

# SUPPLEMENTARY INFORMATION

In format provided by Watson *et al.* (OCTOBER 2013)

Supplementary information S2 (figure) | **Recurrent and significantly mutated genes identified from analysis of whole-exome and whole-genome sequencing studies of haematologic malignancies.** Recurrently mutated genes (Recurrent Mut.) and significantly mutated genes (SMGs) demonstrated to possess a higher mutation rate than the calculated background mutation rate (BMR) are shown for whole-exome/whole-genome sequencing (WES/WGS) studies for a number of haematologic malignancies where available. Approaches to identify SMGs (Sig. approaches) and False Discovery Rate (FDR), a statistical method used to correct for multiple hypothesis testing indicating the expected proportion of "false discoveries", are shown where available.

