

Haematologica
HAEMATOL/2019/228478
Version 3

Analysis of retrotransposon subfamily DNA methylation reveals novel early epigenetic changes in chronic lymphocytic leukaemia

Timothy M. Barrow, Nicole Wong Doo, Roger L. Milne, Graham G. Giles, Elaine Willmore, Gordon Strathdee, and Hyang-Min Byun

Disclosures: This work was supported by funding from Bright Red (awarded to Timothy Barrow) and the JGW Patterson Foundation (grant number 30015.088.045/PA/IXS, awarded to Gordon Strathdee). The authors report no conflicts of interest.

Contributions: TB and HB conceived the study. TB identified HM450K loci mapping to retrotransposons and performed all data analysis. NWD, RM and GG provided the HM450K data from the MCCS, and EW and GS provided HM450K data from the validation cohort. TB and HB performed the data interpretation, with input from NWD, RM, GG, EW and GS. TB and HB drafted the manuscript, which was then revised by all authors. All authors had final approval of the submitted manuscript.