Analysis of Mice Lacking DNaseI Hypersensitive Sites at the 5’ End of the IgH Locus

Introduction

The variable region of an immunoglobulin heavy chain (IgH) is assembled from V (variable), D (diversity), and J (joining) gene segments that lie upstream of several IgH constant (C) region exons in a process called V(D)J recombination [1]. The mouse IgH locus contains large numbers of V\textsubscript{H} segments and multiple D and J\textsubscript{H} segments but an individual IgH V(D)J exon is assembled from only one V\textsubscript{H}, one D, and one J\textsubscript{H} segment. V(D)J recombination of the IgH locus takes place in pro-B cells in an ordered way such that D to J\textsubscript{H} recombination precedes V\textsubscript{H} to DJ\textsubscript{H} recombination [2]. In this regard, activation of the IgH locus is thought to progress in a stepwise manner [3]. D to J\textsubscript{H} rearrangement efficiently occurs on both alleles, however, allelic exclusion ensures that VH to DJ\textsubscript{H} recombination results in rearrangement efficiently occurs on both alleles, however, allelic exclusion ensures that VH to DJ\textsubscript{H} recombination results in expression of a functional heavy chain (HC) from only one of the two alleles [4]. Mature B-cells can undergo further alterations of their HCs. IgH class switch recombination (CSR) causes expression of different immunoglobulin isotypes which confer different effector functions. During this recombination process one of several sets of downstream C\textsubscript{H} exons replaces the C\textsubscript{J} exons and the intervening sequence is deleted from the chromosome, which results in expression of a new C region without changing the specificity of the IgH variable region [5].

A large effort has been made to elucidate mechanisms of IgH locus regulation and a number of cis-regulatory elements have been described and characterized. The IgH intronic enhancer (E\textsubscript{I}) resides in the J\textsubscript{H} – C\textsubscript{H} intron and was shown to be necessary for efficient V(D)J recombination by promoting both D to J\textsubscript{H} and V\textsubscript{H} to DJ\textsubscript{H} recombination [6,7]. Downstream of the C\textsubscript{H} genes at the very 3’ end of the IgH locus a cluster of DNaseI hypersensitive sites was described, termed 3’ IgH regulatory region (3’IgH RR). So far two main functions have been assigned to this regulatory region: the 3’IgH RR plays an important role in promoting CSR to most IgH isotypes, and the 3’IgH RR was shown to be necessary for high level expression of the functionally assembled HC gene from the promoter 5’ of the V\textsubscript{H}DJ\textsubscript{H} exon [8].

An additional potential regulatory region was identified at the 5’ end of the IgH locus, consisting of four DNaseI hypersensitive sites [9]. One of these sites, HS1, was shown to be pro-B cell specific, the stage during which IgH V(D)J recombination takes place, and was suggested to include binding sites for the transcription factors PU.1, Pax5 and E2A [9]. These observations led to the suggestion that this region might represent a new regulatory region for IgH rearrangements. In this regard, the 5’ end of the IgH locus is an attractive location for a regulatory element because it would not be deleted during the course of V(D)J recombination, and it might explain control of several unresolved phenomena in the IgH locus. Among these is the regulation of V\textsubscript{H} germline transcripts as so far
no cis-regulatory element has been identified that controls activity of the bulk of unrearranged $V_{H}$ promoters. Furthermore, it is not known how it is achieved that proximal and distal $V_{H}$ segments are activated independently or why usage of distal versus proximal $V_{H}$ gene families varies significantly.

Here we report the targeted deletion of the pro-B cell specific 5’$IgH$ HS1 as well as combined deletion of HS1, HS2, HS3a,b in mice. We analyzed potential implications on B cell development, V(D)J recombination, and IgH CSR.

Methods

Targeted deletion of 5’$IgH$ DnaseI hypersensitive sites in ES cells and generation of mutant mice

All mouse were handled in strict accordance with good animal practice as defined by the relevant national and/or local animal welfare bodies, and all animal work was approved by Animal Research of Children’s Hospital Boston (Protocol # 08 11 1253R). The RHS1 targeting vector was assembled in pLNTK [10]. As a 5’ homology arm a 2.2 kb PCR product was generated with primers 5’ GTGACCGAGTTAGGAGGATACACAAC 3’ and 5’ GTGACCATTTGGAAACACAGAATCTCG 3’ containing a Sall site at their 5’ ends, which facilitate cloning of the PCR product into the Sall site of pLNTK. As a 3’ homology arm a 7.3 kb AatII - Apal fragment was blunt end cloned into the Xhol site of pLNTK. The R3’HSs targeting vector was generated by blunt end cloning a 4.4 kb EcoRI fragment into the Sall site of pLNTK as a 5’ homology arm, and a 7.0 kb KpnI fragment into the Xhol site as the 3’ homology arm. Correct targeting events and locoP deletion events were confirmed by Southern blotting (Fig 1).

Probe 1 is a 830 bp PCR product amplified with primers 5’ GTCGACGGATTTAGGAGGATACACAAC 3’ and 5’ GTACCATTTGGAAACACAGAATCTCG 3’. Probe 2 is a 1.2 kb PstI – EcorI fragment 5’ of HS2. Probe 3 is a 0.8 kb PstI – XbaI fragment about 11 kb 3’ of HS3b. To confirm single integration of the targeting vectors a 525 bp Neo5 probe was used, amplified with primers 5’ GCAGCCGATTGAGGATACACAAC 3’ and 5’ GTTCGGCTGGCGCGAGCCCC 3’.

EF1 heterozygous $IgH^{+/w}$ embryonic stem (ES) cells, generated in the Alt laboratory, were transfected with PvuI linearized RHS1 targeting vector to obtain RHS1/+ ES cells. To obtain RHS1/+ ES cells, the PGK-Neo5 cassette was deleted by applying a Cre – expressing adenovirus vector. AHS1/+ ES cells were transfected with PvuI linearized R3’HSs targeting vector to obtain R3’HSs/+ ES cells. R3’HSs/+ ES cells were selected for homozygocity of the targeted allele through increasing concentration of G418 to obtain R3’HSs/+ R3’HSs ES cells. Cre – loxP mediated deletion of the PGK-Neo5 cassette resulted in AHSs/AHSs ES cells. Targeted ES cells were injected into Rag2-/- blastocysts to obtain RDBC chimera [11] or into C57BL/6/blastocysts to obtain chimeras that could be crossed to 129Sv mice to achieve germline transmission of the targeted allele.

B cell hybridomas

CD43 splenocytes were isolated by MACS, cultured with LPS or IL4/α-CD40, and analyzed by flow cytometry as described previously [13].

RT-PCR analysis

RNA was extracted using TriPure Isolation Reagent (Roche). 200 ng – 1 µg of total RNA was reverse transcribed for one hour at 50°C using random hexamers (Roche) and Superscript III (Invitrogen) reverse transcriptase. PCR was performed at 94°C for 4’, 30–39 cycles of 94°C for 30’, annealing temperature (Table S1) for 30’, 72°C for 30’, followed by 72°C for 5’. cDNA input amount was normalized upon PCR amplification of β-actin cDNA. PCR products were visualized on ethidium bromide gels and/or subsequently transferred to nylon membranes and visualized with end labeled oligonucleotide probes (Table S1).

Flow cytometry and cell sorting

Single cell suspensions from spleen, thymus, or bone marrow were stained in PBS 2% FBS with various antibodies: FITC-αIgM, PE-Cy5-αB220, PE-αCD8a, PE-αCD43, FITC-αLy9.1, APC-αIgM, APC-Cy7-αB220 (BD Pharmingen), PE-αAA4.1, FITC-αCD4 (eBioscience). FACS analysis was performed on a FACSCalibur (BD Biosciences) and a FACSaria (BD Biosciences) apparatus. Cell sorts were performed on a FACSaria (BD Biosciences) apparatus.

Results

Generation of mice with targeted deletion of 5’$IgH$

DnaseI hypersensitive sites

To determine the in vivo function of the cluster of DnaseI hypersensitive sites described at the 5’ end of the IgH locus [9] we first replaced a ~340 bp Bcl-1 – AatII fragment, harboring HS1, with a loxp flanked PGK-Neo5 cassette. All targeting experiments were performed in heterozygous $IgH^{+/w}$ EF1 ES cells which have the advantage that $IgH^{+}$ (129 strain) and $IgH^{w}$ (C57BL/6 strain) alleles can be distinguished by antibodies against the different allootypes or by detection of restriction fragment length polymorphisms (RFLP). Targeting vector homology arms were cloned from 129 strain genomic DNA, resulting in correct targeting events only on the $IgH^{w}$ allele. In heterozygous targeted ES cells, the $IgH^{w}$ allele always remained in the untargeted wildtype configuration.

Targetings were performed with the RHS1 targeting vector (Fig 1A) to obtain the RHS1 allele and, upon cre/loxP deletion, PCR assay for V(D)J rearrangements

Pro-B cells (IgM+ B220+ CD43+), pre B-cells (IgM+ B220+ CD43+), and double positive T-cells (B220+ CD4+ CD8+) were isolated by FACS on a FACSaria (BD Biosciences) and genomic DNA was extracted. 30 ng DNA or 3-fold dilutions were analyzed by PCR for DJb-Jb, Vbx-Jb, and Vb2-Jb rearrangements with primers listed in Table S1. Input DNA amounts were normalized upon PCR amplification within DLG5. PCR was performed at 95°C for 4’, 30 cycles of 95°C for 30’, 60°C for 90’, and 72°C for 2’, followed by 72°C for 3’. PCR products were transferred from ethidium bromide gels to nylon membranes and visualized with end labeled oligonucleotide probes (Table S1). CDR 3 lengths were generated from IgH VDH rearrangements from mature B cells using oligonucleotides for V558 and JH4.
Figure 1. Targeting strategy for the generation of the RHS1, ΔHS1, and ΔHSs alleles. (A) the wildtype (wt) IgH locus and its 5' flanking region are shown. VH, DH, JH indicate representative IgH V, D, and J segments. Exons 1, 2, and 3 of Zfp386 are shown as grey rectangles, DNaseI hypersensitive sites HS1, HS2, HS3a, and HS3b are shown as black ovals. Correct targeting events of the RHS1 targeting vector were identified by Southern blotting on BglII digested ES cell DNA using probe 1, which results in a 15.8 kb band (lane 1) in addition to the 14.2 kb wildtype band (lane 2). Cre - loxP (black triangles) mediated deletion of the PGK-NeoR cassette (NeoR) from the RHS1 allele results in the ΔHS1 allele. Deletions were identified by Southern analysis of SacI digested DNA utilizing probe 2. A targeted clone before Cre - mediated deletion exhibits a 6.7 kb RHS1 band and a 5.1 kb wildtype band (lane 3). Upon deletion of the PGK-NeoR cassette, a 4.8 kb ΔHS1 band and a 5.1 kb wildtype band are visible (lane 4). Lane 5 shows untargeted wildtype DNA. (B) The ΔHS1 allele was targeted with the R3'HSs targeting vector to introduce a PGK-NeoR cassette flanked by loxP sites. Correct targeting events were confirmed by Southern blotting on SphI digested ES cell DNA with probe 1, resulting in a 2.6 kb band for the wildtype IgHb allele and a 7.2 kb band for the R3'HSs, the targeted IgHa allele (lane 6). Cre - mediated recombination between the first and the third loxP site generates the ΔHSs allele (14.1 kb, lane 8). Homozygous R3'HSs ES cells were generated under increasing concentrations of G418, resulting in a single 7.2 kb R3'HSs band (lane 7). Southern analysis on SphI digested DNA with probe 3 confirms correct targeting events of the R3'HSs targeting vector. ΔHS1 ES cells exhibit a 15.7 kb ΔHS1 band and a 26.3 kb band for the wildtype IgHb allele (lane 10). All targeting events occurred on the IgHa allele, whereas the IgHb allele remained in wildtype configuration. Drawings not to scale. B - BglII; S - SacI; P - SphI.

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theΔHS1 allele. Correct targeting events (Fig1) and single integration of the targeting vector (Figure S1) were confirmed by Southern blotting. Subsequently, targeted ES cells were injected into Rag2-/- blastocysts to obtain Rag-deficient blastocyst complementation (RDBC) chimeras, and into wildtype blastocysts to generate mice that carry the RHS1 or ΔHS1 allele in their germline. In order to delete all four hypersensitivity sites (HS1, HS2, HS3a, and HS3b), ES cells containing the ΔHS1 allele were targeted with the R3HS2, HS3a, and HS3b), ES cells containing the ΔHS1 allele were targeted with the R3HS1 targeting vector to obtain the R3HS1 allele (Fig. 1B). Cre/loxP recombination between the loxP site originating from the ΔHS1 allele and the loxP site 3’ of the PGK-Neo cassette results in the replacement of a 8.9 kb region, harboring all described 5’ IgH DNAse hypersensitive sites, with a single loxP site, referred to as the ΔHS1 allele. Germline transmission could not be achieved for either of the R3HS1 or ΔHS1 heterozygous ES cell lines. Therefore, we placed ES cells containing the R3HS1 allele under increasing concentrations of G418 to select for homozygous mutant ES cells. The homozygous mutant ES cells were subsequently subjected to cre/loxP recombination to delete the Neo gene and generate ES cells homozygous for the ΔHS1 allele. The homozygous mutant ΔHS1 ES cells were injected into Rag2-/- blastocysts, and chimeras generated by RDBC and lymphocytes were analyzed.

Development of homozygous RHS1, ΔHS1, and ΔHSs lymphocytes

Lymphocytes of different developmental stages can be identified by FACS analysis of cells from lymphoid tissues such as bone marrow, thymus, or spleen. We analyzed 8 week old wildtype mice, homozygous RHS1, and homozygous ΔHS1 mice that carry the mutant alleles in their germline, as well as lymphocytes from RDBC chimeras generated from homozygous ΔHSs ES cells (Fig. 2). In wildtype bone marrow, pro-B cells can be identified as IgM B220-CD43low and pre-B cells as IgM+ B220+ CD43low cells, respectively. Defects in B-cell development can be revealed by the increase or decrease of certain lymphocyte populations. In this regard, impaired IgH V(D)J recombination leads to an accumulation of pro-B cells and to reduced numbers of pre-B cells [7]. We performed FACS analyses of bone marrow from three mice of each genotype to measure the percentage of pro- and pre-B cells in the lymphocyte gate. These analyses revealed the average percentage (± standard deviation) of pro-B and pre-B cells, respectively of B220-CD43low events in the total lymphocyte gate were 14±2 and 50±20 for wildtype, 9±3 and 56±6 for RHS1, and 9±3 and 42±11 for ΔHS1 mice (Fig. 2A). Thus, there were no obvious differences in early B-cell development in wildtype and mutant mice. However we cannot exclude minor developmental defects not readily detectable by such analyses. Homozygous mutant ΔHS1 bone marrow cells were analyzed in a similar fashion, but only Ly9.1+ cells were included in the analysis. Ly9.1 is exclusively expressed on cells derived from the ΔHS1 ES cells but not on cells derived from the Rag2-/- blastocyst. The presence of a large compartment of blastocyst derived Rag-deficient pro-B cells in the bone marrow can interfere with development of ES cell derived B-lymphocytes. However, FACS analysis of ΔHSs bone marrow B cells indicated the presence of both pro- and pre-B cells and did not suggest a block in B-cell development (Fig. 2A).

Next we analyzed spleens for IgM+ B220+ AA4.1+ transitional B-cells and IgM+ B220- AA4.1+ mature B-cells (Fig. 2B). In homozygous RHS1, and homozygous ΔHS1 mice transitional (19.7%–27.5%) and mature (65.3%–72.7%) B-cell compartments similar to wildtype were identified, whereas, in spleens from RDBC chimeras generated from homozygous ΔHS1 ES cells strongly reduced numbers of transitional B-cells were observed (6.44%). This reduction in the transitional B-cell compartment compared to the mature B-cell compartment (75%) might be due to overall reduced numbers of developing B cells in the obtained RDBC chimeras and to the accumulation of mature B-cells in the periphery of these mice and not to a defect in B cell development. Finally, we observed normal development of T-lymphocytes in the thymi of wildtype, homozygous RHS1, and homozygous ΔHS1 mice as well as RDBC chimeras generated from homozygous ΔHSs ES cells (Fig. 2C).

The ΔHS1, RHS1, and ΔHSs alleles show no significant defect in V(D)J recombination

The data indicating that HS1 is pro-B cell specific and contains binding sites for the transcription factors PU.1, Pax3, and E2A led to the suggestion that HS1 could be involved in regulation of V(D)J recombination at the IgH locus [9]. We utilized a PCR based assay to assess V(D)J recombination efficiencies in developing lymphocytes from mice with homozygous deletion of RHS1. FACS-sorted pro-B cells (IgM+ B220-CD43low) and pre-B cells (IgM- B220+CD43low) from bone marrow and double positive (DP) T-cells (B220+CD43low) from thymus were analyzed for D to JH, V to DJh, V to Jc, and Vc to Jc rearrangements. Intensities of PCR bands for DαQ52 to JH (Fig. 3A) and DSP to JH rearrangements (Fig. 3B) were comparable in pro-B cells, pre-B cells, and DP T-cells from wildtype, homozygous RHS1, and homozygous ΔHS1 mice indicating that deletion of the pro-B cell specific HS1 site does not detectably affect the D to JH recombination step. DNA input amounts were normalized to the presence of a genomic sequence within the murine DLG5 gene (Fig. 3H).

It was speculated that HS1 might regulate the differential activation of distal versus proximal VHV families [9]; therefore, we analyzed the rearrangement efficiencies of the proximal VHV183 family (Fig. 3C), the distal VHV558 family (Fig. 3D), and the distal most VHV segment VHV558.55 (Fig. 3E). We found that pro-B cells and pre-B cells from wildtype, homozygous RHS1, and homozygous ΔHS1 mice rearranged the proximal VHV183 family at similar levels (Fig. 3C). Also, the distal family VHV558 (Fig. 3D) as well as the distal most VHV segment VHV558.55 (Fig. 3E) rearranged at comparable efficiencies in pro-B cells and pre-B cells from the three different genotypes. VHV to DJH recombination was absent in DP T-cells from wildtype, homozygous RHS1, and homozygous ΔHS1 mice as the VHV to DJH recombination step is restricted to the B-lineage (Fig. 3C, D, E). These data show that HS1 is not
Figure 3. V(D)J recombination in ΔHS1 and RHS1 mice. Pro-B cells, pre-B cells and double positive (DP) T-cells from wildtype 129 mice, from homozygous ΔHS1, and homozygous RHS1 mice were sorted by FACS. 5-fold dilutions of genomic DNA were subjected to PCR analysis. IgH V(D)J recombination efficiencies were assessed using a reverse primer downstream of JH4 and a forward primer recognizing DQ52 (A), DSPs (B), the VH7183 family (C), the VH558 family (D), or the VH558.55 segment (E). Rearrangements can occur to JH1, JH2, JH3, or JH4 as indicated. GL indicates PCR product from germline configuration. Igκ rearrangements were quantified (F), rearrangements can occur to Jκ1, Jκ2, Jκ3, or Jκ4 as indicated. Igλ rearrangement efficiency was analyzed (G). Bands correspond to Vλ2 - Jλ2, Vλ3 - Jλ3, or Vλ1 - Jλ1 rearrangements as indicated. DNA input was normalized to DLG5 PCR products (H).

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necessary for rendering the distal part of the VH cluster accessible and, therefore, suggest that HS1 does not play a major role in regulation of usage or accessibility of distal versus proximal VH families.

Recently, it has been shown that IgH and Igk loci can colocalize during B-cell development, mainly at the pre-B cell stage, and it was suggested that this colocalization induces decontraction of the IgH locus [14]. We therefore performed an assay to evaluate Igk (Fig. 3F) and Igk (Fig. 3G) V(D)J recombination efficiencies. Both Igk and Igk loci show similar V(D)J recombination levels in the analyzed developing B cells from wildtype, homozygous RHS1, and homozygous DHS1 mice, while light chain rearrangements were absent in DP T-cells from the three different genotypes. Therefore, we conclude that deletion of HS1 does not markedly affect Ig light chain gene rearrangements.

As an independent method to evaluate D to JH and VH to DJH recombination efficiencies, we generated clonal hybridoma lines from splenic B-cells of IgH<sup>ab</sup> heterozygous RHS1, RHS1 mice carrying the mutant allele in their germline and of RDBC chimeras generated from heterozygous AHSs ES cells (Table 1). In each case the IgH<sup>+</sup> allele was the mutant allele while the IgH<sup>+</sup> allele was the wildtype allele. In splenic B-cells, one allele exists as a functional V<sub>H</sub>D<sub>JH</sub> rearrangement, while the second allele can either be in germline configuration or it exists as a DJH or a nonproductive V<sub>H</sub>D<sub>JH</sub> rearrangement. The rearrangement status of the second IgH allele was assessed by Southern blot analysis. Consequently, hybridomas expressing the mutant IgH<sup>+</sup> allele can be analyzed for rearrangement efficiency of the wildtype IgH<sup>+</sup> allele, and vice versa, in hybridomas expressing the wildtype IgH<sup>+</sup> allele, the rearrangement status of the mutant IgH<sup>+</sup> allele can be assessed.

Wildtype B cells undergo D to JH rearrangements on both alleles; but still, consistent with earlier studies, about 5% of hybridomas harbor an IgH allele in germline configuration which presumably originates from tripartite fusions involving non-B-cells [12] (not shown). The number of mutant alleles in germline configuration was not increased compared to wildtype indicating that RHS1, RHS1, and DHS alleles can undergo efficient D to JH recombination (not shown). In 30–60% of wildtype B-cells the nonproductive allele is in DJH configuration; whereas in 40–50% the nonproductive allele is in V<sub>H</sub>D<sub>JH</sub> configuration [13]. An increased percentage of DJ<sub>H</sub> alleles could indicate less efficient VH to DJH recombination: in contrast, an increased percentage of V<sub>H</sub>D<sub>JH</sub> alleles might indicate a break in allelic exclusion. IgMa expressing hybridomas generated from B-cells heterozygous for RHS1, RHS1, and DHS were analyzed for their rearrangement status of the wildtype IgM<sup>+</sup> allele and show ratios of DJH (56%–61%), and V<sub>H</sub>D<sub>JH</sub> alleles (39%–44%) in the expected range (Table 1). IgM<sup>+</sup> expressing hybridomas were analyzed for the

### Table 1. AHS1, RHS1, and AHSs hybridoma analysis.

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<td>AHS1</td>
<td>IgM&lt;sup&gt;+&lt;/sup&gt; 66 (61%) 43 (39%)</td>
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<td>RHS1</td>
<td>IgM&lt;sup&gt;+&lt;/sup&gt; 52 (57%) 39 (43%)</td>
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<td>AHSs</td>
<td>IgM&lt;sup&gt;+&lt;/sup&gt; 62 (56%) 49 (44%)</td>
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Hybridomas were generated from heterozygous IgM<sup>ab</sup> AHS1, RHS1, and AHSs splenic B-cells. In each case, IgM<sup>+</sup> is the wildtype allele and IgM<sup>+</sup> is the mutant allele. IgM<sup>+</sup> expressing hybridomas (IgM<sup>+</sup>) and IgM<sup>+</sup> expressing hybridomas (IgM<sup>+</sup>) of each genotype were analyzed for the rearrangement status of their nonproductive allele. Numbers for D to JH rearranged alleles (DJ) and nonproductive V<sub>H</sub> to DJH rearranged alleles (VDJ-) are shown.

Figure 4. IgM<sup>+</sup> versus IgM<sup>+</sup> expression in AHS1, RHS1, and AHSs B cells. Heterozygous IgM<sup>ab</sup> B-cells from spleen (A) and bone marrow (B) of 129 wildtype (wt) or AHS1, RHS1, and AHSs RDBC chimeras were analyzed IgMa and IgMb expression. In AHS1, RHS1, and AHSs B-cells the IgM<sup>+</sup> allele is in wildtype configuration whereas the IgM<sup>+</sup> allele is the mutant allele.

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Figure 4. IgM<sup>+</sup> versus IgM<sup>+</sup> expression in AHS1, RHS1, and AHSs B cells. Heterozygous IgM<sup>ab</sup> B-cells from spleen (A) and bone marrow (B) of 129 wildtype (wt) or AHS1, RHS1, and AHSs RDBC chimeras were analyzed IgMa and IgMb expression. In AHS1, RHS1, and AHSs B-cells the IgM<sup>+</sup> allele is in wildtype configuration whereas the IgM<sup>+</sup> allele is the mutant allele.

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rearrangement status of their mutant IgM* allele. \textit{RHS1}, \textit{AHS1}, and \textit{AHSs} alleles do not show significantly increased or decreased (Fisher’s exact test) rearrangement ratios compared to wt alleles, as 52\%–69\% of mutant alleles were in DJH configuration while 31\%–48\% were in V\textsubscript{H}DJH configuration.

FACS analysis was performed on B-cells from spleens (Fig. 4A) and bone marrow (Fig. 4B) of RDBC chimeras generated from heterozygous \textit{RHS1}, \textit{AHS1}, and \textit{AHSs} ES cells. IgM* expressing populations, representing the targeted allele, and IgM+ expressing populations, representing the wildtype allele, were of similar size both in bone marrow and in spleen from \textit{RHS1}, \textit{AHS1}, and \textit{AHSs} chimeras, suggesting that the \textit{RHS1}, \textit{AHS1}, and \textit{AHSs} alleles can undergo V(D)J recombination at the IgH locus at similar efficiencies as wildtype alleles.

The \textit{AHS1}, \textit{RHS1}, and \textit{AHSs} alleles do not affect allelic exclusion

FACS analysis of wt B cells from spleen (Fig. 4A) and bone marrow (Fig. 4B) shows distinct populations of similar size for B cells that are single positive for either IgH or IgH, but intact allelic exclusion prevents the appearance of an obvious IgH, IgH- double producing population. Similarly, RDBC chimeras generated from heterozygous \textit{RHS1}, \textit{AHS1}, and \textit{AHSs} ES cells exhibited IgH+ or IgH single positive B-cell populations of similar size in spleen (Fig. 4A) and bone marrow (Fig. 4B) but no IgH+, IgH- double producing population. These data indicate that the deleted sequences of the targeted alleles do not contain a regulatory element that is necessary for implementation of allelic exclusion.

Furthermore, data from hybridoma analysis (Tab. 1) support this notion as in the case of a break in allelic exclusion increased numbers of hybridomas with V\textsubscript{H} to DJH rearrangements on both alleles would be expected. Such an increase compared to wildtype alleles could not be observed (Tab. 1), which indicates intact allelic exclusion of \textit{RHS1}, \textit{AHS1}, and \textit{AHSs} alleles.

The 5’IgH DNaseI hypersensitive sites are not required for efficient class switch recombination

To assess a potential effect of the 5’IgH DNaseI hypersensitive sites on CSR, B-cells were stimulated to undergo CSR and analyzed by FACS (Fig. 5). Stimulation with LPS induces IgH isotype switching to \gamma\textsubscript{3}, while stimulation with IL4+ αCD40 promotes switching to \gamma\textsubscript{1}. B-cells from AID-/- mice served as negative controls, while wildtype B-cells represented a positive control and therefore switched to the appropriate isotypes under LPS or IL4+ αCD40 stimulation. CSR in homozygous \textit{AHSs} B-cells occurs at similar levels as in wildtype B-cells implying that the cluster of 5’IgH DNaseI hypersensitive sites is not required for efficient CSR to \gamma\textsubscript{1} (Fig. 5A) and \gamma\textsubscript{3} (Fig. 5B).

Complex phenotypes without an obvious relation to the IgH locus in \textit{AHS1} mice

We performed targeted deletion experiments of the 5’IgH DNaseI hypersensitive sites to test their suggested function in IgH locus regulation. So far no major IgH related phenotype was identified. However, about 20\% of homozygous \textit{AHS1} mice develop a complex neurological phenotype and die at 3–5 weeks of

Figure 5. Ig class switch recombination in absence of the 5’IgH DNaseI hypersensitive sites. MACS purified splenic B-cells were stimulated in culture with LPS or IL4+ αCD40 as indicated. FACS analysis shows B-cells that underwent CSR as B220+ IgG1* or B220+ IgG3* cells, respectively. AID-/- B-cells served as negative controls, wildtype (wt) 129 B-cells as positive controls. Homozygous \textit{AHSs} B-cells were isolated from RDBC chimeras.

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age, likely due to a lack of food intake. These mice exhibit an abnormal limp grasping phenotype, i.e. mice clasp their front and hind feet almost immediately upon being lifted by their tail (Fig. 6A, B). Furthermore, these mice develop a hydrocephalus, which is already visible at about one week of age and is enlarged over the following weeks (Fig. 6C, D). Histological analysis confirmed the presence of a hydrocephalus, revealed abnormal hindbrain development, and revealed retinal abnormalities (Fig. 6E, F, G). The wildtype retina is organized in a delicate layer system (Fig. 6E): stratum opticum and ganglionic layer (1), inner plexiform layer (2), inner nuclear layer (3), outer plexiform layer (4), outer nuclear layer (5), layer of rods and cones (6), pigment layer (7). In the ΔHS1 mutant mice, the organization of retinal layers is impaired in such a way that nuclei from the outer nuclear layer are aberrantly located in the layer of rods and cones (Fig. 6F). In some more severe cases, rosette formation in the outer nuclear layer is evident (Fig. 6G). Currently, we do not know what causes these phenotypes, but we exclude that this phenotype is caused by a second integration of the targeting vector at an undefined site in the genome (Figure S1). The deletion in the ΔHS1 allele deletes 340 bp within intron 1 of Zfp386. Therefore, misregulation of that poorly described gene might cause the described phenotypes although other possibilities are conceivable.

**Discussion**

This study aimed for elucidating the potential regulatory functions of a cluster of recently described DNaseI hypersensitive sites at the 5’ end of the IgH locus [9]. We performed targeted deletion of either the pro-B cell specific site HS1 (ΔHS1) or deletion of the entire cluster of hypersensitive sites (ΔHSs) in mice or in their lymphocytes, respectively. A potential regulatory element at the 5’ end of the IgH locus was speculated to regulate processes such as IgH allelic exclusion, VH germline transcription, differential accessibility or usage of distal versus proximal VH gene families. Furthermore, it was suggested that the 5’ end of the IgH locus might play a role in positioning the IgH locus in distinct subnuclear compartments [16,17,18], and it was suggested to harbor insulator or boundary capacity [19].

B- and T-lymphocytes homozygous for the ΔHS1, RHS1, and ΔHSs alleles appear to proceed through lymphocyte development in an unimpaired way. Data from RDBC chimeras generated from

Figure 6. Complex phenotypes of homozygous ΔHS1 mice. Homozygous ΔHS1 mice exhibit an abnormal limp grasping phenotype (B) whereas wildtype (wt) mice do not (A). ΔHS1 mice can develop severe hydrocephalus as indicated by arrows in (C) and (D). A wildtype mouse without hydrocephalus is shown in (C). The wildtype retina is organized in distinct layers (E): Stratum opticum and ganglionic layer (1), inner plexiform layer (2), inner nuclear layer (3), outer plexiform layer (4), outer nuclear layer (5), layer of rods and cones (6), pigment layer (7). The retina of homozygous ΔHS1 mice shows external nuclei from the outer nuclear layer (5) in the layer of rods and cones (6) indicated by arrows in (F), or rosette formation of the outer nuclear layer (5) indicated by arrows in (G).

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heterozygous \( \text{AHSI}, \ \text{RHSI}, \ \text{and AHSs} \) ES cells indicated that allelic exclusion is not affected in mutant B-cells and that mutant IgH alleles can undergo efficient V(DJ) recombination of their IgH locus. Furthermore, data from PCR assays to analyze V(DJ) recombination efficiency in mice with HS1 deleted on both alleles supports the notion that HS1 is not necessary for neither the D to JH nor the VH to DJH recombination step. Both proximal and distal VH families as well as the distal most VH segment \( \text{VH556.55} \) rearrange as efficiently as on wildtype alleles. Similarly, IgL loci in HS1 deleted B-cells rearrange at the same efficiency as wildtype IgL loci. Analysis of IgH V(DJ) rearrangement status in hybridomas generated from heterozygous \( \text{AHSI}, \ \text{RHSI}, \ \text{and AHSs} \) B-cells also strengthens the idea that the deleted DNaseI hypersensitive sites would not regulate IgH V(DJ) recombination. We tested for potential alterations associated with DNA end processing during V(DJ) recombination by examining the CDR3 sequence obtained from homozygous \( \text{AHSI} \) B cells and found a distribution in length that was similar to wildtype B cells [20] (Figure S2).

We tested a potential effect of the cluster of DNaseI hypersensitive site on the process of IgH CSR. Assaying class switching upon different in vitro stimulations in wildtype and homozygous \( \text{AHSs} \) B-cells let us conclude that the cluster of 5 IgH DNaseI hypersensitive sites does not play a crucial role in CSR.

The only observed phenotypes so far occurred in homozygous \( \text{AHSI} \) mice and seem to be independent of the IgH locus. \( \text{AHSI} \) mice show abnormal limb grasping indicating a neurological abnormality, \( \text{AHSI} \) mice can develop severe hydrocephalus and exhibit retinal impairments. A possible explanation for these phenotypes is a potential defect in regulation of the zinc finger protein \( \text{Zfp386}. \ \text{AHSI} \) deletes a 340 bp region from intron 1 of \( \text{Zfp386}. \) which might result in different splice forms, impaired expression levels, or expression patterns of this gene.

Overall, our analysis of the deletion of the pro-B cell specific site HS1 or the whole cluster of 5 IgH DNaseI hypersensitive sites did not support the existence of a cis-regulatory function of these elements regarding the IgH locus.

### Supporting Information

**Figure S1** Single integration of the RHS1 targeting vector. The targeting vector (targeting vector RHS1), the targeted locus (RHS1), and the wildtype (wt) IgH locus with its 5’ flanking region are shown. VH, DH, JH indicate representative IgH V, D, and J segments. Exons 1, 2, and 3 of Zfp386 are shown as grey rectangles, DNaseI hypersensitive sites HS1, HS2, HS3a, and HS3b are shown as black ovals, the NeoR specific Southern probe shows a single 16.0 kb band. No bands are visible from untargeted wildtype ES cell DNA (lane 3). M - Fermentas 1 kb ladder.

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**Figure S2** CDR3 length in \( \text{AHSI} \) B cells. Peripheral B cells were isolated from one \( \text{AHSI} \) mouse and a wildtype mouse and amplified for V558-JH4 rearrangements. Heavy Chain CDR3 lengths were calculated as the number of nucleotides between the consensus Cys residue and the Trp residue. 23 individual sequences were analyzed from \( \text{AHSI} \) B cells and 10 from wildtype.

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### Table S1

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### Author Contributions

Conceived and designed the experiments: TP IP PB FWA. Performed the experiments: TP IP. Analyzed the data: TP IP JPM AZ PB. Wrote the paper: TP IP FWA.

### References