Transcriptome and epigenome profile of B cells in patients with Transient Hypogammaglobulinemia of Infancy

Brittany Howell

Hypothesis

Patients with Transient Hypogammaglobulinemia of Infancy (THI) will exhibit delayed loss of methylation in B cell lymphopoiesis genes, resulting in a deficiency of mature B cell subpopulations.

1 Background

Antibodies are a vital component of the adaptive immune system[1]. The production of antibodies occurs when naïve B cells are activated in response to foreign antigens (figure 1). During gestation, maternal antibodies (mAbs) are passed to the foetus through the placenta[2]. At birth, B cells do not fully mature, so as mAbs are degraded, serum antibody concentration decreases[3,4]. Physiologic hypogammaglobulinemia refers to the point when serum antibody concentration reaches its lowest level. In normal infants, the hypogammaglobulinemia subsides as the B cells are able to mature into antibody producing cells, commonly at 4 to 6 months of age[5]. Transient Hypogammaglobulinemia of infancy (THI) is a disorder where regular hypogammaglobulinemia is prolonged or exacerbated then spontaneously alleviated.[5–14]. The mechanism causing low serum immunoglobulin in THI patients is unknown[6].

Cause of THI

Studies investigating THI have found that levels of circulating B cells are normal and subpopulations of B cells are intact[5,11,13–16]. With no obvious B cell deficiency, the cause of THI has been speculated extensively, but no proposed cause has been supported by replicated evidence[9,10,13,15–21]. In regards to genetic inheritance, THI was initially thought to be familial[19]. Soothill[20] proposed that THI was a manifestation of genetic heterozygosity for other immunodeficiency diseases, noting the high number of patients who had immunodeficient relatives. While it remains a possibility, no proceeding studies have shown supporting evidence[13,16,21]. With no obvious deficiencies or genetic links, THI is most often speculated to be caused by some kind of delay in B cell maturation or activation[10,11,22,23].

B cell development

Immunoglobulin deficiency can result from B cell precursors failing to develop into mature B cells or mature B cells failing to differentiate into antibody secreting plasma cells[16]. All antibodies are produced by mature B cells, developed from haematopoietic stem cells in a pathway shown in figure 1. First, the hematopoietic stem cells differentiate into common lymphoid progenitors, which commit to the B cell lineage. B cells gradually rearrange their immunoglobulin genes and differentiate into mature naïve B cells which leave the bone marrow to enter the periphery. Resting naive B cells transit through lymph nodes where they encounter specific antigen, activating them and inducing the germinal centre reaction. Further rearrangement of immunoglobulin genes occurs followed by rapid proliferation and differentiation into plasma and memory cells. Plasma cells produce the antibodies required for humoral immunity. The isotype (IgM/G/A/E) of the antibodies is determined by the environmental signals present at the activated B cell stage.

B lymphocyte differentiation is tightly regulated by transcription factors (TFs) functioning in a complex network of auto-regulation, cross regulation, and positive and negative feedback loops. The transcriptional regulation of B cell development is not a single hierarchical cascade,

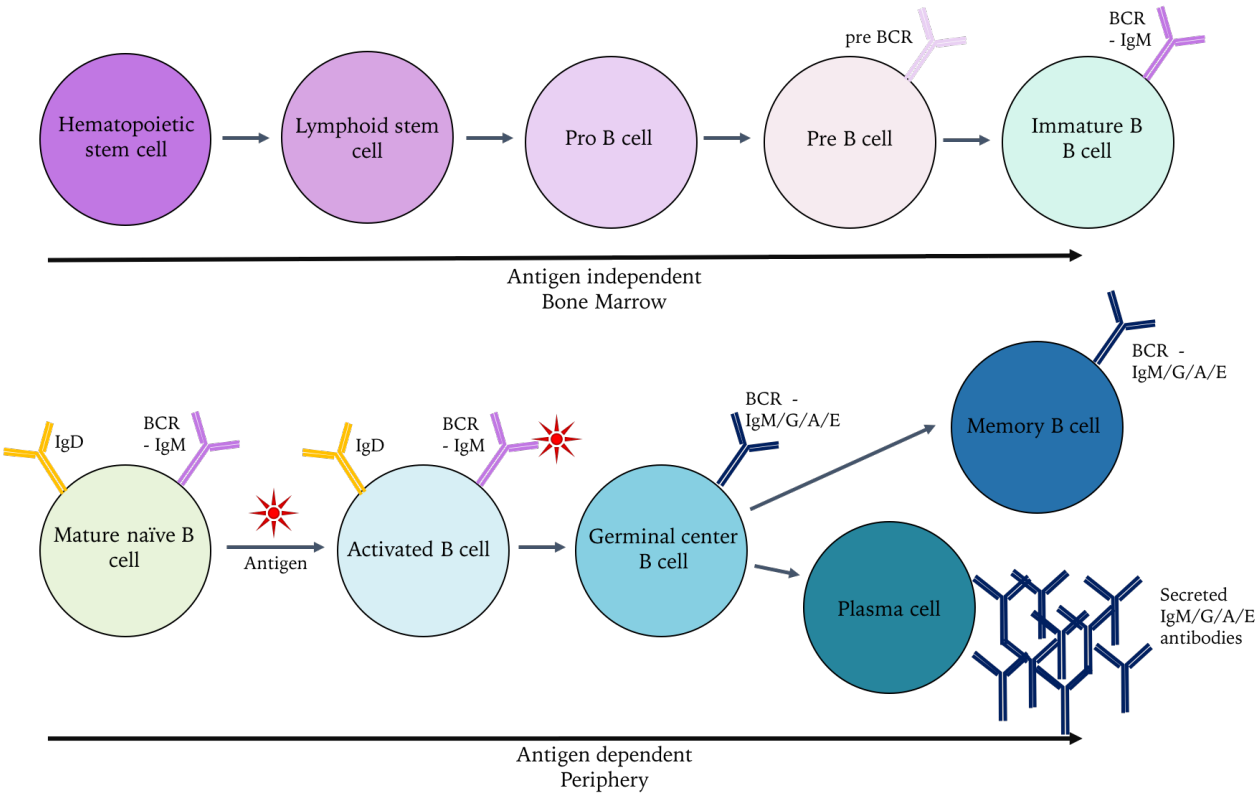


Figure 1: B cell development from hematopoietic stem cell to memory and plasma cells. Phases are shown as antigen independent or dependent and location (bone marrow or periphery) is indicated. IGM/G/A/E indicates option of antibody isotype. BCR: B cell receptor.

many transcription factors work cooperatively to direct the regulation and expression of genes and other TFs (figure 2). Transcription factors prominent in early stages of B cell specification and commitment include E2A, Ebf1, Pax5 and FoxO1. They influence B cell development by promoting changes in chromatin remodelling, facilitating DNA methylation or demethylation and interacting with other factors[24–31]. Ikaros, PU.1, E2A and FoxO1 are also involved in lineage fate determination, but are not restricted to the B cell lineage. Loss of function studies involving the aforementioned TFs show some defect in B cell lineage commitment, resulting in a loss of a B cell subset or the entire B cell lineage[32].

FACS

Previous investigations into THI have claimed that subpopulations of B cells are the same in THI patients as controls[5,11,13–16]. The claim is supported by rosette-formation and single

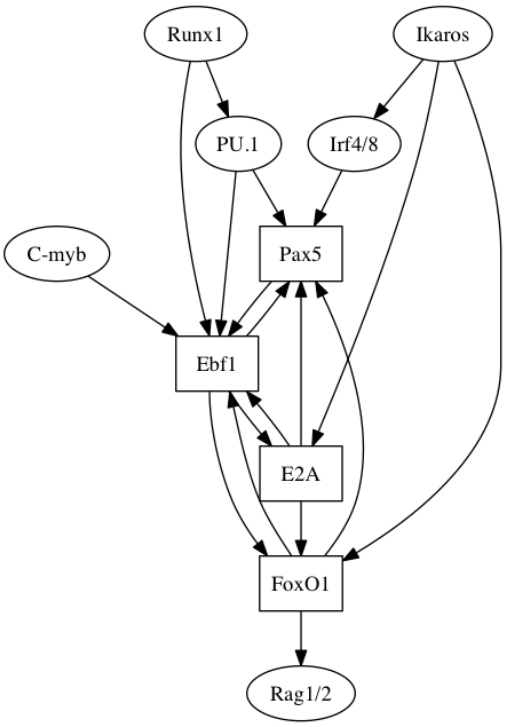


Figure 2: Schematic representation of interactions between early B cell transcription factors. Adapted from Choukrallah and Matthias[32].

or two-colour membrane immunofluorescence studies. The immunofluorescence studies distinguished only between mature and immature B cells, using the observed combinations of surface IgM and IgG. Analysis techniques have improved immensely since 1989, when the most recent study took place. Flow cytometry (FACS) in particular has developed extensively, allowing the measurement of an increasing number of parameters per cell[35]. In a FACS analysis, cells are stained with fluorochrome-conjugated antibodies that bind to cell surface markers or intracellular targets. Cells are then placed into a flow cytometer which passes cells individually through lasers. The light emitted by the lasers excites the fluorochromes on the cell which produces a signal proportional to the concentration of the target[36]. 18-parameter flow cytometry is now routinely used, 30-parameter flow cytometers are becoming commercially available, and 50-parameter flow cytometry is predicted to be available soon[35]. The number of parameters measurable per cell has increased dramatically since 1989, and thence, the potential to distinguish B cell subpopulations is now immensely greater.

1.1 Lineage commitment

Epigenetic modifications act in concert with transcription factors to confer the phenotype of many cell subsets of the immune system[37–39]. A prominent example is the activation and differentiation of the many T cell subsets[40,41]. Confirmation of the T regulatory cell (Treg) lineage relies on stable expression of FOXP3. A substantial amount of evidence suggests that FOXP3 expression itself is not sufficient to establish and maintain the Treg phenotype. In fact, FOXP3 expression occurs in all T cell subsets upon activation[42,43]. The distinguishing factor between Tregs and other subsets is the methylation status of the FOXP3 gene, otherwise known as the Treg-specific demethylated region (TSDR)[44]. When the T cell receptor is engaged in Tregs, demethylation occurs at the TSDR. FOXP3 can then bind to its own gene stabilising expression and hence reinforcing commitment to the Treg lineage. Contrastingly, in other subsets the TSDR remains methylated and so FOXP3 expression is transient[42]. Hence methylation status of key genes can permit lineage commitment.

Aberrant epigenetics have recently been implicated as the cause of common variable immunodeficiency (CVID), a disease similar to THI[45]. CVID is a late-onset primary immunodeficiency characterised by dysfunction or loss of B lymphocytes, blockage of B cell development at pro-B cell stage and decreased immunoglobulin production. Diagnosis most often occurs between the ages of 20 and 40 years, with patients presenting with recurring bacterial infection[46]. RNA-Seq analysis identified 103 genes which were differentially expressed between healthy controls and CVID patients[45]. The most severely down-regulated gene was the transcription factor Pax5. Pax5 is essential to commit a cell to the B cell identity through activation of 170 B cell specific genes and repression of at least 110 lineage inappropriate genes[47–49]. Tallmadge et al.[45] hypothesised that Pax5 is silenced by aberrant epigenetic mechanisms in lymphocyte progenitors. Epigenome analysis revealed that the Pax5 enhancer was hypermethylated. Silencing induced by enhancer methylation would result in a decline in B lymphopoiesis in the bone marrow, followed by a depletion of B cells. Furthermore, that the methylation is epigenetic substantiates the late-onset nature of CVID. The prolonged antibody deficiency

exhibited in THI patients could be the result of dysfunctional B cells. An epigenetic cause such as methylation

2 Summary and experimental aims

- THI is a self-limited disorder characterised by prolonged deficient levels of serum antibody IgG which gradually subside with no obvious stimulus[5–15,20,50].
- Furthermore, the lack of evidence supporting a genetic basis suggests that the cause of THI is not within the genome[13,16,21].
- Tallmadge et al.[45] showed that in CVID, aberrant methylation of key B cell maturation region, Pax5, was the cause of late onset dysfunctional B lymphopoiesis.
- It is possible that the limited IgG production exhibited in THI is caused by delayed B cell maturation as a result of inappropriate methylation.

2.1 Experimental aims

Aim 1: Using FACS, describe the B cell subpopulations in THI patients and normal individuals throughout early development.

Aim 2: Using whole genome bisulphite sequencing, identify regions of the genome which are differentially methylated in THI samples and controls.

Aim 3: Using RNA-Seq, identify differentially expressed regions in THI samples.

3 Data collection and management

3.1 Collecting samples

Members from the Pediatric Department at Wolfson Medical centre have kindly agreed to provide whole blood and tonsil samples they have collected from 26 THI patients (see table 1). Further peripheral blood, bone marrow and tonsil samples will be obtained from the Women's and Children's Hospital Immunodeficiency clinic. Blood will be taken from THI patients between initial presentation and normalisation of IgG levels. Bone marrow will be taken first upon initial presentation, then in six monthly intervals following, until normalisation of IgG levels Control samples will come from donations by healthy subjects. A full clinical record will be kept for every control and experimental sample collected to allow the best possible matching of THI patients with healthy controls.

3.1.1 Matching controls

To determine B cell maturation changes caused by THI, it is imperative to compare samples that are at the closest possible environmental stage. Maturation of B cells integrates numerous internal and environmental signals, so controlling for developmental stage has significant challenges. Where possible, THI samples will be fully matched to control samples. The most important criteria to match will be age, as it is the most prominent indicator of immune system development. Secondly, the method of both birth (vaginal or caesarian) and feeding (bottle or breastfed) will be considered, as both have large influence over the immune system[51–55]. Further factors such as gender and ethnicity will be matched if possible. Finally the diet of patients will be standardised to reduce the environmental effect on B cell maturation. In the best scenario, all of the above criteria will be matched between control and experimental sam-

ples. However, there are limitations in the scope of the matching. In the samples provided, there are already gaps in the clinical history of samples (table 1). Without information such as ethnicity or mode of birth, it is impossible to match a sample to an appropriate control. Additionally, the control samples will be taken from participants' donations which may not match the clinical history of the THI samples. Even if it is possible to match samples according to stringent criteria, there are a myriad more external factors that will affect the dynamic nature of the immune system.

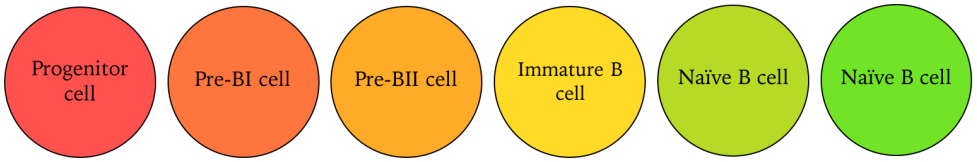
4 Aim 1:

Hypothesis THI samples will be deficient in activated B cells and plasma cells.

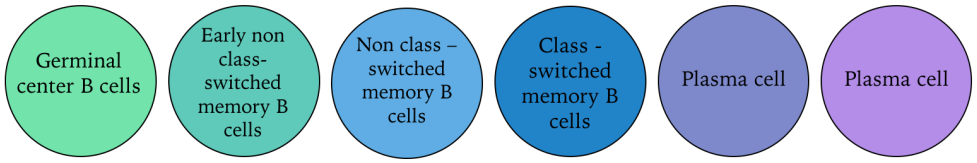
4.1 Proposed experiment

4.2 Segregation of B cells

To analyse the distribution of B cell subpopulations, we will segregate the B cells using flow cytometry as in Kulis et al.[56] and Oakes et al.[57]. B cells will be isolated from bone marrow, peripheral blood and tonsil samples. B cell populations sorted will include progenitor, pre-BI, pre-BII, immature and plasma cells isolated from bone marrow, naïve and memory B cells sorted from peripheral blood and plasma cells, germinal centre and naïve B cells isolated from tonsils. FACS will be used for all three tissues to sort populations using the surface markers in figure 3.



Source	Bone marrow	Bone marrow	Bone marrow	Bone marrow	Blood	Tonsil
Surface markers	$CD34^{++}$ $CD19^{-}$	$CD34^{+}$ $CD19^{+}$	$CD34^{-}$ $CD19^{+}$ $sIgM^{-}$	$CD34^{-}$ $CD19^{+}$ $sIgM^{+}$	$CD19^{+}$ IgD^{+} $CD27^{-}$	$CD19^{+}$ IgD^{+} $CD27^{-}$



Source	Tonsil	Blood	Blood	Blood	Bone marrow	Tonsil
Surface markers	$CD19^{+}$ $CD20^{++}$ $CD38^{+}$	$CD19^{+}$ $CD27^{-}$ $CD23^{-}$ Rhodamine 123^{+}	$CD19^{+}$ $CD27^{+}$ IgM^{+} IgD^{+}	$CD19^{+}$ IgG^{+} $CD27^{+}$	$CD138^{+}$	$CD19^{+}$ $CD20^{+}$ $CD38^{++}$

Figure 3: B cell populations

Figure 4: Description of the FACS sorting markers used to segregate B cell populations.

4.3 Possible outcomes and interpretations

Segregating samples into B cell subpopulations serves two purposes. Firstly, sorting allows greater confidence in any observed differences. We are attempting to find developmental differences between THI and normal patients. It is imperative that any changes observed are explained by THI rather than normal B cell maturation changes. After sorting, we can compare THI and control cells that at the same maturation stage. While there are always limitations when applying discrete stages to continuous processes, segregating B cells into such specific subtypes significantly reduces the chance of detecting differences which are due to developmental stage. Secondly, as the cells will be separated based on maturity, we are able to compare the prevalence of each cell subtype. If there is a block in the B cell development pathway, as in Tallmadge et al.[45], we will see lower numbers of mature B cells in THI samples compared to controls. Alternatively, the distribution of B cell subpopulations could be intact, as previously claimed[5,11,13–16]. A lack of deficient subpopulations indicates that the problem

is not in the development of the B cell lineage but instead in IgG production by plasma cells.

5 Aim 2:

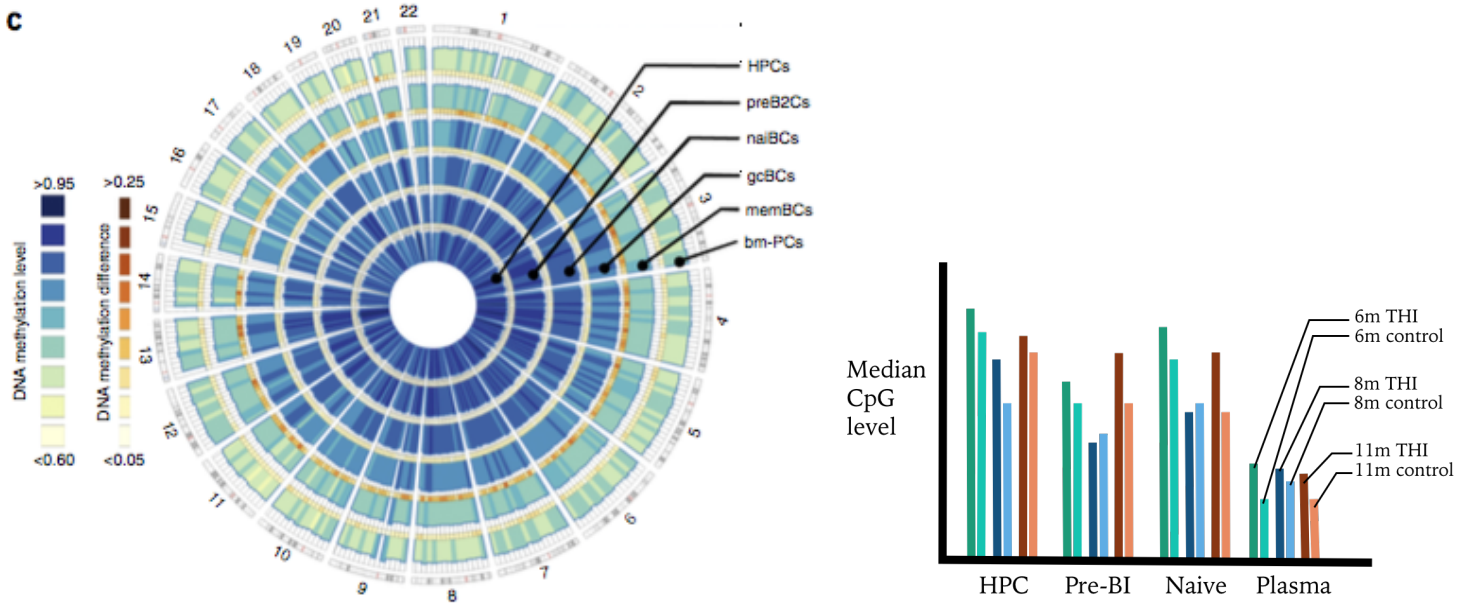
Hypothesis: DNA of B cells from THI patients will have regions which are differentially methylated to normal individuals.

5.1 Proposed experiment

To investigate global methylation of THI and control samples, we will produce full methylomes of the B cell lineages in figure 3. Whole genome bisulfite sequencing will be used such that we can obtain base-pair resolution of all methylated cytosines within the genome. To perform the analysis, we will use two sets of biological replicates for each of the samples. Samples will undergo two rounds of bisulfite conversion to ensure a cytosine to thymine conversion rate of over 99%. Treated samples will then be sequenced on an Illumina HiSeq 2000 platform and mapped to the genome using the STAR algorithm (v2.4.2a)[58].

We will then use ChIP-seq data from the ENCODE project[59] to analyse methylation status in the context of transcription factor binding sites. The relative enrichment of each TFBS in any differentially methylated regions will be calculated in comparison to background reads. A Fisher's exact test will be used to assign an odds ratio and P value to each comparison. Of particular focus will be the genes which are specific to B lymphopoiesis such as those in figure 2.

The high degree of variation between each individual in the development of the immune system at such a young age provides a limitation to our analysis. To ensure changes are due to THI and not normal development, plots such as those in figure 5 need to keep not only developmental stage separate, but other factors such as age and gender as well. As well as plotting each paired sample separately, we would need to combine samples, as in figure 5b, to



(a) Methylome map produced by Kulis et al. [56].

(b) Theoretical methylation plot

Figure 5: Methylation analysis. A: Cytosine methylation status is shown for six stages of B cell development. Concentric circles are labelled with developmental stage. B: Theoretical presentation of median methylation data. Each column represents the developmentally similar group of samples labelled.

visualise significant changes between THI and normal individuals. So even with excellently matched individuals, we may have to compare dissimilar samples.

5.2 Possible outcomes and interpretations

The methylation data will allow us to produce unbiased DNA methylation maps of each of the sorted cell populations as in figure 5a. The map clearly shows the gradual change in methylation exhibited by the cell subsets. It is expected that in both THI and control samples in all age groups, global methylation decreases as the B cells mature, as previously observed [56,60–62]. If THI causes aberrant methylation, it would manifest as lines in the methylation map that are not in the control samples. Furthermore, with multiple samples from the same THI patients, we expect that regions which show hypermethylation will eventually lose their methylation and begin to resemble the controls as serum IgG concentration increases.

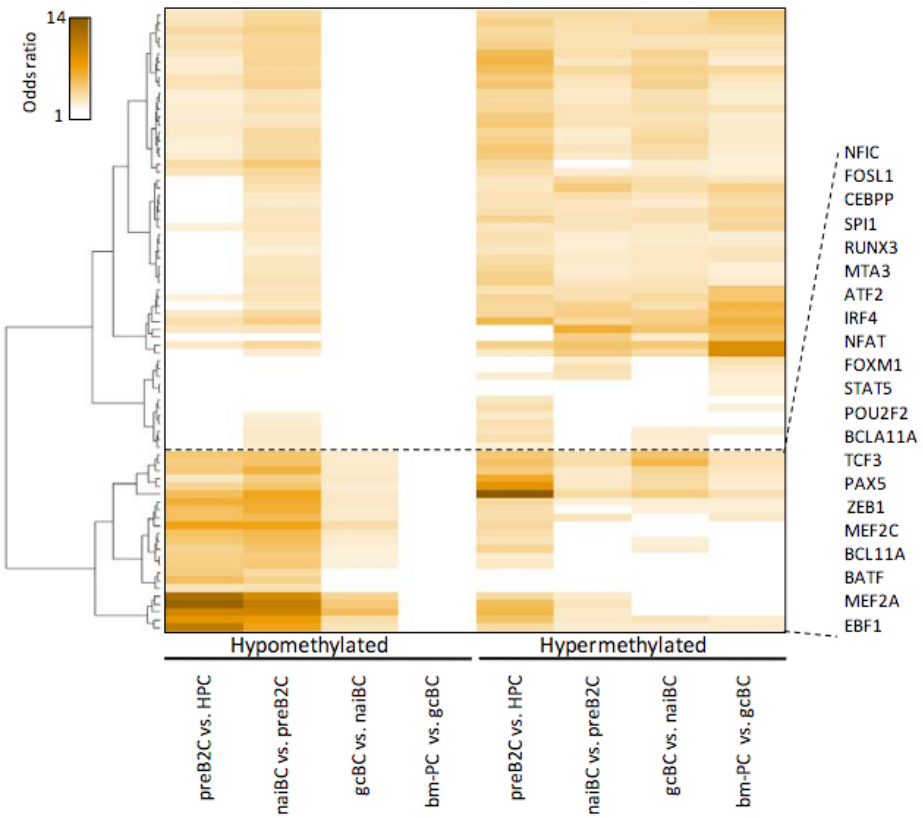


Figure 6: Association of differentially methylated regions (DMRs) and transcription factor binding sites (TFBSs). From Kulis et al.[56].

The ChIP-Seq data provides a more detailed view of key regions such as transcription factor binding sites (TFBSs). We will produce a heatmap such as that in figure 6 which displays the correlations between TFBSs and differentially methylated regions. In the THI samples, we expect to find that regions related to B cell maturation or IgG production will be hypermethylated compared to background levels. The location of differentially methylated regions (DMR) will indicate any potential causes of THI. If a region associated with B cell maturation, such as Pax5, is found to be differentially methylated it indicates that THI could be a result of a developmental block like that seen in CVID[45]. Alternatively if there is a DMR associated with gene rearrangement, THI could be caused by a lack of B cell diversity. Any DMRs identified will be further investigated with expression analysis.

6 Aim 3:

6.1 Hypothesis

Samples from THI patients will show decreased expression for B cell commitment associated genes compared to controls.

6.2 Proposed experiment

To investigate expression changes across the genome of THI samples, we will conduct RNA-Seq analysis on each of the B cell subsets in figure 3.

RNA-Seq libraries will be generated using the TruSeq Stranded Total RNA kit (Illumina). Sequenced reads will be aligned to the genome using the STAR algorithm (v2.4.2a)[58] and RPKM values will be calculated for each gene. qPCR analysis of gene expression will then be undertaken. RNA will be reverse transcribed into cDNA and analysed using the Universal Probe Library System. Target gene expression will be presented relative to average expression for the housekeeping genes *GAPDH*, *ACTB* and *HPRT1*.

6.3 Possible outcomes and interpretations

Expression analysis will allow us to both further investigate any DMRs found in methylation analysis and find other genes which are differentially expressed. Heatmaps will be generated to display the genes which change expression between THI and control samples. Genes which show significant difference will be presented as in figure 7.

Primarily, we expect to see differentially expressed regions associated with IgG production. For example, if the Fox01 region shows significantly decreased expression, we can expect a developmental block at the pro-B cell stage[32], leading to a lack of antibody producing mature B cells.

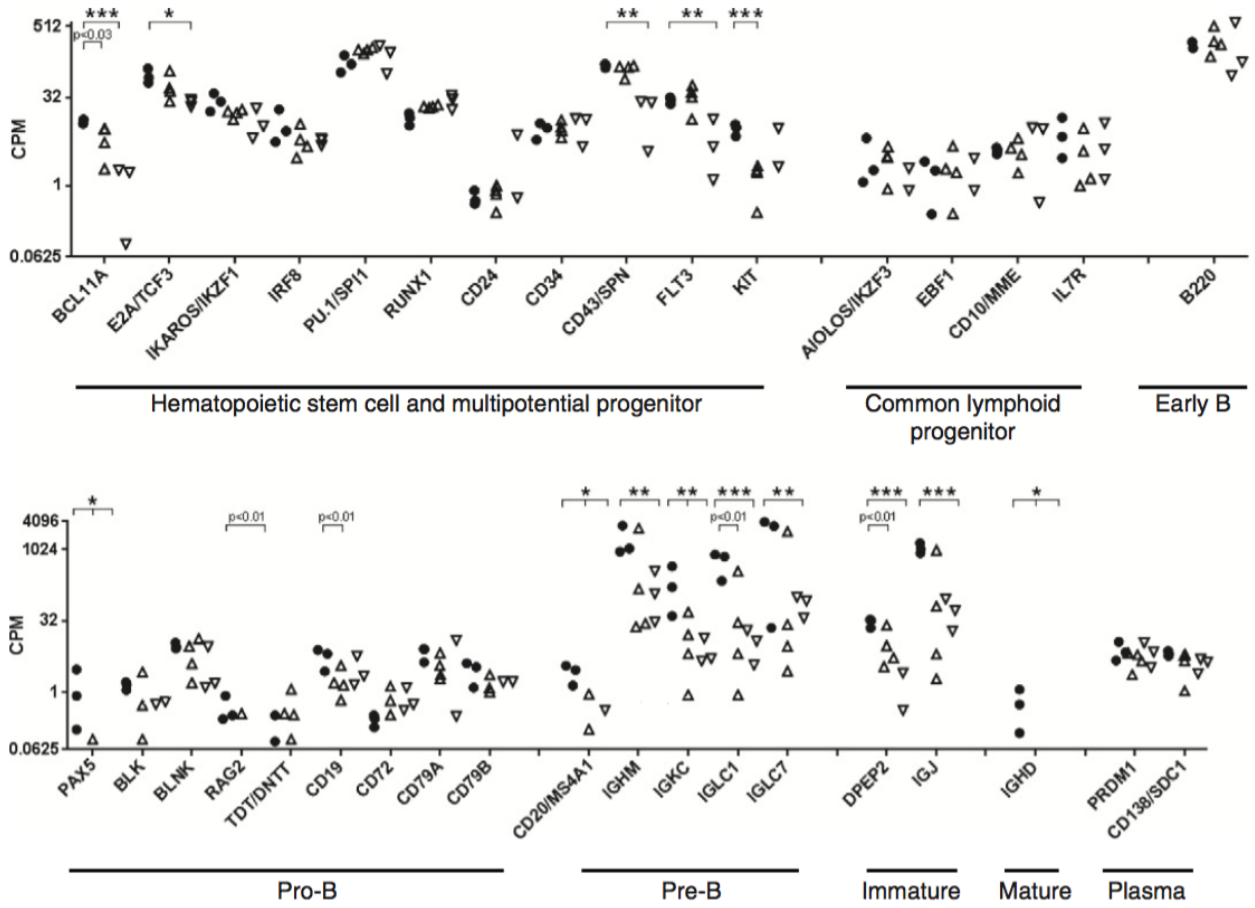


Figure 7: Expression of B lymphocyte-specific genes during development from hematopoietic stem cells to plasma cells. From Tallmadge et al. [45]. Gene expression presented in counts per million reads (CPM)

Furthermore, we expect genes which show hypermethylation in methylation analysis to have lower expression in THI samples than controls. Similarly, any hypomethylated genes are expected to have higher expression in THI samples. If we see expression changes in regions that are not differentially methylated, the implicated region could possibly be affected by a different epigenetic mechanism such as a chromatin modification. Any changes that aren't correlated with methylation changes should be further investigated as potential causes of THI.

A Appendices

A.1 Sample information

Table 1: Clinical details of patients with THI. Abbreviations: m, months; y, years; CVI, common variable immunodeficiency; -, unknown; def, d.

Individual	Tissue	Age at test	Gender	Ethnicity	Breastfeeding status	Mode of birth	Family history of PID
1	Whole Blood Tonsils	7m, 11m, 1y 7m, 2y 1m 2y 1m	Female	Caucasian	Breastfed	Vaginal	None
2	Whole Blood Tonsils	8m, 11m, 1y 3m, 1y 6m, 1y 8m, 2y 1m, 2y 4m, 2y 6m, 2y 8m 2y 6m	Male	Caucasian	Breastfed	Vaginal	None
3	Whole Blood Tonsils	9m, 1y 3m, 1y 9m, 2y 6m, 2y 9m, 3y 2m, 3y 6m 3y 2m	Male	Jewish	Bottle fed	Caesarian section	None
4	Whole Blood	10m, 1y 1m, 1y 8m	Male	Caucasian	Bottle fed	Vaginal	None
5	Whole Blood	9m, 11m, 1y 3m, 1y 5m, 1y 8m	Male	Asian	Breastfed	Vaginal	Brother with CVI
6	Whole Blood	7m, 9m, 11m, 1y 8m	Female	Jewish	Breastfed	Vaginal	None
7	Whole Blood	9m, 11m, 1y 2m, 1y 6m	Male	-	Breastfed	-	-
8	Whole Blood	7m, 9m,	Female	-	Breastfed	-	-
9	Whole Blood	7m, 9m, 11m, 1y 3m 1y 8m	Male	-	Breastfed	-	-
10	Whole Blood	7m, 9m, 11m, 1y 2m, 1y 6m	Male	-	Breastfed	-	-

Individual	Tissue	Age at test	Gender	Ethnicity	Breastfeeding status	Mode of birth	Family history of PID
11	Whole Blood	9m, 11m, 1y 1m, 1y 3m 1y 8m	Male	-	Bottle fed	-	-
12	Whole Blood Tonsils	7m, 11m, 1y 2m, 1y 11m, 2y 6m, 2y 9m, 3y 4m, 3y 7m, 4y 2y 11m	Female	Jewish	Breastfed	Vaginal	None
13	Whole Blood	9m, 11m, 1y 2m, 1y 6m, 2y 4m, 2y 8m	Male	Jewish	Bottle fed	Vaginal	None
14	Whole Blood Tonsils	9m, 1y 1m, 1y 7m, 2y 2m, 2y 9m, 3y 2m 3y 2m	Female	Caucasian	Bottle fed	Vaginal	None
15	Whole Blood	7m, 11m, 1y 1m	Male	Caucasian	Breastfed		Sister with IgA def.
16	Whole Blood	8m, 1y 1m, 1y 4m, 1y 6m	Male	-	-	Vaginal	-
17	Whole Blood	9m, 1y 2m, 1y 6m	Male	-	-	Vaginal	-
18	Whole Blood	7m, 9m, 1y 1m	Female	-	-	Caesarian section	-
19	Whole Blood	7m, 9m, 11m, 1y 2m, 1y 6m	Male	-	-	Vaginal	-
20	Whole Blood	9m, 11m, 1y 2m, 1y 6m	Male	-	-	Vaginal	-
21	Whole Blood	11m, 1y 3m, 1y 5m, 1y 8m	Male	-	-	Caesarian section	-
22	Whole Blood	7m, 9m, 11m, 1y 8m	Female	-	-	-	None
23	Whole Blood	9m, 1y 2m, 1y 6m	Male	-	-	-	None

Individual	Tissue	Age at test	Gender	Ethnicity	Breastfeeding status	Mode of birth	Family history of PID
24	Whole Blood Tonsils	7m, 9m, 1y 1m, 1y 6m, 1y 11m, 2y 1m 2y 4m	Female	-	-	-	None
25	Whole Blood	7m, 11m, 1y 3m, 1y 5m, 1y 8m	Male	-	-	-	Sister with IgA def.
26	Whole Blood	8m, 1y 1m,	Male	-	-	-	None

References

[1] Simon, A. K., Hollander, G. A., and McMichael, A. (2015). Evolution of the immune system in humans from infancy to old age. *Proceedings. Biological sciences / The Royal Society*, 282(1821):20143085.

[2] Hasselquist, D. and Nilsson, J.-A. (2009). Maternal transfer of antibodies in vertebrates: trans-generational effects on offspring immunity. *Philosophical transactions of the Royal Society of London. Series B, Biological sciences*, 364(1513):51–60.

[3] Martin, R., Nauta, A. J., Ben Amor, K., Knippels, L. M. J., Knol, J., and Garssen, J. (2010). Early life: gut microbiota and immune development in infancy. *Beneficial microbes*, 1(4):367–82.

[4] Rechavi, E., Lev, A., Lee, Y. N., Simon, A. J., Yinon, Y., Lipitz, S., Amariglio, N., Weisz, B., Notarangelo, L. D., and Somech, R. (2015). Timely and spatially regulated maturation of B and T cell repertoire during human fetal development. *Science translational medicine*, 7(276):276ra25.

[5] Dressler, F., Peter, H. H., Müller, W., and Rieger, C. H. (1989). Transient hypogammaglobulinemia of infancy: Five new cases, review of the literature and redefinition. *Acta paediatrica Scandinavica*, 78(5):767–74.

[6] Al-Herz, W., Bousfiha, A., Casanova, J.-L., Chatila, T., Conley, M. E., Cunningham-Rundles, C., Etzioni, A., Franco, J. L., Gaspar, H. B., Holland, S. M., Klein, C., Nonoyama, S., Ochs, H. D., Oksenhendler, E., Picard, C., Puck, J. M., Sullivan, K., and Tang, M. L. K. (2014). Primary immunodeficiency diseases: an update on the classification from the international union of immunological societies expert committee for primary immunodeficiency. *Frontiers in immunology*, 5:162.

[7] Gitlin, D. and Janeway, C. A. (1956). Agammaglobulinemia, congenital, acquired and transient forms. *Progress in hematology*, 1:318–29.

[8] Al-Herz, W., Bousfiha, A., Casanova, J.-L., Chapel, H., Conley, M. E., Cunningham-Rundles, C., Etzioni, A., Fischer, A., Franco, J. L., Geha, R. S., Hammarström, L., Nonoyama, S., Notarangelo, L. D., Ochs, H. D., Puck, J. M., Roifman, C. M., Seger, R., and Tang, M. L. K. (2011). Primary immunodeficiency diseases: an update on the classification from the international union of immunological societies expert committee for primary immunodeficiency. *Frontiers in immunology*, 2:54.

[9] Rosen, F. S. and Janeway, C. A. (1966). The gamma globulins: the antibody deficiency syndromes. *New England Journal of Medicine*, 275(13):709–715.

[10] McGeady, S. J. (1987). Transient hypogammaglobulinemia of infancy: need to reconsider name and definition. *The Journal of pediatrics*, 110(1):47–50.

[11] Stiehm, E. R. and Fulginity, V. A. (1980). *Immunologic Disorders in Infants and Children*, chapter The immunodeficiencies of immaturity, pages 219–238. W.B Saunders Company, Philadelphia, second edition.

[12] Dalal, I., Reid, B., Nisbet-Brown, E., and Roifman, C. M. (1998). The outcome of patients with hypogammaglobulinemia in infancy and early childhood. *The Journal of pediatrics*, 133(1):144–6.

[13] Tiller, Jr, T. L. and Buckley, R. H. (1978). Transient hypogammaglobulinemia of infancy: review of the literature, clinical and immunologic features of 11 new cases, and long-term follow-up. *The Journal of pediatrics*, 92(3):347–53.

[14] Buckley, R. H. (1983). Immunodeficiency. *The Journal of allergy and clinical immunology*, 72(6):627–41.

[15] Siegel, R. L., Issekutz, T., Schwaber, J., Rosen, F. S., and Geha, R. S. (1981). Deficiency of t helper cells in transient hypogammaglobulinemia of infancy. *The New England journal of medicine*, 305(22):1307–13.

[16] Fiorilli, M., Crescenzi, M., Carbonari, M., Tedesco, L., Russo, G., Gaetano, C., and Aiuti, F. (1986). Phenotypically immature igg-bearing b cells in patients with hypogammaglobulinemia. *Journal of clinical immunology*, 6(1):21–5.

[17] Fudenberg, H. H. and Fudenberg, B. R. (1964). Antibody to hereditary human gammaglobulin (GM) factor resulting from maternal-fetal incompatibility. *Science*, 145(3628): 170–1.

[18] Nathenson, G., Schorr, J. B., and Litwin, S. D. (1971). Gm factor fetomaternal gamma globulin incompatibility. *Pediatric Research*, 5(1):2–9.

[19] Willenbockel, U. (1960). Transitorisch-protrahiertes Antikörpermangelsyndrom bei zweieiigen Zwillingen. *Zeitschrift für Kinderheilkunde*, 84(5):477–83.

[20] Soothill, J. F. (1968). Immunoglobulins in first-degree relatives of patients with hypogammaglobulinaemia. transient hypogammaglobulinaemia: a possible manifestation of heterozygosity. *Lancet*, 1(7550):1001–3.

[21] Ovadia, A. and Dalal, I. (2014). Transient hypogammaglobulinemia of infancy. *LymphoSign Journal*, 1(1):1–9.

[22] Walker, A. M., Kemp, A. S., Hill, D. J., and Shelton, M. J. (1994). Features of transient hypogammaglobulinaemia in infants screened for immunological abnormalities. *Archives of disease in childhood*, 70(3):183–6.

[23] Rosen, F. S., Cooper, M. D., and Wedgwood, R. J. (1984). The primary immunodeficiencies (1). *The New England journal of medicine*, 311(4):235–42.

[24] Gao, H., Lukin, K., Ramírez, J., Fields, S., Lopez, D., and Hagman, J. (2009). Opposing effects of SWI/SNF and Mi-2/NuRD chromatin remodeling complexes on epigenetic reprogramming by EBF and Pax5. *Proceedings of the National Academy of Sciences of the United States of America*, 106(27):11258–63.

[25] Maier, H., Ostraat, R., Gao, H., Fields, S., Shinton, S. A., Medina, K. L., Ikawa, T., Murre, C., Singh, H., Hardy, R. R., and Hagman, J. (2004). Early B cell factor cooperates with Runx1 and mediates epigenetic changes associated with mb-1 transcription. *Nature immunology*, 5(10):1069–77.

[26] Walter, K., Bonifer, C., and Tagoh, H. (2008). Stem cell-specific epigenetic priming and B cell-specific transcriptional activation at the mouse Cd19 locus. *Blood*, 112(5):1673–82.

[27] Decker, T., Pasca di Magliano, M., McManus, S., Sun, Q., Bonifer, C., Tagoh, H., and Busslinger, M. (2009). Stepwise activation of enhancer and promoter regions of the B cell commitment gene Pax5 in early lymphopoiesis. *Immunity*, 30(4):508–20.

[28] Lin, Y. C., Jhunjhunwala, S., Benner, C., Heinz, S., Welinder, E., Mansson, R., Sigvardsson, M., Hagman, J., Espinoza, C. A., Dutkowski, J., Ideker, T., Glass, C. K., and Murre, C. (2010). A global network of transcription factors, involving E2A, EBF1 and Foxo1, that orchestrates B cell fate. *Nature immunology*, 11s(7):635–43.

[29] McManus, S., Ebert, A., Salvagiotto, G., Medvedovic, J., Sun, Q., Tamir, I., Jaritz, M., Tagoh, H., and Busslinger, M. (2011). The transcription factor Pax5 regulates its target genes by recruiting chromatin-modifying proteins in committed B cells. *The EMBO journal*, 30(12):2388–404.

[30] Treiber, T., Mandel, E. M., Pott, S., Györy, I., Firner, S., Liu, E. T., and Grosschedl, R. (2010). Early B cell factor 1 regulates B cell gene networks by activation, repression, and transcription-independent poising of chromatin. *Immunity*, 32(5):714–725.

[31] Zandi, S., Mansson, R., Tsapogas, P., Zetterblad, J., Bryder, D., and Sigvardsson, M. (2008). EBF1 is essential for B-lineage priming and establishment of a transcription factor network in common lymphoid progenitors. *Journal of immunology*, 181(5):3364–72.

[32] Choukrallah, M. A. and Matthias, P. (2014). The interplay between chromatin and

transcription factor networks during B cell development: Who pulls the trigger first? *Frontiers in immunology*, 5:156.

[33] Griffin, D. O., Holodick, N. E., and Rothstein, T. L. (2011). Human B1 cells in umbilical cord and adult peripheral blood express the novel phenotype CD20+ CD27+ CD43+ CD70-. *The Journal of experimental medicine*, 208(1):67–80.

[34] Montecino-Rodriguez, E. and Dorshkind, K. (2012). B-1 B cell development in the fetus and adult. *Immunity*, 36(1):13–21.

[35] Saeys, Y., Gassen, S. V., and Lambrecht, B. N. (2016). Computational flow cytometry: helping to make sense of high-dimensional immunology data. *Nature reviews. Immunology*, 16(7):449–62.

[36] Aghaeepour, N., Finak, G., FlowCAP Consortium, DREAM Consortium, Hoos, H., Mosmann, T. R., Brinkman, R., Gottardo, R., and Scheuermann, R. H. (2013). Critical assessment of automated flow cytometry data analysis techniques. *Nature methods*, 10 (3):228–38.

[37] Lara-Astiaso, D., Weiner, A., Lorenzo-Vivas, E., Zaretsky, I., Jaitin, D. A., David, E., Keren-Shaul, H., Mildner, A., Winter, D., Jung, S., et al. (2014). Chromatin state dynamics during blood formation. *Science*, 345(6199):943–949.

[38] Zan, H. and Casali, P. (2015). Epigenetics of peripheral B-cell differentiation and the antibody response. *Frontiers in immunology*, 6:631.

[39] Mercer, E. M., Lin, Y. C., Benner, C., Jhunjhunwala, S., Dutkowski, J., Flores, M., Sigvardsson, M., Ideker, T., Glass, C. K., and Murre, C. (2011). Multilineage priming of enhancer repertoires precedes commitment to the B and myeloid cell lineages in hematopoietic progenitors. *Immunity*, 35(3):413–25.

[40] Bégin, P. and Nadeau, K. C. (2014). Epigenetic regulation of asthma and allergic disease. *Allergy Asthma Clinical Immunology*, 10(1):27.

[41] Zeng, W.-p. (2013). 'all things considered': transcriptional regulation of T helper type 2 cell differentiation from precursor to effector activation. *Immunology*, 140(1):31–8.

[42] Ohkura, N., Kitagawa, Y., and Sakaguchi, S. (2013). Development and maintenance of regulatory T cells. *Immunity*, 38(3):414–423.

[43] Polansky, J. K., Kretschmer, K., Freyer, J., Floess, S., Garbe, A., Baron, U., Olek, S., Hamann, A., von Boehmer, H., and Huehn, J. (2008). Dna methylation controls Foxp3 gene expression. *European journal of immunology*, 38(6):1654–63.

[44] Shimazu, Y., Shimazu, Y., Hishizawa, M., Hamaguchi, M., Nagai, Y., Sugino, N., Fujii, S., Kawahara, M., Kadowaki, N., Nishikawa, H., Sakaguchi, S., and Takaori-Kondo, A. (2016). Hypomethylation of the Treg-specific demethylated region in FOXP3 is a hallmark of the regulatory T-cell subtype in adult T-cell leukemia. *Cancer immunology research*, 4(2):136–45.

[45] Tallmadge, R. L., Shen, L., Tseng, C. T., Miller, S. C., Barry, J., and Felippe, M. J. B. (2015). Bone marrow transcriptome and epigenome profiles of equine common variable immunodeficiency patients unveil block of B lymphocyte differentiation. *Clinical immunology*, 160(2):261–76.

[46] Cunningham-Rundles, C. (2012). The many faces of common variable immunodeficiency. *Hematology / the Education Program of the American Society of Hematology. American Society of Hematology. Education Program*, 2012:301–5.

[47] Schebesta, A., McManus, S., Salvagiotto, G., Delogu, A., Busslinger, G. A., and Busslinger, M. (2007). Transcription factor Pax5 activates the chromatin of key genes involved in B cell signaling, adhesion, migration, and immune function. *Immunity*, 27(1): 49–63.

[48] Delogu, A., Schebesta, A., Sun, Q., Aschenbrenner, K., Perlot, T., and Busslinger, M.

(2006). Gene repression by Pax5 in B cells is essential for blood cell homeostasis and is reversed in plasma cells. *Immunity*, 24(3):269–81.

[49] Roessler, S., Györy, I., Imhof, S., Spivakov, M., Williams, R. R., Busslinger, M., Fisher, A. G., and Grosschedl, R. (2007). Distinct promoters mediate the regulation of Ebf1 gene expression by interleukin-7 and Pax5. *Molecular and cellular biology*, 27(2):579–94.

[50] Kowalczyk, D., Mytar, B., and Zembala, M. (1997). Cytokine production in transient hypogammaglobulinemia and isolated IgA deficiency. *The Journal of allergy and clinical immunology*, 100(4):556–62.

[51] Jakobsson, H. E., Abrahamsson, T. R., Jenmalm, M. C., Harris, K., Quince, C., Jernberg, C., Björkstén, B., Engstrand, L., and Andersson, A. F. (2014). Decreased gut microbiota diversity, delayed Bacteroidetes colonisation and reduced Th1 responses in infants delivered by caesarean section. *Gut*, 63(4):559–66.

[52] Cho, C. E. and Norman, M. (2013). Cesarean section and development of the immune system in the offspring. *American journal of obstetrics and gynecology*, 208(4):249–54.

[53] Brandtzaeg, P. (2003). Mucosal immunity: integration between mother and the breast-fed infant. *Vaccine*, 21(24):3382–8.

[54] Rogier, E. W., Frantz, A. L., Bruno, M. E., Wedlund, L., Cohen, D. A., Stromberg, A. J., and Kaetzel, C. S. (2014). Lessons from mother: Long-term impact of antibodies in breast milk on the gut microbiota and intestinal immune system of breastfed offspring. *Gut Microbes*, 5(5):663–8.

[55] Gómez-Gallego, C., Frias, R., Pérez-Martínez, G., Bernal, M. J., Periago, M. J., Salminen, S., Ros, G., and Collado, M. C. (2014). Polyamine supplementation in infant formula: Influence on lymphocyte populations and immune system-related gene expression in a Balb/cOlaHsd mouse model. *Food Research International*, 59:8–15.

[56] Kulis, M., Merkel, A., Heath, S., Queirós, A. C., Schuyler, R. P., Castellano, G., Beekman, R., Raineri, E., Esteve, A., Clot, G., et al. (2015). Whole-genome fingerprint of the DNA methylome during human B cell differentiation. *Nature genetics*, 47(7):746–756.

[57] Oakes, C. C., Seifert, M., Assenov, Y., Gu, L., Przekopowitz, M., Ruppert, A. S., Wang, Q., Imbusch, C. D., Serva, A., Koser, S. D., Brocks, D., Lipka, D. B., Bogatyrova, O., Weichenhan, D., Brors, B., Rassenti, L., Kipps, T. J., Mertens, D., Zapatka, M., Lichter, P., Döhner, H., Küppers, R., Zenz, T., Stilgenbauer, S., Byrd, J. C., and Plass, C. (2016). DNA methylation dynamics during B cell maturation underlie a continuum of disease phenotypes in chronic lymphocytic leukemia. *Nature genetics*, 48(3):253–64.

[58] Dobin, A., Davis, C. A., Schlesinger, F., Drenkow, J., Zaleski, C., Jha, S., Batut, P., Chaisson, M., and Gingeras, T. R. (2013). STAR: ultrafast universal RNA-seq aligner. *Bioinformatics*, 29(1):15–21.

[59] ENCODE Project Consortium (2012). An integrated encyclopedia of DNA elements in the human genome. *Nature*, 489(7414):57–74.

[60] Lai, A. Y., Mav, D., Shah, R., Grimm, S. A., Phadke, D., Hatzi, K., Melnick, A., Geigerman, C., Sobol, S. E., Jaye, D. L., et al. (2013). DNA methylation profiling in human B cells reveals immune regulatory elements and epigenetic plasticity at alu elements during B-cell activation. *Genome research*, 23(12):2030–2041.

[61] Kulis, M., Heath, S., Bibikova, M., Queirós, A. C., Navarro, A., Clot, G., Martínez-Trillos, A., Castellano, G., Brun-Heath, I., Pinyol, M., Barberán-Soler, S., Papasaikas, P., Jares, P., Beà, S., Rico, D., Ecker, S., Rubio, M., Royo, R., Ho, V., Klotzle, B., Hernández, L., Conde, L., López-Guerra, M., Colomer, D., Villamor, N., Aymerich, M., Rozman, M., Bayes, M., Gut, M., Gelpí, J. L., Orozco, M., Fan, J.-B., Quesada, V., Puente, X. S., Pisano, D. G., Valencia, A., López-Guillermo, A., Gut, I., López-Otín, C., Campo, E., and Martín-Subero, J. I. (2012). Epigenomic analysis detects widespread gene-body DNA hypomethylation in chronic lymphocytic leukemia. *Nature genetics*, 44(11):1236–42.

[62] Shaknovich, R., Cerchietti, L., Tsikitas, L., Kormaksson, M., De, S., Figueroa, M. E., Ballon, G., Yang, S. N., Weinhold, N., Reimers, M., Clozel, T., Luttrop, K., Ekstrom, T. J., Frank, J., Vasanthakumar, A., Godley, L. A., Michor, F., Elemento, O., and Melnick, A. (2011). DNA methyltransferase 1 and DNA methylation patterning contribute to germinal center B-cell differentiation. *Blood*, 118(13):3559–69.