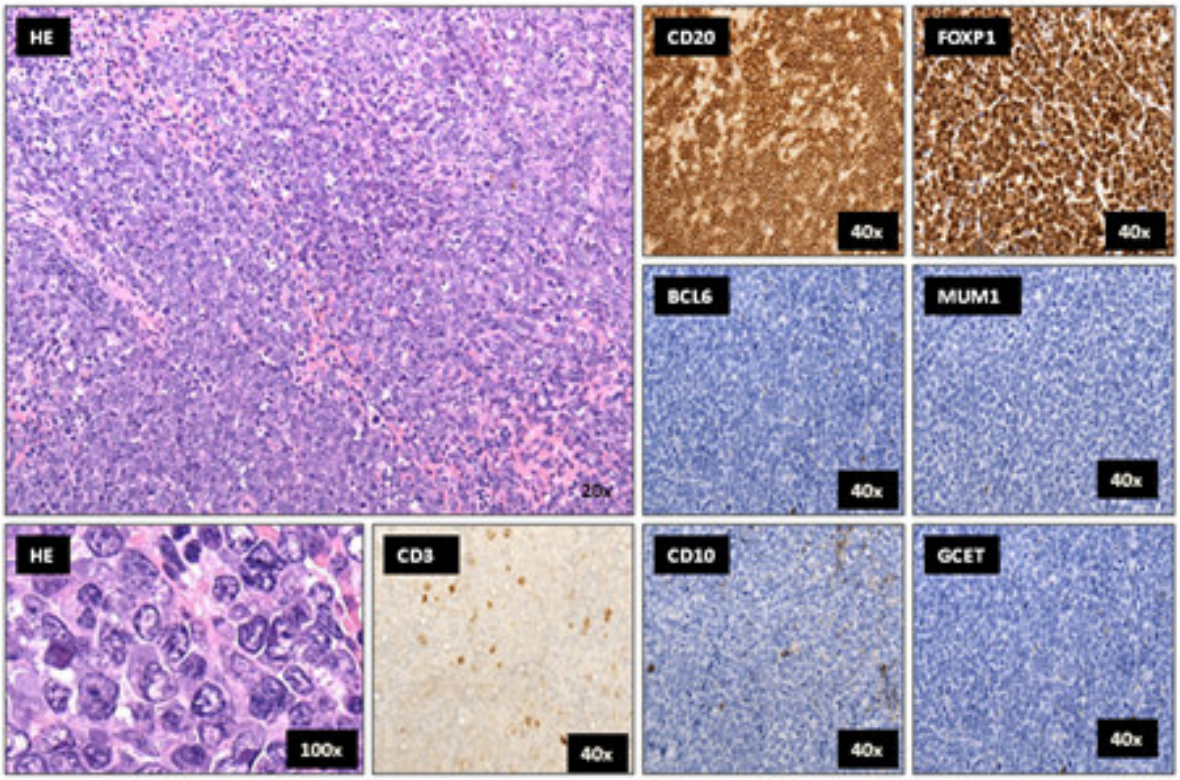
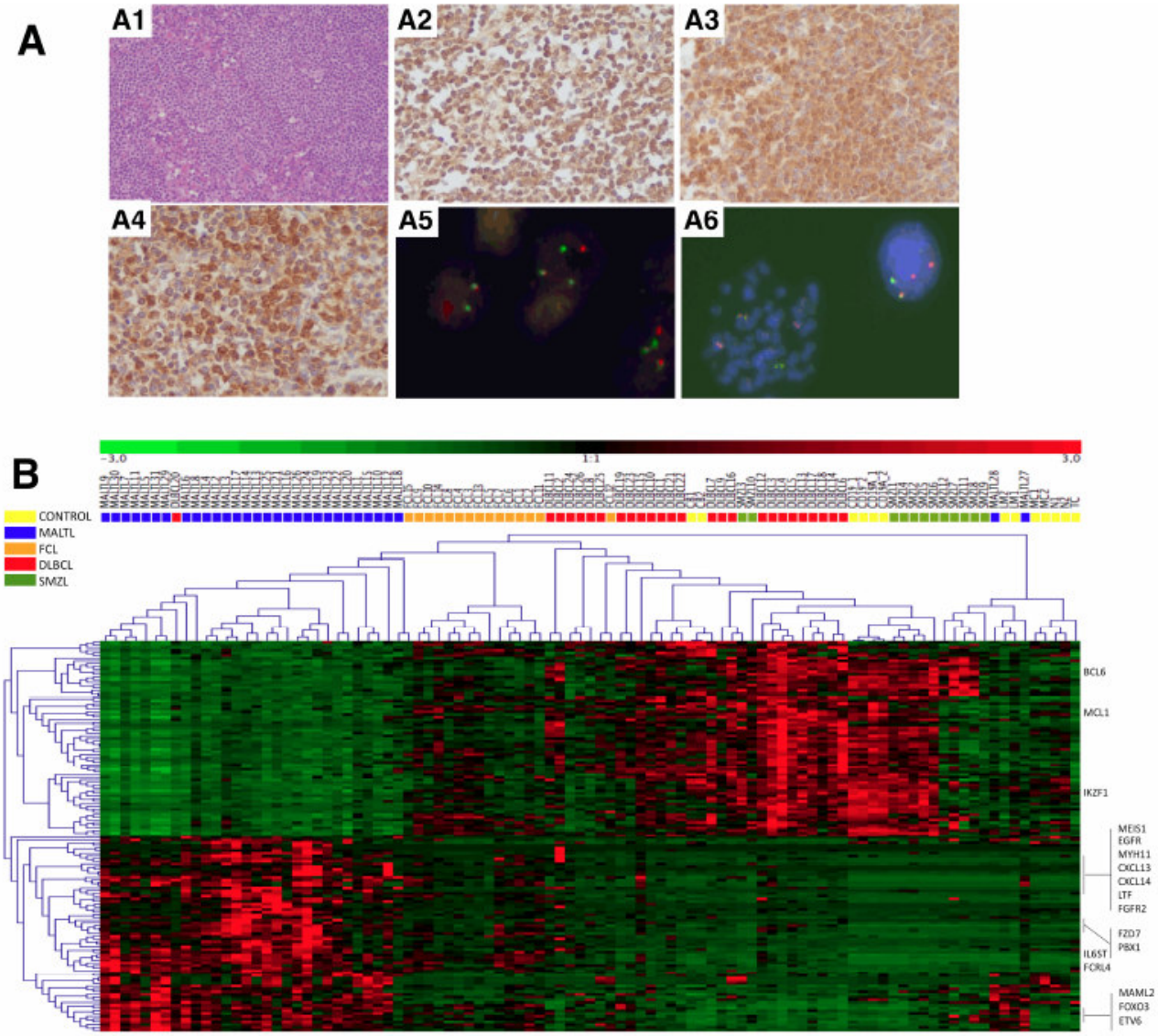
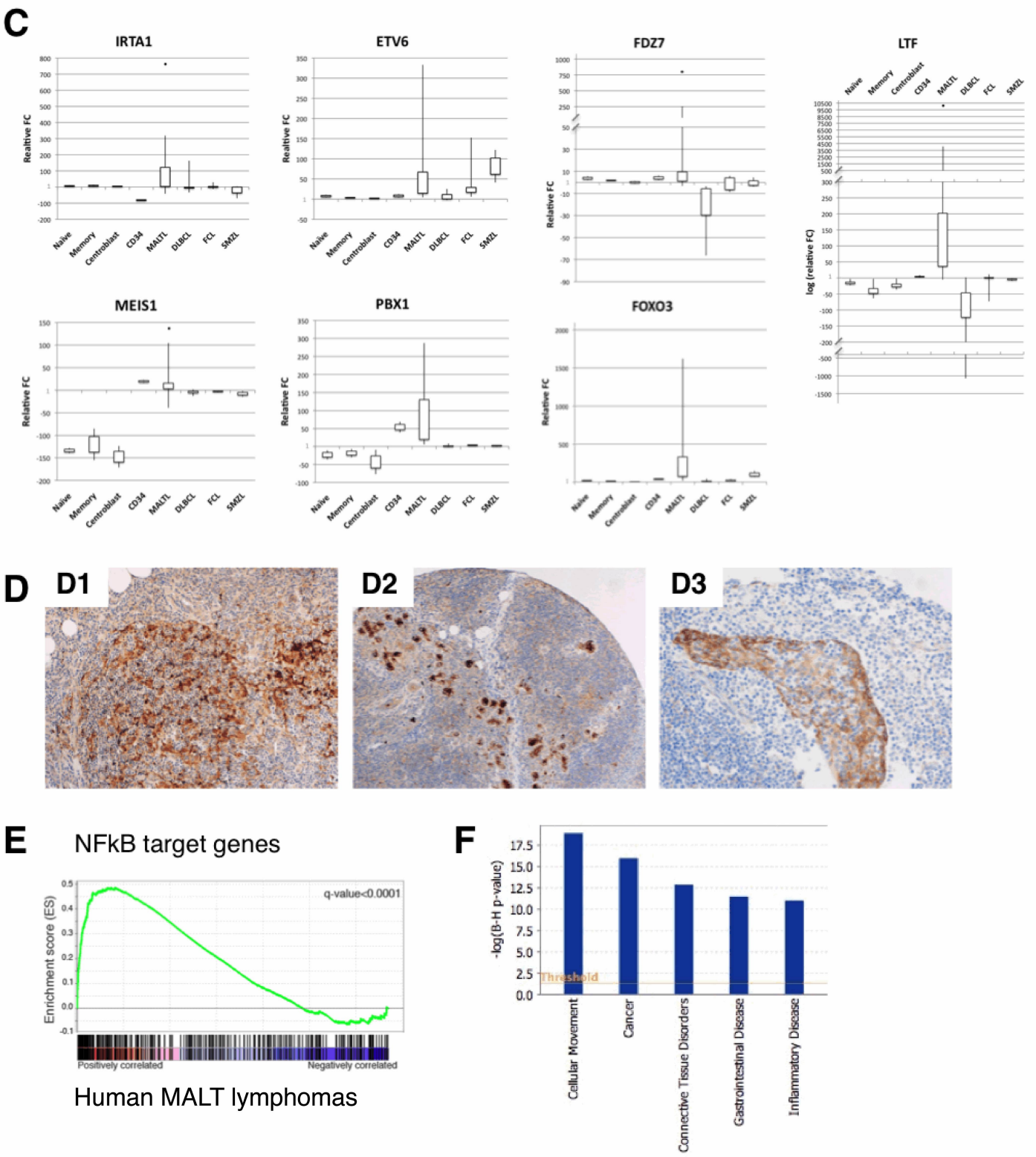
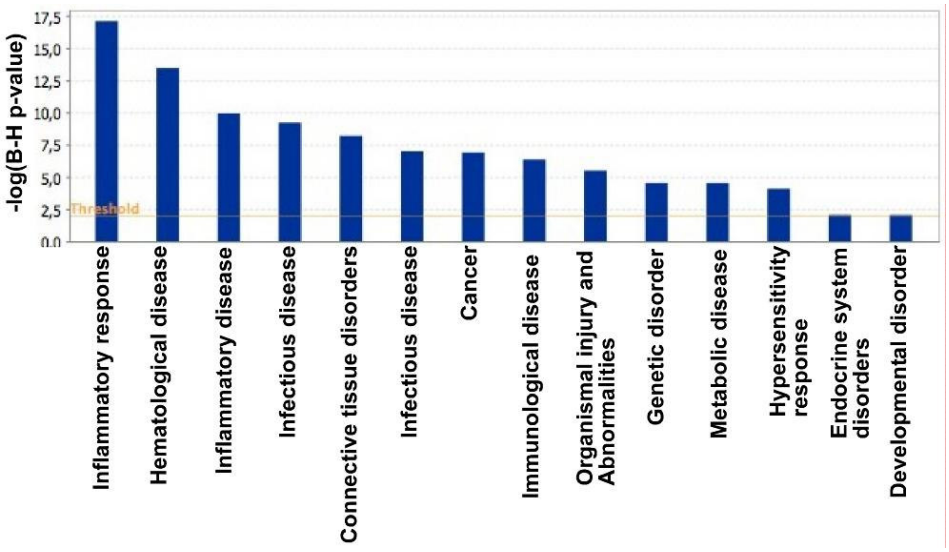

HE
20x
CD20
40x
FOXP1
40x
BCL6
40x
MUM1
40x
HE
100x
CD3
40x
CD10
40x
GCET
40x

Figure S4. Histological and molecular characterization of human MALT lymphoma samples.

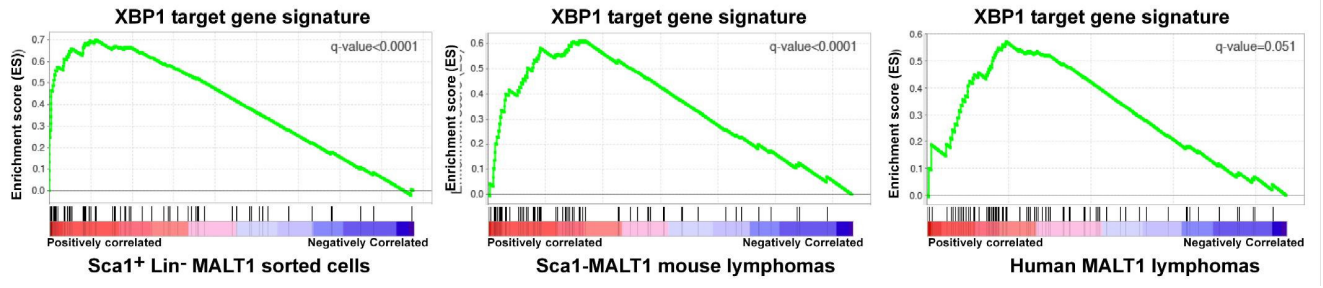



C
IRTA1
ETV6
FDZ7
LTF
MEIS1
PBX1
FOXO3
Realtive FC
Relative FC
log (relative FC)
Naive
Memory
Centroblast
CD34
MALTL
DLBCL
FCL
SMZL
D
D1
D2
D3
E
NFkB target genes
q-value<0.0001
Enrichment score (ES)
Positively correlated
Negatively correlated
Human MALT lymphomas
F
-log(B-H p-value)
Threshold
Cellular Movement
Cancer
Connective Tissue Disorders
Gastrointestinal Disease
Inflammatory Disease

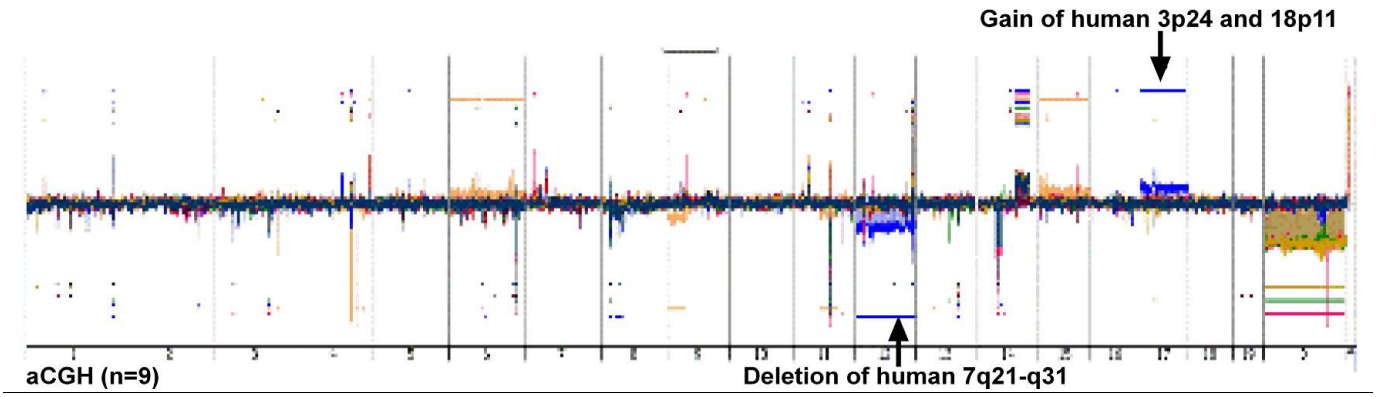
G


-log(B-H p-value)
17,5
15,0
12,5
10,0
7,5
5,0
2,5
Threshold
0,0
Inflammatory response
Hematological disease
Inflammatory disease
Infectious disease
Connective tissue disorders
Infectious disease
Cancer
Immunological disease
Organismal injury and Abnormalities
Genetic disorder
Metabolic disease
Hypersensitivity response
Endocrine system disorders
Developmental disorder

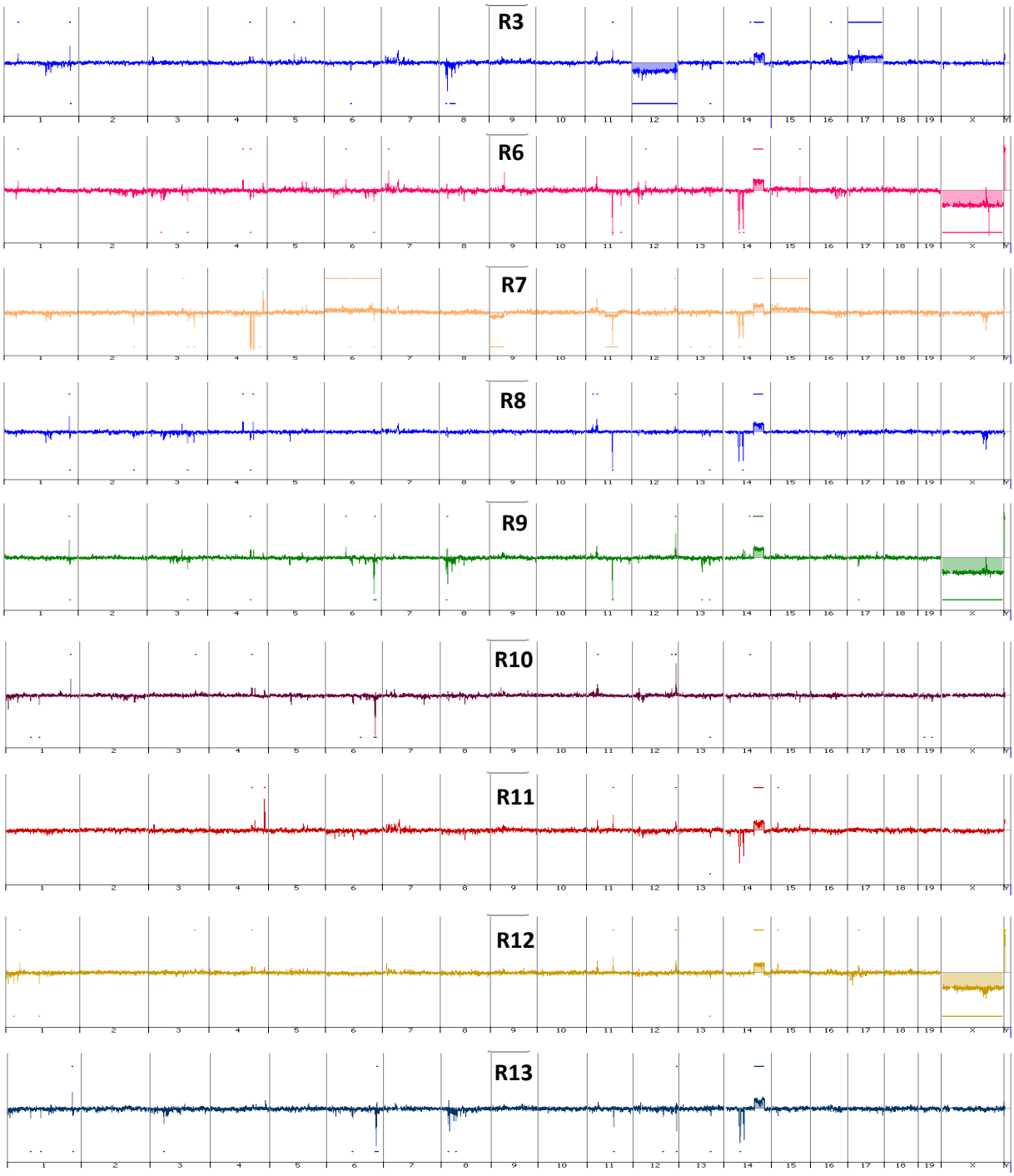
H


XBP1 target gene signature
q-value<0.0001
Enrichment score (ES)
Positively correlated
Negatively Correlated
Sca1+ Lin- MALT1 sorted cells
XBP1 target gene signature
q-value<0.0001
Enrichment score (ES)
Positively correlated
Negatively Correlated
Sca1-MALT1 mouse lymphomas
XBP1 target gene signature
q-value=0.051
Enrichment score (ES)
Positively correlated
Negatively Correlated
Human MALT1 lymphomas

I

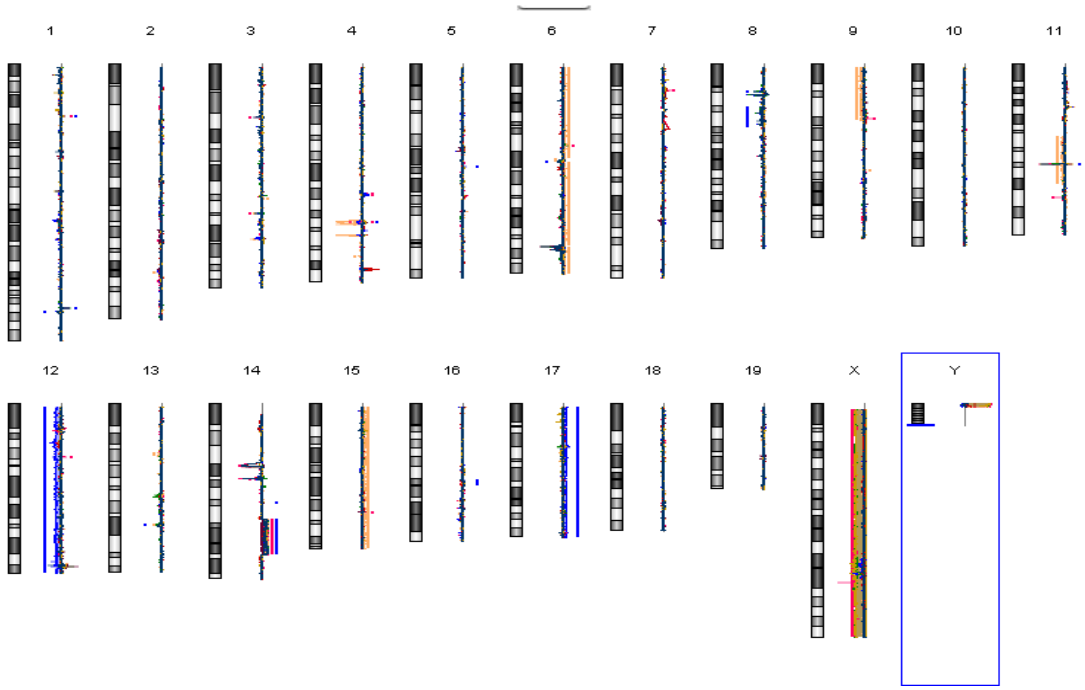

Gain of human 3p24 and 18p11
aCGH (n=9)
Deletion of human 7q21-q31

J

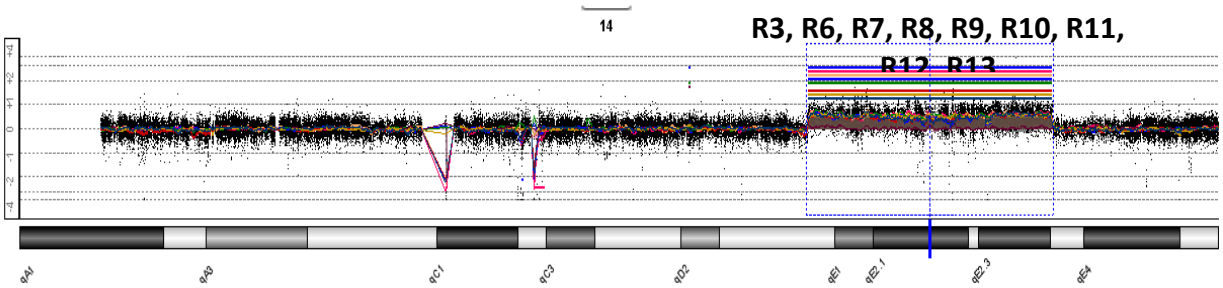


Sca1-MALT1 lymphomas

MERGE



Common regions of gain and loss



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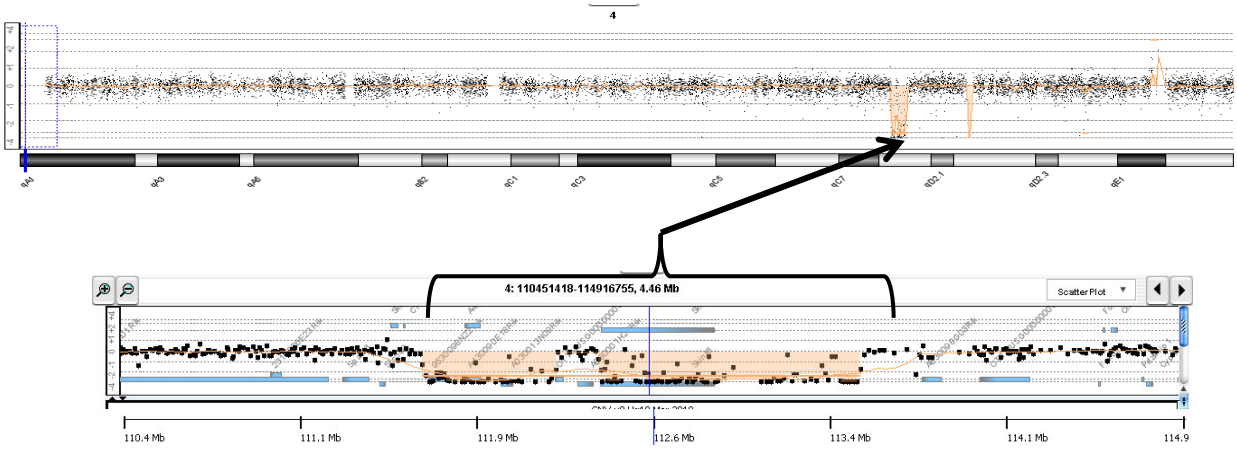
chr14	qD3 - qE3	82388732	107858855	1230	0.456773	0	0	Pcdh17, Diap3, Tdrd3, Pcdh20, Pcdh9, 4921530L21Rik, Klhl1, Dach1, 2410129H14Rik, 6720463M24Rik, Dis3, Pibf1, Pibf1, Klf5, Klf12, 1700110M21Rik, Tbc1d4, Commd6, Uchl3, Lmo7, Kctd12, Irg1, Cln5, Fbxl3, Mycbp2, Scel, Slain1, Ednrb, Pou4f1, Rnf219, Rbm26, Ndfip2, Spry2, Trim52

R7


4
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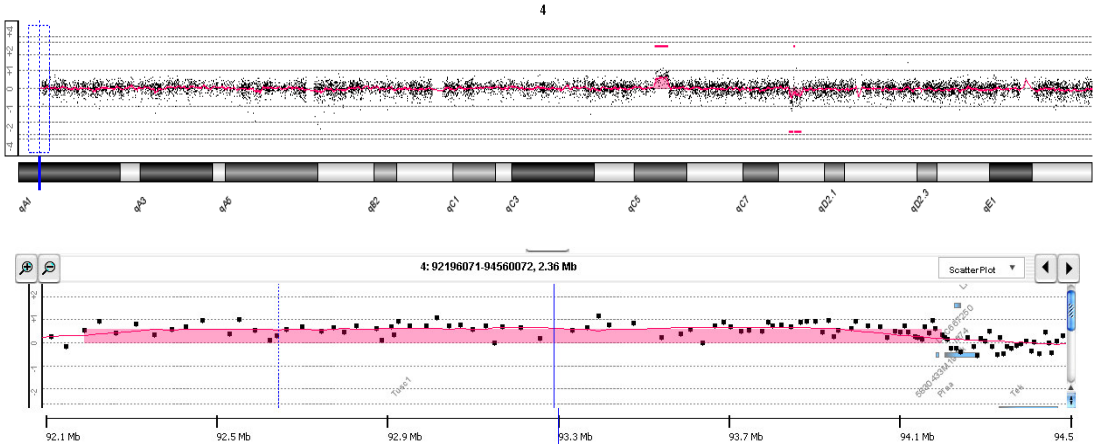
Scatter Plot
110.4 Mb
111.1 Mb
111.9 Mb
112.6 Mb
113.4 Mb
114.1 Mb
114.9

R6


4
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Scatter Plot
92.1 Mb
92.5 Mb
92.9 Mb
93.3 Mb
93.7 Mb
94.1 Mb
94.5

R8

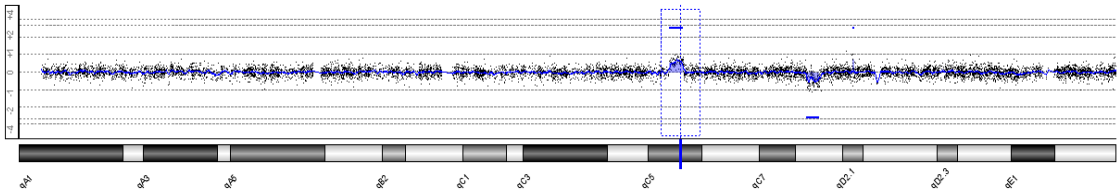
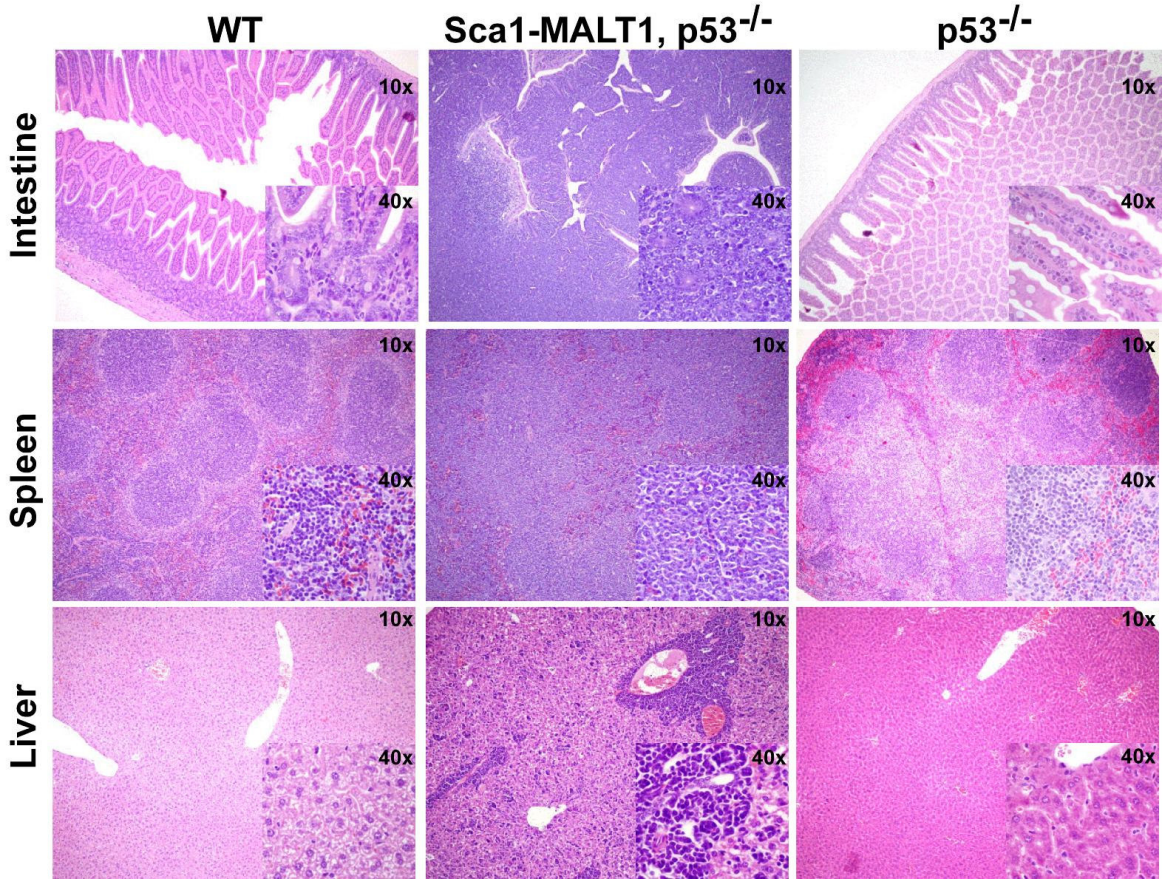
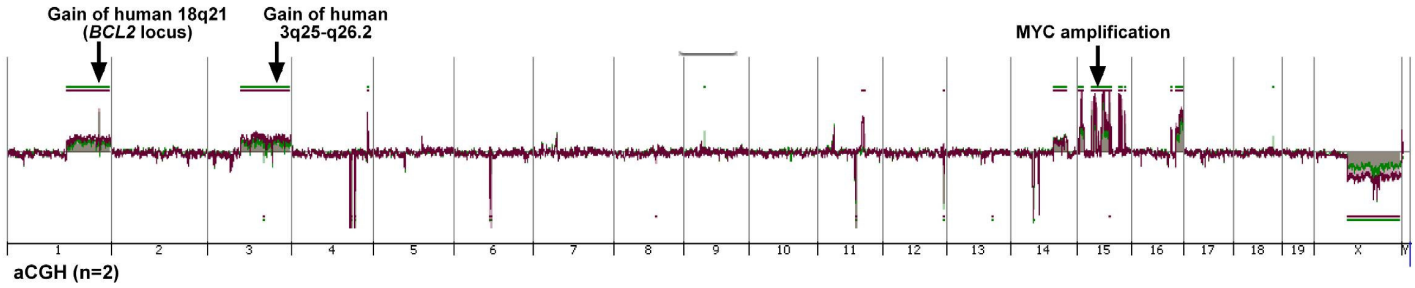

4

Figure S5. Characterization of diffuse large B-cell lymphomas in Sca1-MALT1,p53$^{-/-}$ mice.

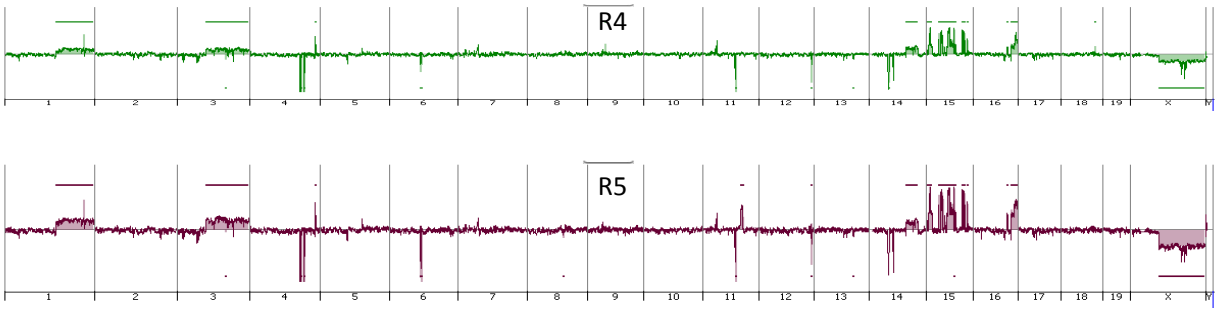
A



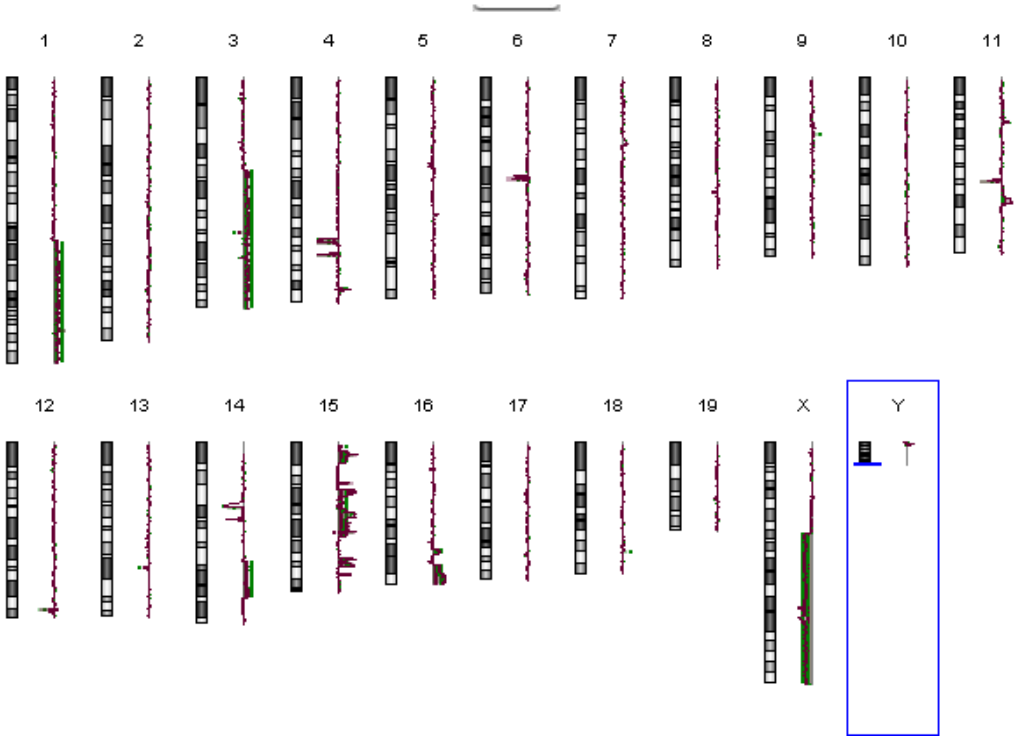
B



C



Sca1-MALT1,p53$^{-/-}$ lymphomas



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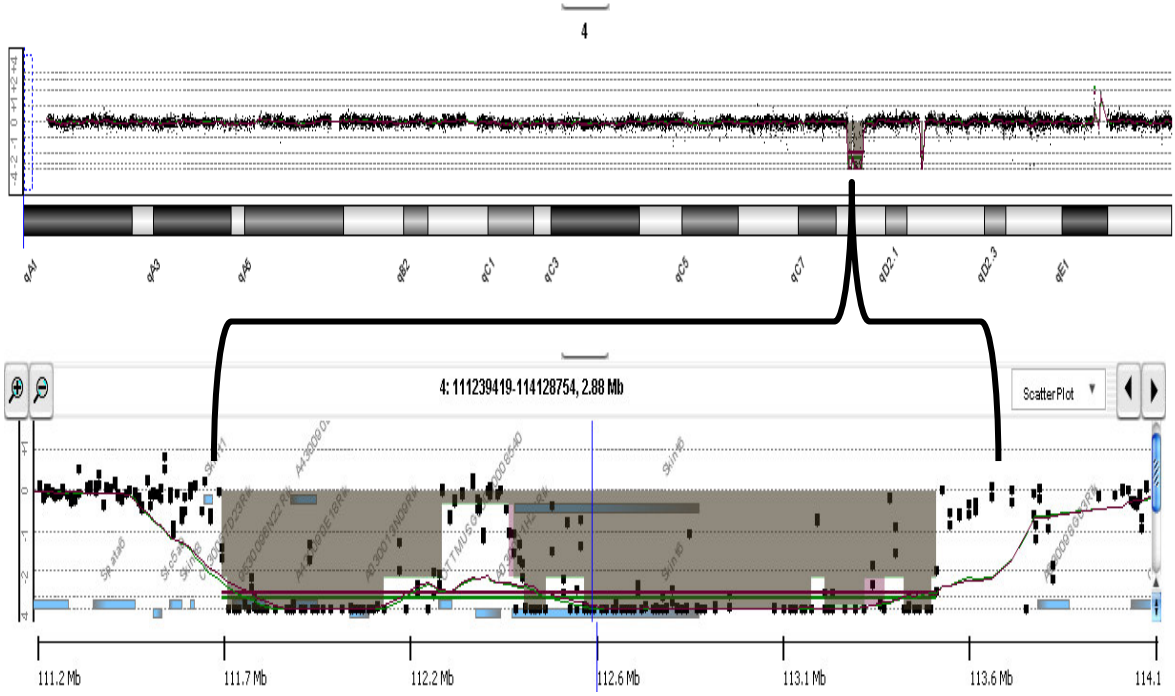
chr3	qE1 - qH4	64403644	159587309	6226	0.364418	0	0	Vmn2r7, Kcnab1, Ssr3, Tiparp, EG624866, Ccnl1, Veph1, Veph1, Ptx3, Shox2, Rsrc1, Mlf1, Gfm1, Lxn, Mfsd1, EG208426, Schip1, Schip1, Schip1, Il12a, Ift80, Smc4, Trim59, Kpna4, Ppm1l, B3galnt1, Nmd3, 1110032A04Rik, Gm414, 2010204N08Rik, Slitrk3, Bche, Zbbx, Serpini2, Pdcd10, Serpini1, Golim4, Fstl5, Rapgef2, Ppid, Etfdh, Rxfp1, Tmem144, 1110032E23Rik, Gria2, Gria2, Glrb, Pdgfc, Ctso, Tdo2, Accn5, Gucy1b3, Gucy1a3, Mtap9, Npy2r, Lrat, Fgg, Fga, Fgb, Plrg1, Sfrp2, Tlr2, D930015E06Rik, Mnd1, Trim2, Fhdc1, Arfip1, Tigd4, Tmem154, Fbxw7, Dear1, Pet112l, 9930021J17Rik, Glt28d2, Gm1019, Sh3d19, Rps3a, Lrba, Lrba, Lrba, Mab21l2, Dclk2, Cd1d2, Cd1d1, Kirrel, Fcrls, Cd5l, Fcrl1, Fcrl1, Fcrl5, Fcrl5, Etv3, Arhgef11, Pear1, Ntrk1, Insrr, Sh2d2a, Sh2d2a, Prcc, Hdgf, Mrpl24, BC023814, Isg20l2, Crabp2, Nes, Bcan, Bcan, Hapln2, Gpatch4, Apoa1bp, Ttc24, Iqgap3, Mef2d, Rhbg, 1700021C14Rik, Cct3, 0610031J06Rik, Tmem79, Smg5, Paqr6, Bglap-rs1, Bglap2, Bglap1, Bglap1, Pmf1, Slc25a44, Sema4a, Lmna, Lmna, Lmna, Mex3a, Rab25, Mapbpip, Ubqln4, Ssr2, Arhgef2, Rxfp4, 2810403A07Rik, Rit1, Syt11, Msto1, Dap3, Ash1l, Rusc1, Rusc1, Fdps, Pklr, Pklr, Hcn3, Clk2, Scamp3, 1110013L07Rik, Gba, Gba, Mtx1, Thbs3,



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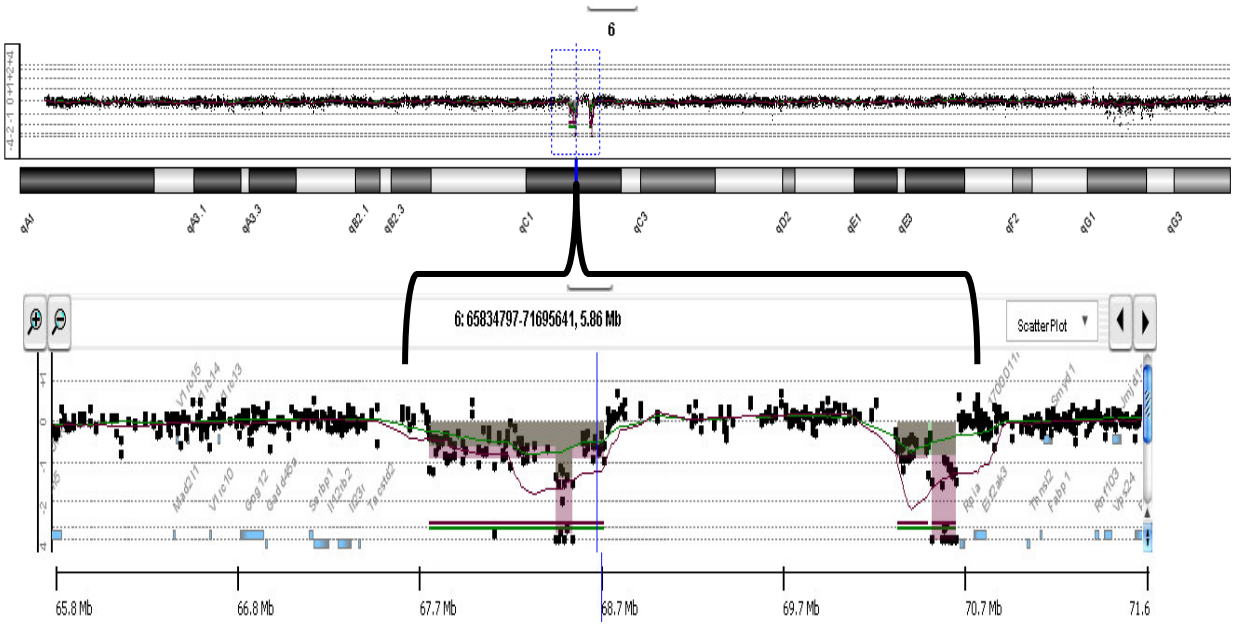
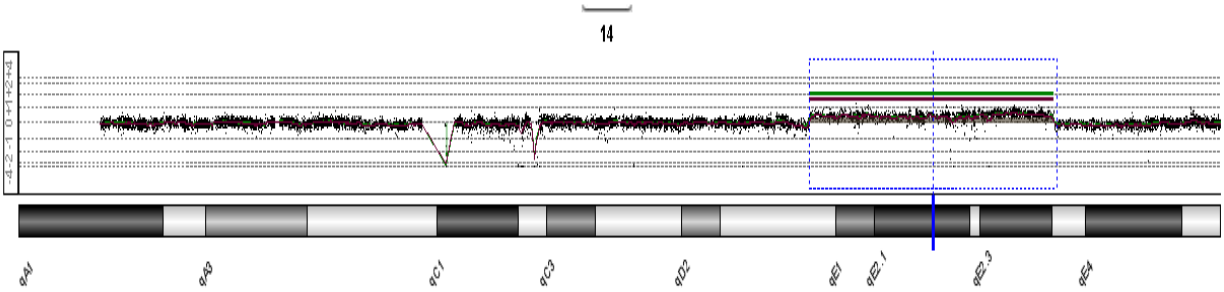
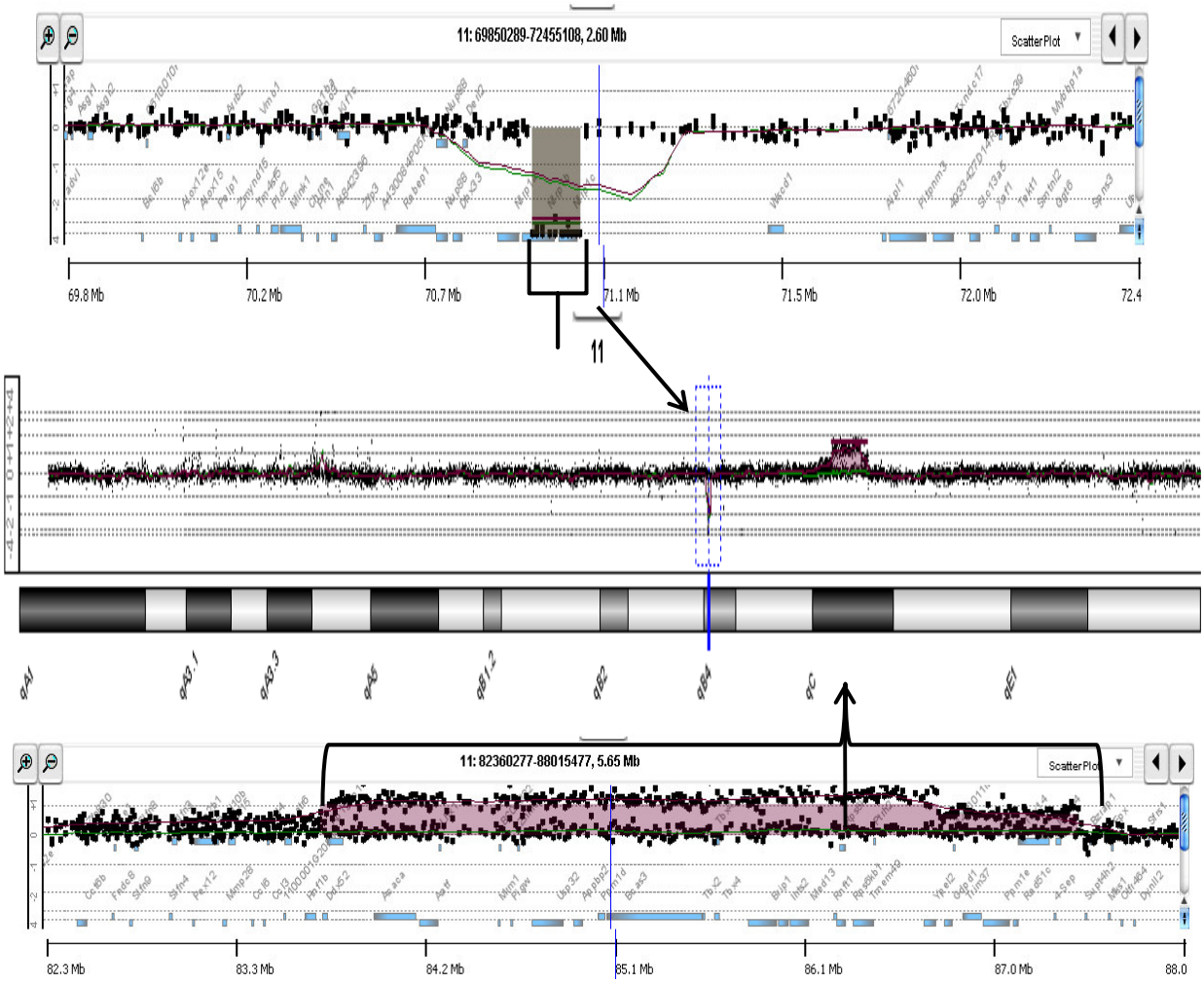
chr4	qD1	111742687	112147158	33	0	-4.369621	3.91E-135	9530098N22Rik, A430090E18Rik, A430090E18Rik, A030013N09Rik
chr4	qD1	112296890	112480784	15	0	-0.307544	3.30E-271	OTTMUSG00000008540, A030001H23Rik, Skint6
chr4	qD1	112510005	112564441	6	0	-5.012057	8.46E-37	Skint6, Skint6
chr4	qD1	112664800	113252080	37	0	-4.033403	1.81E-130	Skint6, Skint6
chr4	qD1	113286038	113388679	6	0	-4.318962	3.85E-25	
chr4	qD1	113491523	113561350	6	0	-4.861999	4.86E-34	
chr4	qE1	144993751	145193074	10	0.674165	0	1.79E-23	



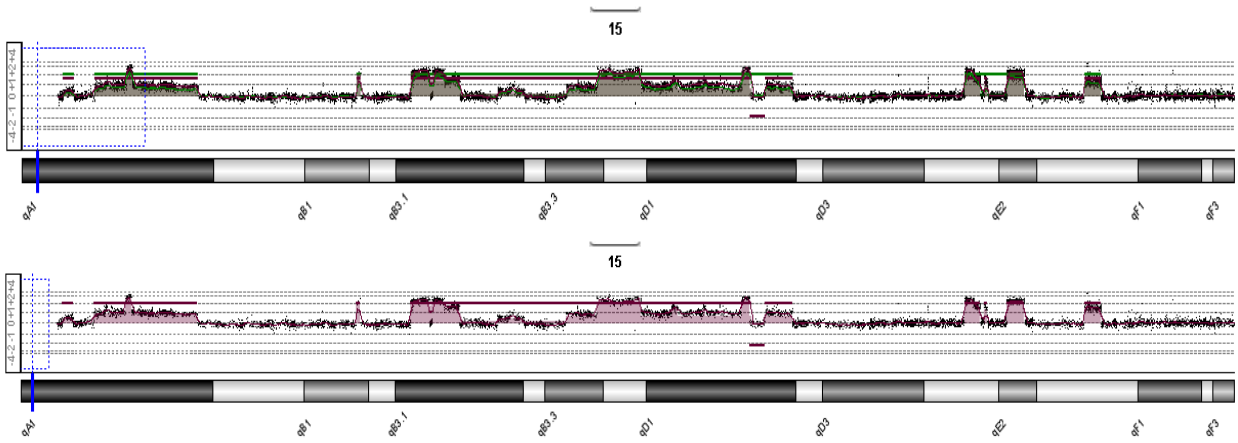
Chr	Cytoband	Start	Stop	#Probes	Amplificatio	Deletion	pval	Gene Names
chr6	qC1	67865262	68805355	45	0	-0.868511	2.34E-127	
chr6	qC1	68546691	68637451	7	0	-3.271456	1.34E-56	
chr6	qC1	70381126	70545481	11	0	-0.873585	3.76E-37	
chr6	qC1	70565020	70697520	11	0	-4.337567	4.83E-185	



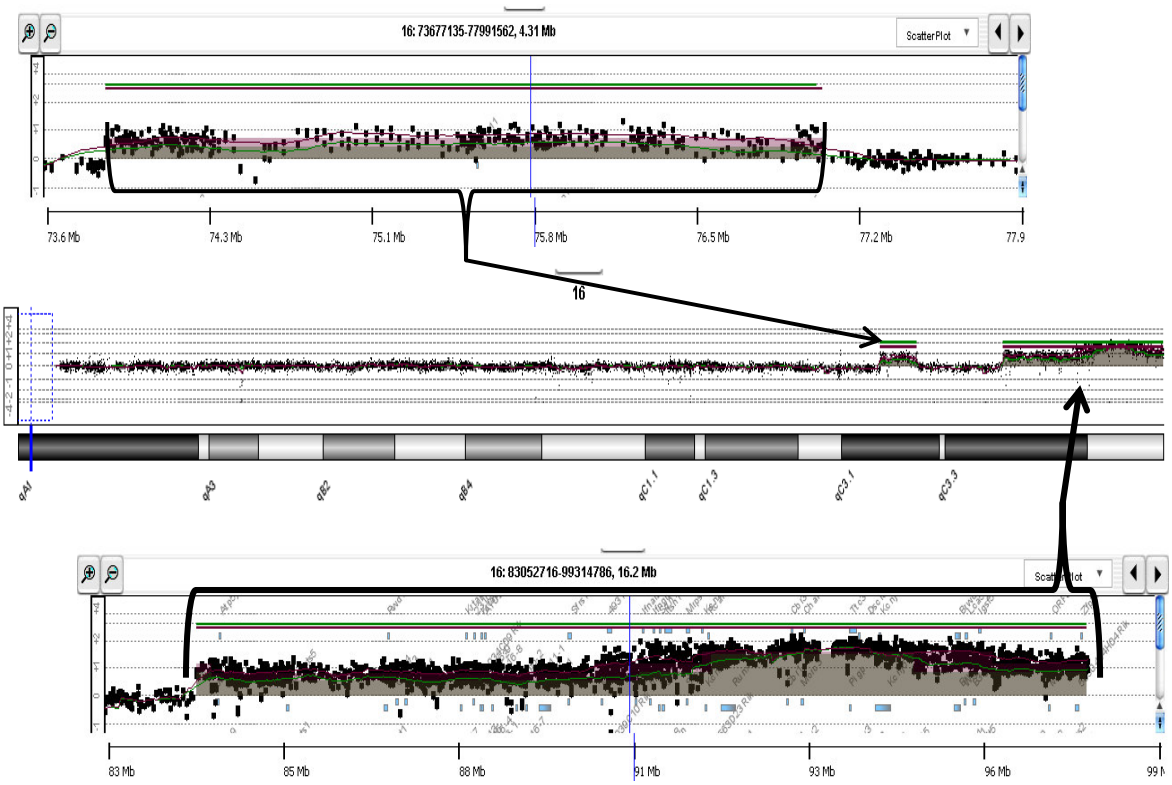
Chr	Cytoband	Start	Stop	#Probes	Amplification	Deletion	pval	Gene Names
chr14	qD3 - qE3	82388732	107858855	1230	0.44771	0	0	Pcdh17, Diap3, Tdrd3, Pcdh20, Pcdh9, 4921530L21Rik, Klhl1, Dach1, 2410129H14Rik, 6720463M24Rik, Dis3, Pibf1, Pibf1, Klf5, Klf12, 1700110M21Rik, Tbc1d4, Commd6, Uchl3, Lmo7, Kctd12, Irg1, Cln5, Fbxl3, Mycbp2, Scel, Slain1, Ednrb, Pou4f1, Rnf219, Rbm26, Ndfip2, Spry2, Trim52



Chr	Cytoband	Start	Stop	#Probes	Amplification	Deletion	pval	Gene Names
chr11	qB4	70989662	71107244	11	0	-4.148097	1.43E-172	Nlrp1b, Nlrp1c
chr11	qC	83745508	87514339	341	1.107702	0	0	Ddx52, Ap1gbp1, Ap1gbp1, Dusp14, Tada2l, OTTMUSG00000000997, Acaca, Aatf, Lhx1, Mrm1, BC022224, Ggnbp2, Pigw, Pigw, Znhit3, Car4, Usp32, Appbp2, Ppm1d, Bcas3, Tbx2, Tbx4, Tbx4, Brip1, Ints2, Med13, Rnft1, Rps6kb1, Rps6kb1, Tubd1, Tmem49, Ptrh2, Ptrh2, Cltc, Dhx40, Ypel2, Gdpd1, 1200011M11Rik, Prr11, 1110001A07Rik, Trim37, Ppm1e, Rad51c, Tex14, 4-Sep, Mtmr4, Hsf5, Rnf43
chr11	qC	86820974	87514339	74	0.744524	0	8.97E-47	Gdpd1, 1200011M11Rik, Prr11, 1110001A07Rik, Trim37, Ppm1e, Rad51c, Tex14, 4-Sep, Mtmr4, Hsf5, Rnf43

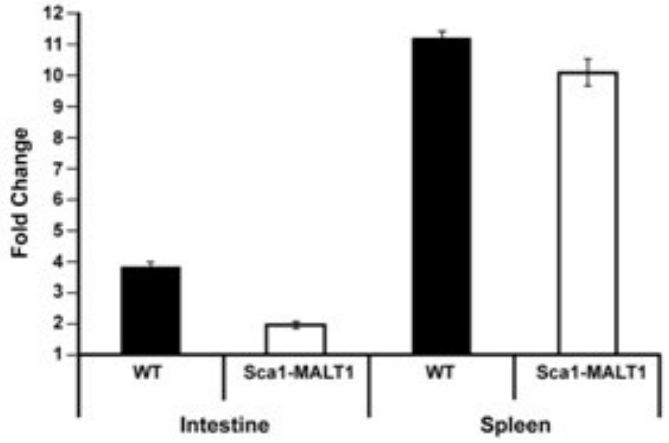


Chr	Cytoband	Start	Stop	#Probes	Amplification	Deletion	pval	Gene Names
chr15	qA1	3561477	4474038	55	0.533169	0	4.17E-77	Fbxo4, AW549877, Oxct1, Plcxd3
chr15	qA1	6284550	15075364	560	1.060266	0	0	Dab2, Dab2, C9, Fyb, 4921505C17Rik, Osmr, Lifr, Lifr, Egflam, Gdnf, Wdr70, Nup155, Nipbl, Nipbl, Slc1a3, Ranbp3l, 1110020G09Rik, Skp2, Lmbrd2, Ugt3a1, Ugt3a2, Capsl, Il7r, Spef2, Prlr, Agxt2, Bxdc2, Rad1, Rai14, C1qtnf3, Amacr, Slc45a2, Rxfp3, Adamts12, Tars, Npr3, Sub1, Zfr, Mtmr12, Golph3, Pdzd2, 6030458C11Rik, Rnasen, Cdh6
chr15	qA1	8984564	9439270	40	2.734695	0	7.18E-231	Ranbp3l, 1110020G09Rik, Skp2, Lmbrd2, Ugt3a1, Ugt3a2, Capsl, Il7r
chr15	qB1	28641546	28916730	7	2.114164	0	1.54E-87	
chr15	qB3.1 - qD1	33264452	65789656	2005	0.835258	0	0	Pgcp, Tspyl5, Mtdh, Laptm4b, Matn2, Rpl30, BC030476, Hrsp12, Pop1, Pop1, Npal2, Kcns2, Stk3, Osr2, Cox6c, Fbxo43, Polr2k, Polr2k, Spag1, Rnf19a, Ankrd46, Snx31, Pabpc1, Ywhaz, Zfp706, Grhl2, Ncald, Rrm2b, Ubr5, Odf1, Klf10, Azin1, Atp6v1c1, Baalc, Fzd6, Cthrc1, Slc25a32, Wdsof1, Rims2, Tm7sf4, Dpys, Lrp12, Zfpm2, Oxr1, Abra, Angpt1, Rspo2, Eif3e, Ttc35, Tmem74, Trhr, Nudcd1, Eny2, Pkhd1l1, Ebag9, 5730410E15Rik, 5730410E15Rik, Kcnv1, Csmd3, Trps1, Eif3h, D530033C11Rik, Rad21, Aard, Slc30a8, Med30, Ext1, Samd12, Tnfrsf11b, Colec10, Mal2, Nov, Enpp2, Taf2, Dscc1, Depdc6, Depdc6, Col14a1, Mrpl13, Mtbp, Sntb1, Has2, BC026439, Zhx2, Derl1, Wdr67, BC030396, 9130401M01Rik, Zhx1, Atad2, 2410187C16Rik, Fbxo32, 8230402K04Rik, Anxa13, D15Ertd621e, Tmem65, Trmt12, Rnf139, Tatdn1, Ndufb9, Mtss1, Sqle, E430025E21Rik, Nsmce2, Trib1, A1bg, Myc, Gsdmc1, Gsdmc2, Gsdmc3, 0910001A06Rik, Ddef1, Adcy8, Efr3a, Oc90
chr15	qB3.1	33264452	37388651	331	1.794359	0	0	Pgcp, Tspyl5, Mtdh, Laptm4b, Matn2, Rpl30, BC030476, Hrsp12, Pop1, Pop1, Npal2, Kcns2, Stk3, Osr2, Cox6c, Fbxo43, Polr2k, Polr2k, Spag1, Rnf19a, Ankrd46, Snx31, Pabpc1, Ywhaz, Zfp706, Grhl2, Ncald
chr15	qB3.1	33264452	34857455	124	2.30756	0	5.10E-84	Pgcp, Tspyl5, Mtdh, Laptm4b, Matn2, Rpl30, BC030476, Hrsp12, Pop1, Pop1, Npal2, Kcns2, Stk3
chr15	qB3.1	34866505	35083328	23	0.040706	0	0	Stk3
chr15	qB3.1	35090592	36071488	88	2.276155	0	8.17E-54	Osr2, Cox6c
chr15	qB3.1 - qB3.3	37394555	46487614	559	0.09945	0	0	Ncald, Rrm2b, Ubr5, Odf1, Klf10, Azin1, Atp6v1c1, Baalc, Fzd6, Cthrc1, Slc25a32, Wdsof1, Rims2, Tm7sf4, Dpys, Lrp12, Zfpm2, Oxr1, Abra, Angpt1, Rspo2, Eif3e, Ttc35, Tmem74, Trhr, Nudcd1, Eny2, Pkhd1l1, Ebag9, 5730410E15Rik, 5730410E15Rik, Kcnv1
chr15	qB3.1 - qB3.2	40624646	42912677	148	0.502803	0	1.32E-117	Zfpm2, Oxr1, Abra, Angpt1, Rspo2
chr15	qB3.3 - qC	49112548	52907210	158	2.217433	0	0	Trps1, Eif3h, D530033C11Rik, Rad21, Aard, Slc30a8, Med30, Ext1
chr15	qD1	55521643	56016942	32	1.53328	0	6.59E-28	Sntb1
chr15	qD1	58177361	58426547	18	1.534425	0	3.12E-16	Anxa13, D15Ertd621e
chr15	qD1	61469044	62160788	50	2.613372	0	0	Myc
chr15	qD1	62170990	63439285	51	0	-0.034062	4.91E-193	
chr15	qE1	80458970	81817702	134	2.039802	0	0	Grap2, AW544981, Tnrc6b, Tnrc6b, Adsl, Sgsm3, Mkl1, Mkl1, Mchr1, Slc25a17, St13, Xpnpep3, Dnajb7, Rbx1, Ep300, L3mbtl2, Rangap1, Zc3h7b, Tef, Tef, Tob2, Phf5a, Aco2, Polr3h, Csdc2, Pmm1, 1700029P11Rik
chr15	qE1	81266634	81817702	51	1.639894	0	5.66E-30	Xpnpep3, Rbx1, Ep300, L3mbtl2, Rangap1, Zc3h7b, Tef, Tef, Tob2, Phf5a, Aco2, Polr3h, Csdc2, Pmm1, 1700029P11Rik
chr15	qE1	82169768	82398252	17	1.453349	0	7.04E-132	C920005C14Rik, 1500032L24Rik, Ndufa6, Cyp2d22, Cyp2d11, Cyp2d10, Cyp2d9, Cyp2d12
chr15	qE2	84047434	85587164	133	2.222249	0	0	Parvb, Parvg, Ldoc1l, Arhgap8, 3110043J09Rik, Phf21b, Nup50, 5031439G07Rik, Upk3a, 3110048E14Rik, 3110048E14Rik, Smc1b, Fbln1, Atxn10, Wnt7b, Ppara, Ppara
chr15	qE3	90682420	92115151	131	1.494769	0	0	Kif21a, Abcd2, Slc2a13, Lrrk2, Muc19, Smgc, Cntn1

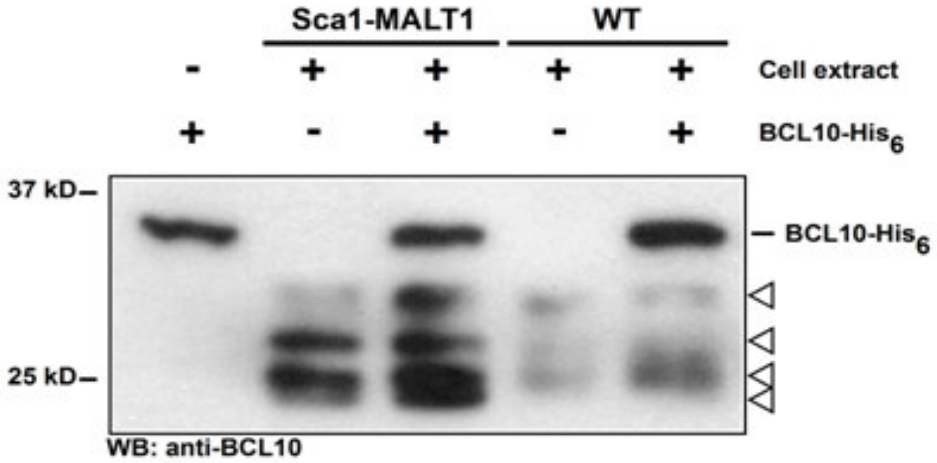


Chr	Cytoband	Start	Stop	#Probes	Amplification	Deletion	pval	Gene Names
chr16	qC3.1	73950448	77127683	171	0.763341	0	0	Robo2, Lipi, Rbm11, Stch, Samsn1, Nrip1, Usp25
chr16	qC3.3 - qC4	84472549	98263853	1014	1.170326	0	0	Mrpl39, Jam2, Atp5j, Gabpa, App, Cyyr1, Adamts1, Adamts5, N6amt1, Zfp294, Rwdd2b, Usp16, Cct8, ORF63, Bach1, Grik1, Cldn17, Cldn8, Krtap26-1, Krtap13-1, Krtap13, 2310034C09Rik, 2310057N15Rik, Krtap14, Krtap15, Krtap16-9, Krtap16-1, Krtap16-5, Krtap16-4, Krtap8-2, AY026312, Krtap16-10, Krtap6-1, Krtap16-8, Krtap16-7, Krtap6-2, Krtap11-1, Tiam1, Sod1, Sfrs15, Hunk, 2610039C10Rik, Mrap, 4931408A02Rik, 1110004E09Rik, 4932438H23Rik, Olig2, Olig1, Ifnar2, Ifnar2, Il10rb, Ifnar1, Ifngr2, Tmem50b, ORF28, Gart, Son, Son, Donson, Cryzl1, Itsn1, Itsn1, Itsn1, Atp5o, Slc5a3, Mrps6, Kcne2, 1190017O12Rik, 4930563D23Rik, Kcne1, Rcan1, Rcan1, Clic6, Runx1, Runx1, Setd4, Cbr1, Cbr3, Dopey2, Dopey2, Morc3, Chaf1b, Cldn14, Sim2, Hlcs, Ripply3, Pigp, Ttc3, Dscr3, Dyrk1a, Dyrk1a, Kcnj6, Kcnj6, Kcnj6, Kcnj6, Kcnj15, Erg, Ets2, Psmg1, Brwd1, Brwd1, Brwd1, Hmgn1, Wrb, Lca5l, Sh3bgr, B3galt5, B3galt5, Igsf5, Itgb2l, Pcp4, Dscam, Bace2, Mx1, ORF9, Mx2, Tmprss2, Ripk4, 5830404H04Rik, Zfp295
chr16	qC3.3	84714007	90639795	395	0.836185	0	4.68E-198	Mrpl39, Jam2, Atp5j, Gabpa, App, Cyyr1, Adamts1, Adamts5, N6amt1, Zfp294, Rwdd2b, Usp16, Cct8, ORF63, Bach1, Grik1, Cldn17, Cldn8, Krtap26-1, Krtap13-1, Krtap13, 2310034C09Rik, 2310057N15Rik, Krtap14, Krtap15, Krtap16-9, Krtap16-1, Krtap16-5, Krtap16-4, Krtap8-2, AY026312, Krtap16-10, Krtap6-1, Krtap16-8, Krtap16-7, Krtap6-2, Krtap11-1, Tiam1, Sod1, Sfrs15, Hunk
chr16	qC4	92303567	96812418	348	1.610889	0	1.64E-229	1190017O12Rik, 4930563D23Rik, Kcne1, Rcan1, Rcan1, Clic6, Runx1, Runx1, Setd4, Cbr1, Cbr3, Dopey2, Dopey2, Morc3, Chaf1b, Cldn14, Sim2, Hlcs, Ripply3, Pigp, Ttc3, Dscr3, Dyrk1a, Dyrk1a, Kcnj6, Kcnj6, Kcnj6, Kcnj6, Kcnj15, Erg, Ets2, Psmg1, Brwd1, Brwd1, Brwd1, Hmgn1, Wrb, Lca5l, Sh3bgr, B3galt5, B3galt5, Igsf5, Itgb2l, Pcp4

D


Fold Change
12
11
10
9
8
7
6
5
4
3
2
1
WT
Sca1-MALT1
WT
Sca1-MALT1
Intestine
Spleen

E


Sca1-MALT1
WT
Cell extract
BCL10-His6
37 kD
25 kD
BCL10-His6
WB: anti-BCL10

F

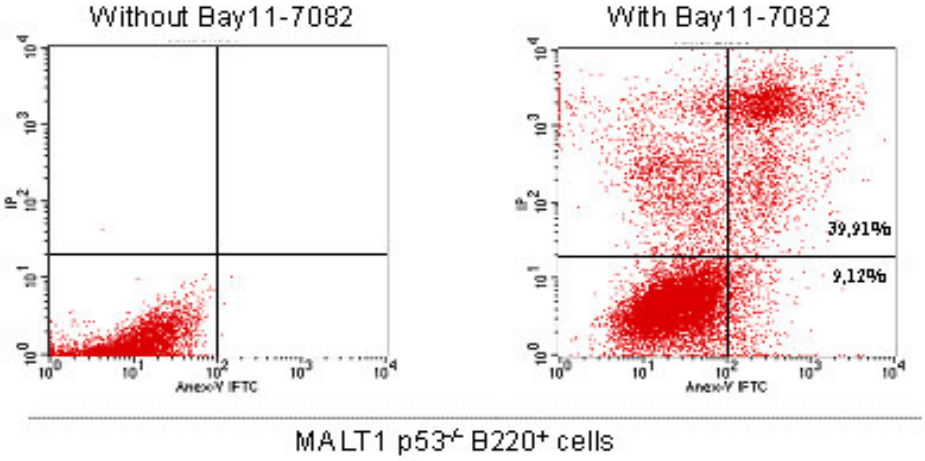
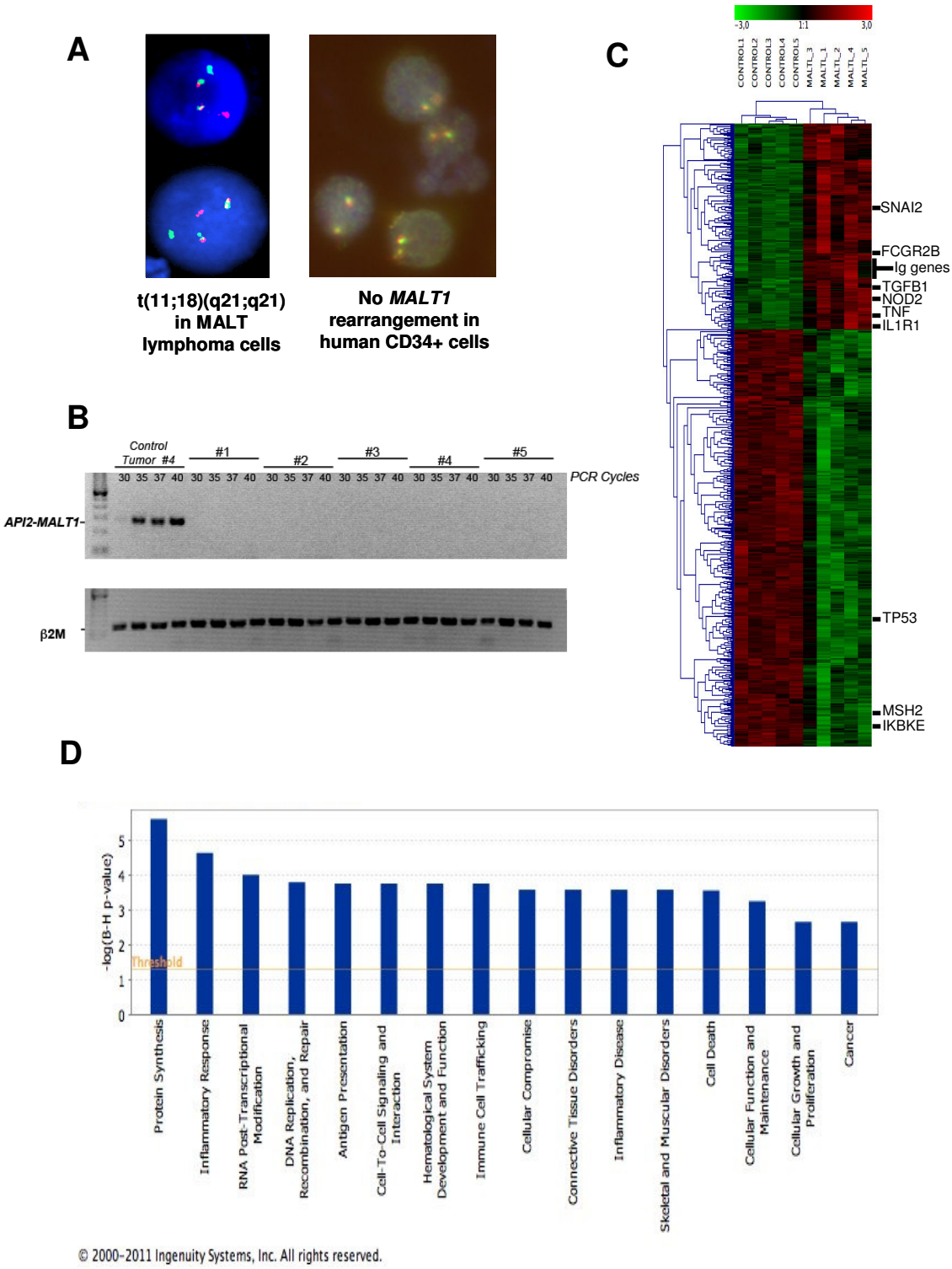
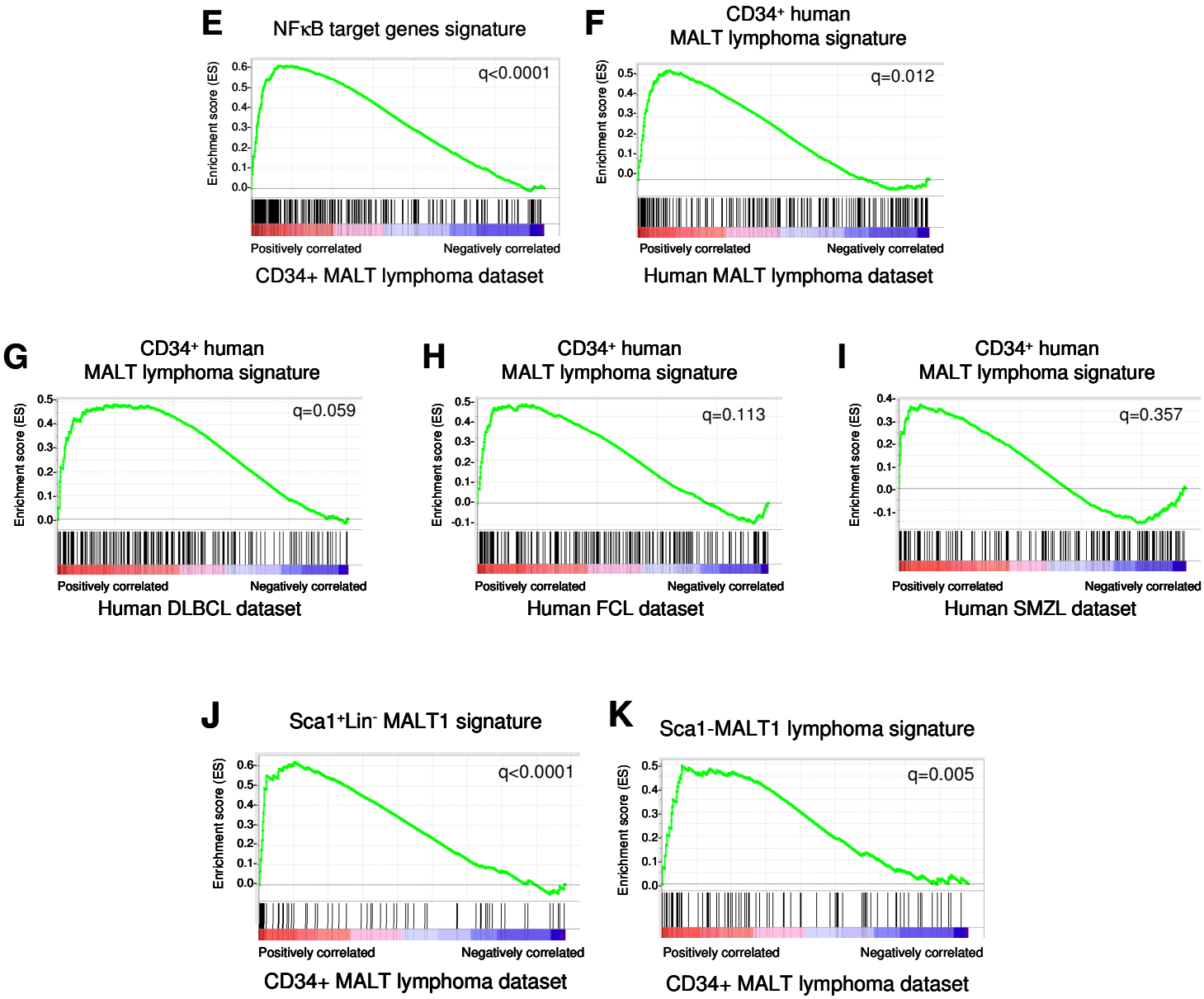

Without Bay11-7082
With Bay11-7082
39,91%
9,12%
Annex-V FITC
Annex-V FITC
MALT1 p53-/- B220+ cells

Figure S6. Characterization of human bone marrow CD34+ cells isolated from patients with MALT lymphoma.




E
NFκB target genes signature
q<0.0001
Enrichment score (ES)
Positively correlated
Negatively correlated
CD34+ MALT lymphoma dataset
F
CD34+ human
MALT lymphoma signature
q=0.012
Enrichment score (ES)
Positively correlated
Negatively correlated
Human MALT lymphoma dataset
G
CD34+ human
MALT lymphoma signature
q=0.059
Enrichment score (ES)
Positively correlated
Negatively correlated
Human DLBCL dataset
H
CD34+ human
MALT lymphoma signature
q=0.113
Enrichment score (ES)
Positively correlated
Negatively correlated
Human FCL dataset
I
CD34+ human
MALT lymphoma signature
q=0.357
Enrichment score (ES)
Positively correlated
Negatively correlated
Human SMZL dataset
J
Sca1+Lin- MALT1 signature
q<0.0001
Enrichment score (ES)
Positively correlated
Negatively correlated
CD34+ MALT lymphoma dataset
K
Sca1-MALT1 lymphoma signature
q=0.005
Enrichment score (ES)
Positively correlated
Negatively correlated
CD34+ MALT lymphoma dataset

SUPPLEMENTAL TABLES (S1-S4)

Table S1. The mouse Sca1^{+}Lin^{-} MALT1 signature. List of the differentially expressed genes in Sca1^{+}Lin^{-} MALT1 *vs.* WT using LIMMA (B>0; 142 probes, 110 genes), defining the Sca1^{+}Lin^{-} MALT1 transcriptional signature

Probeset	Name	logFC	B
1420176_x_at	Igll1	-3.92	5.5
1424631_a_at	Ighg	6.49	5.44
1449283_a_at	Mapk12	1.71	5.18
1452463_x_at	Igk-V1	2.85	4.9
1426174_s_at	Igh-3	8.16	4.79
1433716_x_at	Gfra2	-3.25	4.59
1422610_s_at	Igf2bp3	-1.69	4.47
1436836_x_at	LOC100047856	-1.8	4.23
1449869_at	Vpreb1	-5.55	4.22
1428942_at	Mt2	2.89	4.16
1450680_at	Rag1	-5.88	4.14
1457728_at	Bcnp1	-3.18	4.04
1427576_at	Igk-V1	4.13	4.01
1427577_x_at	Igk-V1	4.05	3.64
1427455_x_at	Igk-V1	1.52	3.45
1452417_x_at	NA	1.15	3.44
1424305_at	Igj	2.58	3.36
1456380_x_at	Cnn3	-1.78	3.29
1427660_x_at	Igk-V1	1.07	3.19
1433934_at	Sec24a	1.39	3.15
1429381_x_at	Igh	6.44	2.88
1455570_x_at	Cnn3	-2.14	2.86
1422416_s_at	Vpreb2	-1.93	2.69
1423746_at	Txndc5	3.81	2.67
1438030_at	Rasgrp3	2.12	2.65
1418531_at	Oosp1	3.65	2.63
1418065_at	Rag2	-2.46	2.49
1434245_a_at	Cybasc3	-1.01	2.42
1417435_at	Large	1.77	2.29
1420442_at	Cacna1s	2.79	2.27
1425247_a_at	Igh-6	6.63	2.23
1452492_a_at	Slc37a2	-0.92	2.12
1422557_s_at	Mt1	3.07	1.98
1427183_at	Efemp1	1.6	1.97
1425738_at	Igk-V1	5.47	1.95
1425324_x_at	Igh-6	6.87	1.9
1419758_at	Abcb1a	2.81	1.9
1436759_x_at	LOC100047856	-1.79	1.85
1454729_at	Tmem108	-1.11	1.81
1423909_at	Tmem176a	1.12	1.8
1425763_x_at	Igh	6.03	1.78
1427870_x_at	Igh-6	5.39	1.76

1451342_at	Spon1	3.19	1.71
1448192_s_at	Prps1	0.82	1.68
1451596_a_at	Sphk1	1.63	1.66
1429891_at	Capsl	-2.06	1.64
1438651_a_at	Aplnr	-3.42	1.57
1440574_at	Rag1	-0.78	1.55
1422120_at	Eaf2	2.55	1.53
1455867_at	Sox4	-0.84	1.52
1426724_at	Cnn3	-1.32	1.51
1456156_at	Lepr	2.57	1.5
1416468_at	Aldh1a1	1.58	1.5
1442050_at	Zfp608	-1.55	1.48
1455642_a_at	Tspan17	1.25	1.45
1423621_a_at	Slc33a1	0.93	1.43
1418601_at	Aldh1a7	1.41	1.39
1435582_at	Wdfy4	-1.27	1.37
1427857_x_at	Igk-V38	3.01	1.37
1446745_at	EG433637	1.61	1.36
1434553_at	Tmem56	2.47	1.35
1422710_a_at	Cacna1h	2.99	1.33
1449270_at	Plxdc2	-0.94	1.32
1435948_at	100040525	1.04	1.32
1425494_s_at	Bmpr1a	1.85	1.22
1427242_at	Ddx4	-4.01	1.22
1425187_at	Sel1l	2.6	1.19
1427757_at	Igk-V21	4.01	1.05
1426910_at	Pawr	2.14	1.04
1455817_x_at	Zxdb	0.95	1.03
1426201_at	Gm1499	2.66	1.03
1417191_at	Dnajb9	1.35	1.01
1419155_a_at	Sox4	-2.19	0.99
1441811_x_at	Tmem176a	0.98	0.98
1448891_at	Fcrls	0.77	0.96
1434463_at	Bfsp2	-1.35	0.91
1451091_at	Txndc5	2.35	0.84
1427851_x_at	Igh-VJ558	4.32	0.8
1441039_at	4930532J02Rik	-0.96	0.79
1437223_s_at	Xbp1	1.32	0.79
1424065_at	Edem1	2.82	0.78
1418126_at	Ccl5	1.93	0.77
1421653_a_at	Igh	5.93	0.74
1457426_at	1700048O20Rik	-1.06	0.71
1460247_a_at	Skp2	-1.13	0.71
1428129_at	Lman1	2.05	0.69
1424090_at	Sdcbp2	0.86	0.66
1427329_a_at	Igh-6	1.21	0.66
1419192_at	Il4i1	-1.13	0.66
1439015_at	Gfra1	-2.04	0.65
1453677_a_at	Derl3	2.88	0.65
1419276_at	Enpp1	2.85	0.64
1442368_at	Kctd12b	-1.65	0.62
1419759_at	Abcb1a	2.14	0.59

1425493_at	Bmpr1a	1.93	0.59
1437765_at	Cpeb3	1.12	0.57
1452418_at	1200016E24Rik	1.35	0.56
1419298_at	Pon3	2.38	0.54
1427860_at	Igk-V19-14	5.97	0.54
1458663_at	NA	2.34	0.51
1426804_at	Smarca4	-0.86	0.49
1434036_at	Mtss1	-1.05	0.49
1427756_x_at	Igh-6	5.42	0.48
1423902_s_at	Arhgef12	1.2	0.46
1426852_x_at	Nov	-1.71	0.46
1434233_at	2610030H06Rik	0.78	0.46
1425492_at	Bmpr1a	1.86	0.45
1449147_at	Chst1	3.51	0.45
1437203_at	Cbll1	-1.01	0.44
1426200_at	Igk-V1	2.88	0.42
1454631_at	6330549H03Rik	1.22	0.41
1449124_at	Rgl1	-0.91	0.38
1420011_s_at	Xbp1	1.79	0.38
1440665_at	NA	-0.89	0.38
1430435_at	Aff3	-1.01	0.37
1441579_at	Dmrta1	2.38	0.37
1420425_at	Prdm1	2.76	0.34
1457319_at	A130038J17Rik	1.23	0.33
1459546_s_at	Enpp1	2.27	0.32
1460423_x_at	Igkv1-117	5.57	0.3
1417128_at	Plekho1	-0.96	0.29
1417437_at	Xrcc6	-1	0.28
1457039_at	Cecr2	-1.57	0.27
1425454_a_at	Il12a	-1.59	0.27
1460416_s_at	100040213	0.75	0.26
1455372_at	Cpeb3	1.79	0.25
1456212_x_at	Socs3	1.82	0.23
1426851_a_at	Nov	-1.66	0.22
1451730_at	Zfp62	-0.61	0.21
1429543_at	6230424C14Rik	1.41	0.2
1444207_at	Alms1	-0.85	0.2
1416193_at	Car1	2.45	0.2
1435857_s_at	Aplp1	0.83	0.16
1437025_at	Cd28	2.47	0.15
1451212_at	Ccdc21	0.85	0.14
1420714_at	Lbx2	0.91	0.14
1427764_a_at	Tcfe2a	-0.87	0.09
1420886_a_at	Xbp1	1.71	0.09
1428333_at	2900062L11Rik	-1.69	0.08
1452535_at	Igh-6	3.48	0.06
1430097_at	8430436C05Rik	1	0.04
1438354_x_at	Cnn3	-1.38	0.02

Table S2

Table S2A. Sca1-MALT1 lymphomas developed in the three different founder lines

TRANSGENIC LINE	MICE AUTOPSIED	MICE WITH TUMOR (%)	AGE AT TUMOR ONSET (Months)	TUMOR TYPE (%)
86A (Sca1-Malt1)	7	5 (71.42)	16.1±2.8	MALT lymphoma
86B (Sca1-Malt1)	39	15 (38.46)	16.2±5.3	MALT lymphoma
86C (Sca1-Malt1)	14	6 (42.85)	18.5±5.9	MALT lymphoma
	n= 60	**n= 26 (43.3)**		

Table S2B. Locations of lymphomas developed in Sca1-MALT1 mice

ID	Line	Small Intestine	Spleen	Salivary Gland	Kidney	Lung	Stomach	Liver	Eye	Age (months)
1191206	86A	X								11
1141206	86A	X	X		X					17.5
1070307	86A	X	X	X						18
1240608	86A		X	X	X					17
1100608	86A			X	X					15.5
1010807	86B			X						17
1040706	86B	X								6
1110809	86B	X								29
1290806	86B	X			X					10.5
1200109	86B	X	X					X		21.5
1220108	86B	X	X		X					20
1020708	86B	X	X	X	X	X	X			16.5
3300507	86B	X		X						21
1060808	86B	X		X	X					19.5
2211008	86B	X		X				X		22
1300908	86B	X		X	X	X		X		17.5
2220108	86B	X			X	X				20
3110809	86B		X	X		X		X		25
1181108	86B		X		X	X				9.5
1211008	86B		X	X	X					22
2300506	86C	X								7
1150708	86C	X								20.5
1090708	86C	X								24
1030807	86C				X					16
1010708	86C				X					18.5
2150708	86C			X	X			X	X	25
n=26										

Table S2C. Characteristics of the patients with MALT lymphoma included in the study (n=73)

Patient		Gender	Age	Localization	% Cases	Chromosomal Translocation	GEM	IHC study	QRT-PCR
1	MALTL30	F	58	Bowel	6.8		X	X	
2	MALTL19	M	92	Bowel			X		
3	MALTL32	F	62	Cecum					X
4	MALTL34	M	60	Duodenum					X
5	MALTL36	M	77	duodenum					X
6	MALTL35	M	35	epidural	4.1				X
7	MALTL33	F	74	dura		11;18			X
8	MALTL37	F	68	brain					X
9	MALTL22	F	58	breast	4.1		X	X	
10	MALTL29	F	52	breast			X		
11	MALTL38	M	56	breast					X
12	MALTL20	M	74	gastric	17.8	11;18	X	X	X
13	MALTL24	M	48	gastric			X	X	X
14	MALTL6	M	55	gastric			X	X	
15	MALTL10	F	57	gastric			X	X	
16	MALTL12	M	38	gastric			X	X	
17	MALTL23	F	72	gastric			X	X	
18	MALTL26	F	77	gastric		3;14	X	X	X
19	MALTL64	M	68	gastric				X	
20	MALTL65	M	67	gastric				X	
21	MALTL66	F	83	gastric				X	
22	MALTL67	F	75	gastric				X	
23	MALTL68	M	66	gastric					X
24	MALTL69	M	44	gastric		11;18			X
25	MALTL39	F	68	liver	1.4				X
26	MALTL21	F	60	lung	13.7		X	X	X
27	MALTL25	F	76	lung			X	X	
28	MALTL40	M	n/a	lung		11;18			X
29	MALTL74*	M	37	lung		11;18	X	X	
30	MALTL75*	M	47	lung		11;18	X	X	
31	MALTL76*	F	66	lung		14;18	X	X	
32	MALTL77*	F	59	lung		11;18	X	X	
33	MALTL78*	F	63	lung		11;18	X	X	
34	MALTL79*	M	72	lung		14;18	X	X	
35	MALTL41	M	46	lung					X
36	MALTL2	F	100	tonsil	16.4		X	X	
37	MALTL9	F	79	tonsil			X	X	
38	MALTL5	M	46	tonsil			X		
39	MALTL7	F	75	tonsil			X		
40	MALTL42	F	75	tonsil				X	X
41	MALTL43	M	62	tonsil		11;18		X	X
42	MALTL44	M	n/a	tonsil				X	
43	MALTL45	M	42	tonsil				X	
44	MALTL46	F	85	tonsil				X	
45	MALTL47	F	76	tonsil					X

46	MALTL48	F	75	tonsil					X
47	MALTL49	F	75	tonsil		11;18			X
48	MALTL28	F	n/a	ocular adnexa	5.5	11;18	X		
49	MALTL27	M	55	ocular adnexa		14;18	X	X	X
50	MALTL51	M	57	ocular adnexa				X	
51	MALTL52	n/a	n/a	ocular adnexa		14;18		X	
52	MALTL11	F	73	parotid	12.0		X	X	X
53	MALTL13	M	49	parotid			X	X	X
54	MALTL17	F	56	parotid			X	X	
55	MALTL3	F	79	parotid			X	X	
56	MALTL4	F	62	parotid			X	X	
57	MALTL8	M	67	parotid			X	X	
58	MALTL53	n/a	n/a	parotid				X	
59	MALTL54	F	71	parotid				X	
60	MALTL55	F	46	parotid				X	
61	MALTL31	M	66	skin	1.4	14;18	X	X	X
62	MALTL15	F	53	soft tissue	4.1	11;18	X	X	X
63	MALTL1	F	59	soft tissue			X		
64	MALTL57	F	82	soft tissue				X	
65	MALTL16	F	76	spleen	9.6		X	X	
66	MALTL58	F	74	spleen				X	
67	MALTL59	F	73	spleen				X	
68	MALTL60	F	64	spleen					X
69	MALTL61	F	76	spleen					X
70	MALTL62	F	62	spleen					X
71	MALTL63	M	43	spleen					X
72	MALTL14	F	47	thyroid	2.7		X	X	X
73	MALTL18	F	85	thyroid			X	X	

n/a: not available. (*) Patients previously reported in in Chng et al; Blood 113:635-645;2009.

Table S2D. Summary of the characteristics of the MALT lymphoma series (n=73)

Gender		***Localization***	***Number of cases (Percentage)***
Female	61%	Bowel	5 (6.8%)
Male	49%	Brain	3 (4.1%)
		Breast	3 (4.1%)
Age		Gastric	13 (17.8%)
	61 (35-100)	Liver	1 (1.4%)
		Lung	10 (13.7%)
Translocation (52 evaluable)	***Number of cases (Percentage)***	Tonsil	12 (16.4%)
t(14;18)(q32;q21)	5 (10%)	Ocular adnexa	4 (5.5%)
t(11:18)(q21;q21)	12 (23%)	Parotid	9 (12%)
t(3;14)(p14;q32)	1 (2%)	Skin	1 (1.4%)
All	18 (35%)	Soft tissue	3 (4.1%)
		Spleen	7 (9.6%)
		Thyroid	2 (2.7%)

Table S3

Table S3A. Molecular classifier for MALT lymphoma. Bioinformatic analysis of microarray data using the Prediction Analysis for Microarrays (PAM) software defined the defining the human MALT lymphoma transcriptional signature. This included 132 genes that distinguished MALT lymphoma from other B-cell lymphomas

Probeset	Name	Description
202018_s_at	LTF	lactotransferrin
224403_at	FCRL4	Fc receptor-like 4
1558093_s_at	MATR3	matrin 3
215565_at	DTNB	dystrobrevin, beta
206917_at	GNA13	guanine nucleotide binding protein (G protein), alpha 13
204964_s_at	SSPN	sarcospan (Kras oncogene-associated gene)
224402_s_at	FCRL4	Fc receptor-like 4
232541_at	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)
212328_at	LIMCH1	LIM and calponin homology domains 1
1557910_at	HSP90AB1	heat shock protein 90kDa alpha (cytosolic), class B member 1
1564053_a_at	YTHDF3	YTH domain family, member 3
201497_x_at	MYH11	myosin, heavy chain 11, smooth muscle
227021_at	AOF1	amine oxidase (flavin containing) domain 1
1553725_s_at	ZNF644	zinc finger protein 644
213872_at	C6orf62	chromosome 6 open reading frame 62
224407_s_at	RP6-213H19.1	serine/threonine protein kinase MST4
222393_s_at	NAT13	N-acetyltransferase 13
203038_at	PTPRK	protein tyrosine phosphatase, receptor type, K
215990_s_at	BCL6	B-cell CLL/lymphoma 6 (zinc finger protein 51)
200641_s_at	YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide
212105_s_at	DHX9	DEAH (Asp-Glu-Ala-His) box polypeptide 9
239661_at	AFF1	AF4/FMR2 family, member 1
214975_s_at	MTMR1	myotubularin related protein 1
213470_s_at	HNRPH1	heterogeneous nuclear ribonucleoprotein H1 (H)
212148_at	PBX1	pre-B-cell leukemia homeobox 1
217022_s_at	IGHA1	immunoglobulin heavy constant alpha 1
209131_s_at	SNAP23	synaptosomal-associated protein, 23kDa
201211_s_at	DDX3X	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked
215711_s_at	WEE1	WEE1 homolog (S. pombe)
1569477_at	FOXO3	forkhead box O3
211737_x_at	PTN	pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1)
210317_s_at	YWHAE	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide

224401_s_at	FCRL4	Fc receptor-like 4
218748_s_at	EXOC5	exocyst complex component 5
215739_s_at	TUBGCP3	tubulin, gamma complex associated protein 3
227662_at	SYNPO2	synaptopodin 2
200606_at	DSP	desmoplakin
204147_s_at	TFDP1	transcription factor Dp-1
213548_s_at	CDV3	CDV3 homolog (mouse)
225720_at	SYNPO2	synaptopodin 2
211090_s_at	PRPF4B	PRP4 pre-mRNA processing factor 4 homolog B (yeast)
1557984_s_at	RPAP3	RNA polymerase II associated protein 3
205727_at	TEP1	telomerase-associated protein 1
209074_s_at	FAM107A	family with sequence similarity 107, member A
217617_at	PBX1	pre-B-cell leukemia homeobox 1
205408_at	MLLT10	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10
233599_at	hCG_2003663	hCG2003663
214190_x_at	GGA2	golgi associated, gamma adaptin ear containing, ARF binding protein 2
214544_s_at	SNAP23	synaptosomal-associated protein, 23kDa
243454_at	ETV6	ets variant gene 6 (TEL oncogene)
208097_s_at	TXNDC1	thioredoxin domain containing 1
207904_s_at	LNPEP	leucyl/cystinyl aminopeptidase
211016_x_at	HSPA4	heat shock 70kDa protein 4
200008_s_at	GDI2	GDP dissociation inhibitor 2
203637_s_at	MID1	midline 1 (Opitz/BBB syndrome)
208109_s_at	C15orf5	chromosome 15 open reading frame 5
225895_at	SYNPO2	synaptopodin 2
1563521_at	MOBKL2B	MOB1, Mps One Binder kinase activator-like 2B (yeast)
1552612_at	CDC42SE2	CDC42 small effector 2
1554450_s_at	MIER3	mesoderm induction early response 1, family member 3
204288_s_at	SORBS2	sorbin and SH3 domain containing 2
225726_s_at	PLEKHH1	pleckstrin homology domain containing, family H (with MyTH4 domain) member 1
1562235_s_at	PBX1	pre-B-cell leukemia homeobox 1
226844_at	MOBKL2B	MOB1, Mps One Binder kinase activator-like 2B (yeast)
228673_s_at	EML4	echinoderm microtubule associated protein like 4
225275_at	EDIL3	EGF-like repeats and discoidin I-like domains 3
219931_s_at	KLHL12	kelch-like 12 (Drosophila)
1555106_a_at	CTDSPL2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase like 2
223315_at	NTN4	netrin 4
222846_at	RAB8B	RAB8B, member RAS oncogene family
227787_s_at	MED30	mediator complex subunit 30
204719_at	ABCA8	ATP-binding cassette, sub-family A (ABC1), member 8
203638_s_at	FGFR2	fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome)
242664_at	PTPRM	protein tyrosine phosphatase, receptor type, M
226765_at	SPTBN1	spectrin, beta, non-erythrocytic 1
210186_s_at	FKBP1A	FK506 binding protein 1A, 12kDa

201504_s_at	TSN	translin
218002_s_at	CXCL14	chemokine (C-X-C motif) ligand 14
1552417_a_at	NEDD1	neural precursor cell expressed, developmentally down-regulated 1
234915_s_at	DENR	density-regulated protein
214464_at	CDC42BPA	CDC42 binding protein kinase alpha (DMPK-like)
228851_s_at	ENSA	endosulfine alpha
210935_s_at	WDR1	WD repeat domain 1
216563_at	ANKRD12	ankyrin repeat domain 12
1555996_s_at	EIF4A2	eukaryotic translation initiation factor 4A, isoform 2
200796_s_at	MCL1	myeloid cell leukemia sequence 1 (BCL2-related)
212151_at	PBX1	pre-B-cell leukemia homeobox 1
204069_at	MEIS1	Meis homeobox 1
227475_at	FOXQ1	forkhead box Q1
202357_s_at	CFB	complement factor B
224970_at	NFIA	nuclear factor I/A
211726_s_at	FMO2	flavin containing monooxygenase 2 (non-functional)
213002_at	MARCKS	myristoylated alanine-rich protein kinase C substrate
1570165_at	CHST11	carbohydrate (chondroitin 4) sulfotransferase 11
221268_s_at	SGPP1	sphingosine-1-phosphate phosphatase 1
231727_s_at	MIF4GD	MIF4G domain containing
222611_s_at	PSPC1	paraspeckle component 1
214971_s_at	ST6GAL1	ST6 beta-galactosamide alpha-2,6-sialyltranferase 1
1565269_s_at	ATF1	activating transcription factor 1
208621_s_at	VIL2	villin 2 (ezrin)
203109_at	UBE2M	ubiquitin-conjugating enzyme E2M (UBC12 homolog, yeast)
203706_s_at	FZD7	frizzled homolog 7 (Drosophila)
237839_at	ANK3	ankyrin 3, node of Ranvier (ankyrin G)
219969_at	CXorf15	chromosome X open reading frame 15
1554508_at	PIK3AP1	phosphoinositide-3-kinase adaptor protein 1
224771_at	NAV1	neuron navigator 1
222484_s_at	CXCL14	chemokine (C-X-C motif) ligand 14
217234_s_at	VIL2	villin 2 (ezrin)
210148_at	HIPK3	homeodomain interacting protein kinase 3
202784_s_at	NNT	nicotinamide nucleotide transhydrogenase
1560754_at	CMTM7	CKLF-like MARVEL transmembrane domain containing 7
222699_s_at	PLEKHF2	pleckstrin homology domain containing, family F (with FYVE domain) member 2
201983_s_at	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)
211559_s_at	CCNG2	cyclin G2
204894_s_at	AOC3	amine oxidase, copper containing 3 (vascular adhesion protein 1)
209653_at	KPNA4	karyopherin alpha 4 (importin alpha 3)
222511_x_at	FAF1	Fas (TNFRSF6) associated factor 1
212016_s_at	PTBP1	polypyrimidine tract binding protein 1
238447_at	RBMS3	RNA binding motif, single stranded interacting protein
242405_at	MAML2	mastermind-like 2 (Drosophila)
214375_at	PPFIBP1	PTPRF interacting protein, binding protein 1 (liprin beta 1)
241897_at	RBPMS	RNA binding protein with multiple splicing
213606_s_at	ARHGDIA	Rho GDP dissociation inhibitor (GDI) alpha

216901_s_at	IKZF1	IKAROS family zinc finger 1 (Ikaros)
220588_at	BCAS4	breast carcinoma amplified sequence 4
234299_s_at	NIN	ninein (GSK3B interacting protein)
201123_s_at	EIF5A	eukaryotic translation initiation factor 5A
212730_at	DMN	desmuslin
208698_s_at	NONO	non-POU domain containing, octamer-binding
235331_x_at	PCGF5	polycomb group ring finger 5
216288_at	CYSLTR1	cysteinyl leukotriene receptor 1
205242_at	CXCL13	chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant)
201435_s_at	EIF4E	eukaryotic translation initiation factor 4E
210432_s_at	SCN3A	sodium channel, voltage-gated, type III, alpha subunit
201043_s_at	ANP32A	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A
204863_s_at	IL6ST	interleukin 6 signal transducer (gp130, oncostatin M receptor)
211801_x_at	MFN1	mitofusin 1
212190_at	SERPINE2	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2
201650_at	KRT19	keratin 19
224311_s_at	CAB39	calcium binding protein 39
218087_s_at	SORBS1	sorbin and SH3 domain containing 1
242551_at	C18orf1	chromosome 18 open reading frame 1
204867_at	GCHFR	GTP cyclohydrolase I feedback regulator
232925_at	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)
239561_at	MED13L	mediator complex subunit 13-like

Table S3B. Sca1-MALT1 lymphoma transcriptional signature. List of the genes differentially expressed in Sca1-MALT1 mouse lymphomas *vs*. WT mice using LIMMA (B>0; 291 probes, 246 genes)

Probeset	Name	logFC	B
1449401_at	C1qc	2.34	6.57
1417381_at	C1qa	1.93	5.93
1424754_at	Ms4a7	1.18	5.73
1437665_at	Il22ra2	-2.44	5.42
1422280_at	Gzmk	3	5.35
1415989_at	Vcam1	0.95	5.31
1447640_s_at	Pbx3	1.01	4.98
1437540_at	Mcoln3	-1.58	4.91
1437726_x_at	C1qb	2.4	4.68
1419627_s_at	Clec4n	1.89	4.67
1427668_at	Siglec1	-1.36	4.58
1448118_a_at	Ctsd	0.98	4.56
1449498_at	Marco	-1.64	4.33
1455301_at	Wipf3	1	4.12
1425951_a_at	Clec4n	2.01	4.1
1424402_at	Rufy3	-0.68	3.91
1457484_at	D930050J11	-0.79	3.89
1432133_at	2210022J03Rik	-0.75	3.87
1442018_at	AI426953	-1.81	3.86
1427427_at	Ryr3	-2.43	3.83
1417063_at	C1qb	2.66	3.76
1421213_at	Edaradd	-1.08	3.75
1434366_x_at	C1qb	2.23	3.74
1418990_at	Ms4a4d	1.01	3.73
1419123_a_at	Pdgfc	1.87	3.7
1415948_at	Creg1	1.15	3.56
1448919_at	Cd302	1.07	3.46
1437800_at	Edaradd	-2.27	3.42
1448732_at	Ctsb	1.01	3.4
1453593_at	Vgll3	1.29	3.38
1419695_at	St8sia1	-0.82	3.36
1450024_at	Sufu	-0.73	3.34
1417492_at	Ctsb	1.04	3.27
1434302_at	Raph1	1	3.17
1448737_at	Tspan7	0.81	3.12
1448162_at	Vcam1	0.77	3.05
1434303_at	Raph1	0.79	2.98
1419598_at	Ms4a6d	2.05	2.97
1426411_a_at	Strbp	-1.01	2.93
1449351_s_at	Pdgfc	1.38	2.93
1448828_at	Smc6	-0.79	2.9

1435836_at	Pdk1	-1.02	2.81
1449500_at	Serpinb7	-1.62	2.79
1419192_at	Il4i1	-1.03	2.77
1449164_at	Cd68	1	2.75
1419599_s_at	Ms4a6d	2.12	2.69
1418243_at	Fcna	1.79	2.64
1440462_at	B930068K11Rik	0.7	2.61
1427318_s_at	Fer1l3	-0.85	2.61
1447946_at	Adam23	-1.47	2.56
1423326_at	Entpd1	0.86	2.52
1427076_at	Mpeg1	0.51	2.51
1420699_at	Clec7a	1.04	2.48
1433133_at	Edaradd	-2.16	2.44
1417491_at	Ctsb	0.91	2.39
1450044_at	Fzd7	1.01	2.36
1417490_at	Ctsb	0.61	2.33
1426808_at	Lgals3	1.11	2.29
1445301_at	BC028528	-0.8	2.28
1419665_a_at	Nupr1	1.26	2.27
1418345_at	Tnfsf13	0.59	2.26
1434196_at	Dnaja4	0.76	2.25
1449155_at	Polr3g	-0.54	2.2
1456010_x_at	Hes5	-0.86	2.2
1418126_at	Ccl5	1.08	2.19
1434112_at	LOC100048050	1.1	2.17
1438766_at	Pnrc2	-1.52	2.12
1456509_at	1110032F04Rik	-0.79	2.12
1448139_at	Mlc1	-1.16	2.09
1460135_at	A930005H10Rik	-1.26	2.06
1456169_at	EG226654	-0.52	2.06
1429206_at	Rhobtb1	0.93	2.06
1449110_at	Rhob	0.67	2.03
1417700_at	Rab38	0.64	1.99
1452014_a_at	Igf1	1.03	1.99
1446968_at	Picalm	-0.88	1.98
1436103_at	Rab3ip	-0.8	1.97
1436530_at	OTTMUSG00000000971	2.21	1.95
1416136_at	Mmp2	1.32	1.94
1457666_s_at	Ifi202b	1.56	1.92
1417268_at	Cd14	1.2	1.9
1460064_at	BC028789	-0.68	1.88
1430596_s_at	Vgll3	1.39	1.87
1441656_at	B930068K11Rik	0.66	1.86
1418847_at	Arg2	1.45	1.83
1428392_at	Rassf2	-0.58	1.82
1419666_x_at	Nupr1	0.98	1.76
1451174_at	Lrrc33	-0.51	1.74
1420361_at	Slc11a1	1.04	1.73
1420715_a_at	Pparg	1.12	1.71
1427532_at	Trat1	-1.49	1.71

1436448_a_at	Ptgs1	1.51	1.71
1439049_at	Dph5	-1.29	1.69
1438296_at	C430010C01	-0.96	1.66
1418366_at	Hist2h2aa1	1	1.66
1436080_at	AW011738	-0.77	1.66
1455328_at	Accn2	-0.57	1.65
1416165_at	Rab31	0.59	1.65
1454632_at	6330442E10Rik	-0.6	1.62
1436788_at	Acp2	0.49	1.59
1430516_at	4930428B01Rik	-0.53	1.57
1423493_a_at	Nfix	0.48	1.57
1420664_s_at	Procr	-0.55	1.57
1416688_at	Snap91	-2.55	1.54
1452061_s_at	Strbp	-0.87	1.51
1450138_a_at	Serpinb6a	0.72	1.5
1441549_at	Pi4kb	-0.51	1.49
1422948_s_at	Hist1h3a	1.64	1.48
1425632_a_at	Pqlc2	-0.57	1.46
1457240_at	Cdk9	-0.73	1.46
1417604_at	Camk1	0.82	1.45
1418555_x_at	Spic	0.94	1.44
1420621_a_at	App	0.65	1.42
1448239_at	Hmox1	1.63	1.42
1457709_a_at	A930005H10Rik	-1.25	1.42
1417061_at	Slc40a1	1.21	1.4
1428783_at	Prkar2a	0.52	1.39
1423586_at	Axl	0.78	1.37
1442566_at	C78878	-0.7	1.37
1421835_at	Mtap7	-0.75	1.37
1421193_a_at	Pbx3	0.72	1.33
1445639_at	9130014G24Rik	-1.34	1.32
1419601_at	Kcnj10	1.13	1.32
1417533_a_at	Itgb5	1.22	1.32
1453402_at	6430500C12Rik	-1	1.31
1417876_at	Fcgr1	1.37	1.31
1455425_at	BB001228	-1.61	1.3
1439331_at	4932439E07Rik	-0.55	1.29
1419537_at	Tcfec	0.91	1.29
1451809_s_at	Rwdd3	-1.15	1.29
1419638_at	Efnb2	-0.86	1.27
1424354_at	Tmem140	0.68	1.26
1454762_at	Xkrx	-1.3	1.22
1451716_at	Mafb	1.14	1.21
1416985_at	Sirpa	0.67	1.21
1429898_at	2310008M10Rik	-0.52	1.2
1438055_at	Rarres1	1.11	1.2
1451353_at	Tm6sf1	-0.77	1.19
1416613_at	Cyp1b1	0.55	1.17
1428444_at	Asb2	-0.58	1.13
1419639_at	Efnb2	-0.7	1.12

1436363_a_at	Nfix	0.7	1.1
1434763_at	Orai2	-0.5	1.07
1448694_at	Jun	0.78	1.07
1421182_at	Clec1b	1.67	1.07
1452533_at	Ryr3	-0.57	1.06
1418174_at	Dbp	-1.07	1.06
1452279_at	Cfp	0.68	1.06
1455299_at	Vgll3	1.45	1.06
1418998_at	Kmo	-1.39	1.04
1423704_at	Lypla3	0.61	1.03
1450852_s_at	F2r	0.75	1.03
1451789_a_at	Ryk	0.78	1.03
1436130_s_at	4930523C11Rik	-0.61	1.02
1416021_a_at	Fabp5	1.03	1
1457593_at	2610202C22Rik	-0.6	0.99
1448620_at	Fcgr3	1.64	0.99
1449402_at	Chst7	0.57	0.98
1440162_x_at	A630043P06	-2.26	0.98
1424489_a_at	Trit1	-0.67	0.97
1457825_x_at	Tcn2	0.65	0.96
1443188_at	Ube2w	-0.64	0.96
1429777_at	Dnajb6	-0.72	0.94
1439276_at	Adar	-0.61	0.93
1430421_a_at	Tmem205	0.74	0.93
1417932_at	Il18	0.58	0.92
1451263_a_at	Fabp4	3	0.92
1422437_at	Col5a2	0.99	0.92
1416022_at	Fabp5	1.32	0.91
1421836_at	Mtap7	-0.59	0.89
1426388_s_at	Ryk	0.51	0.89
1438928_x_at	Ninj1	0.89	0.87
1426188_s_at	BC005685	0.95	0.84
1458879_at	C76798	-0.5	0.83
1438306_at	Rnf180	0.78	0.83
1417010_at	Zfp238	-0.55	0.83
1423722_at	Tmem49	0.77	0.81
1436122_at	Zfp667	-0.48	0.8
1438666_at	Ldlrad3	-0.64	0.79
1452942_at	Tmem65	0.74	0.78
1444343_at	A130064L14Rik	-0.75	0.78
1448521_at	Brd7	-0.41	0.76
1423021_s_at	Insl3	0.72	0.76
1449130_at	Cd1d1	-0.98	0.74
1456775_at	Ints8	-0.85	0.73
1449924_at	Prg3	-1.24	0.73
1440268_at	Trim41	-0.48	0.73
1438658_a_at	S1pr3	-0.85	0.71
1435781_at	Cand1	-0.41	0.71
1452207_at	Cited2	0.52	0.71
1429954_at	Clec4a3	1.49	0.69

1449134_s_at	Spic	1.38	0.68
1460192_at	Osbpl1a	0.81	0.66
1448566_at	Slc40a1	1.62	0.66
1450444_a_at	Nr1h3	0.71	0.65
1450029_s_at	Itga9	1.01	0.6
1448233_at	Prnp	0.58	0.59
1457218_at	6430510M02Rik	-0.98	0.56
1448323_a_at	Bgn	1	0.55
1428580_at	Blvra	0.38	0.53
1437889_x_at	Bgn	0.82	0.53
1449193_at	Cd5l	2.58	0.53
1427655_a_at	A630038E17Rik	-1.32	0.52
1450945_at	Prkca	0.72	0.52
1440874_at	Slco5a1	-0.81	0.51
1418401_a_at	Dusp16	-0.66	0.51
1428643_at	Mgat5	0.5	0.5
1460285_at	Itga9	0.71	0.5
1419519_at	Igf1	0.67	0.49
1449141_at	Fblim1	0.77	0.49
1458459_a_at	E230029C05Rik	1.2	0.48
1423436_at	Gsta3	0.89	0.48
1416405_at	Bgn	0.89	0.48
1460287_at	Timp2	0.81	0.47
1458888_at	OTTMUSG00000003456	-0.53	0.47
1439364_a_at	Mmp2	1.29	0.46
1439256_x_at	Gpr137b-ps	0.71	0.45
1440778_x_at	Zfp712	-0.48	0.44
1448327_at	Actn2	-0.73	0.42
1434473_at	Slc16a5	-1.12	0.42
1417534_at	Itgb5	0.9	0.41
1418892_at	Rhoj	0.84	0.41
1441100_at	Mbtd1	-0.42	0.41
1429324_at	1700012A16Rik	-0.55	0.41
1436364_x_at	Nfix	0.67	0.4
1448269_a_at	Klhl13	0.99	0.4
1436515_at	Bach2	-0.89	0.38
1453568_at	Dapl1	-1.52	0.38
1450234_at	Ms4a6c	1.05	0.38
1425493_at	Bmpr1a	0.75	0.38
1428914_at	2310014D11Rik	-0.48	0.38
1438051_at	Ttc14	-0.67	0.36
1460227_at	Timp1	0.65	0.35
1430886_at	1700112E06Rik	0.75	0.35
1439641_at	LOC553090	-0.96	0.33
1441552_at	Tcra	-1.31	0.3
1448200_at	Tcn2	0.52	0.29
1423414_at	Ptgs1	1.16	0.29
1423378_at	Adam23	-0.76	0.28
1429448_s_at	Tet1	-0.9	0.28
1435331_at	Pyhin1	-1.09	0.28

1455146_at	C230082I21Rik	-1.09	0.26
1427183_at	Efemp1	1	0.25
1422603_at	Rnase4	1.07	0.25
1438091_a_at	H2afz	0.47	0.24
1426925_at	Rc3h2	-0.94	0.24
1443044_at	A830091E24	-0.56	0.24
1430167_a_at	Rwdd3	-0.95	0.23
1433716_x_at	Gfra2	0.42	0.23
1437667_a_at	Bach2	-0.88	0.21
1428644_at	Mgat5	0.57	0.2
1440739_at	Vegfc	1	0.19
1457072_at	Bcl11a	-0.89	0.18
1455237_at	Usp36	-0.8	0.18
1417023_a_at	Fabp4	2.78	0.17
1432337_at	Fancl	-0.68	0.15
1416617_at	Acss1	-0.5	0.14
1424133_at	Tmem98	0.71	0.12
1415806_at	Plat	0.88	0.12
1417031_at	Tmem206	-0.43	0.12
1438454_at	B430203M17Rik	-0.52	0.12
1456632_at	Bcl11a	-0.77	0.11
1448417_at	Ninj1	0.94	0.11
1455455_at	Glt28d2	0.9	0.1
1429381_x_at	Igh	1.48	0.1
1452839_at	Dph5	-0.9	0.09
1417588_at	Galnt3	1.06	0.08
1449183_at	Comt1	0.59	0.07
1454722_at	Pten	-0.42	0.07
1438842_at	Mtch2	-0.55	0.07
1417730_at	Ext1	0.55	0.06
1417494_a_at	Cp	1.08	0.06
1428340_s_at	Atp13a2	0.47	0.06
1422541_at	Ptprm	0.46	0.06
1457482_at	Jarid1b	-0.58	0.06
1434325_x_at	Prkar1b	0.91	0.05
1442499_at	Cdv3	-0.51	0.05
1449106_at	Gpx3	1.67	0.05
1418804_at	Sucnr1	-0.74	0.05
1419202_at	Cst7	0.99	0.04
1424674_at	Slc39a6	-0.47	0.04
1416289_at	Plod1	0.54	0.03
1416827_at	Tbxas1	0.97	0.03
1417605_s_at	Camk1	0.57	0.03
1439330_at	D230040J21Rik	-0.54	0.03
1451019_at	Ctsf	0.68	0.02
1450330_at	Il10	1.68	0.01
1434500_at	Ttyh2	0.77	0.01
1425025_at	Tmem106a	0.8	0.01
1426223_at	Ttc39c	0.77	0.01
1416343_a_at	Lamp2	0.62	0.01

Table S3C. The transcriptional profile of Sca1-MALT1,p53$^{-/-}$ lymphomas. Bioinformatic analysis using LIMMA (B>0) identified defined a list of the genes differentially expressed in Sca1-MALT1,p53$^{-/-}$ mouse lymphomas *vs*. WT mice, which included 34 probes (34 genes) corresponding to the Sca1-MALT1,p53$^{-/-}$ lymphomas transcriptional signature

Probeset	Name	logFC	B
10353849	4632411B12Rik	-0.88	2.20
10389717	NA	-2.25	2.16
10375145	Lcp2	1.56	2.07
10439744	Cd96	1.51	1.87
10440926	Dnajc28	-0.69	1.67
10593024	Cd3e	1.82	1.67
10385428	Itk	1.72	1.57
10422760	Fyb	2.08	1.55
10390328	Tbx21	0.79	1.51
10472235	Dapl1	1.95	1.51
10469255	Prkcq	1.88	1.49
10504759	NA	1.42	1.48
10457168	Cd226	1.01	1.39
10439845	Gm5486	0.72	1.37
10593015	Cd3g	2.47	1.10
10372652	Lyz1	0.73	0.86
10372648	Lyz2	2.19	0.84
10360367	Gm4955	-1.44	0.82
10487208	Atp8b4	1.03	0.78
10547894	Cd4	1.07	0.62
10362350	Themis	1.45	0.60
10586076	NA	-3.41	0.60
10401244	Actn1	0.91	0.55
10360373	E030037K03Rik	-1.32	0.49
10351873	Pyhin1	-0.58	0.47
10441115	Brwd1	-0.64	0.46
10403978	Gm11277	1.17	0.39
10360398	Ifi202b	1.68	0.39
10389207	Ccl5	2.05	0.31
10538979	Cd8b1	2.10	0.28
10489569	Pltp	1.08	0.19
10547985	Cd27	1.07	0.18
10461605	Ms4a4b	1.87	0.16
10601583	Mthfd2l	0.64	0.03

Table S4A. Characterization of human CD34$^+$ cells. Clinical and biological features of MALT patients who underwent BM aspirate for isolation of CD34+ cells and RNA extraction for gene expression microarrays (patients #1 to 5) and FISH (patient #6).

Case	Sex	Age	Diagnosis	Location	Cytogenetics	*MALT1* rearrangement by FISH	*API2-MALT1* rearrangement
1	M	68	MALT lymphoma	Intestine	Not done	Negative	Negative
2	M	54	MALT lymphoma	Stomach	Not done	Negative	Negative
3	F	70	MALT lymphoma	Lung	Not done	Negative	Negative
4	M	80	MALT lymphoma	Lung	46,XY,t(11;18)(q21;q21)	Positive	Positive
5	F	87	MALT lymphoma	Ocular adnexa	46,XX	Negative	Negative
6	F	48	MALT lymphoma	Stomach	46,XX,t(11;18)(q21;q21)	Positive	Positive

Table S4B. Human CD34^{+} MALT lymphoma transcriptional signature. List of the genes differentially expressed in human BM-isolated CD34+Lin- from patients with MALT lymphoma *vs*. healthy individuals using LIMMA (B>0, 743 gene probes)

Probeset	Name	logFC	B
8054344	RFX8	-1.30	9.17
7991766	HBA1	4.69	7.35
8106743	VCAN	3.21	7.15
7974461	LGALS3	2.20	6.30
7960165	ZNF268	-0.81	5.48
7899346	CCDC72	-1.22	5.29
8133314	NCF1	3.06	5.17
7961440	PLBD1	4.06	5.03
8039692	ZNF814	-1.16	4.76
8110055	CPEB4	2.05	4.56
8110427	NA	-0.74	4.50
8020411	SNRPD1	-0.90	4.50
8018189	CD300E	0.95	4.47
8001104	NA	3.10	4.42
8171392	ASB9	-0.61	4.42
7974695	NA	-0.86	4.39
8089015	PROS1	2.15	4.37
8133876	CD36	2.87	4.22
8042637	DYSF	2.84	4.19
7898582	RPS14P3	-0.63	4.19
8109093	ABLIM3	1.62	4.11
7918768	DENND2C	1.74	4.04
8025421	MARCH3	1.08	4.02
7946033	HBB	4.08	4.01
8114239	C5orf20	-0.82	3.98
8097679	LSM6	-0.65	3.98
8179683	NRM	-0.84	3.90
8161563	NA	3.22	3.85
8043474	NA	3.31	3.84
8171879	LOC100508181	-0.73	3.84
7981728	NA	4.17	3.80
8037205	CEACAM1	3.07	3.76
7981722	IGHA1	3.61	3.75
8057517	NCKAP1	1.53	3.71
8102998	GYPA	5.65	3.70
8043932	RPL31	-1.16	3.61
8119159	NA	-0.74	3.55
8043480	NA	3.75	3.55
8161242	EXOSC3	-0.74	3.52
8148304	TRIB1	1.77	3.50
8058765	FN1	0.83	3.43
8166730	CYBB	3.14	3.43
8163896	STOM	1.13	3.42

8023526	LOC100132992	-0.68	3.38
8005200	SNORD49B	-1.13	3.34
8153223	PTK2	1.09	3.33
7985202	PSMA4	-0.58	3.28
8053690	IGK@	3.64	3.26
7944560	ARHGEF12	1.48	3.26
7960865	SLC2A3	2.41	3.25
8112582	NA	-0.89	3.21
7995263	IGHV3-48	3.12	3.19
7981387	CDC42BPB	1.43	3.17
8038899	FPR1	2.55	3.15
8093141	WDR53	-0.63	3.11
8004144	MIS12	-0.84	3.08
8046628	RBM45	-0.62	3.03
7950597	CLNS1A	-0.75	3.00
7907249	FMO3	1.42	3.00
7981068	SERPINA1	2.78	3.00
7929511	ENTPD1	2.86	2.99
7989915	TIPIN	-0.82	2.98
8035831	ZNF98	-0.74	2.95
8140840	STEAP4	1.90	2.92
7913357	ECE1	1.44	2.85
7969533	SLAIN1	-0.82	2.85
7939839	PTPRJ	2.55	2.84
8003204	GINS2	-0.97	2.83
7942204	CTTN	1.59	2.83
8139203	C7orf11	-0.49	2.83
8157605	NA	1.24	2.80
7904751	RBM8A	-0.74	2.80
7941639	BBS1	-0.56	2.78
7968632	NA	-1.25	2.78
7935011	CPEB3	0.63	2.77
8101449	HPSE	1.20	2.77
7951140	LOC100131541	1.31	2.75
8039236	LILRA5	2.35	2.75
8158961	GTF3C5	-0.52	2.72
8030978	ZNF845	-0.66	2.70
8048703	LLPH	-0.66	2.68
8131867	NA	-1.38	2.66
8057045	FKBP7	-0.81	2.64
7922773	NCF2	2.48	2.64
8150698	SNAI2	1.65	2.62
7947928	C1QTNF4	-1.11	2.62
8026047	JUNB	1.44	2.62
8146334	NA	-0.68	2.60
8006477	ZNF830	-0.58	2.60
8179704	IER3	1.58	2.59
8180265	NA	-1.01	2.58
8005202	SNORD49A	-0.98	2.58
8069620	MRPL39	-0.69	2.57
8043322	ANAPC1	-0.75	2.55
8123717	RPP40	-1.15	2.54

8103684	C4orf27	-0.64	2.52
8074909	IGLL1	-0.83	2.50
8058614	LANCL1	-0.72	2.48
8129458	ARHGAP18	1.17	2.47
8098556	CCDC111	-0.90	2.47
8043902	PDCL3	-0.85	2.45
7997662	KIAA0513	1.57	2.45
8027247	ZNF93	-1.12	2.45
8048283	SLC11A1	1.44	2.44
8113504	C5orf13	-1.15	2.43
8005557	EPN2	0.75	2.43
8080964	GXYLT2	-0.80	2.42
7981740	IGHA1	3.15	2.41
8042283	HSPC159	2.48	2.40
8072946	EIF3L	-0.62	2.38
8026679	USE1	-0.62	2.37
8043465	IGKC	2.99	2.36
8043476	LOC652493	3.45	2.35
8077270	CHL1	0.90	2.32
8027260	ZNF486	-1.06	2.32
8102728	NA	-0.96	2.31
8034217	EPOR	0.92	2.31
7916356	HSPB11	-0.53	2.30
8016909	MKS1	-0.71	2.29
7920128	S100A11	1.75	2.28
8009301	PRKCA	1.20	2.27
7954810	LRRK2	2.15	2.26
8027363	ZNF726	-1.01	2.24
8094169	CPEB2	1.13	2.23
8152465	EIF3H	-0.47	2.23
8029065	BCKDHA	-0.69	2.22
7903457	PRMT6	-0.55	2.20
7902787	NA	-0.74	2.20
7989037	CCPG1	1.08	2.20
8122732	NA	-0.88	2.19
8001048	C16orf58	-0.47	2.19
8038877	SIGLEC5	1.29	2.17
8008454	ABCC3	2.12	2.16
7917634	HFM1	-0.89	2.16
8015991	SLC4A1	4.45	2.15
8147447	PTDSS1	-0.52	2.15
7939411	C11orf74	-1.00	2.14
7990555	NRG4	-1.36	2.13
8064502	SNRPB	-0.59	2.13
8030925	ZNF880	-0.82	2.11
8042107	NA	-0.68	2.11
7909390	CR1L	2.46	2.10
7902617	SAMD13	-0.76	2.10
7965152	NA	-0.83	2.09
7906435	DARC	0.76	2.09
8013109	NA	-0.81	2.09
8082350	MCM2	-0.75	2.08

8119926	TMEM63B	1.23	2.08
7939424	API5	-0.50	2.08
8077370	SETMAR	-0.80	2.08
8055492	NA	0.51	2.05
8154727	LOC138412	-0.57	2.04
8043470	IGKV3D-11	4.18	2.03
8101489	FAM175A	-0.96	2.02
8006762	MRPL45	-0.60	2.02
7964828	NA	-0.72	2.02
8043583	LOC285033	-0.54	2.01
8035847	ZNF675	-0.77	2.01
7977319	PLD4	-1.26	2.01
8122457	STX11	1.60	1.99
7978527	C14orf126	-0.87	1.99
7961022	PTMA	-0.57	1.99
8149137	DEFA3	5.43	1.97
8121601	FAM26E	1.13	1.97
7962203	YARS2	-0.57	1.97
8049088	COPS7B	-0.63	1.97
8087283	QARS	-0.60	1.96
8043995	IL1R1	2.19	1.96
8116316	MGAT4B	0.53	1.96
7919984	SELENBP1	2.63	1.95
8067722	STMN3	-0.79	1.95
8163637	TNC	0.86	1.94
8079229	ZNF501	-0.56	1.94
8135235	PMPCB	-0.56	1.93
7900576	PPIH	-0.53	1.92
7991777	C4orf46	-0.85	1.92
8044375	BCL2L11	1.09	1.92
7979886	NA	-0.81	1.90
8121510	RPF2	-0.78	1.90
8133114	VKORC1L1	-0.68	1.90
7941243	DPF2	-0.50	1.89
8114225	H2AFY	-0.46	1.87
7920244	S100A8	3.61	1.87
8029399	ZNF226	-0.62	1.86
8031768	ZIK1	-0.75	1.86
7908988	SNRPE	-0.91	1.86
8089988	CCDC58	-0.70	1.84
8149475	CNOT7	-0.60	1.84
8038624	C19orf48	-0.81	1.84
8154388	NA	-0.76	1.84
7913252	PINK1	-0.73	1.83
7938154	ILK	0.88	1.83
8028916	SNRPA	-0.59	1.82
8027297	ZNF738	-0.93	1.82
8122440	LTV1	-0.82	1.82
8111739	FYB	1.83	1.82
7908777	NA	-0.63	1.82
8052866	FAM136A	-0.65	1.81
8073890	GRAMD4	-0.51	1.80

8100532	C4orf14	-0.55	1.80
8053036	TPRKB	-0.77	1.79
8018114	SDK2	-1.47	1.78
8037387	NA	1.60	1.76
8143341	JHDM1D	1.88	1.75
8170418	NA	-0.58	1.73
7982597	THBS1	3.03	1.72
8027241	ZNF253	-1.11	1.71
8103951	ACSL1	1.23	1.71
8036777	FBL	-0.83	1.71
7981377	ANKRD9	0.56	1.71
7973056	APEX1	-0.66	1.70
8008885	MIR21	2.46	1.69
7978335	SDR39U1	-0.51	1.66
8017850	WIPI1	1.94	1.66
7971513	ESD	-0.61	1.65
7937892	PGAP2	-0.71	1.63
8123819	EEF1E1	-0.75	1.63
7918323	SORT1	1.69	1.62
7907124	TIPRL	-0.53	1.62
8029907	C5AR1	2.50	1.61
8151310	EYA1	0.70	1.60
8051396	NLRC4	2.20	1.60
8111677	LIFR	0.97	1.60
8150253	STAR	-0.68	1.60
8001876	NAE1	-0.67	1.59
7948910	SNORD25	-1.09	1.59
8012891	NA	-0.79	1.59
7953603	C1S	0.62	1.59
7974531	RPL13AP3	-0.63	1.56
8089011	PROS1	1.56	1.56
8085058	NA	-0.79	1.55
8145782	MAK16	-0.65	1.54
8166065	TLR8	1.71	1.54
8168366	PIN4	-0.60	1.54
8040142	CPSF3	-0.65	1.53
7917779	GCLM	0.89	1.53
7960850	SLC2A14	1.67	1.53
8117888	RAN	-0.59	1.50
8036913	BLVRB	2.02	1.49
7965956	NFYB	-0.68	1.49
8141395	MCM7	-0.69	1.49
8179575	TRIM27	-0.47	1.49
8055426	MCM6	-0.81	1.48
8034589	FARSA	-0.67	1.48
8014100	C17orf75	-0.52	1.48
8022418	NA	-0.68	1.48
8131666	ITGB8	-0.99	1.48
8179263	TNF	1.13	1.47
8028200	ZNF567	-0.63	1.46
8069633	ATP5J	-0.54	1.46
8160981	KIAA1539	1.22	1.46

8068478	CHAF1B	-0.72	1.46
8017039	SEPT4	0.49	1.44
8118824	NA	-0.66	1.44
7909188	IKBKE	-0.66	1.44
8086555	LZTFL1	-0.75	1.43
7898276	NA	-0.42	1.43
8105061	NA	1.79	1.43
7954006	PTMA	-0.61	1.42
8174026	YWHAQP8	-0.53	1.42
7905571	S100A9	3.73	1.42
8180373	NA	-0.62	1.42
8088151	ACTR8	-0.55	1.41
8165974	CLCN4	1.02	1.40
8002312	NOB1	-0.87	1.40
7906767	FCGR2C	2.03	1.40
8020110	RAB31	2.10	1.40
8161288	CNTNAP3	1.02	1.39
7899675	TMEM39B	-0.44	1.39
8043449	IGK@	3.62	1.39
8106271	NSA2	-0.60	1.38
8041867	MSH2	-0.73	1.36
8053231	LOXL3	0.64	1.34
7998251	C16orf13	-0.41	1.34
8043438	IGKV1-5	3.22	1.34
8079224	ZNF502	-1.07	1.34
7918223	C1orf59	-0.87	1.33
8180286	NA	-0.61	1.33
7901418	BTF3L4	-0.46	1.32
8127031	MCM3	-0.81	1.32
8143035	NA	-0.61	1.31
8053715	NA	2.14	1.31
7997099	SF3B3	-0.57	1.30
8045142	MZT2B	-0.44	1.30
8105842	CENPH	-0.81	1.29
8135514	IFRD1	0.64	1.28
8104825	BRIX1	-0.73	1.27
8133902	NA	-0.88	1.25
7920238	S100A12	3.92	1.25
8040415	NA	-0.69	1.25
8136347	CALD1	1.53	1.24
8046488	CDCA7	-1.08	1.24
7914184	PTAFR	1.06	1.24
7927108	BMS1	-0.53	1.23
8022882	ZNF24	-0.54	1.23
8111524	UGT3A2	-1.05	1.22
8129637	VNN2	1.59	1.22
7925320	NID1	2.00	1.21
7915594	NA	-0.68	1.20
8078569	GOLGA4	0.62	1.20
8135688	NAA38	-0.51	1.20
8142886	UBE2H	0.93	1.20
7969179	RNASEH2B	-0.67	1.20

8107234	MAN2A1	0.53	1.19
8078227	KAT2B	1.33	1.19
7924923	NUP133	-0.50	1.18
7960900	CLEC4E	1.59	1.18
8018482	WBP2	0.84	1.18
8103975	SLED1	0.91	1.16
8091385	CP	1.64	1.16
8114612	CD14	3.11	1.16
8140227	NCF1	1.46	1.15
7989834	C15orf44	-0.60	1.15
8081657	CD200	-0.91	1.15
8143307	HIPK2	0.62	1.15
7927202	ZNF22	-0.71	1.14
7905163	MRPS21	-0.57	1.13
8025895	PRKCSH	-0.59	1.13
8136631	SSBP1	-0.63	1.13
8163525	POLE3	-0.52	1.13
8036395	ZNF569	-0.54	1.12
8077103	TYMP	0.80	1.12
8169701	MCTS1	-0.55	1.11
8167656	MAGED1	-0.70	1.11
8115957	HK3	1.44	1.11
8087254	IMPDH2	-0.88	1.11
7915861	MOBKL2C	1.06	1.11
7961507	ART4	1.95	1.11
7983228	MAP1A	-0.94	1.10
7958666	C12orf24	-1.24	1.10
7964145	TIMELESS	-0.48	1.10
8013071	FLCN	0.69	1.09
7954243	NA	-0.79	1.09
8014081	UTP6	-0.62	1.09
8090448	RUVBL1	-0.86	1.09
7946957	SAAL1	-0.73	1.09
8022972	RPL7A	-0.66	1.09
8111892	OXCT1	-0.73	1.09
8168843	RPL36A	-0.62	1.09
8169920	RBMX2	-0.49	1.09
8075569	SLC5A4	0.69	1.08
8088526	THOC7	-0.60	1.08
7986323	GLTSCR2	-0.55	1.08
7977482	TTC5	-0.60	1.08
8145454	BNIP3L	0.73	1.07
8085233	RPUSD3	-0.74	1.07
8062377	SRC	0.79	1.07
8121043	ORC3	-0.50	1.07
8081786	QTRTD1	-0.52	1.07
7973352	LRP10	1.06	1.06
7925480	FH	-0.60	1.06
7995069	FUS	-0.40	1.05
8084742	LPP	0.58	1.05
8110486	ZNF879	-0.52	1.04
8146579	CHD7	1.41	1.04

7966183	ALKBH2	-0.43	1.03
7964271	PRIM1	-0.81	1.03
8057933	GTF3C3	-0.53	1.03
7924733	PARP1	-0.55	1.03
8138912	LSM5	-0.71	1.02
7910790	NA	-0.67	1.01
8106181	BTF3	-0.46	1.00
7932069	NUDT5	-0.56	1.00
7956639	TSFM	-0.54	0.99
8009784	MRPS7	-0.44	0.99
8106193	UTP15	-0.67	0.98
8035773	ZNF506	-0.77	0.98
8014115	MYO1D	1.22	0.98
7985493	TM6SF1	2.54	0.98
8009366	NOL11	-0.71	0.97
7962427	PUS7L	-0.62	0.97
7939137	EIF3M	-0.63	0.97
8179559	PFDN6	-0.60	0.96
8121212	NA	-0.78	0.94
8152323	EIF3E	-0.75	0.94
8142930	TSGA14	-0.94	0.94
8162514	FANCC	-0.48	0.92
8017143	PTRH2	-0.63	0.92
7924582	WDR26	0.79	0.92
8111989	NA	-0.61	0.91
8104838	DNAJC21	-0.53	0.91
7917912	DPYD	0.69	0.91
8063942	NTSR1	-0.65	0.90
7901038	RPS8	-0.67	0.89
8011027	MYO1C	1.14	0.89
8092970	APOD	1.03	0.89
8042326	CEP68	-0.65	0.89
8157216	UGCG	2.15	0.88
8009008	METTL2A	-0.44	0.88
8139889	NA	-0.78	0.88
8064471	SIRPB1	1.95	0.87
8123658	SLC22A23	1.49	0.87
8005141	TTC19	-0.52	0.87
8180410	NA	-0.59	0.86
8084945	NA	-0.63	0.86
8040774	AGBL5	-0.56	0.86
8163839	C5	-0.80	0.85
7950501	GDPD5	0.63	0.85
8028332	KCNK6	0.55	0.85
8128726	PPIL6	-0.91	0.84
8160033	SNRPE	-0.83	0.84
8043459	IGKC	2.56	0.84
8114536	TMEM173	-0.78	0.84
8062174	ERGIC3	-0.53	0.83
8119088	CDKN1A	0.96	0.83
8033899	EIF3G	-0.50	0.83
7907271	FMO2	1.14	0.83

7904469	SRGAP2	0.75	0.83
8072004	IGLL3P	-0.61	0.82
7904482	SRGAP2P2	0.73	0.82
8161056	TLN1	0.68	0.82
8098150	C4orf43	-0.73	0.82
7938286	RPL27A	-0.67	0.81
8086784	C3orf75	-0.62	0.81
7983910	AQP9	2.48	0.81
8072584	NA	-0.84	0.81
7900201	UTP11L	-0.63	0.81
8180403	NA	-0.51	0.80
8179055	ZNRD1	-0.76	0.80
8000399	ZKSCAN2	-0.60	0.80
7989759	PARP16	-0.59	0.80
7931168	ACADSB	-0.59	0.80
7969428	UCHL3	-0.49	0.80
8031483	RPL28	-0.52	0.80
8036656	SARS2	-0.58	0.79
8010086	C17orf95	-0.55	0.79
8116532	SNORD95	-0.68	0.78
8012257	TP53	-0.87	0.78
8170166	HTATSF1	-0.54	0.77
8117207	ALDH5A1	-0.61	0.77
8099107	LYAR	-0.67	0.77
8026182	MRI1	-0.76	0.76
7928630	EIF5AL1	-0.85	0.76
7917676	GLMN	-0.67	0.76
7960716	PHB2	-0.59	0.76
7947396	CSTF3	-0.73	0.76
8179019	HLA-F	0.78	0.76
8097128	EXOSC9	-0.49	0.76
8014047	C17orf42	-0.58	0.76
8125750	RPL12	-0.53	0.76
8180217	NA	-0.68	0.75
8161580	NA	1.58	0.75
8093256	NA	-0.65	0.75
8043981	IL1R2	0.72	0.74
7923007	UCHL5	-0.48	0.74
8118974	RPL10A	-0.72	0.74
8145244	TNFRSF10C	0.77	0.73
7994603	SPN	-0.76	0.73
8151917	MTERFD1	-0.54	0.72
8050060	TSSC1	-0.49	0.72
7917707	EVI5	1.17	0.71
8147012	PKIA	-0.63	0.71
7921344	ELL2	2.09	0.70
8173135	ALAS2	4.26	0.70
7951467	ALKBH8	-0.71	0.69
8170468	HMGB3	-0.52	0.69
7942985	NA	0.50	0.69
8157139	NA	-0.68	0.69
8000932	C16orf93	-0.59	0.69

8112892	NA	-0.59	0.68
7916225	NA	-0.57	0.68
7936011	CUEDC2	-0.62	0.68
8050763	CENPO	-0.61	0.68
7948476	PRPF19	-0.65	0.67
7924476	TAF1A	-0.65	0.67
8142307	PNPLA8	0.52	0.66
7923503	ADIPOR1	0.84	0.66
8148263	TRMT12	-0.55	0.66
7915444	LEPRE1	-0.46	0.66
8073343	NA	-0.65	0.65
7961208	MAGOHB	-0.67	0.65
7994237	LCMT1	-0.49	0.65
8037679	DMWD	0.56	0.64
8021101	HAUS1	-0.73	0.64
7941985	TCIRG1	0.72	0.64
7904364	WDR3	-0.87	0.63
7909441	G0S2	1.27	0.63
7990253	NPTN	0.84	0.63
8059689	NCL	-0.57	0.63
7926170	DHTKD1	-0.48	0.63
8075709	APOL4	0.93	0.62
8138988	DPY19L2P1	-1.04	0.62
8027272	ZNF85	-0.62	0.62
8061471	GINS1	-0.75	0.62
7995237	AHSP	3.90	0.61
8058927	TMBIM1	1.30	0.61
7897632	APITD1-CORT	-0.46	0.60
8176263	TAF9B	-0.58	0.60
8102065	BDH2	-0.81	0.59
7916727	ITGB3BP	-0.63	0.59
8179839	LSM2	-0.64	0.59
8174576	AMOT	-0.76	0.58
8029710	VASP	0.67	0.58
7940147	FAM111B	-0.98	0.58
8158714	EXOSC2	-0.79	0.58
7999520	RSL1D1	-0.75	0.57
8021768	TSHZ1	-0.47	0.57
8069561	BTF3L4	-0.43	0.57
8064844	PCNA	-0.58	0.57
8134079	GTPBP10	-0.59	0.57
8070567	TFF3	1.00	0.57
8119898	VEGFA	1.04	0.56
7915563	NA	-0.71	0.56
7937476	RPLP2	-0.46	0.56
8088478	NA	-0.67	0.56
7919787	HORMAD1	1.14	0.56
8034395	ZNF709	-0.47	0.55
8053713	NA	2.85	0.55
8002057	ACD	-0.49	0.55
7956949	NUP107	-0.62	0.55
8066822	SULF2	0.94	0.55

8062286	C20orf4	-0.55	0.54
8129045	HDAC2	-0.46	0.54
8114733	ARAP3	0.57	0.54
8071301	C22orf25	1.01	0.54
8075263	NIPSNAP1	-0.83	0.53
8020508	RIOK3	0.90	0.52
8104607	NA	1.69	0.52
8103431	C4orf46	-0.60	0.52
7924144	RPL21P28	-0.73	0.52
7913869	STMN1	-0.54	0.52
7938368	NA	-0.68	0.51
8119492	BYSL	-0.53	0.51
8020468	RBBP8	-0.61	0.51
8032380	BTBD2	-0.53	0.51
8026339	SNRPG	-0.69	0.50
8101718	PIGY	-0.45	0.50
8001102	NA	1.89	0.50
8150014	INTS9	-0.54	0.50
8115806	UBTD2	-0.57	0.50
8110450	HNRNPAB	-0.50	0.50
8080198	PPM1M	0.99	0.49
7914851	CLSPN	-0.57	0.48
8152453	TRPS1	0.56	0.47
7972674	C13orf27	-0.79	0.47
7981718	IGHM	2.81	0.47
8037298	CD177	4.25	0.47
7919645	SV2A	-0.93	0.47
8001423	RPGRIP1L	-0.77	0.47
7922219	SELL	-0.82	0.47
7933659	CSTF2T	-0.59	0.46
8094271	MED28	-0.42	0.46
8167305	EBP	-0.57	0.46
7950294	CHCHD8	-0.74	0.45
8120826	IRAK1BP1	-0.83	0.45
7978644	NFKBIA	0.94	0.45
8066668	NCOA5	-0.51	0.45
7967021	PXN	0.69	0.45
8006715	TADA2A	-0.57	0.45
8035838	ZNF724P	-0.89	0.45
8130408	IPCEF1	1.83	0.44
8160935	FANCG	-0.58	0.44
8146130	GINS4	-0.61	0.44
8041000	GPN1	-0.49	0.43
8157362	ZNF618	-0.56	0.42
7981601	IGHA2	2.17	0.41
8032491	LMNB2	-0.49	0.41
8171896	CXorf21	-0.73	0.41
8085412	IQSEC1	0.76	0.41
7954196	MGST1	-0.99	0.40
8000323	NDUFAB1	-0.47	0.39
8039226	LILRA3	2.21	0.39
7990528	SNUPN	-0.50	0.39

7901376	RNF11	0.73	0.39
8171373	GEMIN8	-0.91	0.38
7950197	ARAP1	0.95	0.38
8010082	SNORD1A	-1.11	0.38
7974471	NA	-0.58	0.37
8171876	METTL1	-0.96	0.37
7916590	AK2	-0.69	0.37
7994280	IL4R	1.19	0.37
7918050	RPSA	-0.76	0.37
8071655	NA	1.42	0.37
8037005	TGFB1	0.62	0.37
8052654	PELI1	1.39	0.36
8030860	FPR2	2.17	0.36
8180212	NA	-0.43	0.36
7949518	FIBP	-0.53	0.35
8109576	THG1L	-0.68	0.34
7906777	FCGR2B	1.32	0.34
8026533	HSH2D	-0.90	0.34
8117922	PRR3	-0.67	0.34
8151898	C8orf37	-0.76	0.34
7951246	MMP8	5.32	0.34
7973924	KIAA0391	-0.43	0.33
8131067	GPR146	1.22	0.33
8102141	PPA2	-0.45	0.32
8155268	POLR1E	-0.81	0.32
8026971	IFI30	2.73	0.32
8107691	PHAX	-0.55	0.32
8049689	RNPEPL1	0.58	0.32
7996393	CBFB	-0.44	0.32
8142084	YBX1P2	-0.42	0.32
8039645	ZNF772	-0.88	0.31
8165698	NA	0.49	0.31
7900157	RPS27	-0.77	0.31
8160968	STOML2	-0.56	0.31
8071212	CDC45	-0.63	0.31
8052022	NA	-0.47	0.30
7949344	NAALADL1	-0.46	0.30
7957540	MRPL42	-0.69	0.30
7969263	HNRNPA1L2	-0.86	0.30
8061668	HCK	2.07	0.30
7906305	NA	-0.56	0.30
8043251	PTCD3	-0.55	0.30
8133108	SNORA15	-0.54	0.29
7973116	METT11D1	-0.43	0.28
7992795	THOC6	-0.52	0.28
8051215	RBKS	-0.55	0.28
8082229	UMPS	-0.66	0.28
8130129	NUP43	-0.46	0.28
8002919	KARS	-0.46	0.28
8001371	NA	-0.39	0.28
8132960	NA	-0.66	0.28
8176191	HMGN1	-0.53	0.27

7915130	SF3A3	-0.58	0.27
8151942	HRSP12	-0.66	0.27
8002999	GCSH	-0.74	0.27
8031646	LOC100128252	-1.14	0.27
7989516	HERC1	0.37	0.27
7929901	C10orf2	-0.81	0.26
7990361	UBL7	-0.56	0.26
8027254	ZNF90	-0.93	0.26
8147262	OTUD6B	-0.58	0.26
7935002	SRP9	-0.34	0.26
7936320	RPL13AP6	-0.53	0.26
7983890	GCOM1	1.69	0.25
7960143	ZNF84	-0.61	0.25
7917906	RPL7	-0.97	0.25
7927215	ALOX5	2.07	0.24
8048171	PK155	-0.71	0.24
8112570	MRPS27	-0.60	0.24
8117572	ZNF391	-1.06	0.24
8153930	ZNF16	-0.52	0.24
7929243	NHP2	-0.78	0.24
8100085	GNPDA2	-0.77	0.24
8169868	UTP14A	-0.56	0.24
8000236	CDR2	0.39	0.23
8016825	COX11	-0.51	0.23
8073680	NA	0.99	0.23
7950654	ALG8	-0.72	0.23
7916562	HNRNPA1	-0.57	0.22
7989365	RORA	1.22	0.22
8130403	NA	-0.63	0.22
7990700	WDR61	-0.57	0.22
8067822	IGHV1OR21-1	0.74	0.22
7972867	PCID2	-0.60	0.21
7982620	EIF2AK4	-0.47	0.21
8121418	SMPD2	-0.50	0.21
8121757	HSF2	-0.45	0.20
7938263	EIF3F	-1.20	0.20
8098904	SLBP	-0.51	0.20
8062444	BPI	4.64	0.19
8059770	TIGD1	-0.65	0.19
7984008	NA	-1.07	0.19
8103309	NA	-0.88	0.19
7975971	SAMD15	-0.45	0.18
8048523	DNAJB2	0.53	0.18
8096771	OSTC	-0.51	0.18
7932744	ARMC4	-0.91	0.18
7920123	S100A10	1.45	0.18
8046360	METAP1D	-0.93	0.18
7940349	CCDC86	-0.44	0.18
8131661	RPL21	-0.61	0.17
8071332	RANBP1	-0.60	0.17
7990674	CIB2	-0.79	0.17
7995539	NOD2	0.88	0.17

8065569	BCL2L1	1.13	0.16
8175393	ARHGEF6	-0.38	0.16
7959052	RFC5	-0.64	0.16
8178939	WDR46	-0.52	0.16
8173912	RPSAP15	-0.58	0.16
7901460	GPX7	-0.87	0.16
8112622	GFM2	-0.48	0.15
8103289	PLRG1	-0.37	0.15
8105801	SLC30A5	-0.54	0.15
7985224	TBC1D2B	0.77	0.15
8123695	PECI	-0.61	0.14
7981730	IGLJ3	3.23	0.13
8154359	RPL18A	-0.56	0.13
8082816	SRPRB	-0.74	0.13
8048340	RQCD1	-0.43	0.13
7956401	SHMT2	-0.69	0.13
7906662	UFC1	-0.49	0.13
8177601	MCCC2	-0.60	0.12
7995574	HNRNPA1	-0.56	0.12
7945071	FOXRED1	-0.57	0.12
7954061	NA	-0.55	0.12
8083260	CPA3	-1.88	0.12
8039212	LILRB2	1.68	0.11
8080419	GNL3	-0.80	0.11
7969703	IPO5	-0.64	0.11
8102877	CLGN	-1.16	0.11
8079563	DHX30	-0.39	0.11
8062023	MAP1LC3A	0.39	0.11
8045171	IMP4	-0.54	0.11
8041508	QPCT	1.60	0.10
8043431	IGKC	3.67	0.10
8063115	MMP9	3.56	0.09
8031374	FCAR	2.53	0.09
8025973	ZNF700	-0.43	0.09
8093096	TCTEX1D2	-0.58	0.09
8086498	KIAA1143	-0.61	0.08
8158998	SNORD36C	-0.79	0.08
8089000	CGGBP1	-0.44	0.08
8131583	BZW2	-0.82	0.08
7967987	MRP63	-0.67	0.08
8106107	PTCD2	-0.67	0.08
8152582	DSCC1	-0.66	0.07
8151871	CCNE2	-0.72	0.07
7965846	CCDC53	-0.51	0.07
8180297	NA	-0.44	0.07
7959354	BCL7A	-0.52	0.07
8005943	RPL23A	-0.77	0.06
7926207	CDC123	-0.38	0.06
7951325	DCUN1D5	-0.52	0.05
8166580	NA	-0.69	0.05
8133690	MDH2	-0.59	0.05
7906720	FCER1G	2.33	0.05

8095269	POLR2B	-0.35	0.05
8124430	HIST1H1D	-0.56	0.04
8039017	ZNF816	-0.61	0.04
8033801	ZNF562	-0.53	0.04
7952869	THYN1	-0.46	0.04
8023868	LOC400657	-0.40	0.04
8015741	AARSD1	-0.39	0.04
8052413	NA	-0.41	0.04
7981732	IGHV4-59	2.75	0.03
8111814	RPL37	-0.45	0.03
7969640	CLDN10	-1.35	0.03
8028186	ZNF146	-0.78	0.03
8019308	MAFG	0.52	0.03
8054329	RNF149	0.84	0.03
8081277	NIT2	-0.66	0.03
8046306	GORASP2	-0.46	0.02
8180196	NA	1.46	0.02
8032588	C19orf77	-0.59	0.02
7920317	ILF2	-0.49	0.01
8046815	ZNF804A	-1.05	0.01
8090678	MRPL3	-0.62	0.01
8065762	PIGU	-0.60	0.01
8089034	ARMC10	-0.64	0.01
7977749	METTL3	-0.54	0.00