

Supplemental material: Multiomic mapping of acquired chromosome 1 copy number and structural variants to identify therapeutic vulnerabilities in multiple myeloma.

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Supplemental Methods***DepMap analysis***

Functional genomics, DepMap genome wide CRISPR knockout library (24), was applied to 19 myeloma cell lines and 15 non myeloma cell lines selected and clustered based on their dependency score to generate a heatmap (heatmap.2) (25) Enrichment for SV on 1q and 1p was analysed by comparing the proportion of positive cases or measures of the mean value in one subgroup with the remaining samples using dependency as a continuous variable. Absolute fold change (FC) greater than 0.15 with p-value less than 0.05 were considered significant.

Statistical analysis

Proportional testing was performed using Kruskal-Wallis or Fisher's exact tests to compare the median of a continuous variable or the distribution of discrete variables across groups, when appropriate.