Supplementary Table 1. List of probes and primers.

Quantitative PCR	
Ccnd3-Fw	5’-CGC TGC GAG GAG GAT GTC TT-3’
Ccnd3-Rev	5’-CAA CTG CCA TGG AGC CAC AG-3’
Ccnd2-Fw	5’-AGC TGT CCC TGA TCC GCA AG-3’
Ccnd2-Rev	5’-GCA GCT CTG TCA GGG CAT CA-3’
Brwd1-Fw1	5’-GCCTGGTGTTCAGATGCTGTG-3’
Brwd1-Rev1	5’-GCTGTTCCATCTCGGCTACCA-3’
Brwd1-Fw2	5’-TTGCTTCTGGCAGTGGGATTT-3’
Brwd1-Rev2	5’-GCTTTCAAGCTCGGCGATTT-3’
Brwd1-Fw3	5’-GTGGACGGAAACCCTCATCC-3’
Brwd1-Rev3	5’-CCATTTGCAGTCCCATCCTG-3’
Brwd1-Fw4	5’-GATCCAGCGACTGGCAGACT-3’
Brwd1-Rev4	5’-TGGGGTTGATACGGTTCTTGA-3’
Brwd1-Fw5	5’- CGCCAATGGATTTTGGAACA-3’
Brwd1-Rev5	5’- CACCAGGGACAGCACCGTTA-3’
Rag1-Fw	5’-CTG CAG ACA TTC TAG CAC TC-3’
Rag1-Rev	5’-AAC TGA AGC TCA GGG TAG AC-3’
Rag2-Fw	5’- TCA TAA GTG AGA AGC CTG GT-3’
Rag2-Rev	5’-CCT TCA GTG CCA AAA TAA GA-3’
Tcfe2a-Fw	5'-TCCTTTGACCCTAGCCGGACATAC-3'
Tcfe2a-Rev	5'-CCAACACTGGTGTCTCTCCCAAAG-3'
Pax5-Fw	5'-CGCGTGTTTGAGAGACAGCACTACT-3'
Pax5-Rev	5'-GTCTCGGCCTGTGACAATAGGGTAG-3'
Ikzf1-Fw	5'-CACTACCTCTGGAGCACAGC-3'
Ikzf1-Rev	5'-ATAGGGCATGTCTGACAGGCA-3'
Irf4-Fw	5'-CTACCCCATGACAGCACCTT-3'
Irf4-Rev	5'-CCAAACGTCACAGGACATTG-3'
Irf8-Fw	5'-GAGCGAAGTTCCTGAGATGG-3'
Irf8-Rev	5'-TGGGCTCCTCTTGGTCATAC-3'
Smarca4-Fw	5'-AGAAGCTGATTCCTCCGCAAC-3'
Smarca4-Rev	5'-AAGCCTGTACTCCCGCTCTTG-3
Myc-Fw	5′-GCCCCCAAGGTAGTGATCCT-3′
Myc-Rev	5′-GTGCTCGTCTGCTTGAATGG-3′
B-2 Microglobulin-F	5’-AGACTGATACATACGCCTGCA-3’
B-2 Microglobulin-R	5’-GCAGGTTCAAATGAATCTTCA-3’
Igk-Germline-F	5’-GAGGGGGTTAAGCTTTCGCCTACCCAC-3’
Igk-Germline-R	5’-GTTATGTCGTTCATACTCGTCCTTGGTCAA-3’
ChIP- Quantitative PCR	
$V\kappa_{21-1}$-F	5’- TTGTGCTCACCCAATCTCCAG-3’
$V\kappa_{21-1}$-R	5’- GGCTGTCCTGGTTTCTGTTGG-3’
$J\kappa_{1-}$ $J\kappa_2$ -F	5’-AGGCACCAAGCTGGAAATCAA-3’
$J\kappa_{1-}$ $J\kappa_2$ -R	5’-TGCCTTGGAGAGTGCCAGAAT-3’
$J\kappa_{4-}$ $J\kappa_5$ - F	5’- GCTCGGGGACAAAGTTGGAA-3’

Jκ$_{4-}$ Jκ$_5$ —-R	5’- GATGCACAGGTTGCCAGGAAT-3’
Jκ$_5$- Eκi- F	5’- TGTTTTAATGGCCACGGTTTTG-3’
Jκ$_5$- Eκi- R	5’- AGAAGAGGTTGCGGACCGTTT-3’
Eκi- F	5’- GCAGGTGGCCCAGATTACAGT-3’
Eκi- R	5’- AGGGCCTTAAGCCAGGGTCT-3’
Cκ-F	5’- TCTGGAGGTGCCTCAGTCGT-3’
Cκ- R	5’-CCAACTGTTCAGGACGCCATT-3’
3’Eκ- F	5’- CCCCACCTCCATCTTGTTTGA-3’
3’Eκ- R	5’- GGGCCCAGTGACCATATCAGA-3’
Actin γ1-F	5’-CCTCCTCCAATAAAGGGACA-3’
Actin γ1-R	5’-GCCATCACATCCCAGTCA-3’
β-globin-F	5’-GCTGCTGGTTGTCTACCCTT-3’
β-globin-R	5’-GCAGAGGCAGAGGATAGGTC-3’
Eλ1-3-F	5’-AAGCTCTGTGGAGGAGGTTG -3’
Eλ1-3-R	5’-AGCTTGTGGACTCTCAAGGG-3’
Eλ2-4-F	5’-TAGGTTGGGGCAGAGAGATG-3’
Eλ2-4-R	5’-GCTTGTGGATTCTCAAGGGT-3’
IgλJ1-F	5’-GATCTTTCAGTGATGTCACCACC-3’
IgλJ1-R	5’-GCACCTCAAGTCTTGGAGAGAAC-3’
IgλJ2-F	5’-CCACCCACTGCTTCTCAAGTG-3’
IgλJ2-R	5’-AGACAACAAGGGCTGGGCTTA-3’

Short Hairpin RNA Constructs

shRNA-Brwd1-4 (target seq)	5’-CGGATCTGTATCACTAGAGAA-3’
shRNA-Brwd1-4 (97mer)	5’-GCTGTTGACAGTGAGCGCCGGATCTGTATCACTAGAGAATAGTGAAGCCACAGATGTATTCTCTAGTGATACAGATCCGTTGCCTACTGCCTCGGA -3'

Kappa Recombination

degVκ	5’-GGC TGC AGS TTC AGT GGC AGT GGR TCW GGR AC-3’
MAR (Igκ intron)	5’-AAC ACT GGA TAA AGC AGT TTA TGC CCT TTC-3’
κ-meth-F	5’-ATG ACC CAG AGG ATG AAA C-3’
κ-J1-R	5’-AGC ATG GTC TGA GCA CCG AGT AAA GG-3’
Eκi-F	5’-AGA AGT GAA GTC TGC CAG TT-3’
Eκi-R	5’-GTA ACC ACA TGG GAC AAT TT-3’

Jκ Usage

Vκ-FW	5’-AGCTTCAGTGGCAGTGGRTCWGGRAC-3’
Cκ	5’-CTTCCACTTGACATTGATGTC-3’

Supplementary Table 2. ATAC-seq alignment statistics.

	WT1		WT2		Mut1		Mut2	
Raw reads-pair 1	70156781		83648534		86821861		96234426	
Raw reads - Pair 2	70156781		83648534		86821861		96234426	
Trimmed reads - Pair 1	70066574	99.9%	83511078	99.8%	86710495	99.9%	96048959	99.8%
Trimmed reads - Pair2	69455097	99.0%	82600240	98.7%	85797411	98.8%	95175630	98.9%
Complete pairs after trimming	67865040	97.7%	80604130	97.6%	83726404	97.6%	92736672	97.4%
Aligned reads	132317198	97.5%	157384650	97.5%	163040856	97.4%	181760794	98.0%
High quality, unique aligned reads	105123120	77.5%	123169530	76.4%	97989782	58.5%	111467428	60.1%
High quality, unique, paired alignments	50530138	74.5%	58928062	73.1%	46873182	56.0%	53354561	57.5%

From WT and *Brwd1*^{mut} (Mut) small pre-B cells, duplicate samples were obtained. The WT samples had 1.3-1.6 x 10^8 aligned reads (~97.5% of total sequences) and *Brwd1*^{mut} samples had 1.6-1.8 x 10^8 aligned reads (~97.7%). ATAC-Seq profiles were highly reproducible between biological replicates (Spearman's r=0.99).

Supplementary Table 3. Cryptic RSS (cRSS) and GAGA motifs in open+6-ChIP-seq peaks ($P<10^{-7}$).

Sequence under common region of peaks	Location	Gene	Where the peak is	Chromatin remodeling
AGGAATGTCGAAATTACTGAAAAACGTGAAAAATGAGAAATGCACACTGCAGGACCTGGAATATGGCGAGAAAACTGAACATCACGGAAAATGAGAATAACACTCTTTAGGTAGTGAAATATGACGAGAAATATTGAAAAATAAGC No RSS	chr4 70039147 To 70039293	*Cdk5rap2* (Protein coding)	Intron 4 of 36	Yes (Nucleosome shifting)
CCAACGGATGTGTTTTTCAGTGTAACTCACTCATCTAATATGTTCTACAGTGTGGTTTTTATCATTTTCCATGTTCCTCATTGTAACTCATTGATATACACTGTTCTACAATTCCCGTTTCCAACGAATGTGTTTTTCAGTGTAACTCACTCATCTAATATGTTCTACAGTGTGGTTTTTATCATTTTCCATGTTTCTCATTGTAACTCATTGATATACACTGTTCTACAAATCCCGTTTCTATA (RIC score -38.02)- RSS12 sequence; + strand	chr6 103599044 to 103599290	*Chl* (Protein coding)	Intron 4 of 26	No
NNNNGATCCTACAGTGTGCATTTCTCATTTTTCACGTTTTTCAGTGATTTCGTCATTTTTCAAGTCATCAAGTGGCTGTTTCTCATTTTCCATGATTTTCAGTTTTCTTGCCATATTCCTTGTCCTACAGTGGACATTTCTAAATTTTCCACCTTTTTCAGTTTTCCTTGTCATATTTCAGGTCCTACAGTGTGTATTTCTCATTTTTCACGTTTTTCATTGATTTCGTCATTTTTCAAGTTGTCAAGTGCATGTTTCTCATTTTCCATGATTTTCAGTTTTCTTGCCATA No RSS	chr9 2999996 To 3000287	Mir101c miscRNA	Intergenic	No
GTGTATTTCTCATTTTCCGTGATTTTCAGTTTTCTCGACATATTCCAGGTCCTACAGTGTGCATTTCTCATTTTTCACGTTTTTCAGTGATTTCGTCATTTTTCACGTCGTCAAGTGGATGTTTCTCATTTTCCATGATTTTCAGTTTTCTTGCCAT No RSS	chr9 3000363 to 3000520	Mir101c	Intergenic	No
TATTTCACGTCCTAAAGTGTGTATTTCTCATTTTCCGTGATTTTCAGTTTTATCGCCAGATTCCAGGTCCTACGGTGTGCA No RSS	chr9 3000989 to 3001070	Mir101c	Intergenic	No

TGGAAAATGATAAAAACCACACTGTAGAACAGAGTAGATGAGTGAGTTACACTGAAAAACACAATTCGTTGGAAACGGGAATTGTGTATATCAATGAGTTACTAGGAGAAACATGGAAAATGATAAAAAC No RSS	chr9 24346459 to 24346589	*Dpy19l1* (Protein coding)	Intergenic	No
TTTTGAGGTGCACACTGAAGGACCTGGAATTATGCGAGAAAACTGAAAATCACGGAAAATGAGAAATACACACTTTAGGACGTGAAAAATGGCGAGGAAAACTGAAAAAGGTGGAAAATTTAGAAATGTCCTCTGTAGGACATGGAATATGGCAAGAAAACTGAAAATCATGGAAAATGAGAAACATCCACTTGATGACTTGAAAAATGACGAAATCATTAAAAAACGTGAAAAATGAGAAATGCCCACTGAAGGACCTGGAATATGGGGAGAAAACTGAAAATCACGGAAAATGAGAAATACACACTTTAGGACGTGAAATATGGCGAGGAAAACTGAAAAAGGTGGAATATTTAGAAATGTCCACTGTAGGACGTGGAATATAAGT No RSS	chr9 35112792 to 35113180	Rik 4933422A05	Intergenic	Yes (Nucleosome Depletion)
GTTTTACCTACATTGTTCCAACATGCCAGAGGCTGTTCACCTTGGAGACCTGCTGCGGATATGGGTACGGCCCGGAGATTTACAAGCTCTCCCCCGGATTTTCAAGGGCCAGCGAGAGCTCACCGGATGCCGCCGGAACCATGACGCTTTCCAAGGCACGTGCCCCTCTCTCAGGGCGAACCCATTCCAGGGCGCCCTGCCCTTCACAAAGAAAAGAGAACTCTCCCCGGGGCTTCTCCGGGATCGGTCGCGTTACCGCACTGGACGCCTCGCGGCGCCCATCTCCGCCACTCTGGATTTGGGGATCTGAACCCGACTCCCCTTCAATCGGCCGAGGGCAACGGAGGCCATCGCCCATCCCTTCGGAACGGCACTCACCCATCTCTCAGGACTGACTGACCCATGTTTAAC No RSS	chr11 108872956 to 108873367	*Axin2* (Protein coding)	Intergenic	Yes, Nucleosome shifting and depletion
CTGAAAATCATGGAAAATGAGAAACATCCACTTGACGACTTGAAAAATGACAAAATCACTGAAAAAGGTGAAAAATGAGAAATGCACACTGTAGGACTTGGAATATGGCGAGAAAACTGAAAATCACGGAAGTGAGGG No RSS	chr12 3109990 to 3110128	Rik 1700012B15	Intergenic	Yes Nucleosome depletion
AGAGTCTGCTATTTCAAAGCATAAGGAAAAAGTAGGAGAAAAACGTGAGGCTGTTTGTGGATGGTCGAGGCTGCTTTAGGGAGCCTCCTCACCATTCTGCACTTGCAAACCGGGCCACTAGAACCCGGTGAAGGGAGAAACCAAAGCGACCTGAAACAATAGGTCACATGAAGGCCAGCCACCTCCATCTTGTTGTGCAGGAGTTCAGTTAGCAGACAAGATGGCTGCCATCCACATGTCACCTTTCATCTTGGTGAGGTCAATGTGCAGCCGAGTGACAGGACAAGGAAGTAGACATGCAGACAACAGACATGCAGGCGAACCACCTCCCTTCTGTGTTTGGATAAAAGACATACAACAATTTTTATTTTTTACAGTAAGCCTTAAAAAGCACTCTGACAGCCACTCAGATATCTACCTTCTATGT No RSS	chr15 74917050 To 74917477	*Ly6c2* (Protein coding)	Intergenic	Yes Nucleosome depletion

CTCTAGATAACCTCGGGCCGATCGCACGCCCCCGTGGCGGCGACGACCCATTCGAACGTCTGCCCTATCAACTTTCGATGGTAGTCGCCGTGCCTACCATGGTGACCACGGGTGACGGGGAATCAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCACTCCCGACCCGGGGAGGTAGTGACGAAAAATAACAATACAGGACTCTTTCGAGGCCCTGTAATTGGAATGAGTCCACTTTAAATCCTTTAACGAGGAT No RSS	chr17 39983597 To 39983895_ +	Rn45s Non coding RNA	Intergenic	Yes Nucleosome depletion
CATAAACGATGCCGACTGGCAATGCGGCGGCGTTATTCCCATGACCCGCCGGGCAGCTTCCGGGAAACCAAAGTCTTTGGGTTCCGGGGGGAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCCGGCCCGGACACGGACAGGATTGACAGATTGATAGCTCTTTCTCGATTCCGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGCGATTTGTCTGGTTAATTCCGATAACGAACGAGACTCTGGCATGCTAACTAGTTACGCGACCCCCGAGCGGTCGGCGTCCCCCAACTTCTTAGAGGGACAAGTGGCGTTCAGCCACCCGAGATTGAGCAATAACAGGTCTGTGATGCCCTTAGATGTCCGGGGCTGCACGCGCGCTACACTGACTGGCTCAGCGTGTGCCTACCCTACGCCGGCAGGCGCGGGTAACCCGTTGAACCCCATTCGTGATGGGGATCGGGGATTGCAATTATTCCCCATGAACGAGGAATTCCCAGTAAGTGCGGGCCATAAGCTTGCGTTGATTAAGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGGATGGTTTAGTGAGGCCCACGGCCCTGGTGGAGCGCTGAGAAGACGGTCGAACTTGACTATCTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTAACGGGAGACTGTGGAGGAGCGGCGGCGTGGCTCGCTCTCCCCGTCTTGTGTGTGTCCTCGCCGGGAGGCGCGTGCGTCCCGGG (RIC score -58.24)- RSS23 sequence; - strand	chr17 39984382 To 39985229	Rn45s Non coding RNA	Intergenic	Yes Nucleosome depletion
ATTCACTCACTCATTCCGTCTCTCCCAAGGGTCCTCCCTAGCTCAGGGCGGGGCACTCACGCACACATGACAGAGCAGCGTACCCACCCACCACTTCTCCCGAGTGGCACAAACGGTCCCCATCGTCCCGCCCGAACATAGCGAACACGGGCTGGACTCGGGCACCCAAAAACGAAAGTATGACAGGGAGCTGTGAAAACAGGCGAAATCATT No RSS	chr19 61275523 To 61275736	Gm7102 (Predicted protein coding)	Intergenic	Yes Nucleosome depletion
ACACTGTAGAACATAGTGTGAAATGCACATTGTAAAACACAGTATGTTAATGAGTTGCACTGAAAAACAGAAAATGGGAAATGCACAGTGTAGAACCCAATATATGAGTGAGTTGCACTGAAACACCTAGAAAATCAGACCGGCACATTGTAGAACATAGTGTGAAATGCACATTGTAAAACACAGGATGTTAATGAGTTGCACTGAAAAACATAGAAAATGGGAAATGCACAGTGTAGAACATTGTATATGAGTGCTTTGCACTGAACAACCTAGAAAAAAAAGA (RIC score -37.99), RSS12 sequence; + strand (RIC score -56.25), RSS23 sequence; + strand	chrX 73844194 to 73844480	Rik 4930468A15	Intron 1 of 1	Yes Nucleosome depletion

GAGTTTCTCATTGTAACTCATTGATATACACTGTTCTACAATGCCCGTTTCCAACGTATGTGTTTTTCAGTGTAACTCACTCATCTAATATGTTCTACAGTGTGGTTA (RIC score -38.20), RSS12 sequence; + strand	chrX 139917545 to 139917653	Pak3 (Protein coding)	Intergenic	No

The RIC (RSS Information Content) score goes from -1000 (very bad) to 0 (very good). It has been shown that there is a good correlation between this score and the RSS functionality. For the current version, pass/fail RIC thresholds are from Cowell et al (2002) as follows: 12 RSS: pass with RIC > -38.81; 23 RSS: pass with RIC > -58.45

GAGA motifs: (C/G)A(C/G)A(C/G)A….   or(G/C)T(G/C)T(G/C)T….)