# Highly similar genomic landscapes in monoclonal B-cell lymphocytosis and ultra-stable chronic lymphocytic leukemia with low frequency of driver mutations

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**Supplementary material**


**Study population**

The study cohort comprised 9 individuals with LC-MBL, 13 individuals with HC-MBL, and 7 patients with Rai stage 0 CLL, herein called 'ultra-stable' CLL. All CLL patients were monitored for at least 10 years (median, 16); the median follow-up period for the LC-MBL and HC-MBL cases was 10 and 7 years, respectively. CLL patients were diagnosed according to the iwCLL guidelines(1), while the detection of MBL was based on established criteria(2). Patients with CLL were selected based on the absence of any symptoms of disease progression during the monitoring period, whereas individuals with MBL (both LC and HC) were chosen based on the presence of a stable CD19+CD5+ monoclonal population after examination at different timepoints during the follow-up period.


**Whole-genome sequencing: bioinformatics analysis**

Sequencing reads were aligned to the hg19 reference genome using BWA (v0.7.12) and optical or PCR duplicate reads were marked using Picard (v1.96). BAM-files were locally realigned around small insertions and deletions (indels) using GATK (v3.2.4). Single nucleotide variants (SNV) and indels were identified with FreeBayes (0.9.21-7). A variant allele frequency (VAF) of 10% was used as threshold for variant calling. Subsequent filtering was performed to remove variants located in low complexity regions and potential sequencing artifacts present in at least 10% of the reads in a panel of normal samples. Somatic copy-number alterations (sCNA) were analyzed with Control-FREEC(3). For the pre-telomeric and pre-centromeric repetitive regions, a 50kbp detection cut-off was applied to filter out false positive sCNA due to incorrect genome mapping/assembly.

Analysis of the mutational spectra was performed using the MutationalPatterns package(4). The contribution of different mutational signatures in each sample was estimated using non-negative matrix factorization and signatures were extracted based on the cophenetic correlation coefficient. Hierachical clustering was performed with cosine similarity as distance measure.

NCV were analyzed and prioritized with Funseq2(5). Output data were filtered based on the following criteria: (i) Variants should be identified within regulatory elements that affect the expression of target genes

and represent transcription factor (TF) highly occupied regions ("HOT"). The linkage between NCVs and target genes was based on the Roadmap Epigenomics Project, where, data for both the activity signals and gene expression from bisulfite sequencing, ChIP-Seq, and RNA-Seq were analysed. For each candidate target, the correlations of their activity/inactivity and expression levels across the different tissue types were computed. (ii) Variant hits should be recurrent (i.e. the exact change at the exact gene position) and, thus, included multiple times within the COSMIC and the Funseq2 database that contains mutations from 570 samples of 10 tumor types, among which 28 are CLL samples), and (iii) target genes should be network hubs.

Fishhook(6) was used for unbiased NCV prioritization. Briefly, the genome was divided into 10kb windows with 500bp spacing. Positions with low-complexity, low-mappability were masked from the analysis as described by *Li et al.*(7). The tool calculates the neutral somatic density using Gamma-Posion regression and outputs regions across the sample set with significantly increased mutation rate.

**Targeted re-sequencing: bioinformatics analysis**

Agilent SurecallTrimmer (v3.5.1.46) was used to remove adaptor sequences, mask HaloPlex enzyme footprints, and trim low quality bases. The processed reads were aligned to the hg19 human reference genome using BWA (v.0.7.12). Duplicate reads were marked using the Agilent LocatIt tool (v3.5.1.46). Variants were called using a VAF cutoff of 1% and a minimum of 30 variant reads. Variants had to meet the following conditions to be included in downstream analysis: (i) be located within an exonic or splicing region; (ii) be non-synonymous; and (iii) not be listed in the European 1000 genomes variant database.

**References**

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## Supplementary tables

**Table S1.** Details of the 11 CLL putative driver genes that were included in the targeted re-sequencing analysis.

| Gene | RefSeq | Coding exons | Transcript length |
|------|--------|--------------|-------------------|
| *ATM* | NM_000051 | 62 | 13147 |
| *BIRC3* | NM_001165 | 8 | 4342 |
| *MYD88* | NM_001172567 | 5 | 2871 |
| *NOTCH1* | NM_017617 | 34* | 9374 |
| *SF3B1* | NM_012433 | 25* | 6526 |
| *TP53* | NM_000546 | 10 | 2579 |
| *EGR2* | NM_000399 | 2 | 2968 |
| *POT1* | NM_015450 | 15 | 4080 |
| *NFKBIE* | NM_004556 | 6 | 2581 |
| *XPO1* | NM_003400 | 24* | 4915 |
| *FBXW7* | NM_033632 | 11 | 4976 |

*Only the mutational hotspot regions of the following genes were sequenced: *NOTCH1* (exon 34), *SF3B1* (exons 14-16 and 18) and *XPO1* (exon 15). All coding exons in the remaining 8 genes were sequenced.

**Table S2.** Mean autosomal coverage of all samples in the present study.

| Sample ID | Entity | Mean Coverage |
| --- | --- | --- |
| CLL_1 | CLL | 28 |
| CLL_2 | CLL | 56 |
| CLL_3 | CLL | 31 |
| CLL_4 | CLL | 30 |
| CLL_5 | CLL | 28 |
| HC-MBL_1 | HC-MBL | 29 |
| HC-MBL_2 | HC-MBL | 37 |
| HC-MBL_3 | HC-MBL | 28 |
| HC-MBL_4 | HC-MBL | 34 |
| HC-MBL_5 | HC-MBL | 34 |
| LC-MBL_1 | LC-MBL | 26 |
| LC-MBL_2 | LC-MBL | 28 |
| LC-MBL_3 | LC-MBL | 35 |
| LC-MBL_4 | LC-MBL | 35 |
| LC-MBL_5 | LC-MBL | 56 |
| LC-MBL_6 | LC-MBL | 35 |
| CLL_1-PMN | PMN | 26 |
| CLL_2-PMN | PMN | 32 |
| CLL_3-PMN | PMN | 30 |
| CLL_4-PMN | PMN | 29 |
| CLL_5-PMN | PMN | 28 |
| HC-MBL_1-PMN | PMN | 27 |
| HC-MBL_2-PMN | PMN | 33 |
| HC-MBL_3-PMN | PMN | 28 |
| HC-MBL_4-PMN | PMN | 31 |
| HC-MBL_5-PMN | PMN | 34 |
| LC-MBL_1-PMN | PMN | 31 |
| LC-MBL_2-PMN | PMN | 33 |
| LC-MBL_3-PMN | PMN | 30 |
| LC-MBL_4-PMN | PMN | 34 |
| LC-MBL_5-PMN | PMN | 54 |
| LC-MBL_6-PMN | PMN | 33 |
| CLL_1-BUC | buccal control | 26 |
| CLL_2-BUC | buccal control | 26 |
| CLL_3-BUC | buccal control | 32 |
| CLL_4-BUC | buccal control | 25 |
| CLL_5-BUC | buccal control | 26 |
| HC-MBL_1-BUC | buccal control | 27 |
| HC-MBL_2-BUC | buccal control | 38 |
| HC-MBL_3-BUC | buccal control | 24 |
| HC-MBL_4-BUC | buccal control | 26 |
| HC-MBL_5-BUC | buccal control | 32 |
| LC-MBL_1-BUC | buccal control | 26 |
| LC-MBL_2-BUC | buccal control | 26 |

| | | |
|---|---|---|
| **LC-MBL_3-BUC** | buccal control | 30 |
| **LC-MBL_4-BUC** | buccal control | 31 |
| **LC-MBL_5-BUC** | buccal control | 51 |
| **LC-MBL_6-BUC** | buccal control | 29 |

**Table S3.** Basic biological characteristics for the individuals and patients of the present cohort.

| Sample ID | Entity | Sex | Age | IGHV gene | IGHV mut status | % of cell purity | % of B cells* | % of B cells with CLL immunophenotype** |
|---|---|---|---|---|---|---|---|---|
| **CLL_1** | CLL | F | 85 | IGHV3-23 | MUT | 98.2 | 89.0 | 97.0 |
| **CLL_2** | CLL | M | 69 | IGHV4-38-2 | MUT | 96.3 | 88.0 | 56.0 |
| **CLL_3** | CLL | F | 83 | IGHV1-3 | MUT | 95.9 | 95.0 | 100.0 |
| **CLL_4** | CLL | M | 84 | IGHV3-30 | MUT | 98.4 | 93.0 | 100.0 |
| **CLL_5** | CLL | F | 47 | IGHV3-9 | MUT | 97.3 | 97.0 | 97.0 |
| **HC-MBL_1** | HC-MBL | M | 66 | IGHV1-3 | MUT | 96.6 | 53.0 | 93.0 |
| **HC-MBL_2** | HC-MBL | M | 77 | IGHV3-7 | MUT | 97.6 | 41.0 | 81.0 |
| **HC-MBL_3** | HC-MBL | M | 77 | IGHV1-69 | MUT | 96.4 | 67.0 | 61.0 |
| **HC-MBL_4** | HC-MBL | M | 83 | NA | NA | 98.1 | 77.0 | 94.7 |
| **HC-MBL_5** | HC-MBL | F | 94 | IGHV3-15 | UNMUT | 97.5 | 32.8 | 87.6 |
| **LC-MBL_1** | LC-MBL | M | 68 | IGHV4-31 | MUT | 96.3 | 7.3 | 10.7 |
| **LC-MBL_2** | LC-MBL | F | 68 | IGHV3-7 | MUT | 97.2 | 10.8 | 7.1 |
| **LC-MBL_3** | LC-MBL | M | 71 | IGHV1-8 | MUT | 98.8 | 5.5 | 70.5 |
| **LC-MBL_4** | LC-MBL | M | 70 | IGHV1-8 | MUT | 96.3 | 13.0 | 16.8 |
| **LC-MBL_5** | LC-MBL | M | 59 | IGHV5-51 | MUT | 96.4 | 40.0 | 93.0 |
| **LC-MBL_6** | LC-MBL | F | 76 | IGHV2-5 | MUT | 95.3 | 60.0 | 90.0 |

* % of B cells within the entire lymphocyte population

** % of CLL B cells within the entire B cell population

**Table S4.** Ninety-six substitution mutation classification for CLL, HC-MBL, LC-MBL and PMN samples.

| Mutation Type | Motif | CLL | HC-MBL | LC-MBL | PMN |
|---|---|---|---|---|---|
| C>A | A.A | 1,28192 | 1,19265 | 1,38240 | 1,43129 |
| C>A | A.C | 0,99814 | 1,10559 | 1,02965 | 0,50890 |
| C>A | A.G | 0,28378 | 0,18281 | 0,22881 | 0,28625 |
| C>A | A.T | 1,02749 | 1,02724 | 1,01058 | 0,95419 |
| C>A | C.A | 1,45806 | 1,21876 | 1,41100 | 1,36768 |
| C>A | C.C | 0,81221 | 0,64420 | 0,65783 | 0,95419 |
| C>A | C.G | 0,12721 | 0,13058 | 0,19067 | 0,15903 |
| C>A | C.T | 1,12535 | 1,07077 | 1,02011 | 1,14503 |
| C>A | G.A | 1,04706 | 1,20135 | 1,11545 | 1,04961 |
| C>A | G.C | 0,68499 | 0,54844 | 0,81990 | 0,63613 |
| C>A | G.G | 0,15657 | 0,10446 | 0,14300 | 0,31806 |
| C>A | G.T | 0,91985 | 0,88796 | 1,10592 | 0,66793 |
| C>A | T.A | 1,50699 | 1,19265 | 1,39193 | 2,03562 |
| C>A | T.C | 0,75349 | 0,67032 | 0,87710 | 0,57251 |
| C>A | T.G | 0,09785 | 0,15669 | 0,22881 | 0,15903 |
| C>A | T.T | 1,73206 | 1,70627 | 2,04023 | 1,94020 |
| C>G | A.A | 0,56757 | 0,68773 | 0,63876 | 0,79516 |
| C>G | A.C | 0,42078 | 0,45268 | 0,51482 | 0,44529 |
| C>G | A.G | 0,11742 | 0,08705 | 0,06673 | 0,09541 |
| C>G | A.T | 0,76328 | 0,56585 | 0,58156 | 0,73155 |
| C>G | C.A | 0,34249 | 0,36563 | 0,34321 | 0,73155 |
| C>G | C.C | 0,36207 | 0,33080 | 0,30508 | 0,28625 |
| C>G | C.G | 0,09785 | 0,06093 | 0,04766 | 0,28625 |
| C>G | C.T | 0,51864 | 0,40915 | 0,62923 | 0,47709 |
| C>G | G.A | 0,25442 | 0,40045 | 0,40041 | 0,76335 |
| C>G | G.C | 0,51864 | 0,44398 | 0,43855 | 0,89058 |
| C>G | G.G | 0,10764 | 0,07834 | 0,08580 | 0,15903 |
| C>G | G.T | 0,83178 | 0,64420 | 0,65783 | 0,66793 |
| C>G | T.A | 0,38164 | 0,47880 | 0,46715 | 0,89058 |
| C>G | T.C | 0,53821 | 0,36563 | 0,48622 | 0,76335 |
| C>G | T.G | 0,05871 | 0,09576 | 0,08580 | 0,47709 |
| C>G | T.T | 0,80242 | 0,90537 | 0,86757 | 1,14503 |
| C>T | A.A | 1,97671 | 1,94132 | 1,91629 | 2,79898 |
| C>T | A.C | 1,26235 | 1,14041 | 1,30613 | 1,46310 |
| C>T | A.G | 3,83599 | 4,16993 | 3,38449 | 2,48091 |
| C>T | A.T | 1,45806 | 1,35805 | 1,52540 | 1,87659 |
| C>T | C.A | 1,55592 | 1,66274 | 1,47773 | 1,94020 |
| C>T | C.C | 1,56571 | 1,53216 | 1,75421 | 1,68575 |
| C>T | C.G | 2,47578 | 2,10672 | 2,06883 | 1,49491 |
| C>T | C.T | 1,88863 | 2,08931 | 2,11650 | 2,06743 |
| C>T | G.A | 1,48742 | 1,30582 | 1,25846 | 0,85877 |
| C>T | G.C | 1,82013 | 1,56698 | 1,46820 | 1,27226 |
| C>T | G.G | 3,07270 | 2,75093 | 2,35484 | 1,68575 |

| | | | | | |
|---|---|---|---|---|---|
| **C>T** | G.T | 2,23113 | 1,85427 | 1,76375 | 1,97201 |
| **C>T** | T.A | 1,40913 | 1,27970 | 1,49680 | 1,27226 |
| **C>T** | T.C | 1,63421 | 1,84556 | 1,52540 | 1,43129 |
| **C>T** | T.G | 1,38956 | 1,64533 | 1,44913 | 1,43129 |
| **C>T** | T.T | 1,61463 | 1,72368 | 1,75421 | 2,16284 |
| **T>A** | A.A | 1,01771 | 1,15783 | 1,28706 | 0,92239 |
| **T>A** | A.C | 0,65564 | 0,84443 | 0,82944 | 0,79516 |
| **T>A** | A.G | 0,99814 | 0,82702 | 0,72456 | 0,92239 |
| **T>A** | A.T | 1,40913 | 1,21876 | 1,29659 | 1,01781 |
| **T>A** | C.A | 0,46971 | 0,49621 | 0,75316 | 0,76335 |
| **T>A** | C.C | 0,72414 | 0,56585 | 0,67689 | 1,59033 |
| **T>A** | C.G | 0,54799 | 0,67032 | 0,83897 | 0,95419 |
| **T>A** | C.T | 0,89049 | 0,74867 | 0,81990 | 0,92239 |
| **T>A** | G.A | 0,37185 | 0,36563 | 0,45762 | 0,38167 |
| **T>A** | G.C | 0,34249 | 0,27857 | 0,45762 | 0,60432 |
| **T>A** | G.G | 0,48928 | 0,31339 | 0,45762 | 0,82697 |
| **T>A** | G.T | 0,59692 | 0,47880 | 0,61969 | 0,60432 |
| **T>A** | T.A | 0,91985 | 1,07948 | 1,10592 | 0,63613 |
| **T>A** | T.C | 0,34249 | 0,65291 | 0,46715 | 0,57251 |
| **T>A** | T.G | 0,69478 | 0,52232 | 0,94384 | 0,76335 |
| **T>A** | T.T | 0,97856 | 0,91407 | 1,08685 | 0,92239 |
| **T>C** | A.A | 2,57363 | 2,37659 | 2,06883 | 3,02162 |
| **T>C** | A.C | 1,09599 | 1,02724 | 1,13452 | 1,01781 |
| **T>C** | A.G | 1,68313 | 1,47993 | 1,55400 | 2,09923 |
| **T>C** | A.T | 2,09413 | 2,17637 | 2,31671 | 1,81297 |
| **T>C** | C.A | 1,21342 | 1,04465 | 1,11545 | 0,92239 |
| **T>C** | C.C | 1,31128 | 1,29711 | 1,14405 | 1,17684 |
| **T>C** | C.G | 1,46785 | 1,14041 | 1,18219 | 1,90839 |
| **T>C** | C.T | 1,52656 | 1,93261 | 1,69701 | 1,55852 |
| **T>C** | G.A | 1,09599 | 1,27970 | 1,08685 | 1,14503 |
| **T>C** | G.C | 1,14492 | 0,96630 | 0,94384 | 0,89058 |
| **T>C** | G.G | 1,00792 | 0,78349 | 1,06778 | 1,17684 |
| **T>C** | G.T | 1,25256 | 1,42770 | 1,38240 | 0,98600 |
| **T>C** | T.A | 1,46785 | 1,32323 | 1,19172 | 1,17684 |
| **T>C** | T.C | 1,32106 | 1,27100 | 1,17265 | 1,24045 |
| **T>C** | T.G | 0,95899 | 0,72255 | 1,00104 | 1,01781 |
| **T>C** | T.T | 1,72228 | 1,61051 | 1,97349 | 1,36768 |
| **T>G** | A.A | 1,43849 | 1,20135 | 1,39193 | 0,95419 |
| **T>G** | A.C | 0,26421 | 0,31339 | 0,27648 | 0,19083 |
| **T>G** | A.G | 0,49907 | 0,36563 | 0,43855 | 0,54071 |
| **T>G** | A.T | 0,85135 | 1,05336 | 0,87710 | 0,73155 |
| **T>G** | C.A | 0,86114 | 0,72255 | 1,00104 | 0,38167 |
| **T>G** | C.C | 0,43057 | 0,72255 | 0,52435 | 0,76335 |
| **T>G** | C.G | 0,68499 | 0,62679 | 0,81990 | 0,60432 |
| **T>G** | C.T | 2,33878 | 4,70967 | 2,20230 | 1,01781 |
| **T>G** | G.A | 0,42078 | 0,41786 | 0,41948 | 0,47709 |
| **T>G** | G.C | 0,26421 | 0,25245 | 0,31461 | 0,54071 |

| | | | | | |
|---|---|---|---|---|---|
| **T>G** | G.G | 0,38164 | 0,47009 | 0,50529 | 1,43129 |
| **T>G** | G.T | 0,67521 | 1,78462 | 0,91524 | 0,60432 |
| **T>G** | T.A | 1,85928 | 1,69757 | 2,15463 | 1,14503 |
| **T>G** | T.C | 0,49907 | 0,46139 | 0,34321 | 0,73155 |
| **T>G** | T.G | 0,70456 | 0,58326 | 0,78177 | 0,73155 |
| **T>G** | T.T | 2,06478 | 2,23731 | 2,28811 | 1,74936 |

**Table S5.** Distribution of non-synonymous mutations within CLL, HC-MBL, LC-MBL and PMN samples.

| Sample ID | Entity | nonsyn SNV | missense SNV | nonsense SNV | frameshift indel | nonframeshift indel | unknown |
|---|---|---|---|---|---|---|---|
| CLL_1 | CLL | 14 | 11 | 1 | 2 | 0 | 0 |
| CLL_2 | CLL | 11 | 11 | 0 | 0 | 0 | 0 |
| CLL_3 | CLL | 19 | 16 | 2 | 0 | 1 | 0 |
| CLL_4 | CLL | 6 | 4 | 2 | 0 | 0 | 0 |
| CLL_5 | CLL | 8 | 7 | 0 | 1 | 0 | 0 |
| HC-MBL_1 | HC-MBL | 9 | 7 | 0 | 1 | 0 | 1 |
| HC-MBL_2 | HC-MBL | 13 | 11 | 1 | 1 | 0 | 0 |
| HC-MBL_3 | HC-MBL | 14 | 11 | 1 | 2 | 0 | 0 |
| HC-MBL_4 | HC-MBL | 27 | 22 | 2 | 2 | 0 | 1 |
| HC-MBL_5 | HC-MBL | 11 | 10 | 1 | 0 | 0 | 0 |
| LC-MBL_1 | LC-MBL | 1 | 1 | 0 | 0 | 0 | 0 |
| LC-MBL_2 | LC-MBL | 16 | 14 | 1 | 1 | 0 | 0 |
| LC-MBL_3 | LC-MBL | 11 | 10 | 0 | 1 | 0 | 0 |
| LC-MBL_4 | LC-MBL | 3 | 3 | 0 | 0 | 0 | 0 |
| LC-MBL_5 | LC-MBL | 9 | 8 | 1 | 0 | 0 | 0 |
| LC-MBL_6 | LC-MBL | 13 | 11 | 0 | 2 | 0 | 0 |
| CLL_1-PMN | PMN | 0 | 0 | 0 | 0 | 0 | 0 |
| CLL_2-PMN | PMN | 0 | 0 | 0 | 0 | 0 | 0 |
| CLL_4-PMN | PMN | 1 | 1 | 0 | 0 | 0 | 0 |
| CLL_5-PMN | PMN | 1 | 1 | 0 | 0 | 0 | 0 |
| HC-MBL_1-PMN | PMN | 0 | 0 | 0 | 0 | 0 | 0 |
| HC-MBL_2-PMN | PMN | 0 | 0 | 0 | 0 | 0 | 0 |
| HC-MBL_3-PMN | PMN | 0 | 0 | 0 | 0 | 0 | 0 |
| HC-MBL_4-PMN | PMN | 0 | 0 | 0 | 0 | 0 | 0 |
| HC-MBL_5-PMN | PMN | 6 | 2 | 0 | 4 | 0 | 0 |
| LC-MBL_1-PMN | PMN | 1 | 1 | 0 | 0 | 0 | 0 |
| LC-MBL_2-PMN | PMN | 0 | 0 | 0 | 0 | 0 | 0 |
| LC-MBL_3-PMN | PMN | 4 | 1 | 0 | 3 | 0 | 0 |
| LC-MBL_4-PMN | PMN | 0 | 0 | 0 | 0 | 0 | 0 |
| LC-MBL_5-PMN | PMN | 1 | 0 | 0 | 0 | 1 | 0 |
| LC-MBL_6-PMN | PMN | 1 | 1 | 0 | 0 | 0 | 0 |

**Table S6.** Exonic non-synonymous mutations identified in the present study.

| Sample | Entity | Chr | Start | End | Ref base | Var base | Gene | Mutation type | VAF% | Transcripts |
|---|---|---|---|---|---|---|---|---|---|---|
| **CLL_1** | CLL | 2 | 140992404 | 140992404 | G | A | LRP1B | nonsyn SNV | 0.33 | LRP1B:NM_018557:exon90:c.C13610T:p.A4537V |
| **CLL_1** | CLL | 3 | 193016968 | 193016968 | G | T | ATP13A5 | nonsyn SNV | 0.47 | ATP13A5:NM_198505:exon25:c.C2800A:p.Q934K |
| **CLL_1** | CLL | 4 | 53494171 | 53494171 | T | C | USP46 | nonsyn SNV | 0.18 | USP46:NM_001134223:exon3:c.A256G:p.K86E |
| **CLL_1** | CLL | 9 | 90534209 | 90534209 | C | - | SPATA31C1 | frameshift del | 0.18 | SPATA31C1:NM_001145124:exon2:c.229delC:p.P77fs |
| **CLL_1** | CLL | 9 | 90534212 | 90534212 | A | T | SPATA31C1 | nonsyn SNV | 0.18 | SPATA31C1:NM_001145124:exon2:c.A232T:p.T78S |
| **CLL_1** | CLL | 11 | 66281935 | 66281935 | G | A | BBS1 | nonsyn SNV | 0.43 | BBS1:NM_024649:exon4:c.G218A:p.G73E |
| **CLL_1** | CLL | 11 | 123848299 | 123848299 | C | G | OR10S1 | nonsyn SNV | 0.48 | OR10S1:NM_001004474:exon1:c.G100C:p.A34P |
| **CLL_1** | CLL | 12 | 93148037 | 93148037 | A | G | PLEKHG7 | nonsyn SNV | 0.47 | PLEKHG7:NM_001004330:exon6:c.A487G:p.I163V |
| **CLL_1** | CLL | 12 | 132625056 | 132625056 | C | T | DDX51 | nonsyn SNV | 0.37 | DDX51:NM_175066:exon11:c.G1585A:p.G529S |
| **CLL_1** | CLL | 16 | 5121909 | 5121909 | T | G | ALG1 | nonsyn SNV | 0.44 | ALG1:NM_019109:exon1:c.T59G:p.L20R |
| **CLL_1** | CLL | 17 | 73487171 | 73487171 | - | G | KIAA0195 | frameshift ins | 0.44 | KIAA0195:NM_014738:exon12:c.1171dupG:p.L390fs |
| **CLL_1** | CLL | 20 | 51872693 | 51872693 | G | A | TSHZ2 | stopgain SNV | 0.39 | TSHZ2:NM_001193421:exon2:c.G2687A:p.W896X |
| **CLL_1** | CLL | X | 38262941 | 38262941 | T | C | OTC | nonsyn SNV | 0.49 | OTC:NM_000531:exon6:c.T611C:p.I204T |
| **CLL_1** | CLL | X | 46918093 | 46918093 | C | T | PHF16 | nonsyn SNV | 0.46 | PHF16:NM_001077445:exon11:c.C2086T:p.P696S |
| **CLL_2** | CLL | 2 | 220422581 | 220422581 | C | T | OBSL1 | nonsyn SNV | 0.39 | OBSL1:NM_001173431:exon11:c.G3754A:p.G1252R |
| **CLL_2** | CLL | 3 | 134339623 | 134339623 | C | T | KY | nonsyn SNV | 0.48 | KY:NM_178554:exon7:c.G560A:p.R187H |
| **CLL_2** | CLL | 7 | 6189368 | 6189368 | C | T | USP42 | nonsyn SNV | 0.46 | USP42:NM_032172:exon13:c.C1541T:p.P514L |
| **CLL_2** | CLL | 7 | 100687063 | 100687063 | C | A | MUC17 | nonsyn SNV | 0.31 | MUC17:NM_001040105:exon3:c.C12366A:p.N4122K |
| **CLL_2** | CLL | 10 | 103792869 | 103792869 | T | A | C10orf76 | nonsyn SNV | 0.41 | C10orf76:NM_024541:exon4:c.A220T:p.I74F |
| **CLL_2** | CLL | 14 | 105416323 | 105416323 | T | C | AHNAK2 | nonsyn SNV | 0.28 | AHNAK2:NM_138420:exon7:c.A5465G:p.K1822R |
| **CLL_2** | CLL | 15 | 29398949 | 29398949 | G | A | APBA2 | nonsyn SNV | 0.47 | APBA2:NM_001130414:exon10:c.G1808A:p.G603E |
| **CLL_2** | CLL | 16 | 2814622 | 2814622 | A | G | SRRM2 | nonsyn SNV | 0.27 | SRRM2:NM_016333:exon11:c.A4093G:p.T1365A |
| **CLL_2** | CLL | 17 | 10355349 | 10355349 | C | T | MYH4 | nonsyn SNV | 0.21 | MYH4:NM_017533:exon27:c.G3647A:p.R1216Q |
| **CLL_2** | CLL | 17 | 15508600 | 15508600 | C | T | CDRT1 | nonsyn SNV | 0.46 | CDRT1:NM_006382:exon7:c.G1370A:p.R457Q |
| **CLL_2** | CLL | 19 | 440908 | 440908 | G | A | SHC2 | nonsyn SNV | 0.54 | SHC2:NM_012435:exon2:c.C493T:p.R165C |
| **CLL_3** | CLL | 1 | 37947226 | 37947228 | AGA | - | ZC3H12A | nonframeshift del | 0.56 | ZC3H12A:NM_025079:exon4:c.608_610del:p.203_204del |
| **CLL_3** | CLL | 1 | 160326083 | 160326083 | G | A | NCSTN | nonsyn SNV | 0.45 | NCSTN:NM_015331:exon14:c.G1585A:p.A529T |
| **CLL_3** | CLL | 1 | 173839563 | 173839563 | G | A | ZBTB37 | nonsyn SNV | 0.54 | ZBTB37:NM_001122770:exon3:c.G200A:p.S67N |
| **CLL_3** | CLL | 2 | 216986846 | 216986846 | T | - | XRCC5 | stopgain SNV | 0.38 | XRCC5:NM_021141:exon6:c.553delT:p.L185X |
| **CLL_3** | CLL | 5 | 156641319 | 156641319 | C | T | ITK | nonsyn SNV | 0.59 | ITK:NM_005546:exon4:c.C443T:p.P148L |
| **CLL_3** | CLL | 7 | 84628865 | 84628865 | T | C | SEMA3D | nonsyn SNV | 0.53 | SEMA3D:NM_152754:exon17:c.A2225G:p.Q742R |
| **CLL_3** | CLL | 7 | 99117531 | 99117531 | A | G | ZKSCAN5 | nonsyn SNV | 0.38 | ZKSCAN5:NM_014569:exon4:c.A635G:p.Q212R |
| **CLL_3** | CLL | 7 | 148080936 | 148080936 | T | C | CNTNAP2 | nonsyn SNV | 0.39 | CNTNAP2:NM_014141:exon22:c.T3671C:p.M1224T |
| **CLL_3** | CLL | 8 | 42587175 | 42587175 | T | C | CHRNB3 | nonsyn SNV | 0.51 | CHRNB3:NM_000749:exon5:c.T725C:p.I242T |
| **CLL_3** | CLL | 8 | 118819456 | 118819456 | T | C | EXT1 | nonsyn SNV | 0.50 | EXT1:NM_000127:exon9:c.A1883G:p.K628R |
| **CLL_3** | CLL | 9 | 136323206 | 136323206 | G | A | ADAMTS13 | nonsyn SNV | 0.43 | ADAMTS13:NM_139025:exon28:c.G4067A:p.S1356N |
| **CLL_3** | CLL | 11 | 64374910 | 64374910 | T | A | NRXN2 | nonsyn SNV | 0.50 | NRXN2:NM_138734:exon7:c.A1759T:p.S587C |
| **CLL_3** | CLL | 15 | 33954395 | 33954395 | T | A | RYR3 | nonsyn SNV | 0.59 | RYR3:NM_001036:exon35:c.T4664A:p.M1555K |
| **CLL_3** | CLL | 18 | 28609480 | 28609480 | G | A | DSC3 | stopgain SNV | 0.38 | DSC3:NM_001941:exon4:c.C469T:p.Q157X |
| **CLL_3** | CLL | 19 | 42856556 | 42856556 | T | C | MEGF8 | nonsyn SNV | 0.53 | MEGF8:NM_001410:exon18:c.T3097C:p.C1033R |
| **CLL_3** | CLL | 20 | 14306666 | 14306666 | C | A | FLRT3 | nonsyn SNV | 0.50 | FLRT3:NM_013281:exon2:c.G1487T:p.C496F |
| **CLL_3** | CLL | 21 | 19713763 | 19713763 | T | G | TMPRSS15 | nonsyn SNV | 0.51 | TMPRSS15:NM_002772:exon13:c.A1531C:p.T511P |
| **CLL_3** | CLL | X | 9864575 | 9864575 | A | G | SHROOM2 | nonsyn SNV | 0.38 | SHROOM2:NM_001649:exon4:c.A2627G:p.Y876C |
| **CLL_3** | CLL | X | 86888883 | 86888883 | A | C | KLHL4 | nonsyn SNV | 0.45 | KLHL4:NM_019117:exon8:c.A1684C:p.T562P |

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|---|---|---|---|---|---|---|---|---|---|---|
| CLL_4 | CLL | 1 | 17312817 | 17312817 | G | A | ATP13A2 | nonsyn SNV | 0.39 | ATP13A2:NM_001141974:exon27:c.C3140T:p.P1047L |
| CLL_4 | CLL | 2 | 196825024 | 196825024 | G | A | DNAH7 | stopgain SNV | 0.42 | DNAH7:NM_018897:exon18:c.C2851T:p.R951X |
| CLL_4 | CLL | 7 | 113518059 | 113518059 | C | A | PPP1R3A | stopgain SNV | 0.41 | PPP1R3A:NM_002711:exon4:c.G3088T:p.G1030X |
| CLL_4 | CLL | 11 | 77907590 | 77907590 | C | T | USP35 | nonsyn SNV | 0.58 | USP35:NM_020798:exon2:c.C299T:p.A100V |
| CLL_4 | CLL | 12 | 109541352 | 109541352 | C | T | UNG | nonsyn SNV | 0.54 | UNG:NM_003362:exon5:c.C710T:p.S237L |
| CLL_4 | CLL | 17 | 62007661 | 62007661 | T | C | CD79B | nonsyn SNV | 0.41 | CD79B:NM_000626:exon3:c.A203G:p.N68S |
| CLL_5 | CLL | 1 | 19475118 | 19475118 | A | T | UBR4 | nonsyn SNV | 0.47 | UBR4:NM_020765:exon50:c.T7433A:p.L2478Q |
| CLL_5 | CLL | 1 | 27332923 | 27332923 | G | A | FAM46B | nonsyn SNV | 0.46 | FAM46B:NM_052943:exon2:c.C790T:p.R264C |
| CLL_5 | CLL | 2 | 54133825 | 54133825 | C | - | PSME4 | frameshift del | 0.42 | PSME4:NM_014614:exon26:c.2853delG:p.R951fs |
| CLL_5 | CLL | 9 | 104239142 | 104239142 | T | C | TMEM246 | nonsyn SNV | 0.30 | TMEM246:NM_032342:exon2:c.A233G:p.H78R |
| CLL_5 | CLL | 10 | 5567322 | 5567322 | G | A | CALML3 | nonsyn SNV | 0.48 | CALML3:NM_005185:exon1:c.G274A:p.V92M |
| CLL_5 | CLL | 12 | 18443943 | 18443943 | T | G | PIK3C2G | nonsyn SNV | 0.46 | PIK3C2G:NM_004570:exon4:c.T916G:p.C306G |
| CLL_5 | CLL | 13 | 114434316 | 114434316 | G | C | GRK1 | nonsyn SNV | 0.62 | GRK1:NM_002929:exon5:c.G1194C:p.K398N |
| CLL_5 | CLL | 22 | 23230234 | 23230234 | A | G | IGLL5 | nonsyn SNV | 0.44 | IGLL5:NM_001178126:exon1:c.A1G:p.M1V |
| CLL_5 | CLL | 22 | 23230348 | 23230348 | C | G | IGLL5 | nonsyn SNV | 0.58 | IGLL5:NM_001178126:exon1:c.C115G:p.L39V |
| HC-MBL_1 | HC-MBL | 2 | 138378270 | 138378270 | A | G | THSD7B | unknown | 0.32 | UNKNOWN |
| HC-MBL_1 | HC-MBL | 3 | 10429991 | 10429991 | C | T | ATP2B2 | nonsyn SNV | 0.47 | ATP2B2:NM_001001331:exon6:c.G877A:p.G293S |
| HC-MBL_1 | HC-MBL | 3 | 81692113 | 81692113 | C | - | GBE1 | frameshift del | 0.58 | GBE1:NM_000158:exon7:c.811delG:p.E271fs |
| HC-MBL_1 | HC-MBL | 4 | 40339335 | 40339335 | A | T | CHRNA9 | nonsyn SNV | 0.28 | CHRNA9:NM_017581:exon3:c.A319T:p.I107F |
| HC-MBL_1 | HC-MBL | 4 | 85722851 | 85722851 | C | T | WDFY3 | nonsyn SNV | 0.36 | WDFY3:NM_014991:exon17:c.G2774A:p.R925Q |
| HC-MBL_1 | HC-MBL | 5 | 140051099 | 140051099 | C | G | DND1 | nonsyn SNV | 0.57 | DND1:NM_194249:exon4:c.G841C:p.G281R |
| HC-MBL_1 | HC-MBL | 7 | 89939400 | 89939400 | G | C | C7orf63 | nonsyn SNV | 0.31 | C7orf63:NM_001039706:exon23:c.G2674C:p.V892L |
| HC-MBL_1 | HC-MBL | 11 | 119291066 | 119291066 | G | T | THY1 | nonsyn SNV | 0.38 | THY1:NM_006288:exon3:c.C68A:p.T23N |
| HC-MBL_1 | HC-MBL | 12 | 56565175 | 56565175 | C | T | SMARCC2 | nonsyn SNV | 0.33 | SMARCC2:NM_003075:exon21:c.G2134A:p.V712M |
| HC-MBL_2 | HC-MBL | 1 | 149902701 | 149902701 | C | T | MTMR11 | nonsyn SNV | 0.39 | MTMR11:NM_181873:exon13:c.G1231A:p.G411R |
| HC-MBL_2 | HC-MBL | 2 | 71191572 | 71191572 | - | C | ATP6V1B1 | frameshift ins | 0.38 | ATP6V1B1:NM_001692:exon12:c.1149dupC:p.Y383fs |
| HC-MBL_2 | HC-MBL | 2 | 170592138 | 170592138 | T | C | KLHL23 | nonsyn SNV | 0.48 | KLHL23:NM_144711:exon2:c.T614C:p.I205T |
| HC-MBL_2 | HC-MBL | 2 | 170592180 | 170592180 | T | C | KLHL23 | nonsyn SNV | 0.40 | KLHL23:NM_144711:exon2:c.T656C:p.L219P |
| HC-MBL_2 | HC-MBL | 4 | 153249504 | 153249504 | C | G | FBXW7 | nonsyn SNV | 0.26 | FBXW7:NM_001013415:exon8:c.G920C:p.W307S |
| HC-MBL_2 | HC-MBL | 5 | 137520602 | 137520602 | T | C | KIF20A | nonsyn SNV | 0.18 | KIF20A:NM_005733:exon14:c.T1790C:p.V597A |
| HC-MBL_2 | HC-MBL | 14 | 76431943 | 76431943 | T | C | TGFB3 | nonsyn SNV | 0.28 | TGFB3:NM_003239:exon4:c.A742G:p.I248V |
| HC-MBL_2 | HC-MBL | 16 | 58550456 | 58550456 | T | C | SETD6 | nonsyn SNV | 0.45 | SETD6:NM_001160305:exon4:c.T551C:p.I184T |
| HC-MBL_2 | HC-MBL | 16 | 67854817 | 67854817 | C | T | TSNAXIP1 | stopgain SNV | 0.24 | TSNAXIP1:NM_018430:exon3:c.C61T:p.R21X |
| HC-MBL_2 | HC-MBL | 17 | 4876210 | 4876210 | G | A | CAMTA2 | nonsyn SNV | 0.23 | CAMTA2:NM_001171166:exon14:c.C2363T:p.P788L |
| HC-MBL_2 | HC-MBL | 18 | 32470332 | 32470332 | A | T | DTNA | nonsyn SNV | 0.46 | DTNA:NM_001198938:exon20:c.A2103T:p.L701F |
| HC-MBL_2 | HC-MBL | 20 | 42891891 | 42891891 | C | T | GDAP1L1 | nonsyn SNV | 0.48 | GDAP1L1:NM_001256739:exon3:c.C395T:p.T132M |
| HC-MBL_2 | HC-MBL | 21 | 45550531 | 45550531 | C | T | PWP2 | nonsyn SNV | 0.18 | PWP2:NM_005049:exon21:c.C2638T:p.R880W |
| HC-MBL_3 | HC-MBL | 1 | 24426198 | 24426198 | A | T | MYOM3 | nonsyn SNV | 0.50 | MYOM3:NM_152372:exon6:c.T628A:p.Y210N |
| HC-MBL_3 | HC-MBL | 1 | 103491441 | 103491441 | T | G | COL11A1 | nonsyn SNV | 0.83 | COL11A1:NM_080629:exon6:c.A848C:p.K283T |
| HC-MBL_3 | HC-MBL | 1 | 145457068 | 145457068 | C | T | POLR3GL | nonsyn SNV | 0.36 | POLR3GL:NM_032305:exon7:c.G493A:p.E165K |
| HC-MBL_3 | HC-MBL | 1 | 236205413 | 236205413 | G | A | NID1 | nonsyn SNV | 0.46 | NID1:NM_002508:exon4:c.C932T:p.T311M |
| HC-MBL_3 | HC-MBL | 5 | 154394302 | 154394302 | C | T | KIF4B | stopgain SNV | 0.48 | KIF4B:NM_001099293:exon1:c.C883T:p.R295X |
| HC-MBL_3 | HC-MBL | 6 | 138576640 | 138576640 | G | T | KIAA1244 | nonsyn SNV | 0.56 | KIAA1244:NM_020340:exon10:c.G838T:p.A280S |
| HC-MBL_3 | HC-MBL | 10 | 329247 | 329247 | A | - | DIP2C | frameshift del | 0.61 | DIP2C:NM_014974:exon35:c.4259delT:p.F1420fs |
| HC-MBL_3 | HC-MBL | 11 | 22301109 | 22301109 | A | C | ANO5 | nonsyn SNV | 0.44 | ANO5:NM_001142649:exon22:c.A2537C:p.K846T |
| HC-MBL_3 | HC-MBL | 12 | 96641028 | 96641028 | - | C | ELK3 | frameshift ins | 0.54 | ELK3:NM_005230:exon3:c.519dupC:p.S173fs |
| HC-MBL_3 | HC-MBL | 14 | 79434558 | 79434558 | A | C | NRXN3 | nonsyn SNV | 0.59 | NRXN3:NM_004796:exon11:c.A1892C:p.N631T |
| HC-MBL_3 | HC-MBL | 18 | 14851894 | 14851894 | C | A | ANKRD30B | nonsyn SNV | 0.31 | ANKRD30B:NM_001145029:exon36:c.C3594A:p.N1198K |
| HC-MBL_3 | HC-MBL | 19 | 4182475 | 4182475 | G | A | SIRT6 | nonsyn SNV | 0.39 | SIRT6:NM_001193285:exon1:c.C62T:p.P21L |

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|---|---|---|---|---|---|---|---|---|---|---|
| HC-MBL_3 | HC-MBL | 19 | 14070057 | 14070057 | C | T | DCAF15 | nonsyn SNV | 0.31 | DCAF15:NM_138353:exon7:c.C985T:p.R329C |
| HC-MBL_3 | HC-MBL | 22 | 23230439 | 23230439 | G | A | IGLL5 | nonsyn SNV | 0.52 | IGLL5:NM_001178126:exon1:c.G206A:p.R69K |
| HC-MBL_4 | HC-MBL | 1 | 12429537 | 12429537 | A | G | VPS13D | nonsyn SNV | 0.42 | VPS13D:NM_018156:exon53:c.A10513G:p.T3505A |
| HC-MBL_4 | HC-MBL | 2 | 71743313 | 71743313 | C | A | DYSF | nonsyn SNV | 0.50 | DYSF:NM_001130455:exon8:c.C799A:p.L267I |
| HC-MBL_4 | HC-MBL | 3 | 20027162 | 20027162 | A | C | PP2D1 | nonsyn SNV | 0.32 | PP2D1:NM_001252657:exon3:c.T1603G:p.S535A |
| HC-MBL_4 | HC-MBL | 4 | 74274486 | 74274490 | CTGCT | - | ALB | frameshift del | 0.47 | ALB:NM_000477:exon4:c.446_450del:p.149_150del |
| HC-MBL_4 | HC-MBL | 4 | 184129241 | 184129241 | C | T | WWC2 | nonsyn SNV | 0.47 | WWC2:NM_024949:exon3:c.C377T:p.A126V |
| HC-MBL_4 | HC-MBL | 5 | 131008585 | 131008585 | G | A | FNIP1 | nonsyn SNV | 0.57 | FNIP1:NM_001008738:exon13:c.C1468T:p.R490W |
| HC-MBL_4 | HC-MBL | 5 | 139231273 | 139231273 | T | A | NRG2 | nonsyn SNV | 0.32 | NRG2:NM_001184935:exon7:c.A1490T:p.Y497F |
| HC-MBL_4 | HC-MBL | 6 | 26234902 | 26234902 | C | G | HIST1H1D | nonsyn SNV | 0.50 | HIST1H1D:NM_005320:exon1:c.G260C:p.S87T |
| HC-MBL_4 | HC-MBL | 6 | 138199730 | 138199730 | T | A | TNFAIP3 | nonsyn SNV | 0.49 | TNFAIP3:NM_001270507:exon7:c.T1148A:p.M383K |
| HC-MBL_4 | HC-MBL | 7 | 44099168 | 44099168 | A | G | DBNL | nonsyn SNV | 0.42 | DBNL:NM_001014436:exon11:c.A958G:p.S320G |
| HC-MBL_4 | HC-MBL | 7 | 111368443 | 111368443 | C | T | DOCK4 | nonsyn SNV | 0.35 | DOCK4:NM_014705:exon52:c.G5788A:p.A1930T |
| HC-MBL_4 | HC-MBL | 9 | 139390649 | 139390650 | AG | - | NOTCH1 | frameshift del | 0.20 | NOTCH1:NM_017617:exon34:c.7541_7542del:p.P2514fs |
| HC-MBL_4 | HC-MBL | 9 | 127232807 | 127232807 | G | A | GPR144 | nonsyn SNV | 0.61 | GPR144:NM_001161808:exon17:c.G2593A:p.V865I |
| HC-MBL_4 | HC-MBL | 11 | 20077497 | 20077497 | G | A | NAV2 | nonsyn SNV | 0.39 | NAV2:NM_001111019:exon9:c.G2017A:p.E673K |
| HC-MBL_4 | HC-MBL | 11 | 119027281 | 119027281 | T | A | ABCG4 | nonsyn SNV | 0.48 | ABCG4:NM_001142505:exon8:c.T818A:p.I273N |
| HC-MBL_4 | HC-MBL | 12 | 6184709 | 6184709 | C | T | VWF | stopgain SNV | 0.40 | VWF:NM_000552:exon7:c.G666A:p.W222X |
| HC-MBL_4 | HC-MBL | 12 | 6938098 | 6938098 | A | T | LEPREL2 | unknown | 0.54 | UNKNOWN |
| HC-MBL_4 | HC-MBL | 12 | 38714077 | 38714077 | T | C | ALG10B | nonsyn SNV | 0.43 | ALG10B:NM_001013620:exon3:c.T484C:p.F162L |
| HC-MBL_4 | HC-MBL | 12 | 117610322 | 117610322 | T | A | FBXO21 | nonsyn SNV | 0.40 | FBXO21:NM_015002:exon7:c.A967T:p.N323Y |
| HC-MBL_4 | HC-MBL | 13 | 42393505 | 42393505 | T | C | VWA8 | nonsyn SNV | 0.45 | VWA8:NM_001009814:exon15:c.A1718G:p.H573R |
| HC-MBL_4 | HC-MBL | 14 | 69259667 | 69259667 | G | A | ZFP36L1 | stopgain SNV | 0.52 | ZFP36L1:NM_001244701:exon2:c.C196T:p.R66X |
| HC-MBL_4 | HC-MBL | 14 | 73989372 | 73989372 | C | T | HEATR4 | nonsyn SNV | 0.32 | HEATR4:NM_203309:exon2:c.G485A:p.R162H |
| HC-MBL_4 | HC-MBL | 15 | 39886510 | 39886510 | T | A | THBS1 | nonsyn SNV | 0.48 | THBS1:NM_003246:exon21:c.T3374A:p.M1125K |
| HC-MBL_4 | HC-MBL | 17 | 26733131 | 26733131 | A | G | SLC46A1 | nonsyn SNV | 0.45 | SLC46A1:NM_001242366:exon1:c.T2C:p.M1T |
| HC-MBL_4 | HC-MBL | 18 | 3879897 | 3879897 | C | T | DLGAP1 | nonsyn SNV | 0.38 | DLGAP1:NM_001242761:exon4:c.G172A:p.V58M |
| HC-MBL_4 | HC-MBL | 18 | 59170258 | 59170258 | A | G | CDH20 | nonsyn SNV | 0.41 | CDH20:NM_031891:exon4:c.A734G:p.K245R |
| HC-MBL_4 | HC-MBL | 20 | 62421203 | 62421203 | G | A | ZBTB46 | nonsyn SNV | 0.61 | ZBTB46:NM_025224:exon2:c.C908T:p.S303L |
| HC-MBL_5 | HC-MBL | 2 | 77745761 | 77745761 | C | T | LRRTM4 | nonsyn SNV | 0.20 | LRRTM4:NM_001134745:exon3:c.G1234A:p.G412S |
| HC-MBL_5 | HC-MBL | 2 | 141291664 | 141291664 | C | T | LRP1B | nonsyn SNV | 0.29 | LRP1B:NM_018557:exon47:c.G7688A:p.R2563H |
| HC-MBL_5 | HC-MBL | 5 | 5473726 | 5473726 | T | G | KIAA0947 | stopgain SNV | 0.43 | KIAA0947:NM_015325:exon16:c.T6278G:p.L2093X |
| HC-MBL_5 | HC-MBL | 8 | 2832075 | 2832075 | C | T | CSMD1 | nonsyn SNV | 0.48 | CSMD1:NM_033225:exon56:c.G8638A:p.V2880I |
| HC-MBL_5 | HC-MBL | 8 | 65493578 | 65493578 | G | T | BHLHE22 | nonsyn SNV | 0.41 | BHLHE22:NM_152414:exon1:c.G231T:p.L77F |
| HC-MBL_5 | HC-MBL | 10 | 54042064 | 54042064 | T | C | PRKG1 | nonsyn SNV | 0.47 | PRKG1:NM_001098512:exon14:c.T1652C:p.L551P |
| HC-MBL_5 | HC-MBL | 10 | 93740251 | 93740251 | T | G | BTAF1 | nonsyn SNV | 0.46 | BTAF1:NM_003972:exon15:c.T1691G:p.L564R |
| HC-MBL_5 | HC-MBL | 14 | 37050262 | 37050262 | C | G | NKX2-8 | nonsyn SNV | 0.45 | NKX2-8:NM_014360:exon2:c.G565C:p.V189L |
| HC-MBL_5 | HC-MBL | 18 | 29454651 | 29454651 | C | T | TRAPPC8 | nonsyn SNV | 0.23 | TRAPPC8:NM_014939:exon13:c.G1745A:p.R582H |
| HC-MBL_5 | HC-MBL | 20 | 25462723 | 25462723 | C | T | NINL | nonsyn SNV | 0.55 | NINL:NM_025176:exon14:c.G1691A:p.R564H |
| HC-MBL_5 | HC-MBL | 22 | 23235998 | 23235998 | G | C | IGLL5 | nonsyn SNV | 0.45 | IGLL5:NM_001178126:exon2:c.G325C:p.G109R |
| LC-MBL_1 | LC-MBL | 10 | 125528215 | 125528215 | C | T | CPXM2 | nonsyn SNV | 0.25 | CPXM2:NM_198148:exon9:c.G1126A:p.A376T |
| LC-MBL_2 | LC-MBL | 2 | 73675413 | 73675413 | C | G | ALMS1 | nonsyn SNV | 0.35 | ALMS1:NM_015120:exon8:c.C1756G:p.Q586E |
| LC-MBL_2 | LC-MBL | 2 | 215809726 | 215809726 | T | A | ABCA12 | nonsyn SNV | 0.45 | ABCA12:NM_015657:exon41:c.A6388T:p.S2130C |
| LC-MBL_2 | LC-MBL | 3 | 190127746 | 190127746 | C | T | CLDN16 | nonsyn SNV | 0.50 | CLDN16:NM_006580:exon5:c.C839T:p.A280V |
| LC-MBL_2 | LC-MBL | 4 | 8293128 | 8293128 | C | T | HTRA3 | nonsyn SNV | 0.25 | HTRA3:NM_053044:exon4:c.C740T:p.S247L |
| LC-MBL_2 | LC-MBL | 4 | 158224886 | 158224886 | A | C | GRIA2 | nonsyn SNV | 0.44 | GRIA2:NM_000826:exon3:c.A412C:p.S138R |
| LC-MBL_2 | LC-MBL | 5 | 140719538 | 140719538 | A | G | PCDHGA2 | nonsyn SNV | 0.38 | PCDHGA2:NM_018915:exon1:c.A1000G:p.I334V |
| LC-MBL_2 | LC-MBL | 5 | 168678399 | 168678399 | G | A | SLIT3 | stopgain SNV | 0.38 | SLIT3:NM_001271946:exon2:c.C262T:p.R88X |
| LC-MBL_2 | LC-MBL | 8 | 113241012 | 113241012 | C | A | CSMD3 | nonsyn SNV | 0.39 | CSMD3:NM_052900:exon68:c.G10430T:p.G3477V |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| LC-MBL_2 | LC-MBL | 11 | 55798000 | 55798000 | A | G | OR5AS1 | nonsyn SNV | 0.43 | OR5AS1:NM_001001921:exon1:c.A106G:p.T36A |
| LC-MBL_2 | LC-MBL | 16 | 16271339 | 16271339 | C | A | ABCC6 | nonsyn SNV | 0.50 | ABCC6:NM_001171:exon19:c.G2560T:p.A854S |
| LC-MBL_2 | LC-MBL | 17 | 4848222 | 4848222 | G | - | RNF167 | frameshift del | 0.36 | RNF167:NM_015528:exon10:c.964delG:p.G322fs |
| LC-MBL_2 | LC-MBL | 18 | 24722740 | 24722740 | G | T | CHST9 | nonsyn SNV | 0.55 | CHST9:NM_001256316:exon2:c.C34A:p.Q12K |
| LC-MBL_2 | LC-MBL | 20 | 60318795 | 60318795 | G | A | CDH4 | nonsyn SNV | 0.40 | CDH4:NM_001252338:exon2:c.G235A:p.V79M |
| LC-MBL_2 | LC-MBL | X | 100087817 | 100087817 | C | A | CSTF2 | nonsyn SNV | 0.65 | CSTF2:NM_001325:exon10:c.C1126A:p.P376T |
| LC-MBL_2 | LC-MBL | X | 142596924 | 142596924 | T | G | SPANXN3 | nonsyn SNV | 0.55 | SPANXN3:NM_001009609:exon2:c.A146C:p.Y49S |
| LC-MBL_2 | LC-MBL | X | 152981136 | 152981136 | G | A | BCAP31 | nonsyn SNV | 0.38 | BCAP31:NM_001139441:exon4:c.C202T:p.R68C |
| LC-MBL_3 | LC-MBL | 2 | 26950748 | 26950748 | C | T | KCNK3 | nonsyn SNV | 0.52 | KCNK3:NM_002246:exon2:c.C497T:p.S166L |
| LC-MBL_3 | LC-MBL | 3 | 164755760 | 164755760 | T | C | SI | nonsyn SNV | 0.44 | SI:NM_001041:exon21:c.A2354G:p.D785G |
| LC-MBL_3 | LC-MBL | 4 | 129127603 | 129127603 | T | A | LARP1B | nonsyn SNV | 0.52 | LARP1B:NM_018078:exon18:c.T2330A:p.F777Y |
| LC-MBL_3 | LC-MBL | 9 | 90534209 | 90534209 | C | - | SPATA31C1 | frameshift del | 0.20 | SPATA31C1:NM_001145124:exon2:c.229delC:p.P77fs |
| LC-MBL_3 | LC-MBL | 9 | 90534212 | 90534212 | A | T | SPATA31C1 | nonsyn SNV | 0.20 | SPATA31C1:NM_001145124:exon2:c.A232T:p.T78S |
| LC-MBL_3 | LC-MBL | 12 | 113874582 | 113874582 | C | T | SDSL | nonsyn SNV | 0.41 | SDSL:NM_138432:exon8:c.C698T:p.T233M |
| LC-MBL_3 | LC-MBL | 13 | 86369596 | 86369596 | G | A | SLITRK6 | nonsyn SNV | 0.38 | SLITRK6:NM_032229:exon2:c.C1048T:p.R350C |
| LC-MBL_3 | LC-MBL | 17 | 41891664 | 41891664 | T | A | MPP3 | nonsyn SNV | 0.48 | MPP3:NM_001932:exon15:c.A1075T:p.M359L |
| LC-MBL_3 | LC-MBL | 18 | 13056068 | 13056068 | A | G | CEP192 | nonsyn SNV | 0.44 | CEP192:NM_032142:exon19:c.A3479G:p.E1160G |
| LC-MBL_3 | LC-MBL | 19 | 14523407 | 14523407 | A | G | DDX39A | nonsyn SNV | 0.47 | DDX39A:NM_005804:exon3:c.T292C:p.F98L |
| LC-MBL_3 | LC-MBL | 22 | 23230357 | 23230357 | A | G | IGLL5 | nonsyn SNV | 0.62 | IGLL5:NM_001178126:exon1:c.A124G:p.M42V |
| LC-MBL_4 | LC-MBL | 2 | 32733268 | 32733268 | T | C | BIRC6 | nonsyn SNV | 0.40 | BIRC6:NM_016252:exon51:c.T9922C:p.S3308P |
| LC-MBL_4 | LC-MBL | 19 | 21720566 | 21720566 | G | T | ZNF429 | nonsyn SNV | 0.49 | ZNF429:NM_001001415:exon4:c.G1711T:p.D571Y |
| LC-MBL_4 | LC-MBL | 22 | 23230365 | 23230365 | A | G | IGLL5 | nonsyn SNV | 0.35 | IGLL5:NM_001256296:exon1:c.A26G:p.H9R |
| LC-MBL_5 | LC-MBL | 1 | 63069667 | 63069667 | T | A | ANGPTL3 | nonsyn SNV | 0.30 | ANGPTL3:NM_014495:exon6:c.T959A:p.I320K |
| LC-MBL_5 | LC-MBL | 1 | 63069849 | 63069849 | T | C | ANGPTL3 | nonsyn SNV | 0.36 | ANGPTL3:NM_014495:exon6:c.T1141C:p.F381L |
| LC-MBL_5 | LC-MBL | 3 | 183273170 | 183273170 | G | T | KLHL6 | nonsyn SNV | 0.45 | KLHL6:NM_130446:exon1:c.C272A:p.A91D |
| LC-MBL_5 | LC-MBL | 9 | 123210220 | 123210220 | T | G | CDK5RAP2 | nonsyn SNV | 0.46 | CDK5RAP2:NM_001272039:exon19:c.A2288C:p.E763A |
| LC-MBL_5 | LC-MBL | 10 | 43089689 | 43089689 | G | C | ZNF33B | nonsyn SNV | 0.48 | ZNF33B:NM_006955:exon5:c.C709G:p.R237G |
| LC-MBL_5 | LC-MBL | 12 | 33021968 | 33021968 | G | A | PKP2 | stopgain SNV | 0.64 | PKP2:NM_001005242:exon4:c.C1063T:p.R355X |
| LC-MBL_5 | LC-MBL | 14 | 105517528 | 105517528 | G | A | GPR132 | nonsyn SNV | 0.50 | GPR132:NM_013345:exon4:c.C946T:p.R316C |
| LC-MBL_5 | LC-MBL | 20 | 590434 | 590434 | C | A | TCF15 | nonsyn SNV | 0.58 | TCF15:NM_004609:exon1:c.G448T:p.A150S |
| LC-MBL_5 | LC-MBL | 22 | 39421294 | 39421294 | C | T | APOBEC3D | nonsyn SNV | 0.50 | APOBEC3D:NM_152426:exon3:c.C430T:p.R144W |
| LC-MBL_6 | LC-MBL | 2 | 101604571 | 101604571 | A | - | NPAS2 | frameshift del | 0.42 | NPAS2:NM_002518:exon17:c.1660delA:p.S554fs |
| LC-MBL_6 | LC-MBL | 8 | 11995033 | 11995033 | G | T | USP17L2 | nonsyn SNV | 0.71 | USP17L2:NM_201402:exon1:c.C1237A:p.P413T |
| LC-MBL_6 | LC-MBL | 9 | 77415255 | 77415255 | G | T | TRPM6 | nonsyn SNV | 0.43 | TRPM6:NM_001177310:exon17:c.C2138A:p.P713H |
| LC-MBL_6 | LC-MBL | 9 | 107288862 | 107288862 | G | A | OR13C4 | nonsyn SNV | 0.40 | OR13C4:NM_001001919:exon1:c.C629T:p.P210L |
| LC-MBL_6 | LC-MBL | 11 | 74347276 | 74347276 | G | A | POLD3 | nonsyn SNV | 0.34 | POLD3:NM_006591:exon11:c.G1154A:p.R385H |
| LC-MBL_6 | LC-MBL | 11 | 113101945 | 113101945 | G | A | NCAM1 | nonsyn SNV | 0.47 | NCAM1:NM_001242607:exon11:c.G1117A:p.G373S |
| LC-MBL_6 | LC-MBL | 12 | 94975570 | 94975570 | C | A | TMCC3 | nonsyn SNV | 0.37 | TMCC3:NM_020698:exon2:c.G823T:p.A275S |
| LC-MBL_6 | LC-MBL | 13 | 20716839 | 20716839 | G | A | GJA3 | nonsyn SNV | 0.63 | GJA3:NM_021954:exon2:c.C589T:p.P197S |
| LC-MBL_6 | LC-MBL | 13 | 28498404 | 28498404 | G | C | PDX1 | nonsyn SNV | 0.22 | PDX1:NM_000209:exon2:c.G418C:p.A140P |
| LC-MBL_6 | LC-MBL | 15 | 75499628 | 75499643 | CCAGAGGGCATGCCAG | - | C15orf39 | frameshift del | 0.27 | C15orf39:NM_015492:exon2:c.1239_1254del:p.413_418del |
| LC-MBL_6 | LC-MBL | 16 | 70708357 | 70708357 | C | A | MTSS1L | nonsyn SNV | 0.55 | MTSS1L:NM_138383:exon11:c.G905T:p.S302I |
| LC-MBL_6 | LC-MBL | 19 | 42384965 | 42384965 | A | G | CD79A | nonsyn SNV | 0.53 | CD79A:NM_001783:exon5:c.A599G:p.E200G |
| LC-MBL_6 | LC-MBL | 21 | 22910199 | 22910199 | A | G | NCAM2 | nonsyn SNV | 0.45 | NCAM2:NM_004540:exon18:c.A2435G:p.E812G |
| CLL_4-PMN | PMN | 22 | 29885644 | 29885644 | C | A | NEFH | nonsyn SNV | 0.18 | NEFH:NM_021076:exon4:c.C2015A:p.A672E |
| CLL_5-PMN | PMN | 13 | 114783628 | 114783628 | A | C | RASA3 | nonsyn SNV | 0.24 | RASA3:NM_007368:exon11:c.T1043G:p.V348G |
| HC-MBL_5-PMN | PMN | 3 | 8671350 | 8671350 | - | A | SSUH2 | frameshift ins | 0.19 | SSUH2:NM_001256748:exon7:c.587_588insT:p.T196fs |
| HC-MBL_5-PMN | PMN | 5 | 16703202 | 16703202 | A | C | MYO10 | nonsyn SNV | 0.47 | MYO10:NM_012334:exon23:c.T2342G:p.L781R |

| HC-MBL_5-PMN | PMN | 22 | 29885552 | 29885553 | AA | - | NEFH | frameshift del | 0.25 | NEFH:NM_021076:exon4:c.1923_1924del:p.641_642del |
| HC-MBL_5-PMN | PMN | 22 | 29885554 | 29885554 | C | T | NEFH | nonsyn SNV | 0.25 | NEFH:NM_021076:exon4:c.C1925T:p.T642M |
| HC-MBL_5-PMN | PMN | 22 | 29885557 | 29885558 | AG | - | NEFH | frameshift del | 0.25 | NEFH:NM_021076:exon4:c.1928_1929del:p.643_643del |
| HC-MBL_5-PMN | PMN | 22 | 29885561 | 29885562 | GG | - | NEFH | frameshift del | 0.25 | NEFH:NM_021076:exon4:c.1932_1933del:p.644_645del |
| LC-MBL_1-PMN | PMN | 4 | 9213757 | 9213757 | G | C | USP17L10 | nonsyn SNV | 0.11 | USP17L10:NM_001256852:exon1:c.G1375C:p.V459L |
| LC-MBL_3-PMN | PMN | 22 | 29885552 | 29885553 | AA | - | NEFH | frameshift del | 0.16 | NEFH:NM_021076:exon4:c.1923_1924del:p.641_642del |
| LC-MBL_3-PMN | PMN | 22 | 29885554 | 29885554 | C | T | NEFH | nonsyn SNV | 0.16 | NEFH:NM_021076:exon4:c.C1925T:p.T642M |
| LC-MBL_3-PMN | PMN | 22 | 29885557 | 29885558 | AG | - | NEFH | frameshift del | 0.16 | NEFH:NM_021076:exon4:c.1928_1929del:p.643_643del |
| LC-MBL_3-PMN | PMN | 22 | 29885561 | 29885562 | GG | - | NEFH | frameshift del | 0.16 | NEFH:NM_021076:exon4:c.1932_1933del:p.644_645del |
| LC-MBL_5-PMN | PMN | 4 | 88537069 | 88537069 | - | GATAGCAGC | DSPP | nonframeshift ins | 0.97 | DSPP:NM_014208:exon5:c.3255_3256insGATAGCAGC:p.S1085delinsSDSS |
| LC-MBL_6-PMN | PMN | 17 | 39305760 | 39305760 | C | T | KRTAP4-5 | nonsyn SNV | 0.18 | KRTAP4-5:NM_033188:exon1:c.G260A:p.R87K |

**Table S7.** List of all samples included in the WGS analysis, the targeted re-sequencing analysis or both.

| Sample ID | Entity | WGS and deep-sequencing analysis | Only WGS analysis | Only deep-sequencing analysis |
|---|---|:---:|:---:|:---:|
| CLL_1 | CLL | ✓ | | |
| CLL_2 | CLL | ✓ | | |
| CLL_3 | CLL | ✓ | | |
| CLL_4 | CLL | ✓ | | |
| CLL_5 | CLL | ✓ | | |
| CLL_6 | CLL | | | ✓ |
| CLL_7 | CLL | | | ✓ |
| HC-MBL_1 | HC-MBL | ✓ | | |
| HC-MBL_2 | HC-MBL | ✓ | | |
| HC-MBL_3 | HC-MBL | ✓ | | |
| HC-MBL_4 | HC-MBL | ✓ | | |
| HC-MBL_5 | HC-MBL | ✓ | | |
| HC-MBL_6 | HC-MBL | | | ✓ |
| HC-MBL_7 | HC-MBL | | | ✓ |
| HC-MBL_8 | HC-MBL | | | ✓ |
| HC-MBL_9 | HC-MBL | | | ✓ |
| HC-MBL_10 | HC-MBL | | | ✓ |
| HC-MBL_11 | HC-MBL | | | ✓ |
| HC-MBL_12 | HC-MBL | | | ✓ |
| HC-MBL_13 | HC-MBL | | | ✓ |
| LC-MBL_1 | LC-MBL | ✓ | | |
| LC-MBL_2 | LC-MBL | ✓ | | |
| LC-MBL_3 | LC-MBL | ✓ | | |
| LC-MBL_4 | LC-MBL | | ✓ | |
| LC-MBL_5 | LC-MBL | ✓ | | |
| LC-MBL_6 | LC-MBL | ✓ | | |
| LC-MBL_7 | LC-MBL | | | ✓ |
| LC-MBL_8 | LC-MBL | | | ✓ |
| LC-MBL_9 | LC-MBL | | | ✓ |
| CLL_1-PMN | PMN | ✓ | | |
| CLL_2-PMN | PMN | ✓ | | |
| CLL_4-PMN | PMN | ✓ | | |
| CLL_6-PMN | PMN | | | ✓ |
| CLL_7-PMN | PMN | | | ✓ |
| HC-MBL_1-PMN | PMN | ✓ | | |
| HC-MBL_2-PMN | PMN | ✓ | | |
| HC-MBL_3-PMN | PMN | ✓ | | |
| HC-MBL_4-PMN | PMN | ✓ | | |
| HC-MBL_5-PMN | PMN | ✓ | | |

| | | | | |
|---|---|---|---|---|
| HC-MBL_6-PMN | PMN | | | ✓ |
| HC-MBL_7-PMN | PMN | | | ✓ |
| HC-MBL_9-PMN | PMN | | | ✓ |
| HC-MBL_10-PMN | PMN | | | ✓ |
| HC-MBL_11-PMN | PMN | | | ✓ |
| HC-MBL_12-PMN | PMN | | | ✓ |
| HC-MBL_13-PMN | PMN | | | ✓ |
| LC-MBL_1-PMN | PMN | ✓ | | |
| LC-MBL_2-PMN | PMN | ✓ | | |
| LC-MBL_3-PMN | PMN | ✓ | | |
| LC-MBL_4-PMN | PMN | | ✓ | |
| LC-MBL_5-PMN | PMN | ✓ | | |
| LC-MBL_6-PMN | PMN | ✓ | | |
| LC-MBL_7-PMN | PMN | | | ✓ |
| LC-MBL_8-PMN | PMN | | | ✓ |

**Table S8.** High quality exonic variants identified by targeted re-sequencing.

| Sample ID | Entity | Chr | Start | End | Ref_base | Var_base | Gene | Exonic_type | VAF | Transcripts |
|---|---|---|---|---|---|---|---|---|---|---|
| HC-MBL_2 | HC-MBL | 4 | 153249504 | 153249504 | C | G | FBXW7 | nonsyn SNV | 11.56 | NM_001013415:exon8:c.G920C:p.W307S |
| HC-MBL_2 | HC-MBL | 7 | 124532330 | 124532330 | G | C | POT1 | nonsyn SNV | 6.73 | NM_015450:exon6:c.C114G:p.S38R |
| HC-MBL_4 | HC-MBL | 9 | 139390649 | 139390650 | AG | - | NOTCH1 | frameshift del | 16.82 | NM_017617:exon34:c.7541_7542del:p.P2514fs |
| HC-MBL_5 | HC-MBL | 2 | 198266834 | 198266834 | T | C | SF3B1 | nonsyn SNV | 1.05 | NM_012433:exon15:c.A2098G:p.K700E |
| HC-MBL_5 | HC-MBL | 7 | 124537227 | 124537227 | T | C | POT1 | nonsyn SNV | 4.27 | NM_015450:exon5:c.A1G:p.M1V |
| HC-MBL_5-PMN | PMN | 17 | 7577547 | 7577547 | C | G | TP53 | nonsyn SNV | 2.77 | NM_001126115:exon3:c.G338C:p.G113A |
| LC-MBL_3-PMN | PMN | 11 | 108117798 | 108117798 | C | T | ATM | nonsyn SNV | 20.17 | NM_000051:exon8:c.C1009T:p.R337C |

**Table S9.** Prioritized non-coding variants in our cohort using Funseq2.

| Sample | Entity | Chr | Position | Ref base | Var base | GERP | Gene | Cancer Gene |
|--------|--------|-----|----------|----------|----------|------|------|-------------|
| CLL_1 | CLL | 1 | 203275300 | T | C | -2,83 | BTG2(intr&prom) | BTG2[DNA_repair] |
| CLL_1 | CLL | 1 | 203275399 | T | A | 1,4 | BTG2(intr&prom) | BTG2[DNA_repair] |
| CLL_1 | CLL | 1 | 203275440 | T | C | -2,01 | BTG2(intr&prom) | BTG2[DNA_repair] |
| CLL_1 | CLL | 3 | 186783656 | C | T | 0,361 | ST6GAL1(intr) | - |
| CLL_1 | CLL | 6 | 162170004 | C | T | -5,59 | PARK2(intr) | - |
| CLL_1 | CLL | 12 | 122460851 | T | C | -4,55 | BCL7A(intr&prom) | BCL7A[cancer] |
| CLL_2 | CLL | 1 | 214175915 | T | G | 1 | PROX1(intr) | - |
| CLL_2 | CLL | 14 | 71243089 | A | G | 0,978 | MAP3K9(intr) | - |
| CLL_2 | CLL | 16 | 21611962 | T | C | 2,17 | METTL9(intr&prom) | - |
| CLL_3 | CLL | 1 | 36622448 | C | A | -6,99 | MAP7D1(intr&prom) | - |
| CLL_3 | CLL | 1 | 203275722 | C | T | 2 | BTG2(intr&prom) | BTG2[DNA_repair] |
| CLL_3 | CLL | 2 | 85732494 | G | T | 0,656 | CAPG(dis)MAT2A(dis)RNF181(dis)SFTPB(dis)VAMP5(dis)VAMP8(dis) | - |
| CLL_3 | CLL | 3 | 23936126 | G | A | - | NKIRAS1(intr) | - |
| CLL_3 | CLL | 3 | 186783539 | T | A | 0,597 | ST6GAL1(intr) | - |
| CLL_3 | CLL | 3 | 186783608 | C | G | 0,345 | ST6GAL1(intr) | - |
| CLL_3 | CLL | 3 | 186783685 | T | A | -0,496 | ST6GAL1(intr) | - |
| CLL_3 | CLL | 11 | 48041339 | T | C | -0,082 | PTPRJ(intr) | - |
| CLL_3 | CLL | 15 | 45329320 | A | G | -1,49 | SORD(intr) | - |
| CLL_3 | CLL | 16 | 74700936 | G | A | 4,17 | RFWD3(prom) | RFWD3[DNA_repair] |
| CLL_3 | CLL | 19 | 46464080 | A | C | 2,14 | NOVA2(intr) | - |
| CLL_4 | CLL | 1 | 46993788 | G | C | 2,63 | UQCRH(dis) | - |
| CLL_4 | CLL | 3 | 186783576 | G | A | 3,11 | ST6GAL1(intr) | - |
| CLL_4 | CLL | 3 | 186783579 | G | A | 0,0486 | ST6GAL1(intr) | - |
| CLL_4 | CLL | 14 | 37667115 | C | G | -5,74 | MIPOL1(prom) | - |
| CLL_4 | CLL | 18 | 60988085 | C | T | 0,502 | BCL2(prom) | BCL2[actionable][cancer] |
| CLL_5 | CLL | 1 | 40847880 | A | G | 4,36 | SMAP2(intr) | - |
| CLL_5 | CLL | 1 | 164741374 | A | T | 0,326 | PBX1(intr) | PBX1[cancer] |
| CLL_5 | CLL | 3 | 23936126 | G | A | - | NKIRAS1(intr) | - |
| CLL_5 | CLL | 6 | 106773194 | C | G | 1,27 | ATG5(prom&UTR) | - |
| CLL_5 | CLL | 11 | 102189019 | C | T | 0,846 | BIRC3(intr) | BIRC3[cancer] |
| CLL_5 | CLL | 12 | 32832099 | T | G | 4,46 | DNM1L(prom) | - |

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|---|---|---|---|---|---|---|---|---|
| CLL_5 | CLL | 19 | 2051560 | C | T | 0,147 | MKNK2(prom) | - |
| HC-MBL_1 | HC-MBL | 1 | 203275423 | C | G | 1,9 | BTG2(intr&prom) | BTG2[DNA_repair] |
| HC-MBL_1 | HC-MBL | 1 | 203275443 | T | C | 2,56 | BTG2(intr&prom) | BTG2[DNA_repair] |
| HC-MBL_1 | HC-MBL | 3 | 47823658 | G | C | -0,289 | SMARCC1(prom) | - |
| HC-MBL_1 | HC-MBL | 3 | 47823668 | A | C | -1,7 | SMARCC1(prom) | - |
| HC-MBL_1 | HC-MBL | 3 | 187462358 | A | G | -0,748 | BCL6(intr&prom) | BCL6[actionable][cancer] |
| HC-MBL_1 | HC-MBL | 3 | 187462529 | G | C | 2,12 | BCL6(intr&prom) | BCL6[actionable][cancer] |
| HC-MBL_1 | HC-MBL | 7 | 76178630 | C | T | - | UPK3B(intr) | - |
| HC-MBL_1 | HC-MBL | 7 | 158374412 | G | A | -0,326 | PTPRN2(intr) | - |
| HC-MBL_1 | HC-MBL | 10 | 75654546 | G | A | -0,15 | ADK(dis)AP3M1(dis)C10orf55(dis)CAMK2G(dis)CHCHD1(dis)PLAU(dis)SEC24C(dis)VCL(dis) | - |
| HC-MBL_1 | HC-MBL | 17 | 74734053 | G | A | 2,57 | MFSD11(prom&UTR) | - |
| HC-MBL_1 | HC-MBL | 19 | 14613558 | G | A | 1,36 | DNAJB1(dis)GIPC1(dis)MIR639(dis)PKN1(dis)TECR(dis) | - |
| HC-MBL_1 | HC-MBL | 21 | 45066483 | T | A | -0,477 | HSF2BP(intr) | - |
| HC-MBL_2 | HC-MBL | 1 | 21995326 | T | C | 0,467 | RAP1GAP(intr) | - |
| HC-MBL_2 | HC-MBL | 3 | 126247887 | T | C | 2,33 | C3orf22(intr)CHST13(intr) | - |
| HC-MBL_3 | HC-MBL | 6 | 80657408 | G | A | -0,118 | ELOVL4(prom) | - |
| HC-MBL_3 | HC-MBL | 7 | 44678984 | G | A | 0,263 | OGDH(intr) | - |
| HC-MBL_3 | HC-MBL | 7 | 99067253 | G | A | -0,911 | ZNF789(prom) | - |
| HC-MBL_3 | HC-MBL | 8 | 141521792 | C | T | -0,634 | AC1(intr&prom) | - |
| HC-MBL_3 | HC-MBL | 11 | 69455341 | T | C | -2,41 | CCND1(prom) | CCND1[DNA_repair][actionable][cancer] |
| HC-MBL_3 | HC-MBL | 12 | 52890401 | G | A | -3,1 | IGFBP6(dis)KRT18(dis)KRT4(dis)KRT5(dis)KRT6A(dis)KRT6B(dis)KRT6C(dis)KRT7(dis)KRT75(dis)KRT8(dis) | KRT5[DNA_repair] |
| HC-MBL_3 | HC-MBL | 15 | 72979375 | A | C | 0,0665 | BBS4(intr) | - |
| HC-MBL_3 | HC-MBL | 20 | 43975029 | G | A | 0,57 | SDC4(intr&prom) | SDC4[cancer] |
| HC-MBL_4 | HC-MBL | 1 | 154469618 | T | G | 5,43 | ADAR(dis)SHE(dis&intr)UBAP2L(dis) | - |
| HC-MBL_4 | HC-MBL | 10 | 14051939 | G | A | 1,89 | FRMD4A(intr&prom) | - |
| HC-MBL_4 | HC-MBL | 10 | 73982763 | T | A | 0,331 | ANAPC16(intr&prom)ASCC1(dis)DDIT4(dis)SPOCK2(dis) | - |
| HC-MBL_4 | HC-MBL | 11 | 102188518 | A | C | -4,89 | BIRC3(intr&prom) | BIRC3[cancer] |
| HC-MBL_4 | HC-MBL | 12 | 69754128 | A | G | -0,851 | YEATS4(intr&prom) | - |
| HC-MBL_4 | HC-MBL | 14 | 69259281 | T | A | -2,12 | ZFP36L1(intr&prom) | - |
| HC-MBL_4 | HC-MBL | 14 | 69259510 | T | A | 1,16 | ZFP36L1(intr&prom) | - |
| HC-MBL_4 | HC-MBL | 14 | 96179957 | A | G | 0,314 | TCL1A(intr) | TCL1A[cancer] |
| HC-MBL_4 | HC-MBL | 16 | 75681654 | T | G | -4,17 | KARS(intr&prom)TERF2IP(prom) | TERF2IP[DNA_repair] |
| HC-MBL_4 | HC-MBL | 18 | 4106601 | T | G | 2,44 | DLGAP1(intr) | - |
| HC-MBL_4 | HC-MBL | 18 | 12328135 | G | A | 0,949 | TUBB6(intr) | - |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| HC-MBL_4 | HC-MBL | 2 | 75381295 | C | T | -7,27 | TACR1(intr) | - |
| HC-MBL_4 | HC-MBL | 2 | 202646000 | C | T | 0,991 | ALS2(prom) | - |
| HC-MBL_4 | HC-MBL | 5 | 147051073 | T | C | 0,756 | JAKMIP2(intr) | - |
| HC-MBL_4 | HC-MBL | 8 | 38760365 | A | C | 1,15 | PLEKHA2(intr&prom) | - |
| HC-MBL_4 | HC-MBL | 8 | 38760381 | A | G | -1,3 | PLEKHA2(intr&prom) | - |
| HC-MBL_5 | HC-MBL | 3 | 58015823 | A | G | 1,54 | FLNB(intr) | - |
| HC-MBL_5 | HC-MBL | 4 | 16085748 | T | C | 0,845 | PROM1(prom&UTR) | - |
| HC-MBL_5 | HC-MBL | 9 | 5510779 | T | C | 0,0824 | PDCD1LG2(UTR) | - |
| HC-MBL_5 | HC-MBL | 11 | 16377920 | G | T | 5,7 | SOX6(intr) | - |
| HC-MBL_5 | HC-MBL | 11 | 128425760 | G | C | -0,523 | ETS1(intr) | ETS1[DNA_repair] |
| HC-MBL_5 | HC-MBL | 14 | 65149276 | A | G | 2,53 | GPX2(dis)HSPA2(dis)PLEKHG3(dis) | - |
| HC-MBL_5 | HC-MBL | 17 | 7766319 | T | G | -4,06 | LSMD1(intr) | - |
| LC-MBL_1 | LC-MBL | 7 | 45925242 | C | T | 0,975 | IGFBP1(dis) | - |
| LC-MBL_2 | LC-MBL | 1 | 203275550 | C | G | 3,87 | BTG2(intr&prom) | BTG2[DNA_repair] |
| LC-MBL_2 | LC-MBL | 1 | 203275574 | T | C | -4,78 | BTG2(intr&prom) | BTG2[DNA_repair] |
| LC-MBL_2 | LC-MBL | 1 | 203275871 | A | G | -0,234 | BTG2(intr&prom) | BTG2[DNA_repair] |
| LC-MBL_2 | LC-MBL | 8 | 26307602 | C | A | -2,19 | BNIP3L(intr) | - |
| LC-MBL_2 | LC-MBL | 8 | 67686962 | T | G | -5,34 | C8orf44-SGK3(intr)SGK3(intr&prom) | - |
| LC-MBL_2 | LC-MBL | 17 | 1968643 | C | G | -0,983 | SMG6(intr) | - |
| LC-MBL_2 | LC-MBL | 19 | 17634108 | C | G | -2,06 | FAM129C(prom) | - |
| LC-MBL_2 | LC-MBL | 22 | 47365593 | C | T | -3,23 | TBC1D22A(intr) | - |
| LC-MBL_2 | LC-MBL | 22 | 47365682 | T | C | -0,722 | TBC1D22A(intr) | - |
| LC-MBL_3 | LC-MBL | 5 | 133860532 | G | A | 1,74 | PHF15(intr&prom) | - |
| LC-MBL_3 | LC-MBL | 5 | 134094201 | C | T | -2,29 | DDX46(prom) | - |
| LC-MBL_3 | LC-MBL | 5 | 149184640 | C | T | 0,192 | PPARGC1B(intr) | - |
| LC-MBL_3 | LC-MBL | 6 | 11368027 | T | A | 1,41 | NEDD9(intr) | - |
| LC-MBL_3 | LC-MBL | 16 | 67260703 | A | C | 0,19 | LRRC29(prom&UTR) | - |
| LC-MBL_3 | LC-MBL | 22 | 41252751 | C | T | 5,15 | ST13(prom&UTR) | - |
| LC-MBL_4 | LC-MBL | 3 | 187462700 | G | A | 4,27 | BCL6(intr&prom) | BCL6[actionable][cancer] |
| LC-MBL_4 | LC-MBL | 3 | 187463529 | A | G | 2,11 | BCL6(prom) | BCL6[actionable][cancer] |
| LC-MBL_4 | LC-MBL | 3 | 187463764 | G | A | 4,53 | BCL6(prom) | BCL6[actionable][cancer] |
| LC-MBL_4 | LC-MBL | 6 | 34100411 | T | C | -4,84 | GRM4(intr) | - |
| LC-MBL_4 | LC-MBL | 9 | 20462552 | C | A | -0,344 | MLLT3(intr) | MLLT3[cancer] |
| LC-MBL_5 | LC-MBL | 6 | 91005922 | T | G | 4,04 | BACH2(intr&prom) | - |

| LC-MBL_5 | LC-MBL | 8 | 28266617 | T | C | -0,225 | FBXO16(intr)ZNF395(dis) | - |
| LC-MBL_5 | LC-MBL | 12 | 57078170 | G | C | 2,28 | PTGES3(intr&prom) | - |
| LC-MBL_5 | LC-MBL | X | 119006091 | T | A | -1,19 | NDUFA1(intr)RNF113A(prom) | - |
| LC-MBL_6 | LC-MBL | 2 | 225450786 | T | C | -1,05 | CUL3(prom) | - |
| LC-MBL_6 | LC-MBL | 4 | 103748140 | A | G | -0,842 | UBE2D3(prom&UTR) | UBE2D3[DNA_repair] |
| LC-MBL_6 | LC-MBL | 7 | 30265449 | C | T | 1,11 | C7orf41(dis)GARS(dis)ZNRF2(dis) | - |
| LC-MBL_6 | LC-MBL | 11 | 96000836 | G | A | 1,28 | MAML2(dis&intr) | MAML2[cancer] |

**Table S10.** List of NCV targeting TF binding sites resulting in a motif-breaking event.

| Entity | Chr | Position | Ref base | Var base | Gene | Motif-breaking |
|---|---|---|---|---|---|---|
| CLL | 6 | 162170004 | C | T | PARK2(intr) | CTCF,CTCFL,DHS,RAD21,SMC3 |
| CLL | 12 | 122460851 | T | C | BCL7A(intr&prom) | DHS,ZBTB7A |
| CLL | 1 | 214175915 | T | G | PROX1(intr) | FOS,JUN,JUND,NR3C1 |
| CLL | 14 | 71243089 | A | G | MAP3K9(intr) | DHS,PBX3 |
| CLL | 16 | 21611962 | T | C | METTL9(intr&prom) | CEBPB,CTCF,DHS,STAT3 |
| CLL | 1 | 36622448 | C | A | MAP7D1(intr&prom) | CCNT2,CHD2,DHS,MAX,SIN3A,USF1,USF2 |
| CLL | 1 | 203275722 | C | T | BTG2(intr&prom) | CTCF,DHS,EBF1,GATA1,GATA2,GATA3,MXI1,STAT1,STAT3,TBP,TRIM28,WRNIP1 |
| CLL | 11 | 48041339 | T | C | PTPRJ(intr) | DHS,GATA1 |
| CLL | 15 | 45329320 | A | G | SORD(intr) | CTCF,IRF4,MAX,RAD21,SMC3,SP1,YY1 |
| CLL | 16 | 74700936 | G | A | RFWD3(prom) | CHD2,DHS,E2F1,E2F4,ELF1,ELK4,FOS,FOSL2,GABPA,GATA1,IRF1,IRF3,MAX,NFYA,NFYB,PBX3,RFX5,SIX5,SP1,SP2,TBP,YY1 |
| CLL | 19 | 46464080 | A | C | NOVA2(intr) | CTCF,CTCFL,DHS,JUND,NANOG,POU2F2,POU5F1,RAD21,SP1,TCF12 |
| CLL | 1 | 46993788 | G | C | UQCRH(dis) | CEBPB,CTCF,EGR1,ELF1,FOS,FOSL1,GTF2F1,HDAC2,HMGN3,JUN,JUNB,JUND,MAX,MYC,PAX5,RAD21,SMC3,SPI1,STAT2,YY1,ZNF143,ZNF263 |
| CLL | 14 | 37667115 | C | G | MIPOL1(prom) | CCNT2,DHS,E2F1,E2F6,HDAC2,HMGN3,MAX,MYC,NRF1,STAT2,TAF1,TBP,TFAP2C,USF1,ZBTB7A,ZNF263 |
| CLL | 18 | 60988085 | C | T | BCL2(prom) | CTCF,DHS,EBF1,EGR1,FOXA1,NFKB1,TAF1,ZEB1 |
| CLL | 1 | 40847880 | A | G | SMAP2(intr) | DHS,JUNB |
| CLL | 1 | 164741374 | A | T | PBX1(intr) | CEBPB,DHS,EP300 |
| CLL | 6 | 106773194 | C | G | ATG5(prom&UTR) | DHS,E2F1,EBF1,SMARCB1,TFAP2A,TFAP2C,YY1,ZNF263 |
| CLL | 12 | 32832099 | T | G | DNM1L(prom) | CHD2,CTCF,DHS,EGR1,ELF1,ESR1,ETS1,GABPA,HMGN3,IRF1,JUND,MAX,MYC,NFKB1,NRF1,PAX5,RFX5,SIX5,SP1,TAF1,TBP,TRIM28,USF1,YY1,ZBTB7A,ZEB1,ZNF143 |
| HC-MBL | 3 | 47823658 | G | C | SMARCC1(prom) | BATF,BCL11A,BCLAF1,E2F1,E2F6,EBF1,EGR1,ELF1,ELK4,HMGN3,IRF4,JUNB,MAX,MEF2A,MEF2C,MYC,NFKB1,PAX5,POU2F2,REST,SP1,TAF1,TBP,TCF12,TCF7L2,TFAP2C,YY1 |
| HC-MBL | 3 | 47823668 | A | C | SMARCC1(prom) | BATF,BCL11A,BCLAF1,E2F1,E2F6,EBF1,EGR1,ELF1,ELK4,HMGN3,IRF4,JUNB,MAX,MEF2A,MEF2C,MYC,NFKB1,PAX5,POU2F2,REST,SP1,TAF1,TBP,TCF12,TCF7L2,TFAP2C,YY1 |
| HC-MBL | 7 | 76178630 | C | T | UPK3B(intr) | DHS,E2F6,EGR1,ELF1,ELK4,GABPA,MAX,MYC,NFKB1,NRF1,PAX5,REST,SP1,STAT1,TAF1,ZNF263 |
| HC-MBL | 7 | 158374412 | G | A | PTPRN2(intr) | FOXA1,HNF4G |
| HC-MBL | 10 | 75654546 | G | A | ADK(dis)AP3M1(dis)C10orf55(dis)CAMK2G(dis)CHCHD1(dis)PLAU(dis)SEC24C(dis)VCL(dis) | BATF,CEBPB,DHS,EBF1,EP300,FOS,FOSL1,GATA2,IRF4,JUN,JUND,SRF |
| HC-MBL | 17 | 74734053 | G | A | MFSD11(prom&UTR) | ATF3,BATF,BCL3,BHLHE40,CCNT2,DHS,E2F1,E2F4,E2F6,ELF1,EP300,ETS1,FOS,FOSL1,FOSL2,GABPA,HMGN3,JUN,JUNB,JUND,MAX,MXI1,MYC,NFKB1,NRF1,PAX5,SIN3A,SIX5,SP1,SREBF1,SRF,TAF1,TBP,TCF12,TCF7L2,THAP1,TRIM28,USF1,USF2,YY1,ZBTB7A,ZNF143,ZNF263 |
| HC-MBL | 19 | 14613558 | G | A | DNAJB1(dis)GIPC1(dis)MIR639(dis)PKN1(dis)TECR(dis) | CEBPB,E2F1,EP300,FOXA1,FOXA2,GTF2F1,JUN,JUND,MYC,NR3C1,RFX5,SMARCC1,STAT3,TFAP2A,USF2 |
| HC-MBL | 1 | 21995326 | T | C | RAP1GAP(intr) | CTCF,CTCFL,DHS,HMGN3,SPI1,ZBTB7A |
| HC-MBL | 3 | 126247887 | T | C | C3orf22(intr)CHST13(intr) | ATF3,CEBPB,CTCF,DHS,EP300,FOXA1,FOXA2,HDAC2,HNF4A,HNF4G,MAX,RAD21,RXRA,SP1,TBP |
| HC-MBL | 6 | 80657408 | G | A | ELOVL4(prom) | ATF3,DHS,E2F1,EGR1,MAX,NRF1,TBP,TCF12,USF1,ZNF263 |
| HC-MBL | 7 | 44678984 | G | A | OGDH(intr) | BATF,BCL11A,BCL3,BCLAF1,CEBPB,CHD2,CTCF,DHS,EBF1,EGR1,ELF1,ELK4,EP300,ETS1,FOS,FOSL1,FOSL2,GABPA,GATA2,GTF2F1,IRF4,JUN,JUNB,JUND,MAX,MEF2A,MEF2C,NFKB1,PAX5,POU2F2,RAD21,SIN3A,SIX5,SMARCB1,SMARCC1,SMC3,SP1,SPI1,TAF1,TBP,TCF12,TCF7L2,TFAP2C,YY1,ZEB1 |
| HC-MBL | 7 | 99067253 | G | A | ZNF789(prom) | DHS,TBP,USF1 |
| HC-MBL | 8 | 141521792 | C | T | AC1(intr&prom) | CCNT2,DHS,E2F1,EBF1,EGR1,PAX5,TAF1 |
| HC-MBL | 11 | 69455341 | T | C | CCND1(prom) | E2F1,TCF7L2 |
| HC-MBL | 12 | 52890401 | G | A | IGFBP6(dis)KRT18(dis)KRT4(dis)KRT5(dis)KRT6A(dis)KRT6B(dis)KRT6C(dis)KRT7(dis)KRT75(dis)KRT8(dis) | DHS,NR3C1,SIN3A |
| HC-MBL | 15 | 72979375 | A | C | BBS4(intr) | DHS,E2F1 |
| HC-MBL | 20 | 43975029 | G | A | SDC4(intr&prom) | DHS,MYC,SMARCB1,TFAP2C,ZBTB7A |
| HC-MBL | 1 | 154469618 | T | G | ADAR(dis)SHE(dis&intr)UBAP2L(dis) | DHS,ELF1,FOS,GABPA,GATA2,HDAC2,HNF4A,MAX,PAX5,SPI1,TAL1,ZBTB7A |
| HC-MBL | 2 | 75381295 | C | T | TACR1(intr) | BCL11A,CTCF,DHS,E2F1,ESR1,FOXA1,JUND,RAD21,SP1,TAF1 |
| HC-MBL | 2 | 202646000 | C | T | ALS2(prom) | ATF3,BRCA1,E2F1,ELF1,JUN,JUND,PRDM1,RFX5,SIN3A,SP1,SRF,TAF1,TBP,TCF7L2,YY1,ZNF263 |
| HC-MBL | 5 | 147051073 | T | C | JAKMIP2(intr) | EP300,FOXA1,FOXA2,HNF4A,HNF4G,SP1 |
| HC-MBL | 10 | 14051939 | G | A | FRMD4A(intr&prom) | BCL11A,DHS,NFKB1,PAX5 |
| HC-MBL | 10 | 73982763 | T | A | ANAPC16(intr&prom)ASCC1(dis)DDIT4(dis)SPOCK2(dis) | CTCF,DHS,MEF2A,RAD21,SMC3 |

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|---|---|---|---|---|---|---|
| HC-MBL | 12 | 69754128 | A | G | YEATS4(intr&prom) | E2F1,EBF1,EGR1,ETS1,FOXA1,FOXA2,GATA1,GTF2B,GTF2F1,MXI1,MYC,NFKB1,PBX3,SIN3A,SP1,TAF1,TBP,YY1 |
| HC-MBL | 14 | 69259281 | T | A | ZFP36L1(intr&prom) | EBF1 |
| HC-MBL | 16 | 75681654 | T | G | KARS(intr&prom)TERF2IP(prom) | CCNT2,DHS,E2F1,EGR1,ELF1,ETS1,FOSL2,GABPA,GTF2F1,IRF1,MYC,NFKB1,NR2C2,NRF1,PAX5,REST,SIN3A,SIX5,SP1,TAF1,TAF7,TBP,TRIM28,YY1 |
| HC-MBL | 18 | 4106601 | T | G | DLGAP1(intr) | CTCF,DHS,RAD21,SMC3 |
| HC-MBL | 18 | 12328135 | G | A | TUBB6(intr) | CEBPB,CTCF,CTCFL,DHS,EBF1,ELF1,GABPA,MAX,MYC,RAD21,SIN3A,SMC3,SPI1,TCF12,TFAP2A,TFAP2C,YY1,ZNF143 |
| HC-MBL | 4 | 16085748 | T | C | PROM1(prom&UTR) | DHS,REST,TAF1,TBP |
| HC-MBL | 9 | 5510779 | T | C | PDCD1LG2(UTR) | CHD2,DHS,TBP |
| HC-MBL | 11 | 16377920 | G | T | SOX6(intr) | FOXA1,RAD21 |
| HC-MBL | 11 | 128425760 | G | C | ETS1(intr) | CTCF,DHS,RAD21 |
| HC-MBL | 17 | 7766319 | T | G | LSMD1(intr) | CTCF,NFKB1 |
| LC-MBL | 7 | 45925242 | C | T | IGFBP1(dis) | CEBPB,DHS,EP300,FOSL2,FOXA1,FOXA2,GTF2F1,HDAC2,HNF4A,HNF4G,JUN,JUND,NR3C1,RFX5,RXRA,SMC3,SP1,STAT3,TCF12,TCF7L2,ZBTB33 |
| LC-MBL | 1 | 203275574 | T | C | BTG2(intr&prom) | CCNT2,DHS,E2F6,EGR1,ETS1,GATA1,GATA2,GATA3,JUN,JUND,MAX,MYC,REST,SIRT6,STAT1,STAT3,TAF1,TAL1,USF1,WRNIP1,ZBTB7A |
| LC-MBL | 8 | 26307602 | C | A | BNIP3L(intr) | GATA2,ZBTB7A |
| LC-MBL | 8 | 67686962 | T | G | C8orf44-SGK3(intr)SGK3(intr&prom) | E2F1,TAF1 |
| LC-MBL | 17 | 1968643 | C | G | SMG6(intr) | CTCF,ELF1 |
| LC-MBL | 22 | 47365593 | C | T | TBC1D22A(intr) | BATF,BCL11A,BCL3,DHS,EBF1,EGR1,ELF1,IRF4,MEF2A,NFKB1,PAX5,POU2F2,RAD21,SP1,TCF12,ZBTB33 |
| LC-MBL | 22 | 47365682 | T | C | TBC1D22A(intr) | BATF,BCL11A,BCL3,DHS,EBF1,EGR1,ELF1,IRF4,MEF2A,NFKB1,PAX5,POU2F2,SP1,TCF12,ZBTB33 |
| LC-MBL | 5 | 133860532 | G | A | PHF15(intr&prom) | E2F1,TFAP2A,TFAP2C |
| LC-MBL | 5 | 134094201 | C | T | DDX46(prom) | E2F1,E2F4,E2F6,GATA1,HMGN3,IRF1,MAX,NFKB1,PAX5,STAT1,STAT3,TAF1,TRIM28 |
| LC-MBL | 6 | 11368027 | T | A | NEDD9(intr) | CEBPB,DHS,EBF1,EP300,FOSL2,FOXA1,HDAC2,HNF4A,JUND,RAD21,RXRA,SP1,SRF,TBP,TCF7L2 |
| LC-MBL | 16 | 67260703 | A | C | LRRC29(prom&UTR) | CTCF,GATA1,HMGN3,TFAP2C |
| LC-MBL | 22 | 41252751 | C | T | ST13(prom&UTR) | CTCF,DHS,EP300,ETS1,GATA1,HSF1,MAX,MYC,NRF1,PPARGC1A,TAF1,TBP,USF1,USF2,ZNF263 |
| LC-MBL | 3 | 187463529 | A | G | BCL6(prom) | ATF3,BRCA1,DHS,EGR1,EP300,FOXA1,GTF2B,HDAC2,IRF1,JUND,MAX,NFE2,REST,RFX5,SIX5,SMARCC2,SP1,STAT1,STAT3,TAF1,TAF7,TBP,TCF7L2,TRIM28,USF1,USF2 |
| LC-MBL | 3 | 187463764 | G | A | BCL6(prom) | DHS,EP300,GTF2B,HDAC2,STAT1,TBP,ZBTB7A |
| LC-MBL | 9 | 20462552 | C | A | MLLT3(intr) | CTCF,DHS,RAD21 |
| LC-MBL | 8 | 28266617 | T | C | FBXO16(intr)ZNF395(dis) | DHS,FOXA1 |
| LC-MBL | 12 | 57078170 | G | C | PTGES3(intr&prom) | DHS,HNF4A,HNF4G,MEF2A,SIN3A,SP1,SPI1 |
| LC-MBL | X | 119006091 | T | A | NDUFA1(intr)RNF113A(prom) | CEBPB,DHS,GABPA |
| LC-MBL | 2 | 225450786 | T | C | CUL3(prom) | DHS,STAT1,TBP,TRIM28,ZNF263 |
| LC-MBL | 7 | 30265449 | C | T | C7orf41(dis)GARS(dis)ZNRF2(dis) | DHS,GATA2 |
| LC-MBL | 11 | 96000836 | G | A | MAML2(dis&intr) | BCL11A,DHS,IRF4,NFKB1,PAX5,RAD21,SMC3 |

**Table S11.** Pathway enrichment analysis of transcription factors that were implicated in the NVC-induced TF motif breaks in the MBL and ultra-stable CLL cohort.

| Cohort | Database | Signaling pathways | Adjusted P-value | Genes |
|---|---|---|---|---|
| MBL, ultra stable CLL | KEGG | MAPK | 0.00004398 | *ELK4, JUN, MEF2C, JUND, MAX, MYC, SRF, FOS, NFKB1* |
| | NCI-Nature | AP-1 | 1.165e-22 | *EGR1, TCF7L2, JUN, JUND, FOS, NR3C1, GATA2, ESR1, ETS1, FOSL2, FOSL1, ELF1, SP1, MYC, EP300, JUNB, ATF3* |
| | Panther | WNT | 0.001385 | *TCFL2, SMARCC1, HDAC2, SMARCB1, SMARCC2, MYC, EP300* |
| | BioCarta | MAPK | 9.649e-9 | *MEF2A, JUN, MEF2C, SP1, STAT1, MAX, MYC, FOS* |

**Table S12.** List of non-recurrent shared NCV between MBL/CLL and PMN samples.

| Sample ID | Entity | Chr | Start | End | Reference_base | Variant_base | Gene | Type | Var. ratio% | depth |
|---|---|---|---|---|---|---|---|---|---|---|
| HC-MBL_3 | HC-MBL | chrUn_gl000216 | 20780 | 20780 | C | A | NONE(dist=NONE),NONE(dist=NONE) | intergenic | 0.21 | 170 |
| HC-MBL_3 | PMN | chrUn_gl000216 | 20780 | 20780 | C | A | NONE(dist=NONE),NONE(dist=NONE) | intergenic | 0.20 | 122 |
| LC-MBL_1 | LC-MBL | chrUn_gl000225 | 31493 | 31493 | C | T | NONE(dist=NONE),NONE(dist=NONE) | intergenic | 0.26 | 34 |
| LC-MBL_1 | PMN | chrUn_gl000225 | 31493 | 31493 | C | T | NONE(dist=NONE),NONE(dist=NONE) | intergenic | 0.25 | 36 |
| CLL_4 | CLL | chr17 | 57565 | 57565 | G | C | DOC2B(dist=26145),RPH3AL(dist=4615) | intergenic | 0.48 | 35 |
| CLL_4 | PMN | chr17 | 57565 | 57565 | G | C | DOC2B(dist=26145),RPH3AL(dist=4615) | intergenic | 0.23 | 38 |
| LC-MBL_1 | LC-MBL | chrUn_gl000211 | 59603 | 59603 | - | TA | FLJ43315 | ncRNA_intronic | 0.40 | 44 |
| LC-MBL_1 | PMN | chrUn_gl000211 | 59603 | 59603 | - | TA | FLJ43315 | ncRNA_intronic | 0.35 | 60 |
| LC-MBL_6 | LC-MBL | chrUn_gl000225 | 198000 | 198000 | A | G | NONE(dist=NONE),NONE(dist=NONE) | intergenic | 0.25 | 66 |
| LC-MBL_6 | PMN | chrUn_gl000225 | 198000 | 198000 | A | G | NONE(dist=NONE),NONE(dist=NONE) | intergenic | 0.34 | 69 |
| HC-MBL_2 | HC-MBL | chr12 | 1496286 | 1496287 | CC | - | ERC1 | intronic | 0.28 | 49 |
| HC-MBL_2 | PMN | chr12 | 1496286 | 1496287 | CC | - | ERC1 | intronic | 0.26 | 34 |
| HC-MBL_2 | HC-MBL | chr12 | 1496291 | 1496291 | T | G | ERC1 | intronic | 0.28 | 49 |
| HC-MBL_2 | PMN | chr12 | 1496291 | 1496291 | T | G | ERC1 | intronic | 0.26 | 34 |
| HC-MBL_2 | HC-MBL | chr12 | 1496294 | 1496295 | CT | - | ERC1 | intronic | 0.28 | 49 |
| HC-MBL_2 | PMN | chr12 | 1496294 | 1496295 | CT | - | ERC1 | intronic | 0.26 | 34 |
| CLL_5 | CLL | chr19 | 4085791 | 4085791 | G | C | ZBTB7A(dist=18975),MAP2K2(dist=4529) | intergenic | 0.29 | 31 |
| CLL_5 | PMN | chr19 | 4085791 | 4085791 | G | C | ZBTB7A(dist=18975),MAP2K2(dist=4529) | intergenic | 0.25 | 35 |
| CLL_5 | CLL | chr19 | 4085794 | 4085799 | GGAGGG | - | ZBTB7A(dist=18978),MAP2K2(dist=4521) | intergenic | 0.29 | 31 |
| CLL_5 | PMN | chr19 | 4085794 | 4085799 | GGAGGG | - | ZBTB7A(dist=18978),MAP2K2(dist=4521) | intergenic | 0.25 | 35 |
| CLL_5 | CLL | chr19 | 4085801 | 4085801 | A | C | ZBTB7A(dist=18985),MAP2K2(dist=4519) | intergenic | 0.29 | 31 |
| CLL_5 | PMN | chr19 | 4085801 | 4085801 | A | C | ZBTB7A(dist=18985),MAP2K2(dist=4519) | intergenic | 0.25 | 35 |
| CLL_5 | CLL | chr19 | 4085804 | 4085804 | G | C | ZBTB7A(dist=18988),MAP2K2(dist=4516) | intergenic | 0.29 | 31 |
| CLL_5 | PMN | chr19 | 4085804 | 4085804 | G | C | ZBTB7A(dist=18988),MAP2K2(dist=4516) | intergenic | 0.25 | 35 |
| CLL_5 | CLL | chr19 | 4085805 | 4085805 | G | T | ZBTB7A(dist=18989),MAP2K2(dist=4515) | intergenic | 0.29 | 31 |
| CLL_5 | PMN | chr19 | 4085805 | 4085805 | G | T | ZBTB7A(dist=18989),MAP2K2(dist=4515) | intergenic | 0.25 | 35 |
| CLL_5 | CLL | chr19 | 4085807 | 4085807 | A | C | ZBTB7A(dist=18991),MAP2K2(dist=4513) | intergenic | 0.29 | 31 |
| CLL_5 | PMN | chr19 | 4085807 | 4085807 | A | C | ZBTB7A(dist=18991),MAP2K2(dist=4513) | intergenic | 0.25 | 35 |
| HC-MBL_1 | HC-MBL | chr2 | 4294004 | 4294004 | - | GAATGGAATG GAATGGAATG | LOC100505964(dist=272382),LOC727982(dist=381804) | intergenic | 0.24 | 25 |
| HC-MBL_1 | PMN | chr2 | 4294004 | 4294004 | - | GAATGGAATG GAATGGAATG | LOC100505964(dist=272382),LOC727982(dist=381804) | intergenic | 0.45 | 24 |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| LC-MBL_4 | LC-MBL | chr17 | 5110984 | 5110984 | G | A | LOC100130950 | ncRNA_intronic | 0.11 | 18 |
| LC-MBL_4 | PMN | chr17 | 5110984 | 5110984 | G | A | LOC100130950 | ncRNA_intronic | 0.16 | 25 |
| LC-MBL_4 | LC-MBL | chr17 | 5110987 | 5110987 | G | A | LOC100130950 | ncRNA_intronic | 0.11 | 18 |
| LC-MBL_4 | PMN | chr17 | 5110987 | 5110987 | G | A | LOC100130950 | ncRNA_intronic | 0.16 | 25 |
| LC-MBL_4 | LC-MBL | chr17 | 5110989 | 5110989 | G | A | LOC100130950 | ncRNA_intronic | 0.11 | 18 |
| LC-MBL_4 | PMN | chr17 | 5110989 | 5110989 | G | A | LOC100130950 | ncRNA_intronic | 0.16 | 25 |
| LC-MBL_4 | LC-MBL | chr17 | 5110992 | 5110992 | G | T | LOC100130950 | ncRNA_intronic | 0.11 | 18 |
| LC-MBL_4 | PMN | chr17 | 5110992 | 5110992 | G | T | LOC100130950 | ncRNA_intronic | 0.16 | 25 |
| LC-MBL_4 | LC-MBL | chr17 | 5110993 | 5110993 | G | A | LOC100130950 | ncRNA_intronic | 0.11 | 18 |
| LC-MBL_4 | PMN | chr17 | 5110993 | 5110993 | G | A | LOC100130950 | ncRNA_intronic | 0.16 | 25 |
| LC-MBL_4 | LC-MBL | chr17 | 5110997 | 5110997 | T | C | LOC100130950 | ncRNA_intronic | 0.11 | 18 |
| LC-MBL_4 | PMN | chr17 | 5110997 | 5110997 | T | C | LOC100130950 | ncRNA_intronic | 0.16 | 25 |
| CLL_2 | CLL | chr19 | 8792819 | 8792819 | - | CATTCACCCACTCATT | ADAMTS10(dist=117231),ACTL9(dist=14932) | intergenic | 0.36 | 52 |
| CLL_2 | PMN | chr19 | 8792819 | 8792819 | - | CATTCACCCACTCATT | ADAMTS10(dist=117231),ACTL9(dist=14932) | intergenic | 0.38 | 26 |
| CLL_4 | CLL | chr1 | 9134211 | 9134211 | A | G | SLC2A5(dist=4324),GPR157(dist=30265) | intergenic | 0.36 | 25 |
| CLL_4 | PMN | chr1 | 9134211 | 9134211 | A | G | SLC2A5(dist=4324),GPR157(dist=30265) | intergenic | 0.26 | 23 |
| CLL_4 | CLL | chr21 | 9997440 | 9997440 | A | G | TEKT4P2(dist=28847),TPTE(dist=909303) | intergenic | 0.44 | 36 |
| CLL_4 | PMN | chr21 | 9997440 | 9997440 | A | G | TEKT4P2(dist=28847),TPTE(dist=909303) | intergenic | 0.56 | 25 |
| LC-MBL_5 | LC-MBL | chr20 | 10856216 | 10856247 | AGGCCATGATTCAATCTGAGCCTAGGCCTCAG | - | JAG1(dist=201522),LOC339593(dist=391060) | intergenic | 0.52 | 50 |
| LC-MBL_5 | PMN | chr20 | 10856216 | 10856247 | AGGCCATGATTCAATCTGAGCCTAGGCCTCAG | - | JAG1(dist=201522),LOC339593(dist=391060) | intergenic | 0.48 | 62 |
| CLL_4 | CLL | chr6 | 13403204 | 13403204 | T | C | GFOD1 | intronic | 0.53 | 49 |
| CLL_4 | PMN | chr6 | 13403204 | 13403204 | T | C | GFOD1 | intronic | 0.16 | 59 |
| CLL_2 | CLL | chr18 | 14921306 | 14921316 | CAACCAGCAGA | - | ANKRD30B(dist=68569),LOC644669(dist=392239) | intergenic | 0.41 | 123 |
| CLL_2 | PMN | chr18 | 14921306 | 14921316 | CAACCAGCAGA | - | ANKRD30B(dist=68569),LOC644669(dist=392239) | intergenic | 0.53 | 39 |
| CLL_2 | CLL | chr18 | 14921321 | 14921321 | G | T | ANKRD30B(dist=68584),LOC644669(dist=392234) | intergenic | 0.30 | 134 |
| CLL_2 | PMN | chr18 | 14921321 | 14921321 | G | T | ANKRD30B(dist=68584),LOC644669(dist=392234) | intergenic | 0.37 | 37 |
| LC-MBL_5 | LC-MBL | chr11 | 15231917 | 15231917 | - | GCCTGTTCTGTGGGCTACAGACAT | INSC | intronic | 0.33 | 30 |
| LC-MBL_5 | PMN | chr11 | 15231917 | 15231917 | - | GCCTGTTCTGTGGGCTACAGACAT | INSC | intronic | 0.40 | 37 |
| LC-MBL_4 | LC-MBL | chr3 | 16035091 | 16035091 | G | T | MIR563(dist=119735),GALNT15(dist=181093) | intergenic | 0.21 | 23 |
| LC-MBL_4 | PMN | chr3 | 16035091 | 16035091 | G | T | MIR563(dist=119735),GALNT15(dist=181093) | intergenic | 0.54 | 11 |
| LC-MBL_4 | LC-MBL | chr3 | 16035092 | 16035092 | A | T | MIR563(dist=119736),GALNT15(dist=181092) | intergenic | 0.21 | 23 |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| LC-MBL_4 | PMN | chr3 | 16035092 | 16035092 | A | T | MIR563(dist=119736),GALNT15(dist=181092) | intergenic | 0.54 | 11 |
| LC-MBL_4 | LC-MBL | chr10 | 16445777 | 16445777 | A | C | FAM188A(dist=543258),PTER(dist=33165) | intergenic | 0.17 | 51 |
| LC-MBL_4 | PMN | chr10 | 16445777 | 16445777 | A | C | FAM188A(dist=543258),PTER(dist=33165) | intergenic | 0.21 | 46 |
| LC-MBL_4 | LC-MBL | chr10 | 16445778 | 16445778 | G | T | FAM188A(dist=543259),PTER(dist=33164) | intergenic | 0.17 | 51 |
| LC-MBL_4 | PMN | chr10 | 16445778 | 16445778 | G | T | FAM188A(dist=543259),PTER(dist=33164) | intergenic | 0.21 | 46 |
| LC-MBL_4 | LC-MBL | chr10 | 16445779 | 16445779 | A | T | FAM188A(dist=543260),PTER(dist=33163) | intergenic | 0.17 | 51 |
| LC-MBL_4 | PMN | chr10 | 16445779 | 16445779 | A | T | FAM188A(dist=543260),PTER(dist=33163) | intergenic | 0.21 | 46 |
| LC-MBL_4 | LC-MBL | chr10 | 16445780 | 16445780 | G | T | FAM188A(dist=543261),PTER(dist=33162) | intergenic | 0.17 | 51 |
| LC-MBL_4 | PMN | chr10 | 16445780 | 16445780 | G | T | FAM188A(dist=543261),PTER(dist=33162) | intergenic | 0.21 | 46 |
| CLL_5 | CLL | chr9 | 16958278 | 16958278 | G | T | BNC2(dist=87492),CNTLN(dist=176760) | intergenic | 0.26 | 46 |
| CLL_5 | PMN | chr9 | 16958278 | 16958278 | G | T | BNC2(dist=87492),CNTLN(dist=176760) | intergenic | 0.27 | 40 |
| LC-MBL_5 | LC-MBL | chr8 | 18123545 | 18123545 | T | - | NAT1(dist=42347),NAT2(dist=125210) | intergenic | 0.48 | 113 |
| LC-MBL_5 | PMN | chr8 | 18123545 | 18123545 | T | - | NAT1(dist=42347),NAT2(dist=125210) | intergenic | 0.35 | 96 |
| LC-MBL_5 | LC-MBL | chr8 | 18123547 | 18123547 | A | G | NAT1(dist=42349),NAT2(dist=125208) | intergenic | 0.48 | 113 |
| LC-MBL_5 | PMN | chr8 | 18123547 | 18123547 | A | G | NAT1(dist=42349),NAT2(dist=125208) | intergenic | 0.35 | 96 |
| LC-MBL_5 | LC-MBL | chr6 | 20749006 | 20749006 | - | GAAAACTGGAGAGCCACATGCAAAA | CDKAL1 | intronic | 0.16 | 12 |
| LC-MBL_5 | PMN | chr6 | 20749006 | 20749006 | - | GAAAACTGGAGAGCCACATGCAAAA | CDKAL1 | intronic | 0.18 | 16 |
| CLL_4 | CLL | chrX | 21975165 | 21975165 | A | T | SMS | intronic | 0.94 | 17 |
| CLL_4 | PMN | chrX | 21975165 | 21975165 | A | T | SMS | intronic | 0.36 | 19 |
| LC-MBL_1 | LC-MBL | chr22 | 25152165 | 25152165 | G | C | PIWIL3 | intronic | 0.66 | 15 |
| LC-MBL_1 | PMN | chr22 | 25152165 | 25152165 | G | C | PIWIL3 | intronic | 0.5 | 10 |
| LC-MBL_6 | LC-MBL | chr20 | 25389115 | 25389117 | TAT | - | GINS1 | intronic | 0.4 | 15 |
| LC-MBL_6 | PMN | chr20 | 25389115 | 25389117 | TAT | - | GINS1 | intronic | 0.63 | 33 |
| LC-MBL_4 | LC-MBL | chr20 | 26310418 | 26310418 | C | G | LOC284801(dist=120549),NONE(dist=NONE) | intergenic | 0.31 | 45 |
| LC-MBL_4 | PMN | chr20 | 26310418 | 26310418 | C | G | LOC284801(dist=120549),NONE(dist=NONE) | intergenic | 0.25 | 43 |
| LC-MBL_4 | LC-MBL | chr3 | 29623690 | 29623690 | C | T | RBMS3 | intronic | 0.2 | 55 |
| LC-MBL_4 | PMN | chr3 | 29623690 | 29623690 | C | T | RBMS3 | intronic | 0.29 | 41 |
| LC-MBL_6 | LC-MBL | chr14 | 30932584 | 30932584 | - | GAGGCACAAGGATCGCTTGAACCTGG | PRKD1(dist=535685),G2E3(dist=95745) | intergenic | 0.31 | 22 |
| LC-MBL_6 | PMN | chr14 | 30932584 | 30932584 | - | GAGGCACAAGGATCGCTTGAACCTGG | PRKD1(dist=535685),G2E3(dist=95745) | intergenic | 0.25 | 24 |
| CLL_1 | CLL | chrX | 32462845 | 32462845 | - | GACTTGAGGGGAGTGAGGT | DMD | intronic | 0.38 | 26 |
| CLL_1 | PMN | chrX | 32462845 | 32462845 | - | GACTTGAGGGGAGTGAGGT | DMD | intronic | 0.41 | 12 |

| CLL_1 | CLL | chr13 | 32746053 | 32746053 | A | G | FRY | | intronic | 0.21 | 37 |
|---|---|---|---|---|---|---|---|---|---|---|---|
| CLL_1 | PMN | chr13 | 32746053 | 32746053 | A | G | FRY | | intronic | 0.18 | 33 |
| CLL_1 | CLL | chr13 | 32746055 | 32746055 | - | TGTGGA | FRY | | intronic | 0.21 | 37 |
| CLL_1 | PMN | chr13 | 32746055 | 32746055 | - | TGTGGA | FRY | | intronic | 0.18 | 33 |
| HC-MBL_5 | LC-MBL | chr10 | 33432834 | 33432834 | G | T | ITGB1(dist=185541),NRP1(dist=33585) | | intergenic | 0.21 | 64 |
| HC-MBL_5 | PMN | chr10 | 33432834 | 33432834 | G | T | ITGB1(dist=185541),NRP1(dist=33585) | | intergenic | 0.17 | 63 |
| CLL_4 | CLL | chr8 | 34187757 | 34187757 | G | T | DUSP26(dist=730318),UNC5D(dist=905218) | | intergenic | 0.60 | 58 |
| CLL_4 | PMN | chr8 | 34187757 | 34187757 | G | T | DUSP26(dist=730318),UNC5D(dist=905218) | | intergenic | 0.15 | 66 |
| HC-MBL_3 | HC-MBL | chr12 | 34572304 | 34572304 | - | ACGTTTAATTCTTT | ALG10(dist=391068),NONE(dist=NONE) | | intergenic | 0.12 | 25 |
| HC-MBL_3 | PMN | chr12 | 34572304 | 34572304 | - | ACGTTTAATTCTTT | ALG10(dist=391068),NONE(dist=NONE) | | intergenic | 0.17 | 29 |
| HC-MBL_3 | HC-MBL | chr12 | 34572309 | 34572309 | T | A | ALG10(dist=391073),NONE(dist=NONE) | | intergenic | 0.12 | 25 |
| HC-MBL_3 | PMN | chr12 | 34572309 | 34572309 | T | A | ALG10(dist=391073),NONE(dist=NONE) | | intergenic | 0.17 | 29 |
| CLL_5 | CLL | chr16 | 35276818 | 35276818 | - | AACAGGAAATAACTTCACATA | FLJ26245(dist=285823),NONE(dist=NONE) | | intergenic | 0.27 | 22 |
| CLL_5 | PMN | chr16 | 35276818 | 35276818 | - | AACAGGAAATAACTTCACATA | FLJ26245(dist=285823),NONE(dist=NONE) | | intergenic | 0.30 | 23 |
| LC-MBL_5 | LC-MBL | chr21 | 37281760 | 37281765 | AAACAT | - | MIR802(dist=188654),SETD4(dist=125074) | | intergenic | 0.43 | 37 |
| LC-MBL_5 | PMN | chr21 | 37281760 | 37281765 | AAACAT | - | MIR802(dist=188654),SETD4(dist=125074) | | intergenic | 0.39 | 33 |
| LC-MBL_5 | LC-MBL | chr21 | 37281772 | 37281772 | - | GGG | MIR802(dist=188666),SETD4(dist=125067) | | intergenic | 0.33 | 48 |
| LC-MBL_5 | PMN | chr21 | 37281772 | 37281772 | - | GGG | MIR802(dist=188666),SETD4(dist=125067) | | intergenic | 0.32 | 37 |
| LC-MBL_5 | LC-MBL | chr21 | 37281776 | 37281776 | G | T | MIR802(dist=188670),SETD4(dist=125063) | | intergenic | 0.30 | 52 |
| LC-MBL_5 | PMN | chr21 | 37281776 | 37281776 | G | T | MIR802(dist=188670),SETD4(dist=125063) | | intergenic | 0.30 | 39 |
| LC-MBL_5 | LC-MBL | chr21 | 37281777 | 37281777 | A | C | MIR802(dist=188671),SETD4(dist=125062) | | intergenic | 0.30 | 52 |
| LC-MBL_5 | PMN | chr21 | 37281777 | 37281777 | A | C | MIR802(dist=188671),SETD4(dist=125062) | | intergenic | 0.30 | 39 |
| LC-MBL_6 | LC-MBL | chr12 | 38064665 | 38064665 | C | G | NONE(dist=NONE),ALG10B(dist=645892) | | intergenic | 0.35 | 42 |
| LC-MBL_6 | PMN | chr12 | 38064665 | 38064665 | C | G | NONE(dist=NONE),ALG10B(dist=645892) | | intergenic | 0.35 | 56 |
| LC-MBL_6 | LC-MBL | chr12 | 38064668 | 38064668 | A | T | NONE(dist=NONE),ALG10B(dist=645889) | | intergenic | 0.35 | 42 |
| LC-MBL_6 | PMN | chr12 | 38064668 | 38064668 | A | T | NONE(dist=NONE),ALG10B(dist=645889) | | intergenic | 0.35 | 56 |
| LC-MBL_6 | LC-MBL | chr12 | 38064669 | 38064669 | A | C | NONE(dist=NONE),ALG10B(dist=645888) | | intergenic | 0.35 | 42 |
| LC-MBL_6 | PMN | chr12 | 38064669 | 38064669 | A | C | NONE(dist=NONE),ALG10B(dist=645888) | | intergenic | 0.35 | 56 |
| LC-MBL_6 | LC-MBL | chr12 | 38064670 | 38064670 | T | A | NONE(dist=NONE),ALG10B(dist=645887) | | intergenic | 0.35 | 42 |
| LC-MBL_6 | PMN | chr12 | 38064670 | 38064670 | T | A | NONE(dist=NONE),ALG10B(dist=645887) | | intergenic | 0.35 | 56 |
| LC-MBL_6 | LC-MBL | chr12 | 38064674 | 38064674 | C | G | NONE(dist=NONE),ALG10B(dist=645883) | | intergenic | 0.35 | 42 |
| LC-MBL_6 | PMN | chr12 | 38064674 | 38064674 | C | G | NONE(dist=NONE),ALG10B(dist=645883) | | intergenic | 0.35 | 56 |
| LC-MBL_6 | LC-MBL | chr12 | 38064682 | 38064682 | C | G | NONE(dist=NONE),ALG10B(dist=645875) | | intergenic | 0.31 | 48 |

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|---|---|---|---|---|---|---|---|---|---|---|
| LC-MBL_6 | PMN | chr12 | 38064682 | 38064682 | C | G | NONE(dist=NONE),ALG10B(dist=645875) | intergenic | 0.32 | 68 |
| LC-MBL_6 | LC-MBL | chr12 | 38064688 | 38064688 | T | C | NONE(dist=NONE),ALG10B(dist=645869) | intergenic | 0.3 | 50 |
| LC-MBL_6 | PMN | chr12 | 38064688 | 38064688 | T | C | NONE(dist=NONE),ALG10B(dist=645869) | intergenic | 0.27 | 68 |
| LC-MBL_6 | LC-MBL | chr12 | 38064689 | 38064689 | G | A | NONE(dist=NONE),ALG10B(dist=645868) | intergenic | 0.3 | 50 |
| LC-MBL_6 | PMN | chr12 | 38064689 | 38064689 | G | A | NONE(dist=NONE),ALG10B(dist=645868) | intergenic | 0.27 | 68 |
| HC-MBL_2 | HC-MBL | chr3 | 38129024 | 38129044 | ACACCATCCATCAGCATGCTC | - | DLEC1 | intronic | 0.30 | 52 |
| HC-MBL_2 | PMN | chr3 | 38129024 | 38129044 | ACACCATCCATCAGCATGCTC | - | DLEC1 | intronic | 0.46 | 43 |
| LC-MBL_4 | LC-MBL | chr10 | 38778199 | 38778199 | T | C | LOC399744(dist=37118),ACTR3BP5(dist=211528) | intergenic | 0.19 | 120 |
| LC-MBL_4 | PMN | chr10 | 38778199 | 38778199 | T | C | LOC399744(dist=37118),ACTR3BP5(dist=211528) | intergenic | 0.12 | 99 |
| LC-MBL_6 | LC-MBL | chr10 | 38786152 | 38786152 | G | T | LOC399744(dist=45071),ACTR3BP5(dist=203575) | intergenic | 0.25 | 100 |
| LC-MBL_6 | PMN | chr10 | 38786152 | 38786152 | G | T | LOC399744(dist=45071),ACTR3BP5(dist=203575) | intergenic | 0.18 | 91 |
| LC-MBL_6 | LC-MBL | chr10 | 38786155 | 38786155 | C | A | LOC399744(dist=45074),ACTR3BP5(dist=203572) | intergenic | 0.25 | 100 |
| LC-MBL_6 | PMN | chr10 | 38786155 | 38786155 | C | A | LOC399744(dist=45074),ACTR3BP5(dist=203572) | intergenic | 0.18 | 91 |
| LC-MBL_6 | LC-MBL | chr10 | 38786156 | 38786156 | T | C | LOC399744(dist=45075),ACTR3BP5(dist=203571) | intergenic | 0.25 | 100 |
| LC-MBL_6 | PMN | chr10 | 38786156 | 38786156 | T | C | LOC399744(dist=45075),ACTR3BP5(dist=203571) | intergenic | 0.18 | 91 |
| LC-MBL_6 | LC-MBL | chr10 | 38786159 | 38786159 | T | - | LOC399744(dist=45078),ACTR3BP5(dist=203568) | intergenic | 0.25 | 100 |
| LC-MBL_6 | PMN | chr10 | 38786159 | 38786159 | T | - | LOC399744(dist=45078),ACTR3BP5(dist=203568) | intergenic | 0.18 | 91 |
| HC-MBL_3 | HC-MBL | chr10 | 39112116 | 39112116 | A | T | ACTR3BP5(dist=120745),NONE(dist=NONE) | intergenic | 0.59 | 160 |
| HC-MBL_3 | PMN | chr10 | 39112116 | 39112116 | A | T | ACTR3BP5(dist=120745),NONE(dist=NONE) | intergenic | 0.42 | 99 |
| HC-MBL_3 | HC-MBL | chr10 | 39112121 | 39112121 | A | G | ACTR3BP5(dist=120750),NONE(dist=NONE) | intergenic | 0.59 | 160 |
| HC-MBL_3 | PMN | chr10 | 39112121 | 39112121 | A | G | ACTR3BP5(dist=120750),NONE(dist=NONE) | intergenic | 0.42 | 99 |
| LC-MBL_6 | LC-MBL | chr17 | 41399300 | 41399300 | T | G | LINC00854(dist=18238),LOC100130581(dist=47913) | intergenic | 0.32 | 77 |
| LC-MBL_6 | PMN | chr17 | 41399300 | 41399300 | T | G | LINC00854(dist=18238),LOC100130581(dist=47913) | intergenic | 0.40 | 67 |
| HC-MBL_1 | HC-MBL | chr13 | 41436110 | 41436110 | - | TGTG | TPTE2P5 | ncRNA_intronic | 0.66 | 21 |
| HC-MBL_1 | PMN | chr13 | 41436110 | 41436110 | - | TGTG | TPTE2P5 | ncRNA_intronic | 0.61 | 13 |
| HC-MBL_5 | LC-MBL | chr5 | 42406349 | 42406349 | G | A | FBXO4(dist=464677),GHR(dist=17528) | intergenic | 0.55 | 18 |
| HC-MBL_5 | PMN | chr5 | 42406349 | 42406349 | G | A | FBXO4(dist=464677),GHR(dist=17528) | intergenic | 0.33 | 15 |
| HC-MBL_4 | HC-MBL | chr17 | 43222702 | 43222741 | AGCAGGGCCACCTTGGTGGGGGATGCAGGCCTGGAGCTGA | - | ACBD4(dist=1159),HEXIM1(dist=1943) | intergenic | 0.52 | 21 |
| HC-MBL_4 | PMN | chr17 | 43222702 | 43222741 | AGCAGGGCCACCTTGGTGGGGGATGCAGGCCTGGAGCTGA | - | ACBD4(dist=1159),HEXIM1(dist=1943) | intergenic | 0.41 | 29 |
| LC-MBL_4 | LC-MBL | chr22 | 44010081 | 44010081 | C | A | EFCAB6 | intronic | 0.16 | 24 |
| LC-MBL_4 | PMN | chr22 | 44010081 | 44010081 | C | A | EFCAB6 | intronic | 0.27 | 29 |

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|---|---|---|---|---|---|---|---|---|---|---|
| **LC-MBL_4** | LC-MBL | chr19 | 44021896 | 44021896 | C | A | ETHE1 | intronic | 0.2 | 45 |
| **LC-MBL_4** | PMN | chr19 | 44021896 | 44021896 | C | A | ETHE1 | intronic | 0.25 | 31 |
| **LC-MBL_4** | LC-MBL | chr19 | 44021899 | 44021899 | C | G | ETHE1 | intronic | 0.2 | 45 |
| **LC-MBL_4** | PMN | chr19 | 44021899 | 44021899 | C | G | ETHE1 | intronic | 0.25 | 31 |
| **HC-MBL_2** | HC-MBL | chr3 | 45121901 | 45121901 | T | A | CLEC3B(dist=44338),CDCP1(dist=1868) | intergenic | 0.25 | 47 |
| **HC-MBL_2** | PMN | chr3 | 45121901 | 45121901 | T | A | CLEC3B(dist=44338),CDCP1(dist=1868) | intergenic | 0.12 | 31 |
| **LC-MBL_5** | LC-MBL | chr22 | 48003778 | 48003815 | ATGCCACCACCCCTGGCTAATGCCGCCACACCTGGCTA | - | TBC1D22A(dist=432436),FLJ46257(dist=12977) | intergenic | 0.76 | 38 |
| **LC-MBL_5** | PMN | chr22 | 48003778 | 48003815 | ATGCCACCACCCCTGGCTAATGCCGCCACACCTGGCTA | - | TBC1D22A(dist=432436),FLJ46257(dist=12977) | intergenic | 0.66 | 30 |
| **LC-MBL_1** | LC-MBL | chr19 | 48107325 | 48107325 | - | GGG | ZNF541(dist=48212),GLTSCR1(dist=4128) | intergenic | 0.17 | 35 |
| **LC-MBL_1** | PMN | chr19 | 48107325 | 48107325 | - | GGG | ZNF541(dist=48212),GLTSCR1(dist=4128) | intergenic | 0.20 | 39 |
| **LC-MBL_4** | LC-MBL | chr11 | 48962962 | 48962962 | C | A | OR4A47(dist=451688),TRIM49B(dist=90190) | intergenic | 0.47 | 112 |
| **LC-MBL_4** | PMN | chr11 | 48962962 | 48962962 | C | A | OR4A47(dist=451688),TRIM49B(dist=90190) | intergenic | 0.41 | 130 |
| **LC-MBL_6** | LC-MBL | chr11 | 48962969 | 48962969 | - | A | OR4A47(dist=451695),TRIM49B(dist=90183) | intergenic | 0.44 | 83 |
| **LC-MBL_6** | PMN | chr11 | 48962969 | 48962969 | - | A | OR4A47(dist=451695),TRIM49B(dist=90183) | intergenic | 0.47 | 92 |
| **LC-MBL_6** | LC-MBL | chr5 | 49536053 | 49536053 | C | A | NONE(dist=NONE),EMB(dist=155978) | intergenic | 0.40 | 37 |
| **LC-MBL_6** | PMN | chr5 | 49536053 | 49536053 | C | A | NONE(dist=NONE),EMB(dist=155978) | intergenic | 0.57 | 52 |
| **LC-MBL_6** | LC-MBL | chr5 | 49536070 | 49536070 | A | G | NONE(dist=NONE),EMB(dist=155961) | intergenic | 0.36 | 36 |
| **LC-MBL_6** | PMN | chr5 | 49536070 | 49536070 | A | G | NONE(dist=NONE),EMB(dist=155961) | intergenic | 0.54 | 50 |
| **LC-MBL_6** | LC-MBL | chr11 | 50763731 | 50763731 | G | T | LOC646813(dist=383929),OR4A5(dist=647647) | intergenic | 0.24 | 75 |
| **LC-MBL_6** | PMN | chr11 | 50763731 | 50763731 | G | T | LOC646813(dist=383929),OR4A5(dist=647647) | intergenic | 0.20 | 86 |
| **LC-MBL_4** | LC-MBL | chr11 | 51572224 | 51572224 | T | C | OR4C46(dist=56013),NONE(dist=NONE) | intergenic | 0.41 | 72 |
| **LC-MBL_4** | PMN | chr11 | 51572224 | 51572224 | T | C | OR4C46(dist=56013),NONE(dist=NONE) | intergenic | 0.39 | 58 |
| **LC-MBL_4** | LC-MBL | chr11 | 51572225 | 51572225 | A | C | OR4C46(dist=56014),NONE(dist=NONE) | intergenic | 0.41 | 72 |
| **LC-MBL_4** | PMN | chr11 | 51572225 | 51572225 | A | C | OR4C46(dist=56014),NONE(dist=NONE) | intergenic | 0.39 | 58 |
| **LC-MBL_4** | LC-MBL | chr11 | 51572226 | 51572226 | A | G | OR4C46(dist=56015),NONE(dist=NONE) | intergenic | 0.41 | 72 |
| **LC-MBL_4** | PMN | chr11 | 51572226 | 51572226 | A | G | OR4C46(dist=56015),NONE(dist=NONE) | intergenic | 0.39 | 58 |
| **CLL_5** | CLL | chr13 | 52494296 | 52494296 | - | TGAGCTGCTGCCTGTATTT | CCDC70(dist=53924),ATP7B(dist=12510) | intergenic | 0.32 | 28 |
| **CLL_5** | PMN | chr13 | 52494296 | 52494296 | - | TGAGCTGCTGCCTGTATTT | CCDC70(dist=53924),ATP7B(dist=12510) | intergenic | 0.36 | 22 |
| **LC-MBL_1** | LC-MBL | chr20 | 55594182 | 55594215 | CCGAGGCGGGAGCCTTCTCCGCTGTGGGGCTGTC | - | TFAP2C(dist=379844),BMP7(dist=149594) | intergenic | 0.52 | 17 |
| **LC-MBL_1** | PMN | chr20 | 55594182 | 55594215 | CCGAGGCGGGAGCCTTCTCCGCTGTGGGGCTGTC | - | TFAP2C(dist=379844),BMP7(dist=149594) | intergenic | 0.54 | 22 |

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|---|---|---|---|---|---|---|---|---|---|---|
| CLL_4 | CLL | chr10 | 56045729 | 56045729 | G | T | PCDH15 | intronic | 0.47 | 34 |
| CLL_4 | PMN | chr10 | 56045729 | 56045729 | G | T | PCDH15 | intronic | 0.16 | 37 |
| CLL_4 | CLL | chr1 | 56909789 | 56909789 | G | A | MIR4422(dist=1218393),PPAP2B(dist=50630) | intergenic | 0.51 | 62 |
| CLL_4 | PMN | chr1 | 56909789 | 56909789 | G | A | MIR4422(dist=1218393),PPAP2B(dist=50630) | intergenic | 0.18 | 55 |
| LC-MBL_2 | LC-MBL | chr7 | 57955916 | 57955916 | G | T | ZNF716(dist=422651),NONE(dist=NONE) | intergenic | 0.18 | 32 |
| LC-MBL_2 | PMN | chr7 | 57955916 | 57955916 | G | T | ZNF716(dist=422651),NONE(dist=NONE) | intergenic | 0.13 | 36 |
| LC-MBL_2 | LC-MBL | chr7 | 57955920 | 57955920 | A | T | ZNF716(dist=422655),NONE(dist=NONE) | intergenic | 0.18 | 32 |
| LC-MBL_2 | PMN | chr7 | 57955920 | 57955920 | A | T | ZNF716(dist=422655),NONE(dist=NONE) | intergenic | 0.13 | 36 |
| CLL_4 | CLL | chr11 | 60633987 | 60633987 | A | G | PTGDR2(dist=10543),ZP1(dist=1028) | intergenic | 0.26 | 42 |
| CLL_4 | PMN | chr11 | 60633987 | 60633987 | A | G | PTGDR2(dist=10543),ZP1(dist=1028) | intergenic | 0.23 | 47 |
| HC-MBL_2 | HC-MBL | chr20 | 62845104 | 62845104 | - | TGTGAGTGTACGTGCA | MYT1 | intronic | 0.36 | 47 |
| HC-MBL_2 | PMN | chr20 | 62845104 | 62845104 | - | TGTGAGTGTACGTGCA | MYT1 | intronic | 0.39 | 41 |
| HC-MBL_10 | PMN | chr15 | 66980888 | 66980888 | G | T | LCTL(dist=123053),SMAD6(dist=13786) | intergenic | 0.20 | 29 |
| HC-MBL_4 | HC-MBL | chr15 | 66980888 | 66980888 | G | T | LCTL(dist=123053),SMAD6(dist=13786) | intergenic | 0.28 | 21 |
| HC-MBL_11 | PMN | chr15 | 66980889 | 66980889 | A | T | LCTL(dist=123054),SMAD6(dist=13785) | intergenic | 0.20 | 29 |
| HC-MBL_4 | HC-MBL | chr15 | 66980889 | 66980889 | A | T | LCTL(dist=123054),SMAD6(dist=13785) | intergenic | 0.28 | 21 |
| HC-MBL_12 | PMN | chr15 | 66980890 | 66980890 | G | T | LCTL(dist=123055),SMAD6(dist=13784) | intergenic | 0.20 | 29 |
| HC-MBL_4 | HC-MBL | chr15 | 66980890 | 66980890 | G | T | LCTL(dist=123055),SMAD6(dist=13784) | intergenic | 0.28 | 21 |
| HC-MBL_21 | PMN | chrX | 67924538 | 67924538 | G | A | STARD8 | intronic | 0.22 | 31 |
| HC-MBL_4 | HC-MBL | chrX | 67924538 | 67924538 | G | A | STARD8 | intronic | 1.0 | 23 |
| HC-MBL_4 | HC-MBL | chr7 | 69403285 | 69403285 | T | C | AUTS2 | intronic | 0.48 | 43 |
| HC-MBL_5 | PMN | chr7 | 69403285 | 69403285 | T | C | AUTS2 | intronic | 0.20 | 34 |
| CLL_4 | CLL | chr17 | 72644428 | 72644428 | G | A | CD300E(dist=24531),RAB37(dist=22828) | intergenic | 0.63 | 22 |
| CLL_4 | PMN | chr17 | 72644428 | 72644428 | G | A | CD300E(dist=24531),RAB37(dist=22828) | intergenic | 0.3 | 30 |
| LC-MBL_6 | LC-MBL | chr2 | 73709565 | 73709565 | - | TGGTGGATAAGCTTTTCGGTGTGC | ALMS1 | intronic | 0.14 | 14 |
| LC-MBL_6 | PMN | chr2 | 73709565 | 73709565 | - | TGGTGGATAAGCTTTTCGGTGTGC | ALMS1 | intronic | 0.14 | 21 |
| CLL_5 | CLL | chr18 | 74473944 | 74473966 | TTCCTGTGCTTTGAGTGTGTTTA | - | LOC284276(dist=202160),LOC100131655(dist=32722) | intergenic | 0.66 | 27 |
| CLL_5 | PMN | chr18 | 74473944 | 74473966 | TTCCTGTGCTTTGAGTGTGTTTA | - | LOC284276(dist=202160),LOC100131655(dist=32722) | intergenic | 0.48 | 25 |
| CLL_1 | CLL | chr12 | 75036725 | 75036725 | - | T | ATXN7L3B(dist=101493),KCNC2(dist=397133) | intergenic | 0.45 | 20 |
| CLL_1 | PMN | chr12 | 75036725 | 75036725 | - | T | ATXN7L3B(dist=101493),KCNC2(dist=397133) | intergenic | 0.6 | 25 |
| HC-MBL_22 | PMN | chr3 | 77014932 | 77014932 | - | TG | ZNF717(dist=1180677),ROBO2(dist=74362) | intergenic | 0.55 | 9 |
| HC-MBL_4 | HC-MBL | chr3 | 77014932 | 77014932 | - | TG | ZNF717(dist=1180677),ROBO2(dist=74362) | intergenic | 0.5 | 14 |

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|---|---|---|---|---|---|---|---|---|---|---|
| **HC-MBL_4** | HC-MBL | chr14 | 86942177 | 86942177 | - | GC | FLRT2(dist=847907),LOC283585(dist=429945) | intergenic | 0.18 | 49 |
| **HC-MBL_6** | PMN | chr14 | 86942177 | 86942177 | - | GC | FLRT2(dist=847907),LOC283585(dist=429945) | intergenic | 0.22 | 36 |
| **HC-MBL_4** | HC-MBL | chr14 | 86942178 | 86942178 | - | C | FLRT2(dist=847908),LOC283585(dist=429944) | intergenic | 0.18 | 49 |
| **HC-MBL_7** | PMN | chr14 | 86942178 | 86942178 | - | C | FLRT2(dist=847908),LOC283585(dist=429944) | intergenic | 0.22 | 36 |
| **HC-MBL_4** | HC-MBL | chr14 | 86942179 | 86942179 | - | C | FLRT2(dist=847909),LOC283585(dist=429943) | intergenic | 0.18 | 49 |
| **HC-MBL_8** | PMN | chr14 | 86942179 | 86942179 | - | C | FLRT2(dist=847909),LOC283585(dist=429943) | intergenic | 0.22 | 36 |
| **HC-MBL_4** | HC-MBL | chr14 | 86942180 | 86942180 | T | A | FLRT2(dist=847910),LOC283585(dist=429942) | intergenic | 0.18 | 49 |
| **HC-MBL_9** | PMN | chr14 | 86942180 | 86942180 | T | A | FLRT2(dist=847910),LOC283585(dist=429942) | intergenic | 0.22 | 36 |
| **CLL_4** | CLL | chr9 | 89475535 | 89475535 | T | A | ZCCHC6(dist=506133),GAS1(dist=83742) | intergenic | 0.47 | 34 |
| **CLL_4** | PMN | chr9 | 89475535 | 89475535 | T | A | ZCCHC6(dist=506133),GAS1(dist=83742) | intergenic | 0.20 | 39 |
| **LC-MBL_6** | LC-MBL | chr2 | 89849647 | 89849647 | T | C | MIR4436A(dist=737679),LOC654342(dist=1975062) | intergenic | 0.19 | 110 |
| **LC-MBL_6** | PMN | chr2 | 89849647 | 89849647 | T | C | MIR4436A(dist=737679),LOC654342(dist=1975062) | intergenic | 0.21 | 119 |
| **LC-MBL_6** | LC-MBL | chr2 | 89849648 | 89849648 | T | G | MIR4436A(dist=737680),LOC654342(dist=1975061) | intergenic | 0.19 | 110 |
| **LC-MBL_6** | PMN | chr2 | 89849648 | 89849648 | T | G | MIR4436A(dist=737680),LOC654342(dist=1975061) | intergenic | 0.21 | 119 |
| **LC-MBL_6** | LC-MBL | chr2 | 89849649 | 89849649 | C | G | MIR4436A(dist=737681),LOC654342(dist=1975060) | intergenic | 0.19 | 110 |
| **LC-MBL_6** | PMN | chr2 | 89849649 | 89849649 | C | G | MIR4436A(dist=737681),LOC654342(dist=1975060) | intergenic | 0.21 | 119 |
| **LC-MBL_6** | LC-MBL | chr2 | 89849652 | 89849652 | T | A | MIR4436A(dist=737684),LOC654342(dist=1975057) | intergenic | 0.19 | 110 |
| **LC-MBL_6** | PMN | chr2 | 89849652 | 89849652 | T | A | MIR4436A(dist=737684),LOC654342(dist=1975057) | intergenic | 0.21 | 119 |
| **LC-MBL_6** | LC-MBL | chr2 | 89849653 | 89849653 | C | A | MIR4436A(dist=737685),LOC654342(dist=1975056) | intergenic | 0.19 | 110 |
| **LC-MBL_6** | PMN | chr2 | 89849653 | 89849653 | C | A | MIR4436A(dist=737685),LOC654342(dist=1975056) | intergenic | 0.21 | 119 |
| **LC-MBL_6** | LC-MBL | chr2 | 89849654 | 89849654 | T | A | MIR4436A(dist=737686),LOC654342(dist=1975055) | intergenic | 0.19 | 110 |
| **LC-MBL_6** | PMN | chr2 | 89849654 | 89849654 | T | A | MIR4436A(dist=737686),LOC654342(dist=1975055) | intergenic | 0.21 | 119 |
| **LC-MBL_6** | LC-MBL | chr2 | 89849657 | 89849657 | T | C | MIR4436A(dist=737689),LOC654342(dist=1975052) | intergenic | 0.19 | 110 |
| **LC-MBL_6** | PMN | chr2 | 89849657 | 89849657 | T | C | MIR4436A(dist=737689),LOC654342(dist=1975052) | intergenic | 0.21 | 119 |
| **LC-MBL_6** | LC-MBL | chr2 | 89849663 | 89849663 | C | T | MIR4436A(dist=737695),LOC654342(dist=1975046) | intergenic | 0.26 | 118 |
| **LC-MBL_6** | PMN | chr2 | 89849663 | 89849663 | C | T | MIR4436A(dist=737695),LOC654342(dist=1975046) | intergenic | 0.24 | 129 |
| **LC-MBL_4** | LC-MBL | chr3 | 90403090 | 90403090 | C | G | EPHA3(dist=871806),NONE(dist=NONE) | intergenic | 0.33 | 113 |
| **LC-MBL_4** | PMN | chr3 | 90403090 | 90403090 | C | G | EPHA3(dist=871806),NONE(dist=NONE) | intergenic | 0.27 | 111 |
| **LC-MBL_4** | LC-MBL | chr3 | 90403222 | 90403222 | A | C | EPHA3(dist=871938),NONE(dist=NONE) | intergenic | 0.39 | 148 |
| **LC-MBL_4** | PMN | chr3 | 90403222 | 90403222 | A | C | EPHA3(dist=871938),NONE(dist=NONE) | intergenic | 0.47 | 125 |
| **LC-MBL_3** | LC-MBL | chr15 | 90641805 | 90641805 | C | A | IDH2 | intronic | 0.17 | 93 |
| **LC-MBL_3** | PMN | chr15 | 90641805 | 90641805 | C | A | IDH2 | intronic | 0.22 | 57 |
| **CLL_4** | CLL | chr3 | 99248247 | 99248247 | T | C | DCBLD2(dist=627714),MIR548G(dist=24906) | intergenic | 0.51 | 45 |

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|---|---|---|---|---|---|---|---|---|---|---|
| **CLL_4** | PMN | chr3 | 99248247 | 99248247 | T | C | DCBLD2(dist=627714),MIR548G(dist=24906) | intergenic | 0.2 | 35 |
| **CLL_5** | CLL | chr1 | 100779887 | 100779887 | - | ATCGT | RTCA(dist=21562),CDC14A(dist=38136) | intergenic | 0.55 | 29 |
| **CLL_5** | PMN | chr1 | 100779887 | 100779887 | - | ATCGT | RTCA(dist=21562),CDC14A(dist=38136) | intergenic | 0.34 | 41 |
| **CLL_5** | CLL | chr7 | 101137408 | 101137408 | - | GTTTTATTTTG TTTTGTTTTGT TTTGTTTT | COL26A1 | intronic | 0.28 | 21 |
| **CLL_5** | PMN | chr7 | 101137408 | 101137408 | - | GTTTTATTTTG TTTTGTTTTGT TTTGTTTT | COL26A1 | intronic | 0.36 | 19 |
| **CLL_4** | CLL | chr5 | 107620103 | 107620103 | C | T | FBXL17 | intronic | 0.54 | 57 |
| **CLL_4** | PMN | chr5 | 107620103 | 107620103 | C | T | FBXL17 | intronic | 0.21 | 37 |
| **CLL_5** | CLL | chr7 | 110012280 | 110012280 | C | T | EIF3IP1(dist=412010),IMMP2L(dist=290826) | intergenic | 0.35 | 14 |
| **CLL_5** | PMN | chr7 | 110012280 | 110012280 | C | T | EIF3IP1(dist=412010),IMMP2L(dist=290826) | intergenic | 0.4 | 20 |
| **CLL_2** | CLL | chr4 | 110927393 | 110927424 | CAAGAGACTGAA GCAGGAGGGTC ACTTGAACC | - | EGF | intronic | 0.36 | 44 |
| **CLL_2** | PMN | chr4 | 110927393 | 110927424 | CAAGAGACTGAA GCAGGAGGGTC ACTTGAACC | - | EGF | intronic | 0.38 | 26 |
| **LC-MBL_1** | LC-MBL | chr3 | 111806623 | 111806623 | T | A | C3orf52 | intronic | 0.5 | 36 |
| **LC-MBL_1** | PMN | chr3 | 111806623 | 111806623 | T | A | C3orf52 | intronic | 0.51 | 54 |
| **CLL_1** | CLL | chr10 | 115263134 | 115263134 | G | A | TCF7L2(dist=335698),HABP2(dist=47456) | intergenic | 0.18 | 81 |
| **CLL_1** | PMN | chr10 | 115263134 | 115263134 | G | A | TCF7L2(dist=335698),HABP2(dist=47456) | intergenic | 0.17 | 64 |
| **CLL_4** | CLL | chr11 | 115570083 | 115570084 | CC | - | CADM1(dist=194842),LOC283143(dist=55967) | intergenic | 0.54 | 48 |
| **CLL_4** | PMN | chr11 | 115570083 | 115570084 | CC | - | CADM1(dist=194842),LOC283143(dist=55967) | intergenic | 0.23 | 34 |
| **LC-MBL_4** | LC-MBL | chr5 | 115966442 | 115966442 | - | TCTCTG | SEMA6A(dist=55891),LOC728342(dist=784766) | intergenic | 0.95 | 45 |
| **LC-MBL_4** | PMN | chr5 | 115966442 | 115966442 | - | TCTCTG | SEMA6A(dist=55891),LOC728342(dist=784766) | intergenic | 0.83 | 36 |
| **CLL_4** | CLL | chr11 | 119028401 | 119028401 | C | G | ABCG4 | intronic | 0.23 | 43 |
| **CLL_4** | PMN | chr11 | 119028401 | 119028401 | C | G | ABCG4 | intronic | 0.25 | 36 |
| **CLL_4** | CLL | chr11 | 119028402 | 119028402 | C | A | ABCG4 | intronic | 0.23 | 43 |
| **CLL_4** | PMN | chr11 | 119028402 | 119028402 | C | A | ABCG4 | intronic | 0.25 | 36 |
| **LC-MBL_6** | LC-MBL | chr3 | 119799165 | 119799165 | - | GAAGGAAGAC | GSK3B | intronic | 0.53 | 15 |
| **LC-MBL_6** | PMN | chr3 | 119799165 | 119799165 | - | GAAGGAAGAC | GSK3B | intronic | 0.5 | 26 |
| **HC-MBL_2** | HC-MBL | chr10 | 123912506 | 123912506 | C | T | TACC2 | intronic | 0.33 | 24 |
| **HC-MBL_2** | PMN | chr10 | 123912506 | 123912506 | C | T | TACC2 | intronic | 0.83 | 6 |
| **LC-MBL_5** | LC-MBL | chr11 | 124771650 | 124771650 | T | - | ROBO4(dist=3819),HEPN1(dist=17496) | intergenic | 0.50 | 73 |
| **LC-MBL_5** | PMN | chr11 | 124771650 | 124771650 | T | - | ROBO4(dist=3819),HEPN1(dist=17496) | intergenic | 0.65 | 69 |
| **LC-MBL_5** | LC-MBL | chr11 | 124771651 | 124771651 | G | A | ROBO4(dist=3820),HEPN1(dist=17495) | intergenic | 0.50 | 73 |
| **LC-MBL_5** | PMN | chr11 | 124771651 | 124771651 | G | A | ROBO4(dist=3820),HEPN1(dist=17495) | intergenic | 0.65 | 69 |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| LC-MBL_6 | LC-MBL | chr5 | 132479422 | 132479468 | GGCCTGCTGCTACCTCTGGGCCTTAGGACTTACCATTCCTACTGCCT | - | HSPA4(dist=38713),FSTL4(dist=52684) | intergenic | 0.6 | 35 |
| LC-MBL_6 | PMN | chr5 | 132479422 | 132479468 | GGCCTGCTGCTACCTCTGGGCCTTAGGACTTACCATTCCTACTGCCT | - | HSPA4(dist=38713),FSTL4(dist=52684) | intergenic | 0.51 | 27 |
| CLL_1 | CLL | chr11 | 133961411 | 133961411 | A | G | JAM3 | intronic | 0.23 | 38 |
| CLL_1 | PMN | chr11 | 133961411 | 133961411 | A | G | JAM3 | intronic | 0.4 | 30 |
| CLL_1 | CLL | chr11 | 134249675 | 134249675 | - | CCTTGCCCACCACCCACCG | B3GAT1 | UTR3 | 0.45 | 20 |
| CLL_1 | PMN | chr11 | 134249675 | 134249675 | - | CCTTGCCCACCACCCACCG | B3GAT1 | UTR3 | 0.45 | 11 |
| LC-MBL_3 | LC-MBL | chr8 | 136642756 | 136642756 | - | TA | KHDRBS3 | intronic | 0.31 | 38 |
| LC-MBL_3 | PMN | chr8 | 136642756 | 136642756 | - | TA | KHDRBS3 | intronic | 0.38 | 44 |
| LC-MBL_5 | LC-MBL | chr9 | 139493108 | 139493108 | G | C | MIR4674(dist=52397),EGFL7(dist=64271) | intergenic | 0.13 | 82 |
| LC-MBL_5 | PMN | chr9 | 139493108 | 139493108 | G | C | MIR4674(dist=52397),EGFL7(dist=64271) | intergenic | 0.18 | 77 |
| CLL_1 | CLL | chr5 | 140895092 | 140895092 | T | C | DIAPH1 | UTR3 | 0.30 | 46 |
| CLL_1 | PMN | chr5 | 140895092 | 140895092 | T | C | DIAPH1 | UTR3 | 0.21 | 41 |
| LC-MBL_4 | LC-MBL | chr8 | 144057120 | 144057120 | T | C | CYP11B2(dist=57861),LOC100133669(dist=6328) | intergenic | 0.38 | 34 |
| LC-MBL_4 | PMN | chr8 | 144057120 | 144057120 | T | C | CYP11B2(dist=57861),LOC100133669(dist=6328) | intergenic | 0.4 | 30 |
| LC-MBL_4 | LC-MBL | chr8 | 144057121 | 144057121 | G | T | CYP11B2(dist=57862),LOC100133669(dist=6327) | intergenic | 0.38 | 34 |
| LC-MBL_4 | PMN | chr8 | 144057121 | 144057121 | G | T | CYP11B2(dist=57862),LOC100133669(dist=6327) | intergenic | 0.4 | 30 |
| LC-MBL_5 | LC-MBL | chr2 | 146212608 | 146212608 | C | T | DKFZp686O1327(dist=378317),PABPC1P2(dist=1132017) | intergenic | 0.46 | 28 |
| LC-MBL_5 | PMN | chr2 | 146212608 | 146212608 | C | T | DKFZp686O1327(dist=378317),PABPC1P2(dist=1132017) | intergenic | 0.59 | 22 |
| LC-MBL_5 | LC-MBL | chr2 | 147177726 | 147177726 | A | G | DKFZp686O1327(dist=1343435),PABPC1P2(dist=166899) | intergenic | 0.17 | 35 |
| LC-MBL_5 | PMN | chr2 | 147177726 | 147177726 | A | G | DKFZp686O1327(dist=1343435),PABPC1P2(dist=166899) | intergenic | 0.15 | 38 |
| LC-MBL_5 | LC-MBL | chr2 | 147177727 | 147177727 | A | T | DKFZp686O1327(dist=1343436),PABPC1P2(dist=166898) | intergenic | 0.17 | 35 |
| LC-MBL_5 | PMN | chr2 | 147177727 | 147177727 | A | T | DKFZp686O1327(dist=1343436),PABPC1P2(dist=166898) | intergenic | 0.15 | 38 |
| LC-MBL_5 | LC-MBL | chr2 | 147177728 | 147177728 | C | G | DKFZp686O1327(dist=1343437),PABPC1P2(dist=166897) | intergenic | 0.17 | 35 |
| LC-MBL_5 | PMN | chr2 | 147177728 | 147177728 | C | G | DKFZp686O1327(dist=1343437),PABPC1P2(dist=166897) | intergenic | 0.15 | 38 |
| CLL_4 | CLL | chrX | 153904329 | 153904329 | G | C | GAB3 | UTR3 | 0.87 | 16 |
| CLL_4 | PMN | chrX | 153904329 | 153904329 | G | C | GAB3 | UTR3 | 0.21 | 32 |
| CLL_2 | CLL | chr7 | 153961975 | 153961975 | G | A | DPP6 | intronic | 0.20 | 111 |
| CLL_2 | PMN | chr7 | 153961975 | 153961975 | G | A | DPP6 | intronic | 0.15 | 39 |
| CLL_2 | CLL | chr7 | 153961978 | 153961978 | A | G | DPP6 | intronic | 0.20 | 111 |
| CLL_2 | PMN | chr7 | 153961978 | 153961978 | A | G | DPP6 | intronic | 0.15 | 39 |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| **LC-MBL_4** | LC-MBL | chr6 | 163111165 | 163111168 | ACAA | - | PARK2 | intronic | 0.22 | 22 |
| **LC-MBL_4** | PMN | chr6 | 163111165 | 163111168 | ACAA | - | PARK2 | intronic | 0.26 | 26 |
| **CLL_4** | CLL | chr4 | 169020915 | 169020915 | T | A | ANXA10 | intronic | 0.62 | 40 |
| **CLL_4** | PMN | chr4 | 169020915 | 169020915 | T | A | ANXA10 | intronic | 0.23 | 26 |
| **LC-MBL_1** | LC-MBL | chr1 | 185421404 | 185421404 | - | CTACCCCT | LOC100288079(dist=117233),HMCN1(dist=282279) | intergenic | 0.38 | 13 |
| **LC-MBL_1** | PMN | chr1 | 185421404 | 185421404 | - | CTACCCCT | LOC100288079(dist=117233),HMCN1(dist=282279) | intergenic | 0.25 | 20 |
| **LC-MBL_1** | LC-MBL | chr1 | 185421405 | 185421405 | - | CCCCTGCCCTTC | LOC100288079(dist=117234),HMCN1(dist=282278) | intergenic | 0.38 | 13 |
| **LC-MBL_1** | PMN | chr1 | 185421405 | 185421405 | - | CCCCTGCCCTTC | LOC100288079(dist=117234),HMCN1(dist=282278) | intergenic | 0.25 | 20 |
| **HC-MBL_13** | PMN | chr2 | 190956291 | 190956291 | T | C | MSTN(dist=28836),C2orf88(dist=46195) | intergenic | 0.2 | 10 |
| **HC-MBL_4** | HC-MBL | chr2 | 190956291 | 190956291 | T | C | MSTN(dist=28836),C2orf88(dist=46195) | intergenic | 0.15 | 20 |
| **HC-MBL_14** | PMN | chr2 | 190956293 | 190956293 | G | - | MSTN(dist=28838),C2orf88(dist=46193) | intergenic | 0.2 | 10 |
| **HC-MBL_4** | HC-MBL | chr2 | 190956293 | 190956293 | G | - | MSTN(dist=28838),C2orf88(dist=46193) | intergenic | 0.15 | 20 |
| **HC-MBL_15** | PMN | chr2 | 190956295 | 190956295 | C | A | MSTN(dist=28840),C2orf88(dist=46191) | intergenic | 0.2 | 10 |
| **HC-MBL_4** | HC-MBL | chr2 | 190956295 | 190956295 | C | A | MSTN(dist=28840),C2orf88(dist=46191) | intergenic | 0.15 | 20 |
| **HC-MBL_16** | PMN | chr2 | 190956304 | 190956304 | A | C | MSTN(dist=28849),C2orf88(dist=46182) | intergenic | 0.2 | 10 |
| **HC-MBL_4** | HC-MBL | chr2 | 190956304 | 190956304 | A | C | MSTN(dist=28849),C2orf88(dist=46182) | intergenic | 0.15 | 20 |
| **HC-MBL_17** | PMN | chr2 | 190956305 | 190956305 | C | A | MSTN(dist=28850),C2orf88(dist=46181) | intergenic | 0.2 | 10 |
| **HC-MBL_4** | HC-MBL | chr2 | 190956305 | 190956305 | C | A | MSTN(dist=28850),C2orf88(dist=46181) | intergenic | 0.15 | 20 |
| **HC-MBL_18** | PMN | chr2 | 190956308 | 190956311 | TTTT | - | MSTN(dist=28853),C2orf88(dist=46175) | intergenic | 0.2 | 10 |
| **HC-MBL_4** | HC-MBL | chr2 | 190956308 | 190956311 | TTTT | - | MSTN(dist=28853),C2orf88(dist=46175) | intergenic | 0.15 | 20 |
| **HC-MBL_19** | PMN | chr2 | 190956312 | 190956312 | A | C | MSTN(dist=28857),C2orf88(dist=46174) | intergenic | 0.2 | 10 |
| **HC-MBL_4** | HC-MBL | chr2 | 190956312 | 190956312 | A | C | MSTN(dist=28857),C2orf88(dist=46174) | intergenic | 0.15 | 20 |
| **HC-MBL_20** | PMN | chr2 | 190956314 | 190956314 | G | C | MSTN(dist=28859),C2orf88(dist=46172) | intergenic | 0.2 | 10 |
| **HC-MBL_4** | HC-MBL | chr2 | 190956314 | 190956314 | G | C | MSTN(dist=28859),C2orf88(dist=46172) | intergenic | 0.15 | 20 |
| **HC-MBL_5** | LC-MBL | chr2 | 235777171 | 235777171 | C | G | ARL4C(dist=371478),SH3BP4(dist=83457) | intergenic | 0.28 | 21 |
| **HC-MBL_5** | PMN | chr2 | 235777171 | 235777171 | C | G | ARL4C(dist=371478),SH3BP4(dist=83457) | intergenic | 0.28 | 25 |
| **HC-MBL_5** | LC-MBL | chr2 | 235777173 | 235777173 | T | G | ARL4C(dist=371480),SH3BP4(dist=83455) | intergenic | 0.28 | 21 |
| **HC-MBL_5** | PMN | chr2 | 235777173 | 235777173 | T | G | ARL4C(dist=371480),SH3BP4(dist=83455) | intergenic | 0.28 | 25 |
| **HC-MBL_3** | HC-MBL | chr1 | 246235199 | 246235199 | T | - | SMYD3 | intronic | 0.49 | 93 |
| **HC-MBL_3** | PMN | chr1 | 246235199 | 246235199 | T | - | SMYD3 | intronic | 0.35 | 70 |

**Table S13.** Shared recurrent mutations between MBL/CLL samples and their respective PMN samples.

| Sample ID | Entity | Chr | Start | End | Ref_base | Var_base | Gene | Type | VAF | dbSNP_id |
|-----------|--------|-----|-------|-----|----------|----------|------|------|-----|----------|
| HC-MBL_2 | HC-MBL | 3 | 45121897 | 45121897 | G | A | CLEC3B(dist=44334),CDCP1(dist=1872) | intergenic | 0.22 | rs192693541 |
| HC-MBL_4 | HC-MBL | 3 | 45121897 | 45121897 | G | A | CLEC3B(dist=44334),CDCP1(dist=1872) | intergenic | 0.26 | rs192693541 |
| HC-MBL_1 | HC-MBL | 4 | 26287660 | 26287660 | - | CTGCAGTGCGCTATGATCGTGCCA | SMIM20(dist=356159),RBPJ(dist=33672) | intergenic | 0.59 | - |
| LC-MBL_3 | LC-MBL | 4 | 26287660 | 26287660 | - | CTGCAGTGCGCTATGATCGTGCCA | SMIM20(dist=356159),RBPJ(dist=33672) | intergenic | 0.61 | - |
| LC-MBL_5 | LC-MBL | 2 | 233920626 | 233920626 | - | GATGGCTG | NEU2(dist=20859),INPP5D(dist=4410) | intergenic | 0.69 | - |
| LC-MBL_6 | LC-MBL | 2 | 233920626 | 233920626 | - | GATGGCTG | NEU2(dist=20859),INPP5D(dist=4410) | intergenic | 0.64 | - |
| HC-MBL_3 | HC-MBL | 6 | 54074925 | 54074925 | - | CACCTCACCT | MLIP | intronic | 0.24 | - |
| LC-MBL_3 | LC-MBL | 6 | 54074925 | 54074925 | - | CACCTCACCT | MLIP | intronic | 0.29 | - |
| HC-MBL_2 | HC-MBL | 21 | 44415639 | 44415639 | - | TAGCCAGGTATGGTGGCATGTGCCTA | PKNOX1 | intronic | 0.17 | - |
| LC-MBL_3 | LC-MBL | 21 | 44415639 | 44415639 | - | TAGCCAGGTATGGTGGCATGTGCCTA | PKNOX1 | intronic | 0.19 | - |
| HC-MBL_2 | HC-MBL | 4 | 153579774 | 153579774 | - | CTAAAAATACAAAATTTTTAGCTTTA | TMEM154 | intronic | 0.25 | rs143753374 |
| LC-MBL_5 | LC-MBL | 4 | 153579774 | 153579774 | - | CTAAAAATACAAAATTTTTAGCTTTA | TMEM154 | intronic | 0.13 | rs143753374 |

**Table S14.** Allele specific primers for the 11 cases with available material.

| Primer Name | Primer sequence | Type | Length | Tm | GC% | Self complementarity | Self 3' complementarity |
|---|---|---|---|---|---|---|---|
| HC-MBL_1-For | GCTGGAGTGAGGAAGCCTG | Forward | 19 | 60.08 | 63.16 | 3.00 | 1.00 |
| HC-MBL_1-Rev | CCCAGGGGTCGAACCAGT | Reverse | 18 | 60.93 | 66.67 | 6.00 | 2.00 |
| HC-MBL_3-For | TGGGGCTGAAGTGAAGAAGC | Forward | 20 | 60.25 | 55.00 | 3.00 | 2.00 |
| HC-MBL_3-Rev | CCCTGGCCCCAGTAGTCAAT | Reverse | 20 | 61.28 | 60.00 | 6.00 | 2.00 |
| HC-MBL_4-For | GAAGTGCAGCTGGTGGAGTC | Forward | 20 | 60.95 | 60.00 | 6.00 | 3.00 |
| HC-MBL_4-Rev | GAGACGGTGACCTGGGTTC | Reverse | 19 | 59.71 | 63.16 | 5.00 | 2.00 |
| CLL_1-For | TTCAGCTGTCGGAGTCTGGG | Forward | 20 | 61.54 | 60.00 | 6.00 | 1.00 |
| CLL_1-Rev | GAGACGGTGACCAGGGTTC | Reverse | 19 | 59.71 | 63.16 | 5.00 | 2.00 |
| CLL_2-For | ACTGGTGAAGCCTTCGGAGA | Forward | 20 | 60.83 | 55.00 | 7.00 | 2.00 |
| CLL_2-Rev | CCTGGCCCCAAAAGTCAAAG | Reverse | 20 | 59.32 | 55.00 | 4.00 | 0.00 |
| CLL_4-For | CCTGTGCAGCGTCTGGATT | Forward | 19 | 60.38 | 57.89 | 4.00 | 1.00 |
| CLL_4-Rev | GCCCCAGACGTCCATATCGT | Reverse | 20 | 61.75 | 60.00 | 6.00 | 2.00 |
| CLL_5-For | GAAGTGCAGCTGGTGGAGTC | Forward | 20 | 60.95 | 60.00 | 6.00 | 3.00 |
| CLL_5-Rev | CTGGCCCCAGTAGTCAACAC | Reverse | 20 | 60.32 | 60.00 | 6.00 | 2.00 |
| LC-MBL_1-For | AGATGCAACTGCAGGGGTC | Forward | 19 | 60.0 | 57.89 | 6.00 | 2.00 |
| LC-MBL_1-Rev | CCCAGACGTCCATACCGTAG | Reverse | 20 | 59.33 | 60.00 | 6.00 | 3.00 |
| LC-MBL_4-For | AAGGTCTCCTGCAAGGCTTC | Forward | 20 | 59.96 | 55.00 | 5.00 | 3.00 |
| LC-MBL_4-Rev | GAGACGGTGACCAGGGTTCC | Reverse | 20 | 62.17 | 65.00 | 5.00 | 2.00 |
| LC-MBL_5-For | CAGAGGTGAAAAAGCCCGGA | Forward | 20 | 60.25 | 55.00 | 4.00 | 2.00 |
| LC-MBL_5-Rev | CTGAAGAGACGGTGACCAGG | Reverse | 20 | 59.76 | 60.00 | 5.00 | 3.00 |
| LC-MBL_6-For | TGGTCCTACGCTGGTGAAAC | Forward | 20 | 59.97 | 55.00 | 3.00 | 1.00 |
| LC-MBL_6-Rev | GAGACGGTGACCAGGGTTC | Reverse | 19 | 59.71 | 63.16 | 5.00 | 2.00 |

**Table S15.** Genomic aberrations detected in the present cohort by CNA analysis of WGS data.

| Sample | Entity | chr | Band | Position | chr size | start | end | BP size | copy number | status |
|---|---|---|---|---|---|---|---|---|---|---|
| CLL_1 | CLL | **13** | **q14.2** | q-middle | 115169878 | 50500000 | 50600000 | 100000 | 1 | loss |
| CLL_4 | CLL | 2 | p11.1 | centromeric | 243199373 | 92250000 | 92350000 | 100000 | 1 | loss |
| CLL_4 | CLL | 4 | p11 | centromeric | 191154276 | 49050000 | 49200000 | 150000 | 1 | loss |
| CLL_4 | CLL | 4 | p11 | centromeric | 191154276 | 49600000 | 49700000 | 100000 | 1 | loss |
| CLL_5 | CLL | **13** | **q14.2** | q-middle | 115169878 | 50450000 | 50650000 | 200000 | 1 | loss |
| HC-MBL_1 | HC-MBL | **13** | **q14.2-q14.3** | q-middle | 115169878 | 48400000 | 52100000 | 3700000 | 1 | loss |
| HC-MBL_2 | HC-MBL | **13** | **q14.2-q14.3** | q-middle | 115169878 | 50350000 | 51650000 | 1300000 | 1 | loss |
| HC-MBL_3 | HC-MBL | 9 | q13 | q-arm | 141213431 | 66200000 | 66300000 | 100000 | 1 | loss |
| HC-MBL_3 | HC-MBL | **13** | **q14.2-q14.3** | q-middle | 115169878 | 49000000 | 53400000 | 4400000 | 1 | loss |
| LC-MBL_2 | LC-MBL | 6 | p21.32 | p-middle | 171115067 | 32650000 | 32750000 | 100000 | 1 | loss |
| LC-MBL_5 | LC-MBL | 3 | q29 | q-end | 198022430 | 195450000 | 195550000 | 100000 | 1 | loss |
| LC-MBL_5 | LC-MBL | 8 | p11.22 | centromeric | 146364022 | 39250000 | 39350000 | 100000 | 1 | loss |
| LC-MBL_5 | LC-MBL | 12 | q24.33 | q-end | 133851895 | 132600000 | 133450000 | 850000 | 3 | gain |
| LC-MBL_5 | LC-MBL | **13** | **q14.2-q14.3** | q-middle | 115169878 | 49900000 | 51600000 | 1700000 | 1 | loss |
| LC-MBL_5 | LC-MBL | 15 | q21.2 | q-middle | 102531392 | 52250000 | 52650000 | 400000 | 1 | loss |
| LC-MBL_6 | LC-MBL | **13** | **q14.2-q31.1** | q-middle | 115169878 | 48250000 | 80800000 | 32550000 | 1 | loss |

**Table S16.** Common genomic aberrations in CLL that were also identified in the present study by the analysis of WGS data and FISH.

| Lab Sample ID | Entity | WGS identified CNAs | FISH results | | | |
| --- | --- | --- | --- | --- | --- | --- |
| | | | del(13q) | trisomy 12 | del(11q) | del(17p) |
| CLL_1 | CLL | del(13q) | + | - | - | - |
| CLL_2 | CLL | not available | + | - | - | - |
| CLL_3 | CLL | not available | + | - | - | - |
| CLL_4 | CLL | - | - | - | - | - |
| CLL_5 | CLL | del(13q) | not available | | | |
| HC-MBL_1 | HC-MBL | del(13q) | + | - | - | - |
| HC-MBL_2 | HC-MBL | del(13q) | + | - | - | - |
| HC-MBL_3 | HC-MBL | del(13q) | + | - | - | - |
| HC-MBL_4 | HC-MBL | not available | not available | | | |
| HC-MBL_5 | HC-MBL | not available | - | - | - | - |
| LC-MBL_1 | LC-MBL | - | not available | | | |
| LC-MBL_2 | LC-MBL | - | + | - | - | - |
| LC-MBL_3 | LC-MBL | not available | - | - | - | - |
| LC-MBL_4 | LC-MBL | not available | not available | | | |
| LC-MBL_5 | LC-MBL | del(13q) | not available | | | |
| LC-MBL_6 | LC-MBL | del(13q) | + | - | - | - |

**Figure S1.** Coding and non-coding regions enriched for mutations. Mutational enrichment was observed in the IG loci and within gene sites known to be recurrently affected by off-target somatic hypermutation (e.g. *BTG2*, *BCL6* and *TCL1A*).