

Haematologica
HAEMATOL/2020/249243
Version 4

Epigenetic and functional changes imposed by NUP98-HOXA9 in a genetically engineered model of chronic myeloid leukemia progression

Ivan Sloma, Philip Beer, Christophe Desterke, Elizabeth Bulaeva, Misha Bilenky, Annaïck Carles, Michelle Moksa, Kamini Raghuram, Cedric Brimacombe, Karen Lambie, Ali G. Turhan, Oriane Wagner-Ballon, Philippe Gaulard, Keith Humphries, Martin Hirst, and Connie J. Eaves

Disclosures: The authors have no conflicts of interest to disclose

Contributions: IS and CJE designed the study. IS prepared the vectors with assistance from KR and CB. IS isolated the CD34+ cells, and with EB performed the transductions and with KR, CB and PB carried out the in vitro experiments. IS and PB performed the in vivo experiments and got assistance from PG and OWB for necropsies analysis. MH supervised the RNASeq and ChIP-seq studies. MM prepared RNAseq libraries. MB performed primary RNAseq analysis and differential expression analysis. CD performed variant calling, in silico transcriptomics analysis and integration of RNASeq and ChIP-Seq data. IS and CD contributed to tertiary RNASeq analysis. MM performed ChIP-Seq experiments. AC did the primary and secondary analysis of ChIP-Seq experiments while IS contributed to secondary and tertiary analysis. IS and CJE wrote the manuscript with input from PB, CD, MB and MM and approval from all authors.