

Supplementary Table S5 | Deposited data and analysis

Deposited Data

Resource	Source	Identifier
The Repli-seq dataset	GEO	GSM3759850, GSM3759851
Replication origin dataset	GEO	GSM2125829, GSM2125830
Nascent RNA-seq dataset	GEO	GSM1671336, GSM1671337, GSM1671338, GSM1671339
H3K36me3 and H3K9me3 ChIP-seq datasets	GEO	GSM788076, GSM788078, GSM788069 (Input)
H3K4me3 and H3K27me3 ChIP-seq datasets	GEO	GSM871043, GSM871044, GSM871045 (Input)
H3K9me2 and H3K27ac ChIP-seq datasets	GEO	GSM2341638, GSM2341636, GSM2341640 (Input)
DNase-seq dataset	GEO	GSM4221655
Human evolutionary break points	GitHub Supporting data RECOMB-CG 2019	https://github.com/bioinfoUQA M/RECOMB-CG-2019_supp

Software and Algorithms

Resource	Source	Identifier
Trim Galore	Babraham Bioinformatics	https://www.bioinformatics.babraham.ac.uk/projects/trim_galore/
SRA-Tools	SRA Toolkit Development Team from NCBI	http://ncbi.github.io/sra-tools/
Bowtie2	Langmead, B. & Salzberg, S. L., 2012 ¹	http://bowtie-bio.sourceforge.net/bowtie2/index.shtml
HISAT2	Kim, D. et al., 2015 ²	https://ccb.jhu.edu/software/hisat2/index.shtml
FeatureCounts	Liao, Y. et al., 2014 ³	http://bioinf.wehi.edu.au/featureCounts/
HOMER	Heinz, S. et al., 2010 ⁴	http://homer.ucsd.edu/homer/ngs/ucsc.html
SAMtools	Li, H. et al., 2009 ⁵	http://samtools.sourceforge.net/
Bedtools	Quinlan, A. R. & Hall, I. M., 2010 ⁶	https://bedtools.readthedocs.io/en/latest/
DeepTools2	Ramirez, F. et al., 2016 ⁷	https://deeptools.readthedocs.io/en/develop/index.html#
R	R Development Core Team, 2008	https://www.r-project.org/
SICER2	Zang, C. et al., 2009 ⁸	https://zanglab.github.io/SICER2/
GATK4	McKenna, A. et al., 2010 ⁹	https://software.broadinstitute.org/gatk/
Control-FREEC	Boeva, V. et al., 2012 ¹⁰	http://boevalab.inf.ethz.ch/FREEC/index.html

Circos	Krzywinski, M. et al., 2009 ¹¹	http://www.circos.ca/
ChIPseeker	Yu, G. et al., 2015 ¹²	https://bioconductor.org/packages/release/bioc/html/ChIPseeker.html
ClusterProfiler	Yu, G. et al., 2012 ¹³	http://www.bioconductor.org/packages/release/bioc/html/clusterProfiler.html
IGV (Integrative Genomics Viewer)	Robinson, J. T. et al., 2011 ¹⁴ , Thorvaldsdottir, H. et al., 2013 ¹⁵	http://www.igv.org/
TxDb.Hsapiens.UCSC.hg38.knownGene	Bioconductor core team and Bioconductor package maintainer, 2019	http://www.bioconductor.org/packages/release/data/annotation/html/TxDb.Hsapiens.UCSC.hg38.knownGene.html
Gviz	Hahne, F. & Ivanek, R., 2016 ¹⁶	http://bioconductor.org/packages/release/bioc/html/Gviz.html
ggpubr	A. Kassambara., 2016	https://cran.r-project.org/web/packages/ggpubr/index.html
ggplot2	Ginestet, C., 2011 ¹⁷	https://cran.r-project.org/web/packages/ggplot2/index.html
Stats	R Core Team, 2019	https://www.R-project.org/
DOSE	Yu, G. et al., 2015 ¹⁸	http://www.bioconductor.org/packages/release/bioc/html/DOSE.html
Org.Hs.eg.db	Marc Carlson, 2019	http://www.bioconductor.org/pack

		ages/release/data/annotation/html/org.Hs.eg.db.html
Remap	Remap Development Team from NCBI	https://www.ncbi.nlm.nih.gov/genome/tools/remap
SPADE	Mori, H. et al., 2019 ¹⁹	https://github.com/yachielab/SPADE
BWA	H. Li, 2013	http://bio-bwa.sourceforge.net/index.shtml
Segment.pl	Paulsen, M. T. et al., 2014 ²⁰	http://sourceforge.net/projects/segment-stream/

Supplementary reference

- 1 Langmead, B. & Salzberg, S. L. Fast gapped-read alignment with Bowtie 2. *Nat Methods* **9**, 357-359, doi:10.1038/nmeth.1923 (2012).
- 2 Kim, D., Langmead, B. & Salzberg, S. L. HISAT: a fast spliced aligner with low memory requirements. *Nat Methods* **12**, 357-360, doi:10.1038/nmeth.3317 (2015).
- 3 Liao, Y., Smyth, G. K. & Shi, W. featureCounts: an efficient general purpose program for assigning sequence reads to genomic features. *Bioinformatics* **30**, 923-930, doi:10.1093/bioinformatics/btt656 (2014).
- 4 Heinz, S. *et al.* Simple combinations of lineage-determining transcription factors prime cis-regulatory elements required for macrophage and B cell identities. *Mol Cell* **38**, 576-589, doi:10.1016/j.molcel.2010.05.004 (2010).
- 5 Li, H. *et al.* The Sequence Alignment/Map format and SAMtools. *Bioinformatics* **25**, 2078-2079, doi:10.1093/bioinformatics/btp352 (2009).
- 6 Quinlan, A. R. & Hall, I. M. BEDTools: a flexible suite of utilities for comparing genomic features. *Bioinformatics* **26**, 841-842, doi:10.1093/bioinformatics/btq033 (2010).
- 7 Ramirez, F. *et al.* deepTools2: a next generation web server for deep-

- sequencing data analysis. *Nucleic Acids Res* **44**, W160-165, doi:10.1093/nar/gkw257 (2016).
- 8 Zang, C. *et al.* A clustering approach for identification of enriched domains from histone modification ChIP-Seq data. *Bioinformatics* **25**, 1952-1958, doi:10.1093/bioinformatics/btp340 (2009).
- 9 McKenna, A. *et al.* The Genome Analysis Toolkit: a MapReduce framework for analyzing next-generation DNA sequencing data. *Genome Res* **20**, 1297-1303, doi:10.1101/gr.107524.110 (2010).
- 10 Boeva, V. *et al.* Control-FREEC: a tool for assessing copy number and allelic content using next-generation sequencing data. *Bioinformatics* **28**, 423-425, doi:10.1093/bioinformatics/btr670 (2012).
- 11 Krzywinski, M. *et al.* Circos: an information aesthetic for comparative genomics. *Genome Res* **19**, 1639-1645, doi:10.1101/gr.092759.109 (2009).
- 12 Yu, G., Wang, L. G. & He, Q. Y. ChIPseeker: an R/Bioconductor package for ChIP peak annotation, comparison and visualization. *Bioinformatics* **31**, 2382-2383, doi:10.1093/bioinformatics/btv145 (2015).
- 13 Yu, G., Wang, L. G., Han, Y. & He, Q. Y. clusterProfiler: an R package for comparing biological themes among gene clusters. *Omics : a journal of integrative biology* **16**, 284-287, doi:10.1089/omi.2011.0118 (2012).
- 14 Robinson, J. T. *et al.* Integrative genomics viewer. *Nat Biotechnol* **29**, 24-26, doi:10.1038/nbt.1754 (2011).
- 15 Thorvaldsdottir, H., Robinson, J. T. & Mesirov, J. P. Integrative Genomics Viewer (IGV): high-performance genomics data visualization and exploration. *Brief Bioinform* **14**, 178-192, doi:10.1093/bib/bbs017 (2013).
- 16 Hahne, F. & Ivanek, R. Visualizing Genomic Data Using Gviz and Bioconductor. *Methods in molecular biology (Clifton, N.J.)* **1418**, 335-351, doi:10.1007/978-1-4939-3578-9_16 (2016).
- 17 Ginestet, C. ggplot2: Elegant Graphics for Data Analysis. *J R Stat Soc a*

- Stat* **174**, 245-245, doi:DOI 10.1111/j.1467-985X.2010.00676_9.x (2011).
- 18 Yu, G., Wang, L. G., Yan, G. R. & He, Q. Y. DOSE: an R/Bioconductor package for disease ontology semantic and enrichment analysis. *Bioinformatics* **31**, 608-609, doi:10.1093/bioinformatics/btu684 (2015).
- 19 Mori, H., Evans-Yamamoto, D., Ishiguro, S., Tomita, M. & Yachie, N. Fast and global detection of periodic sequence repeats in large genomic resources. *Nucleic Acids Research* **47**, doi:ARTN e8 10.1093/nar/gky890 (2019).
- 20 Paulsen, M. T. *et al.* Use of Bru-Seq and BruChase-Seq for genome-wide assessment of the synthesis and stability of RNA. *Methods* **67**, 45-54, doi:10.1016/j.ymeth.2013.08.015 (2014).