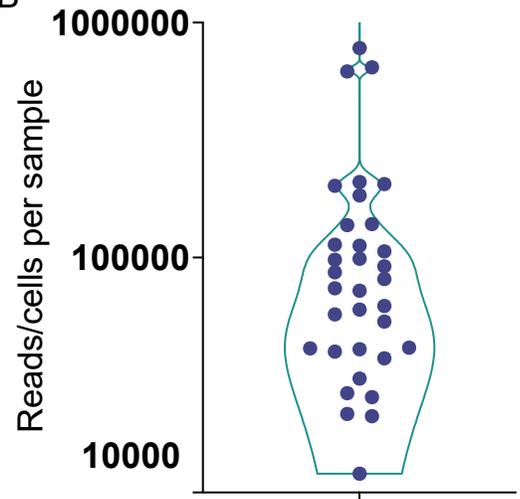


Supplementary Figure 1

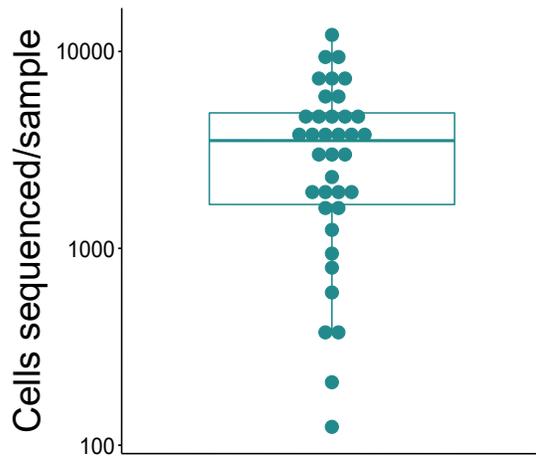
A

<i>ASXL1</i>	<i>DNMT3A</i>	<i>IDH1</i>	<i>MYC</i>	<i>PTPN11</i>	<i>STAG2</i>
<i>ATM</i>	<i>ERG</i>	<i>IDH2</i>	<i>MYD88</i>	<i>RAD21</i>	<i>STAT3</i>
<i>BCOR</i>	<i>ETV6</i>	<i>JAK2</i>	<i>NF1</i>	<i>RUNX1</i>	<i>TET2</i>
<i>BRAF</i>	<i>EZH2</i>	<i>KDM6A</i>	<i>NPM1</i>	<i>SETBP1</i>	<i>TP53</i>
<i>CALR</i>	<i>FLT3</i>	<i>KIT</i>	<i>NRAS</i>	<i>SF3B1</i>	<i>U2AF1</i>
<i>CBL</i>	<i>GATA2</i>	<i>KMT2A</i>	<i>PHF6</i>	<i>SMC1A</i>	<i>WT1</i>
<i>CHEK2</i>	<i>GNAS</i>	<i>KRAS</i>	<i>PPM1D</i>	<i>SMC3</i>	<i>ZRSR2</i>
<i>CSF3R</i>	<i>HRAS</i>	<i>MPL</i>	<i>PTEN</i>	<i>SRSF2</i>	

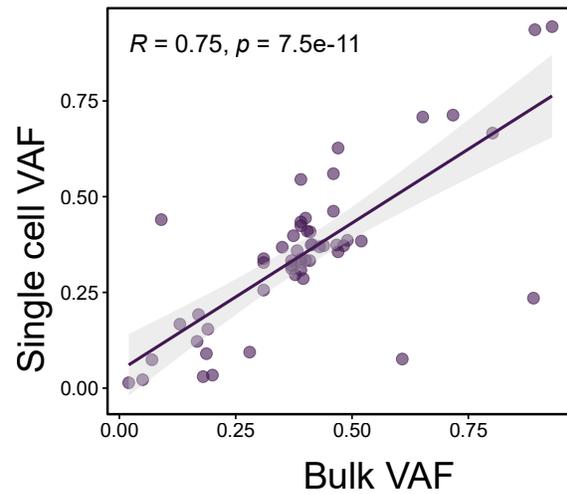
B



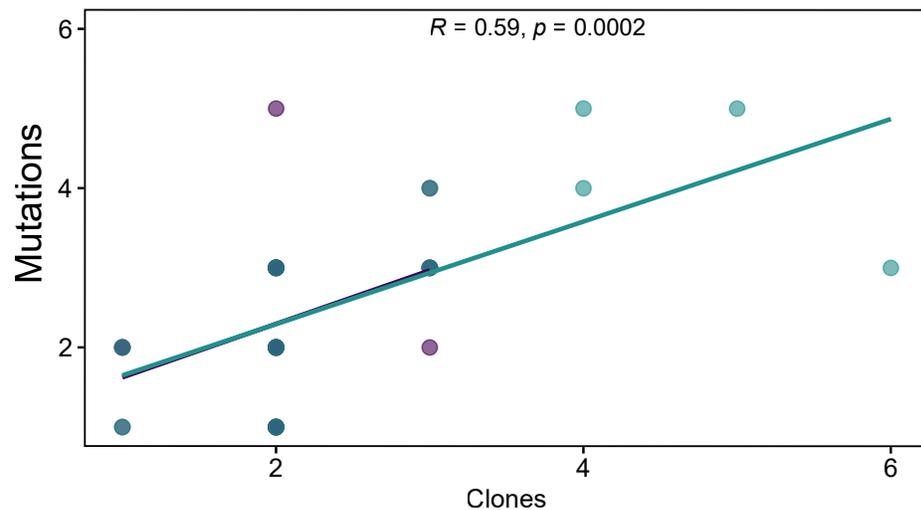
C



D



E



Supplementary Figure 1

a, Genes included in the myeloid single-cell DNA sequencing (scDNAseq) panel from MissionBio. b, Violin plot depicting mean reads per cell detected for all samples during scDNAseq. c, Box and whisker plot depicting the number of cells sequenced per sample (for all boxplots in this figure, center line represents median, box represents interquartile range (IQR), whiskers, 1.5 x IQR). d, Scatterplot shows correlation of scDNA-seq calculated variant allele frequencies (VAFs) and VAFs generated by bulk sequencing. (Note: two *ASXL1* variants are excluded from this calculation) ($R = 0.75$, $p < 0.0001$). e, Scatter plot illustrating the relationship of mutations and clones. ($R = 0.58$, $p = 0.00024$, Pearson).