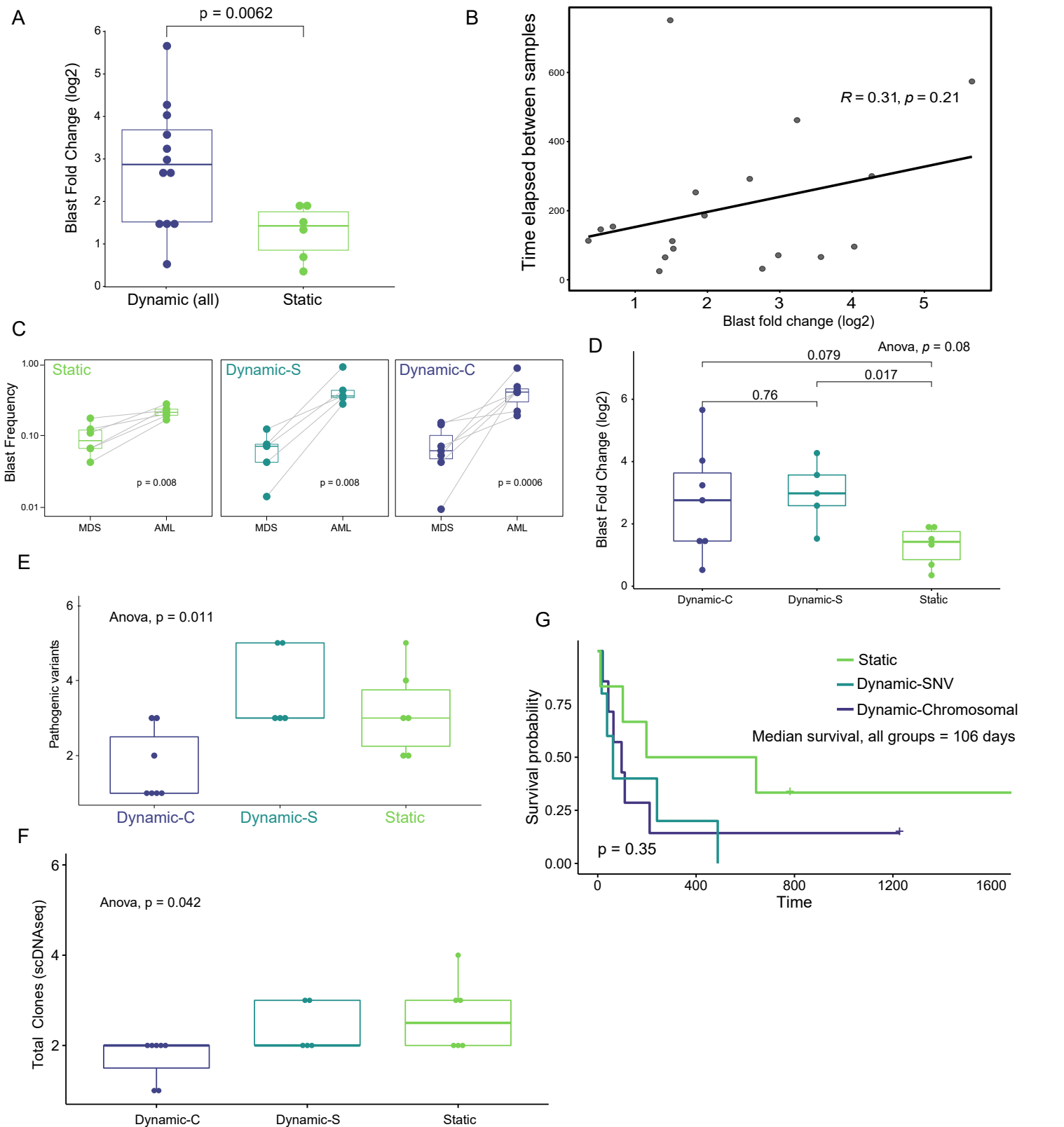# Supplementary Figure 4.

Supplemental Figure 4

a, Box plot illustrating the difference in blast fold change (log2) between the patients with Static clonal progression compared to those with Dynamic clonal progression (p = 0.0062, two-tailed t-test). (For all box plots in this figure center line represents median, box represents interquartile range (IQR), whiskers, 1.5 x IQR). b, Scatterplot of blast fold change (log2) and the time elapsed between MDS and sAML samples with line of best fit (Pearson correlation, R = 0.31, *p* = 0.21) c, Line plots show change in blast frequency during disease progression in each of the three groups (p-values shown for paired, two-tailed t-test). d, Box plot of blast fold change (log2) from MDS to sAML for each patient within the three groups of clonal progression e, Box plot depicting the number of pathogenic mutations identified in each sample in each distinct group (p = 0.011, ANOVA). f , Box plot of total number of distinct clones by scDNAseq in each progression case. g, Kaplan-Meier analysis of the three clonal progression groups (Kaplan Meier log rank test *p* value shown)